METHODS AND SYSTEMS FOR ANALYZING NUCLEIC ACID MOLECULES

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] The instant application claims the benefit of U.S. Provisional Application No. 63/188,410, filed May 13, 2021, and U.S. Provisional Application No. 63/224,795, filed July 22, 2021, and U.S. Patent Application No. 17/308,958, filed May 5, 2021, each of which is incorporated by reference herein in its entirety.

SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on November 3, 2020, is named 58626-702_601_SL.txt and is 307,199 bytes in size.

GOVERNMENT RIGHTS

[0003] This invention was made with Government support under CA233975, CA241076, and CA188298 awarded by the National Institutes of Health. The Government has certain rights in the invention.

BACKGROUND

[0004] Noninvasive blood tests that can detect somatic alterations (e.g., mutated nucleic acids) based on the analysis of cell-free nucleic acids (e.g., cell-free deoxyribonucleic acid (cfDNA) and cell-free ribonucleic acid (cfRNA)) are attractive candidates for cancer screening applications due to the relative ease of obtaining biological specimens (e.g., biological fluids). Circulating tumor nucleic acids (e.g., ctDNA or ctRNA; i.e., nucleic acids derived from cancerous cells) can be sensitive and specific biomarkers in numerous cancer subtypes. However, current methods for minimal residual disease (MRD) detection from ctDNA can be limited by one or more factors, such as low input DNA amounts and high background error rates.

[0005] Recent approaches have improved ctDNA MRD performance by tracking multiple somatic mutations with error-suppressed sequencing, resulting in detection limits as low as 4 parts in 100,000 from limited cfDNA input. Detection of residual disease during or after treatment is a powerful tool, with detectable MRD representing an adverse prognostic sign even during radiographic remission. However, current limits of detection may be insufficient to universally detect residual disease in patients destined for disease relapse or progression.

This 'loss of detection' is exemplified in diffuse large B-cell lymphoma (DLBCL), where ctDNA detection after two cycles of curative-intent therapy is a strong prognostic marker. Despite this, almost one-third of patients experiencing disease progression do not have detectable ctDNA at this landmark, representing 'false-negative' tests. Similar false-negative rates in colon cancer and breast cancer have been observed.

SUMMARY

[0006] The present disclosure provides methods and systems for analyzing nucleic acids, such as cell-free nucleic acids (e.g., cfDNA, cfRNA) from a subject. Methods and systems of the present disclosure can utilize sequencing results derived from the subject to detect cancer-derived nucleic acids (e.g., ctDNA, ctRNA) for, e.g., disease diagnosis, disease monitoring, or determining treatments for the subject. Methods and systems of the present disclosure can exhibit enhanced sensitivity, specificity and/or reliability of detection of cancer-derived nucleic acids.

[0007] In one aspect, the present disclosure provides a method comprising: (a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject; (b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence, wherein at least about 10% of the one or more cell-free nucleic acid molecules comprises a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants that are separated by at least one nucleotide; and (c) analyzing, by the computer system, the identified one or more cell-free nucleic acid molecules to determine a condition of the subject. In some embodiments, cellular DNA is used instead of cell-free DNA (e.g., for detection of leukemia or other hematological cancers).

[0008] In some embodiments of any one of the methods disclosed herein, the at least about 10% of the cell-free nucleic acid molecules comprise at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of the one or more cell-free nucleic acid molecules.

[0009] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and (c) further comprises determining the condition of the subject based at least in part on the identified one or more indels.

[0010] In some embodiments, the method further comprises determining the start position (i.e., the 5'-most nucleotide) and the end position (i.e., the 3'-most nucleotide) in a molecule. In some cases, tumor-derived nucleic acids, such as tumor-derived cfDNA molecules can have stereotyped start/end positions, which may reflect cleavage by tissue-specific nucleases. The start and end positions can be used—in connection with phased variants—to identify a condition of a subject.

[0011] In one aspect, the present disclosure provides a method comprising: (a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject; (b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide; and (c) analyzing, by the computer system, the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

[0012] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and (c) further comprises determining the condition of the subject based at least in part on the identified one or more indels.

[0013] In one aspect, the present disclosure provides a method comprising: (a) obtaining sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject; (b) processing the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules with a limit of detection of less than about 1 out of 50,000 observations from the sequencing data; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

[0014] In some embodiments of any one of the methods disclosed herein, the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 observations from the sequencing data.

[0015] In some embodiments of any one of the methods disclosed herein, each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence. In some embodiments of any one of the methods disclosed herein, a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide.

[0016] In some embodiments of any one of the methods disclosed herein, the processes (a) to (c) are performed by a computer system.

[0017] In some embodiments of any one of the methods disclosed herein, the sequencing data is generated based on nucleic acid amplification. In some embodiments of any one of the methods disclosed herein, the sequencing data is generated based on polymerase chain reaction. In some embodiments of any one of the methods disclosed herein, the sequencing data is generated based on amplicon sequencing.

[0018] In some embodiments of any one of the methods disclosed herein, the sequencing data is generated based on next-generation sequencing (NGS). Alternatively, in some embodiments of any one of the methods disclosed herein, the sequencing data is generated based on non-hybridization-based NGS.

[0019] In some embodiments of any one of the methods disclosed herein, the sequencing data is generated without use of molecular barcoding of at least a portion of the plurality of cell-free nucleic acid molecules. In some embodiments of any one of the methods disclosed herein, the sequencing data is obtained without use of sample barcoding of at least a portion of the plurality of cell-free nucleic acid molecules.

[0020] In some embodiments of any one of the methods disclosed herein, the sequencing data is obtained without in silico removal or suppression of (i) background error or (ii) sequencing error.

[0021] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and (c) further comprises determining the condition of the subject based at least in part on the identified one or more indels.

[0022] In one aspect, the present disclosure provides a method of treating a condition of a subject, the method comprising: (a) identifying the subject for treatment of the condition, wherein the subject has been determined to have the condition based on identification of one or more cell-free nucleic acid molecules from a plurality of cell-free nucleic acid molecules that is obtained or derived from the subject, wherein each of the one or more cell-free nucleic acid molecules identified comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide, and wherein a presence of the plurality of phased variants is indicative of the condition of the subject; and (b) subjecting the subject to the treatment based on the identification in (a).

[0023] In some embodiments, the subject has been determined to have the condition based at least in part on one or more insertions or deletions (indels) identified in the one or more cell-free nucleic acid molecules.

[0024] In one aspect, the present disclosure provides a method of monitoring a progress of a condition of a subject, the method comprising: (a) determining a first state of the condition of the subject based on identification of a first set of one or more cell-free nucleic acid molecules from a first plurality of cell-free nucleic acid molecules that is obtained or derived from the subject; (b) determining a second state of the condition of the subject based on identification of a second set of one or more cell-free nucleic acid molecules from a second plurality of cell-free nucleic acid molecules that is obtained or derived from the subject, wherein the second plurality of cell-free nucleic acid molecules are obtained from the subject subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject; and (c) determining the progress of the condition based on the first state of the condition and the second state of the condition, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide.

[0025] In some embodiments of any one of the methods disclosed herein, the progress of the condition is worsening of the condition.

[0026] In some embodiments of any one of the methods disclosed herein, the progress of the condition is at least a partial remission of the condition.

[0027] In some embodiments of any one of the methods disclosed herein, a presence of the plurality of phased variants is indicative of the first state or the second state of the condition of the subject.

[0028] In some embodiments of any one of the methods disclosed herein, the second plurality of cell-free nucleic acid molecules is obtained from the subject at least about 1 week, at least about 2 weeks, at least about 3 weeks, at least about 4 weeks, at least about 2 months, or at least about 3 months subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject.

[0029] In some embodiments of any one of the methods disclosed herein, the subject is subjected to a treatment for the condition (i) prior to obtaining the second plurality of cell-free nucleic acid molecules from the subject and (ii) subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject.

[0030] In some embodiments of any one of the methods disclosed herein, the progress of the condition is indicative of minimal residual disease of the condition of the subject. In some

embodiments of any one of the methods disclosed herein, the progress of the condition is indicative of tumor burden or cancer burden of the subject.

[0031] In some embodiments of any one of the methods disclosed herein, the one or more cell-free nucleic acid molecules are captured from among the plurality of cell-free nucleic acid molecules with a set of nucleic acid probes, wherein the set of nucleic acid probes is configured to hybridize to at least a portion of cell-free nucleic acid molecules comprising one or more genomic regions associated with the condition.

[0032] In some embodiments, the subject has been determined to have the condition based at least in part on one or more insertions or deletions (indels) identified in the one or more cell-free nucleic acid molecules.

[0033] In one aspect, the present disclosure provides a method comprising: (a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject, wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide, and wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the plurality of phased variants and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants; (b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the plurality of phased variants; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

[0034] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and (c) further comprises determining the condition of the subject based at least in part on the identified one or more indels.

[0035] In one aspect, the present disclosure provides a method comprising: (a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject, wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising a plurality of phased variants relative to a reference

genomic sequence, and wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the plurality of phased variants and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants; (b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the plurality of phased variants, wherein a limit of detection of the identification step is less than about 1 out of 50,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

[0036] In some embodiments of any one of the methods disclosed herein, the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules.

[0037] In some embodiments of any one of the methods disclosed herein, a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide.

[0038] In some embodiments of any one of the methods disclosed herein, the activatable reporter agent is activated upon hybridization of the individual nucleic acid probe to the plurality of phased variants.

[0039] In some embodiments of any one of the methods disclosed herein, the activatable reporter agent is activated upon dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants.

[0040] In some embodiments of any one of the methods disclosed herein, the method further comprises mixing (1) the set of nucleic acid probes and (2) the plurality of cell-free nucleic acid molecules.

[0041] In some embodiments of any one of the methods disclosed herein, the activatable reporter agent is a fluorophore.

[0042] In some embodiments of any one of the methods disclosed herein, analyzing the identified one or more cell-free nucleic acid molecules comprises analyzing (i) the identified one or more cell-free nucleic acid molecules and (ii) other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased

variants as different variables.

[0043] In some embodiments of any one of the methods disclosed herein, the analyzing of the identified one or more cell-free nucleic acid molecules is not based on other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants.

[0044] In some embodiments of any one of the methods disclosed herein, a number of the plurality of phased variants from the identified one or more cell-free nucleic acid molecules is indicative of the condition of the subject. In some embodiments, a ratio of (i) the number of the plurality of phased variants from the one or more cell-free nucleic acid molecules and (ii) a number of single nucleotide variants (SNVs) from the one or more cell-free nucleic acid molecules is indicative of the condition of the subject.

[0045] In some embodiments of any one of the methods disclosed herein, a frequency of the plurality of phased variants in the identified one or more cell-free nucleic acid molecules is indicative of the condition of the subject. In some embodiments, the frequency is indicative of a diseased cell associated with the condition. In some embodiments, the condition is diffuse large B-cell lymphoma, and wherein the frequency is indicative of whether the one or more cell-free nucleic acid molecules are derived from germinal center B-cell (GCB) or activated B-cell (ABC).

[0046] In some embodiments of any one of the methods disclosed herein, genomic origin of the identified one or more cell-free nucleic acid molecules is indicative of the condition of the subject.

[0047] In some embodiments of any one of the methods disclosed herein, the first and second phased variants are separated by at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 nucleotides. In some embodiments of any one of the methods disclosed herein, the first and second phased variants are separated by at most about 180, at most about 170, at most about 160, at most about 150, or at most about 140 nucleotides.

[0048] In some embodiments of any one of the methods disclosed herein, at least about 10%, at least about 20%, at least about 30%, at least about 40%, or at least about 50% of the one or more cell-free nucleic acid molecules comprising a plurality of phased variants comprises a single nucleotide variant (SNV) that is at least 2 nucleotides away from an adjacent SNV.

[0049] In some embodiments of any one of the methods disclosed herein, the plurality of phased variants comprises at least 3, at least 4, at least 5, at least 10, at least 15, at least 20, or at least 25 phased variants within the same cell-free nucleic acid molecule.

[0050] In some embodiments of any one of the methods disclosed herein, the one or more cell-free nucleic acid molecules identified comprises at least 2, at least 3, at least 4, at least 5, at least 10, at least 50, at least 100, at least 500, or at least 1,000 cell-free nucleic acid molecules.

[0051] In some embodiments of any one of the methods disclosed herein, the reference genomic sequence is derived from a reference cohort. In some embodiments, the reference genomic sequence comprises a consensus sequence from the reference cohort. In some embodiments, the reference genomic sequence comprises at least a portion of hg19 human genome, hg18 genome, hg17 genome, hg16 genome, or hg38 genome.

[0052] In some embodiments of any one of the methods disclosed herein, the reference genomic sequence is derived from a sample of the subject.

[0053] In some embodiments of any one of the methods disclosed herein, the sample is a healthy sample. In some embodiments, the sample comprises a healthy cell. In some embodiments, the healthy cell comprises a healthy leukocyte.

[0054] In some embodiments of any one of the methods disclosed herein, the sample is a diseased sample. In some embodiments, the diseased sample comprises a diseased cell. In some embodiments, the diseased cell comprises a tumor cell. In some embodiments, the diseased sample comprises a solid tumor.

[0055] In some embodiments of any one of the methods disclosed herein, the set of nucleic acid probes is designed based on the plurality of phased variants that are identified by comparing (i) sequencing data from a solid tumor, lymphoma, or blood tumor of the subject and (ii) sequencing data from a healthy cell of the subject or a healthy cohort. In some embodiments, the healthy cell is from the subject. In some embodiments, the healthy cell is from the healthy cohort.

[0056] In some embodiments of any one of the methods disclosed herein, the set of nucleic acid probes are designed to hybridize to at least a portion of sequences of genomic loci associated with the condition. In some embodiments, the genomic loci associated with the condition are known to exhibit aberrant somatic hypermutation when the subject has the condition.

[0057] In some embodiments of any one of the methods disclosed herein, the set of nucleic acid probes are designed to hybridize to at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3.

[0058] In some embodiments of any one of the methods disclosed herein, each nucleic acid probe of the set of nucleic acid probes has at least about 70%, at least about 80%, at least about 90% sequence identity, at least about 95% sequence identity, or about 100% sequence identity to a probe sequence selected from Table 6.

[0059] In some embodiments of any one of the methods disclosed herein, the set of nucleic acid probes comprises at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90% of probe sequences in Table 6.

[0060] In some embodiments of any one of the methods disclosed herein, the method further comprises determining that the subject has the condition or determining a degree or status of the condition of the subject, based on the identified one or more cell-free nucleic acid molecules comprising the plurality of phased variants. In some embodiments, the method further comprises determining that the one or more cell-free nucleic acid molecules are derived from a sample associated with the condition, based on performing a statistical model analysis of the identified one or more cell-free nucleic acid molecules. In some embodiments, the statistical model analysis comprises a Monte Carlo statistical analysis.

[0061] In some embodiments of any one of the methods disclosed herein, the method further comprises monitoring a progress of the condition of the subject based on the identified one or more cell-free nucleic acid molecules.

[0062] In some embodiments of any one of the methods disclosed herein, the method further comprises performing a different procedure to confirm the condition of the subject. In some embodiments, the different procedure comprises a blood test, genetic test, medical imaging, physical exam, or tissue biopsy.

[0063] In some embodiments of any one of the methods disclosed herein, the method further comprises determining a treatment for the condition of the subject based on the identified one or more cell-free nucleic acid molecules.

[0064] In some embodiments of any one of the methods disclosed herein, the subject has been subjected to a treatment for the condition prior to (a).

[0065] In some embodiments of any one of the methods disclosed herein, the treatment comprises chemotherapy, radiotherapy, chemoradiotherapy, immunotherapy, adoptive cell therapy, hormone therapy, targeted drug therapy, surgery, transplant, transfusion, or medical surveillance.

[0066] In some embodiments of any one of the methods disclosed herein, the plurality of cell-free nucleic acid molecules comprise a plurality of cell-free deoxyribonucleic acid (DNA) molecules.

[0067] In some embodiments of any one of the methods disclosed herein, condition comprises a disease.

[0068] In some embodiments of any one of the methods disclosed herein, the plurality of cell-free nucleic acid molecules are derived from a bodily sample of the subject. In some embodiments, the bodily sample comprises plasma, serum, blood, cerebrospinal fluid, lymph fluid, saliva, urine, or stool.

[0069] In some embodiments of any one of the methods disclosed herein, the subject is a mammal. In some embodiments of any one of the methods disclosed herein, the subject is a human.

[0070] In some embodiments of any one of the methods disclosed herein, the condition comprises neoplasm, cancer, or tumor. In some embodiments, the condition comprises a solid tumor. In some embodiments, the condition comprises a lymphoma. In some embodiments, the condition comprises a B-cell lymphoma. In some embodiments, the condition comprises a sub-type of B-cell lymphoma selected from the group consisting of diffuse large B-cell lymphoma, follicular lymphoma, Burkitt lymphoma, and B-cell chronic lymphocytic leukemia. In some embodiments of any one of the methods disclosed herein, the condition comprises transplant rejection of or a chromosomal abnormality.

[0071] In some embodiments of any one of the methods disclosed herein, the plurality of phased variants have been previously identified as tumor-derived from sequencing a prior tumor sample or cell-free nucleic acid sample.

[0072] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and (c) further comprises determining the condition of the subject based at least in part on the identified one or more indels.

[0073] In one aspect, the present disclosure provides a composition comprising a bait set comprising a set of nucleic acid probes designed to capture cell-free DNA molecules derived from at least about 5% of genomic regions set forth in (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3.

[0074] In some embodiments of any of the compositions disclosed herein, the set of nucleic acid probes are designed to pull down cell-free DNA molecules derived from at least about

10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of the genomic regions set forth in (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3.

[0075] In some embodiments of any of the compositions disclosed herein, the set of nucleic acid probes are designed to capture the one or more cell-free DNA molecules derived from at most about 10%, at most about 20%, at most about 30%, at most about 40%, at most about 50%, at most about 60%, at most about 70%, at most about 80%, at most about 90%, or about 100% of the genomic regions set forth in (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3.

[0076] In some embodiments of any of the compositions disclosed herein, the bait set comprises at most 5, at most 10, at most 50, at most 100, at most 500, at most 1000, or at most 2000 nucleic acid probes.

[0077] In some embodiments of any of the compositions disclosed herein, an individual nucleic acid probe of the set of nucleic acid probes comprises a pull-down tag.

[0078] In some embodiments of any of the compositions disclosed herein, the pull-down tag comprises a nucleic acid barcode.

[0079] In some embodiments of any of the compositions disclosed herein, the pull-down tag comprises biotin.

[0080] In some embodiments of any of the compositions disclosed herein, each of the cell-free DNA molecules is between about 100 nucleotides and about 180 nucleotides in length.

[0081] In some embodiments of any of the compositions disclosed herein, the genomic regions are associated with a condition.

[0082] In some embodiments of any of the compositions disclosed herein, the genomic regions exhibit aberrant somatic hypermutation when a subject has the condition.

[0083] In some embodiments of any of the compositions disclosed herein, the condition comprises a B-cell lymphoma. In some embodiments, the condition comprises a sub-type of B-cell lymphoma selected from the group consisting of diffuse large B-cell lymphoma, follicular lymphoma, Burkitt lymphoma, and B-cell chronic lymphocytic leukemia.

[0084] In some embodiments of any of the compositions disclosed herein, the composition further comprises a plurality of cell-free DNA molecules obtained or derived from a subject.

[0085] In one aspect, the present disclosure provides a method to perform a clinical procedure on an individual, the method comprising: (a) obtaining or having obtained a targeted sequencing result of a collection of cell-free nucleic acid molecules, wherein the collection of cell-free nucleic acid molecules are sourced from a liquid or waste biopsy of an individual, and wherein the targeting sequencing is performed utilizing nucleic acid probes to pull down sequences of genomic loci known to experience aberrant somatic hypermutation in a B-cell cancer; (b) identifying or having identified a plurality of variants in phase within the cell-free nucleic acid sequencing result; (c) determining or having determined, utilizing a statistical model and the identified phased variants, that the cell-free nucleic acid sequencing result contains nucleotides derived from a neoplasm; and (d) performing a clinical procedure on the individual to confirm the presence of the B-cell cancer, based upon determining that the cell-free nucleic acid sequencing result contains nucleic acid sequences likely derived from the B-cell cancer.

[0086] In some embodiments of any of the compositions disclosed herein, the biopsy is one of blood, serum, cerebrospinal fluid, lymph fluid, urine, or stool.

[0087] In some embodiments of any of the compositions disclosed herein, the genomic loci are selected from (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3.

[0088] In some embodiments of any of the compositions disclosed herein, the sequences of the nucleic acid probes are selected from Table 6.

[0089] In some embodiments of any of the compositions disclosed herein, the clinical is procedure is a blood test, medical imaging, or a physical exam.

[0090] In some embodiments, the method further comprises identifying or having identified one or more insertions or deletions (indels) within the cell-free nucleic acid sequencing result, and determining or having determined, based least in part on the identified one or more indels, that the cell-free nucleic acid sequencing result contains the nucleotides derived from the neoplasm.

[0091] In one aspect, the present disclosure provides a method to treat an individual for a B-cell cancer, the method comprising: (a) obtaining or having obtained a targeted sequencing result of a collection of cell-free nucleic acid molecules, wherein the collection of cell-free nucleic acid molecules are sourced from a liquid or waste biopsy of an individual, and wherein the targeting sequencing is performed utilizing nucleic acid probes to pull down sequences of genomic loci known to experience aberrant somatic hypermutation in a B-cell cancer; (b)

identifying or having identified a plurality of variants in phase within the cell-free nucleic acid sequencing result; (c) determining or having determined, utilizing a statistical model and the identified phased variants, that the cell-free nucleic acid sequencing result contains nucleotides derived from a neoplasm; and (d) treating the individual to curtail the B-cell cancer, based upon determining that the cell-free nucleic acid sequencing result contains nucleic acid sequences derived from the B-cell cancer.

[0092] In some embodiments of any of the compositions disclosed herein, the biopsy is one of blood, serum, cerebrospinal fluid, lymph fluid, urine or stool.

[0093] In some embodiments of any of the compositions disclosed herein, the genomic loci are selected from (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3.

[0094] In some embodiments of any of the compositions disclosed herein, the sequences of the nucleic acid probes are selected from Table 6.

[0095] In some embodiments of any of the compositions disclosed herein, the treatment is chemotherapy, radiotherapy, immunotherapy, hormone therapy, targeted drug therapy, or medical surveillance.

[0096] In some embodiments, the method further comprises identifying or having identified one or more insertions or deletions (indels) within the cell-free nucleic acid sequencing result, and determining or having determined, based least in part on the identified one or more indels, that the cell-free nucleic acid sequencing result contains the nucleotides derived from the neoplasm.

[0097] In one aspect, the present disclosure provides a method to detect cancerous minimal residual disease in an individual and to treat the individual for a cancer, the method comprising: (a) obtaining or having obtained a targeted sequencing result of a collection of cell-free nucleic acid molecules, wherein the collection of cell-free nucleic acid molecules are sourced from a liquid or waste biopsy of an individual, wherein the liquid or waste biopsy is sourced after a series of treatments in order to detect minimal residual disease, and wherein the targeting sequencing is performed utilizing nucleic acid probes to pull down sequences of genomic loci determined to contain a plurality of variants in phase, as determined by a prior sequencing result on a prior biopsy derived from the cancer; (b) identifying or having identified at least one set of the plurality of variants in phase within the cell-free nucleic acid sequencing result; and (c) treating the individual to curtail the cancer, based upon determining that the cell-free nucleic acid sequencing result contains nucleic acid sequences derived from the cancer.

[0098] In some embodiments of any of the compositions disclosed herein, the liquid or waste biopsy is one of blood, serum, cerebrospinal fluid, lymph fluid, urine or stool.

[0099] In some embodiments of any of the compositions disclosed herein, the treatment is chemotherapy, radiotherapy, immunotherapy, hormone therapy, targeted drug therapy, or medical surveillance.

[0100] In some embodiments, the method further comprises identifying or having identified one or more insertions or deletions (indels) within the cell-free nucleic acid sequencing result, and treating the individual to curtail the cancer, based least in part on the identified one or more indels.

[0101] In one aspect, the present disclosure provides a method comprising: (a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject; (b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises one or more insertions or deletions (indels) relative to a reference genomic sequence; and (c) analyzing, by the computer system, the one or more indels to determine a condition of the subject.

[0102] In one aspect, the present disclosure provides a method comprising: (a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject; (b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises one or more insertions or deletions (indels) relative to a reference genomic sequence; and (c) analyzing, by the computer system, the one or more insertions or deletions (indels) to determine a condition of the subject.

[0103] In one aspect, the present disclosure provides a method comprising: (a) obtaining sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject; (b) processing the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules with a limit of detection of less than about 1 out of 50,000 observations from the sequencing data, wherein each of the one or more cell-free nucleic acid molecules comprises one or more insertions or deletions (indels) relative to a reference genomic sequence; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

[0104] In some embodiments, the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 observations from the sequencing data. In some embodiments, (a) to (c) are performed by a computer system. In some embodiments, the sequencing data is generated based on nucleic acid amplification. In some embodiments, the sequencing data is generated based on polymerase chain reaction. In some embodiments, the sequencing data is generated based on amplicon sequencing. In some embodiments, the sequencing data is generated based on next-generation sequencing (NGS). In some embodiments, the sequencing data is generated based on non-hybridization-based NGS. In some embodiments, the sequencing data is generated without use of molecular barcoding of at least a portion of the plurality of cell-free nucleic acid molecules. In some embodiments, the sequencing data is obtained without use of sample barcoding of at least a portion of the plurality of cell-free nucleic acid molecules. In some embodiments, the sequencing data is obtained without in silico removal or suppression of (i) background error or (ii) sequencing error.

[0105] In one aspect, the present disclosure provides a method of treating a condition of a subject, the method comprising: (a) identifying the subject for treatment of the condition, wherein the subject has been determined to have the condition based on identification of one or more cell-free nucleic acid molecules from a plurality of cell-free nucleic acid molecules that is obtained or derived from the subject, wherein each of the one or more cell-free nucleic acid molecules comprises one or more insertions or deletions (indels) relative to a reference genomic sequence, and wherein a presence of the one or more indels is indicative of the condition of the subject; and (b) subjecting the subject to the treatment based on the identification in (a).

[0106] In one aspect, the present disclosure provides a method of monitoring a progress of a condition of a subject, the method comprising: (a) determining a first state of the condition of the subject based on identification of a first set of one or more cell-free nucleic acid molecules from a first plurality of cell-free nucleic acid molecules that is obtained or derived from the subject; (b) determining a second state of the condition of the subject based on identification of a second set of one or more cell-free nucleic acid molecules from a second plurality of cell-free nucleic acid molecules that is obtained or derived from the subject, wherein the second plurality of cell-free nucleic acid molecules are obtained from the subject subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject; and (c) determining the progress of the condition based on the first state of the condition and

the second state of the condition, wherein each of the one or more cell-free nucleic acid molecules comprises one or more insertions or deletions (indels) relative to a reference genomic sequence.

[0107] In some embodiments, the progress of the condition is worsening of the condition. In some embodiments, the progress of the condition is at least a partial remission of the condition. In some embodiments, a presence of the one or more indels is indicative of the first state or the second state of the condition of the subject. In some embodiments, the second plurality of cell-free nucleic acid molecules is obtained from the subject at least about 1 week, at least about 2 weeks, at least about 3 weeks, at least about 4 weeks, at least about 2 months, or at least about 3 months subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject. In some embodiments, the subject is subjected to a treatment for the condition (i) prior to obtaining the second plurality of cell-free nucleic acid molecules from the subject and (ii) subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject. In some embodiments, the progress of the condition is indicative of minimal residual disease of the condition of the subject. In some embodiments, the progress of the condition is indicative of tumor burden or cancer burden of the subject. In some embodiments, the one or more cell-free nucleic acid molecules are captured from among the plurality of cell-free nucleic acid molecules with a set of nucleic acid probes, wherein the set of nucleic acid probes is configured to hybridize to at least a portion of cell-free nucleic acid molecules comprising one or more genomic regions associated with the condition.

[0108] In one aspect, the present disclosure provides a method comprising: (a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject, wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising one or more insertions or deletions (indels) relative to a reference genomic sequence, and wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the one or more indels and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the one or more indels; (b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the one or more indels; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

[0109] In one aspect, the present disclosure provides a method comprising: (a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject, wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising one or more insertions or deletions (indels) relative to a reference genomic sequence, and wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the one or more indels and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the one or more indels; (b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the one or more indels, wherein a limit of detection of the identification step is less than about 1 out of 50,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

[0110] In some embodiments, the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules. In some embodiments, the activatable reporter agent is activated upon hybridization of the individual nucleic acid probe to the one or more indels. In some embodiments, the activatable reporter agent is activated upon dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the one or more indels. In some embodiments, the method further comprises mixing (1) the set of nucleic acid probes and (2) the plurality of cell-free nucleic acid molecules. In some embodiments, the activatable reporter agent is a fluorophore. In some embodiments, analyzing the identified one or more cell-free nucleic acid molecules comprises analyzing (i) the identified one or more cell-free nucleic acid molecules and (ii) other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the one or more indels as different variables. In some embodiments, the analyzing of the identified one or more cell-free nucleic acid molecules is not based on other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the one or more indels. In some embodiments, a number of the one or more indels from the identified one or more cell-free nucleic acid molecules is indicative of the condition of the subject. In

some embodiments, a ratio of (i) the number of the one or more indels from the one or more cell-free nucleic acid molecules and (ii) a number of single nucleotide variants (SNVs) from the one or more cell-free nucleic acid molecules is indicative of the condition of the subject. In some embodiments, a frequency of the one or more indels in the identified one or more cell-free nucleic acid molecules is indicative of the condition of the subject. In some embodiments, the frequency is indicative of a diseased cell associated with the condition. In some embodiments, the condition is diffuse large B-cell lymphoma, and wherein the frequency is indicative of whether the one or more cell-free nucleic acid molecules are derived from germinal center B-cell (GCB) or activated B-cell (ABC). In some embodiments, genomic origin of the identified one or more cell-free nucleic acid molecules is indicative of the condition of the subject.

[0111] In some embodiments, the one or more indels comprises at least 3, at least 4, at least 5, at least 10, at least 15, at least 20, or at least 25 indels within the same cell-free nucleic acid molecule. In some embodiments, the one or more cell-free nucleic acid molecules identified comprises at least 2, at least 3, at least 4, at least 5, at least 10, at least 50, at least 100, at least 500, or at least 1,000 cell-free nucleic acid molecules. In some embodiments, the reference genomic sequence is derived from a reference cohort. In some embodiments, the reference genomic sequence comprises a consensus sequence from the reference cohort. In some embodiments, the reference genomic sequence comprises at least a portion of hg19 human genome, hg18 genome, hg17 genome, hg16 genome, or hg38 genome. In some embodiments, the reference genomic sequence is derived from a sample of the subject. In some embodiments, the sample is a healthy sample. In some embodiments, the sample comprises a healthy cell. In some embodiments, the healthy cell comprises a healthy leukocyte. In some embodiments, the sample is a diseased sample. In some embodiments, the diseased sample comprises a diseased cell. In some embodiments, the diseased cell comprises a tumor cell. In some embodiments, the diseased sample comprises a solid tumor. In some embodiments, the set of nucleic acid probes is designed based on the one or more indels that are identified by comparing (i) sequencing data from a solid tumor, lymphoma, or blood tumor of the subject and (ii) sequencing data from a healthy cell of the subject or a healthy cohort. In some embodiments, the healthy cell is from the subject. In some embodiments, the healthy cell is from the healthy cohort. In some embodiments, the set of nucleic acid probes are designed to hybridize to at least a portion of sequences of genomic loci associated with the condition. In some embodiments, the genomic loci associated with the condition are known to exhibit aberrant somatic hypermutation when the subject has the condition.

[0112] In some embodiments, the set of nucleic acid probes are designed to hybridize to at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of (i) the genomic regions identified in Table 1, or (ii) the genomic regions identified in Table 3. In some embodiments, each nucleic acid probe of the set of nucleic acid probes has at least about 70%, at least about 80%, at least about 90% sequence identity, at least about 95% sequence identity, or about 100% sequence identity to a probe sequence selected from Table 6. In some embodiments, the set of nucleic acid probes comprises at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90% of probe sequences in Table 6.

[0113] In some embodiments, the method further comprises determining that the subject has the condition or determining a degree or status of the condition of the subject, based on the identified one or more cell-free nucleic acid molecules comprising the one or more indels. In some embodiments, the method further comprises determining that the one or more cell-free nucleic acid molecules are derived from a sample associated with the condition, based on performing a statistical model analysis of the identified one or more cell-free nucleic acid molecules. In some embodiments, the statistical model analysis comprises a Monte Carlo statistical analysis. In some embodiments, the method further comprises monitoring a progress of the condition of the subject based on the identified one or more cell-free nucleic acid molecules. In some embodiments, the method further comprises performing a different procedure to confirm the condition of the subject. In some embodiments, the different procedure comprises a blood test, genetic test, medical imaging, physical exam, or tissue biopsy. In some embodiments, the method further comprises determining a treatment for the condition of the subject based on the identified one or more cell-free nucleic acid molecules. In some embodiments, the subject has been subjected to a treatment for the condition prior to (a). In some embodiments, the treatment comprises chemotherapy, radiotherapy, chemoradiotherapy, immunotherapy, adoptive cell therapy, hormone therapy, targeted drug therapy, surgery, transplant, transfusion, or medical surveillance. In some embodiments, the plurality of cell-free nucleic acid molecules comprises a plurality of cell-free deoxyribonucleic acid (DNA) molecules. In some embodiments, the condition comprises a disease. In some embodiments, the plurality of cell-free nucleic acid molecules is derived from a bodily sample of the subject. In some embodiments, the bodily sample comprises plasma, serum, blood, cerebrospinal fluid, lymph fluid, saliva, urine, or stool. In some embodiments, the subject is a

mammal. In some embodiments, the subject is a human. In some embodiments, the condition comprises neoplasm, cancer, or tumor. In some embodiments, the condition comprises a solid tumor. In some embodiments, the condition comprises a lymphoma. In some embodiments, the condition comprises a B-cell lymphoma. In some embodiments, the condition comprises a sub-type of B-cell lymphoma selected from the group consisting of diffuse large B-cell lymphoma, follicular lymphoma, Burkitt lymphoma, and B-cell chronic lymphocytic leukemia. In some embodiments, the one or more indels have been previously identified as tumor-derived from sequencing a prior tumor sample or cell-free nucleic acid sample.

[0114] In one aspect, the present disclosure provides a method to perform a clinical procedure on an individual, the method comprising: obtaining or having obtained a targeted sequencing result of a collection of cell-free nucleic acid molecules, wherein the collection of cell-free nucleic acid molecules are sourced from a liquid or waste biopsy of an individual, and wherein the targeting sequencing is performed utilizing nucleic acid probes to pull down sequences of genomic loci known to experience aberrant somatic hypermutation in a B-cell cancer; identifying or having identified one or more insertions or deletions (indels) within the cell-free nucleic acid sequencing result; determining or having determined, utilizing a statistical model and the identified one or more indels, that the cell-free nucleic acid sequencing result contains nucleotides derived from a neoplasm; and performing a clinical procedure on the individual to confirm the presence of the B-cell cancer, based upon determining that the cell-free nucleic acid sequencing result contains nucleic acid sequences likely derived from the B-cell cancer.

[0115] In some embodiments, the biopsy is one of blood, serum, cerebrospinal fluid, lymph fluid, urine, or stool. In some embodiments, the genomic loci are selected from (i) the genomic regions identified in Table 1, or (ii) the genomic regions identified in Table 3. In some embodiments, the sequences of the nucleic acid probes are selected from Table 6. In some embodiments, the clinical is procedure is a blood test, medical imaging, or a physical exam.

[0116] In one aspect, the present disclosure provides a method to treat an individual for a B-cell cancer, the method comprising: obtaining or having obtained a targeted sequencing result of a collection of cell-free nucleic acid molecules, wherein the collection of cell-free nucleic acid molecules are sourced from a liquid or waste biopsy of an individual, and wherein the targeting sequencing is performed utilizing nucleic acid probes to pull down sequences of genomic loci known to experience aberrant somatic hypermutation in a B-cell cancer; identifying or having identified one or more insertions or deletions (indels) within the cell-free nucleic acid sequencing result; determining or having determined, utilizing a statistical model

and the identified one or more indels, that the cell-free nucleic acid sequencing result contains nucleotides derived from a neoplasm; and treating the individual to curtail the B-cell cancer, based upon determining that the cell-free nucleic acid sequencing result contains nucleic acid sequences derived from the B-cell cancer.

[0117] In some embodiments, the biopsy is one of blood, serum, cerebrospinal fluid, lymph fluid, urine or stool. In some embodiments, the genomic loci are selected from (i) the genomic regions identified in Table 1, or (ii) the genomic regions identified in Table 3. In some embodiments, the sequences of the nucleic acid probes are selected from Table 6. In some embodiments, the treatment is chemotherapy, radiotherapy, immunotherapy, hormone therapy, targeted drug therapy, or medical surveillance.

[0118] In one aspect, the present disclosure provides a method to detect cancerous minimal residual disease in an individual and to treat the individual for a cancer, the method comprising: obtaining or having obtained a targeted sequencing result of a collection of cell-free nucleic acid molecules, wherein the collection of cell-free nucleic acid molecules are sourced from a liquid or waste biopsy of an individual, wherein the liquid or waste biopsy is sourced after a series of treatments in order to detect minimal residual disease, and wherein the targeting sequencing is performed utilizing nucleic acid probes to pull down sequences of genomic loci determined to contain one or more insertions or deletions (indels), as determined by a prior sequencing result on a prior biopsy derived from the cancer; identifying or having identified at least one set of the one or more indels within the cell-free nucleic acid sequencing result; and treating the individual to curtail the cancer, based upon determining that the cell-free nucleic acid sequencing result contains nucleic acid sequences derived from the cancer.

[0119] In some embodiments, the liquid or waste biopsy is one of blood, serum, cerebrospinal fluid, lymph fluid, urine or stool. In some embodiments, the treatment is chemotherapy, radiotherapy, immunotherapy, hormone therapy, targeted drug therapy, or medical surveillance.

[0120] In one aspect, the present disclosure provides a method comprising: (a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject who has received an organ or tissue transplant; (b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence, wherein at least about 10% of the one or more cell-free nucleic acid molecules comprises a first phased variant of the plurality of phased

variants and a second phased variant of the plurality of phased variants that are separated by at least one nucleotide; and (c) analyzing, by the computer system, the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an extent of transplant rejection of the subject.

[0121] In some embodiments, the at least about 10% of the cell-free nucleic acid molecules comprise at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of the one or more cell-free nucleic acid molecules. In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the extent of transplant rejection of the subject based at least in part on the identified one or more indels.

[0122] In one aspect, the present disclosure provides a method comprising: (a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject who has received an organ or tissue transplant; (b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide; and (c) analyzing, by the computer system, the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an extent of transplant rejection of the subject.

[0123] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the extent of transplant rejection of the subject based at least in part on the identified one or more indels.

[0124] In one aspect, the present disclosure provides a method comprising: (a) obtaining sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject who has received an organ or tissue transplant; (b) processing the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules with a limit of detection of less than about 1 out of 50,000 observations from the sequencing data; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an extent of transplant rejection of the subject.

[0125] In some embodiments, the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 observations from the sequencing data. In some embodiments, each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence. In some embodiments, a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide. In some embodiments, (a) to (c) are performed by a computer system. In some embodiments, the sequencing data is generated based on nucleic acid amplification. In some embodiments, the sequencing data is generated based on polymerase chain reaction. In some embodiments, the sequencing data is generated based on amplicon sequencing. In some embodiments, the sequencing data is generated based on next-generation sequencing (NGS). In some embodiments, the sequencing data is generated based on non-hybridization-based NGS. In some embodiments, the sequencing data is generated without use of molecular barcoding of at least a portion of the plurality of cell-free nucleic acid molecules. In some embodiments, the sequencing data is obtained without use of sample barcoding of at least a portion of the plurality of cell-free nucleic acid molecules. In some embodiments, the sequencing data is obtained without in silico removal or suppression of (i) background error or (ii) sequencing error. In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence or the absence of the transplant rejection of the subject based at least in part on the identified one or more indels.

[0126] In one aspect, the present disclosure provides a method of treating a transplant rejection of a subject who has received an organ or tissue transplant, the method comprising: (a) identifying the subject for treatment of the transplant rejection, wherein the subject has been determined to have the transplant rejection based on identification of one or more cell-free nucleic acid molecules from a plurality of cell-free nucleic acid molecules that is obtained or derived from the subject, wherein each of the one or more cell-free nucleic acid molecules identified comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide, and wherein a presence of the plurality of phased variants is indicative of the transplant rejection of the subject; and (b) subjecting the subject to the treatment based on the identification in (a).

[0127] In some embodiments, the subject has been determined to have the transplant rejection based at least in part on one or more insertions or deletions (indels) identified in the one or more cell-free nucleic acid molecules.

[0128] In one aspect, the present disclosure provides a method of monitoring a subject who has received an organ or tissue transplant for a presence, an absence, or an extent of transplant rejection, the method comprising: (a) determining a first state of the presence, the absence, or the extent of transplant rejection of the subject based on identification of a first set of one or more cell-free nucleic acid molecules from a first plurality of cell-free nucleic acid molecules that is obtained or derived from the subject; (b) determining a second state of the presence, the absence, or the extent of transplant rejection of the subject based on identification of a second set of one or more cell-free nucleic acid molecules from a second plurality of cell-free nucleic acid molecules that is obtained or derived from the subject, wherein the second plurality of cell-free nucleic acid molecules are obtained from the subject subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject; and (c) determining a transplant rejection status of the subject based on the first state and the second state, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide.

[0129] In some embodiments, the transplant rejection status is at least a partial transplant rejection. In some embodiments, a presence of the plurality of phased variants is indicative of the first state or the second state. In some embodiments, the second plurality of cell-free nucleic acid molecules is obtained from the subject at least about 1 week, at least about 2 weeks, at least about 3 weeks, at least about 4 weeks, at least about 2 months, or at least about 3 months subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject. In some embodiments, the subject is subjected to a treatment for the transplant rejection (i) prior to obtaining the second plurality of cell-free nucleic acid molecules from the subject and (ii) subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject. In some embodiments, the one or more cell-free nucleic acid molecules are captured from among the plurality of cell-free nucleic acid molecules with a set of nucleic acid probes, wherein the set of nucleic acid probes is configured to hybridize to at least a portion of cell-free nucleic acid molecules comprising one or more genomic regions associated with the transplant rejection. In some embodiments, the subject has been determined to have the presence or the absence of the transplant rejection based at least in part on one or more insertions or deletions (indels) identified in the one or more cell-free nucleic acid molecules.

[0130] In one aspect, the present disclosure provides a method comprising: (a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject who has received an organ or tissue transplant, wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide, and wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the plurality of phased variants and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants; (b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the plurality of phased variants; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an extent of transplant rejection of the subject.

[0131] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence or the absence of the transplant rejection of the subject based at least in part on the identified one or more indels.

[0132] In one aspect, the present disclosure provides a method comprising: (a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject who has received an organ or tissue transplant, wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising a plurality of phased variants relative to a reference genomic sequence, and wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the plurality of phased variants and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants; (b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the plurality of phased variants, wherein a limit of detection of the identification step is less than about 1 out

of 50,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an extent of transplant rejection of the subject.

[0133] In some embodiments, the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules. In some embodiments, a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide. In some embodiments, the activatable reporter agent is activated upon hybridization of the individual nucleic acid probe to the plurality of phased variants. In some embodiments, the activatable reporter agent is activated upon dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants. In some embodiments, the method further comprises mixing (1) the set of nucleic acid probes and (2) the plurality of cell-free nucleic acid molecules. In some embodiments, the activatable reporter agent is a fluorophore. In some embodiments, analyzing the identified one or more cell-free nucleic acid molecules comprises analyzing (i) the identified one or more cell-free nucleic acid molecules and (ii) other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants as different variables. In some embodiments, the analyzing of the identified one or more cell-free nucleic acid molecules is not based on other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants. In some embodiments, a number of the plurality of phased variants from the identified one or more cell-free nucleic acid molecules is indicative of the presence, the absence, or the extent of transplant rejection of the subject. In some embodiments, a ratio of (i) the number of the plurality of phased variants from the one or more cell-free nucleic acid molecules and (ii) a number of single nucleotide variants (SNVs) from the one or more cell-free nucleic acid molecules is indicative of the presence, the absence, or the extent of transplant rejection of the subject. In some embodiments, a frequency of the plurality of phased variants in the identified one or more cell-free nucleic acid molecules is indicative of the presence or the absence of the transplant rejection of the subject. In some embodiments, the frequency is indicative of a diseased cell associated with the presence, the absence, or the extent of transplant rejection. In some embodiments, genomic origin of the identified one or more cell-free nucleic acid molecules is indicative of the presence or the absence of the transplant rejection of the subject. In some embodiments, the first and second phased variants

are separated by at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 nucleotides. In some embodiments, the first and second phased variants are separated by at most about 180, at most about 170, at most about 160, at most about 150, or at most about 140 nucleotides.

[0134] In some embodiments, at least about 10%, at least about 20%, at least about 30%, at least about 40%, or at least about 50% of the one or more cell-free nucleic acid molecules comprising a plurality of phased variants comprises a single nucleotide variant (SNV) that is at least 2 nucleotides away from an adjacent SNV. In some embodiments, the plurality of phased variants comprises at least 3, at least 4, at least 5, at least 10, at least 15, at least 20, or at least 25 phased variants within the same cell-free nucleic acid molecule. In some embodiments, the one or more cell-free nucleic acid molecules identified comprises at least 2, at least 3, at least 4, at least 5, at least 10, at least 50, at least 100, at least 500, or at least 1,000 cell-free nucleic acid molecules. In some embodiments, the reference genomic sequence is derived from a reference cohort. In some embodiments, the reference genomic sequence comprises a consensus sequence from the reference cohort. In some embodiments, the reference genomic sequence comprises at least a portion of hg19 human genome, hg18 genome, hg17 genome, hg16 genome, or hg38 genome. In some embodiments, the reference genomic sequence is derived from a sample of the subject. In some embodiments, the sample is a healthy sample. In some embodiments, the sample comprises a healthy cell. In some embodiments, the healthy cell comprises a healthy leukocyte. In some embodiments, the sample is a diseased sample. In some embodiments, the diseased sample comprises a diseased cell. In some embodiments, the healthy cell is from the subject. In some embodiments, the healthy cell is from the healthy cohort. In some embodiments, the set of nucleic acid probes are designed to hybridize to at least a portion of sequences of genomic loci associated with the presence or the absence of the transplant rejection. In some embodiments, the genomic loci associated with the presence, the absence, or the extent of transplant rejection are known to exhibit aberrant somatic hypermutation when the subject has the transplant rejection.

[0135] In some embodiments, the set of nucleic acid probes are designed to hybridize to at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3. In some embodiments, each nucleic acid probe of the set of nucleic acid probes has at least about 70%, at least about 80%, at least about 90% sequence identity, at least

about 95% sequence identity, or about 100% sequence identity to a probe sequence selected from Table 6. In some embodiments, the set of nucleic acid probes comprises at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90% of probe sequences in Table 6. In some embodiments, the method further comprises determining the presence or the absence of the transplant rejection or determining a degree or status thereof, based on the identified one or more cell-free nucleic acid molecules comprising the plurality of phased variants. In some embodiments, the method further comprises determining that the one or more cell-free nucleic acid molecules are derived from a sample associated with the presence or the absence of the transplant rejection, based on performing a statistical model analysis of the identified one or more cell-free nucleic acid molecules. In some embodiments, the statistical model analysis comprises a Monte Carlo statistical analysis. In some embodiments, the method further comprises monitoring a progress of the presence, the absence, or the extent of transplant rejection of the subject based on the identified one or more cell-free nucleic acid molecules. In some embodiments, the method further comprises performing a different procedure to confirm the presence, the absence, or the extent of transplant rejection of the subject. In some embodiments, the different procedure comprises a blood test, genetic test, medical imaging, physical exam, or tissue biopsy. In some embodiments, the method further comprises determining a treatment for the transplant rejection of the subject based on the identified one or more cell-free nucleic acid molecules. In some embodiments, the subject has been subjected to a treatment for the transplant rejection prior to (a). In some embodiments, the plurality of cell-free nucleic acid molecules comprises a plurality of cell-free deoxyribonucleic acid (DNA) molecules. In some embodiments, the plurality of cell-free nucleic acid molecules are derived from a bodily sample of the subject. In some embodiments, the bodily sample comprises plasma, serum, blood, cerebrospinal fluid, lymph fluid, saliva, urine, or stool. In some embodiments, the subject is a mammal. In some embodiments, the subject is a human. In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the extent of transplant rejection of the subject based at least in part on the identified one or more indels.

[0136] In one aspect, the present disclosure provides a method comprising: (a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a pregnant subject; (b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the

plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence, wherein at least about 10% of the one or more cell-free nucleic acid molecules comprises a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants that are separated by at least one nucleotide; and (c) analyzing, by the computer system, the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an elevated risk of a genetic abnormality of a fetus of the pregnant subject.

[0137] In some embodiments, the at least about 10% of the cell-free nucleic acid molecules comprise at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of the one or more cell-free nucleic acid molecules. In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based at least in part on the identified one or more indels. In some embodiments, the genetic abnormality is a chromosomal aneuploidy. In some embodiments, the chromosomal aneuploidy is in chromosome 13, 18, 21, X, or Y.

[0138] In one aspect, the present disclosure provides a method comprising: (a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a pregnant subject; (b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide; and (c) analyzing, by the computer system, the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an elevated risk of a genetic abnormality of a fetus of the pregnant subject.

[0139] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based at least in part on the identified one or more indels. In some embodiments, the genetic abnormality is a chromosomal aneuploidy. In some embodiments, the chromosomal aneuploidy is in chromosome 13, 18, 21, X, or Y.

[0140] In one aspect, the present disclosure provides a method comprising: (a) obtaining sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a pregnant subject; (b) processing the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules with a limit of detection of less than about 1 out of 50,000 observations from the sequencing data; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an elevated risk of a genetic abnormality of a fetus of the pregnant subject.

[0141] In some embodiments, the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 observations from the sequencing data. In some embodiments, each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence. In some embodiments, a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide. In some embodiments, (a) to (c) are performed by a computer system. In some embodiments, he method of any one of claims 309-313, wherein the sequencing data is generated based on nucleic acid amplification. In some embodiments, the sequencing data is generated based on polymerase chain reaction. In some embodiments, the sequencing data is generated based on amplicon sequencing. In some embodiments, the sequencing data is generated based on next-generation sequencing (NGS). In some embodiments, the sequencing data is generated based on non-hybridization-based NGS. In some embodiments, the sequencing data is generated without use of molecular barcoding of at least a portion of the plurality of cell-free nucleic acid molecules. In some embodiments, the sequencing data is obtained without use of sample barcoding of at least a portion of the plurality of cell-free nucleic acid molecules. In some embodiments, the sequencing data is obtained without in silico removal or suppression of (i) background error or (ii) sequencing error. In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based at least in part on the identified one or more indels. In some embodiments, the genetic abnormality is a chromosomal aneuploidy. In some embodiments, the chromosomal aneuploidy is in chromosome 13, 18, 21, X, or Y.

[0142] In one aspect, the present disclosure provides a method of monitoring a pregnant subject for a presence, an absence, or an elevated risk of a genetic abnormality of a fetus of the pregnant subject, the method comprising: (a) determining a first state of the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based on identification of a first set of one or more cell-free nucleic acid molecules from a first plurality of cell-free nucleic acid molecules that is obtained or derived from the pregnant subject; (b) determining a second state of the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based on identification of a second set of one or more cell-free nucleic acid molecules from a second plurality of cell-free nucleic acid molecules that is obtained or derived from the pregnant subject, wherein the second plurality of cell-free nucleic acid molecules are obtained from the pregnant subject subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the pregnant subject; and (c) determining the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based on the first state and the second state, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide.

[0143] In some embodiments, the transplant rejection status is at least a partial transplant rejection. In some embodiments, a presence of the plurality of phased variants is indicative of the first state or the second state. In some embodiments, the second plurality of cell-free nucleic acid molecules is obtained from the pregnant subject at least about 1 week, at least about 2 weeks, at least about 3 weeks, at least about 4 weeks, at least about 2 months, or at least about 3 months subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the pregnant subject. In some embodiments, the one or more cell-free nucleic acid molecules are captured from among the plurality of cell-free nucleic acid molecules with a set of nucleic acid probes, wherein the set of nucleic acid probes is configured to hybridize to at least a portion of cell-free nucleic acid molecules comprising one or more genomic regions associated with the genetic abnormality. In some embodiments, the fetus has been determined to have the presence, the absence, or the elevated risk of the genetic abnormality based at least in part on one or more insertions or deletions (indels) identified in the one or more cell-free nucleic acid molecules.

[0144] In one aspect, the present disclosure provides a method comprising: (a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a pregnant subject, wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising a plurality of phased variants relative to a

reference genomic sequence that are separated by at least one nucleotide, and wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the plurality of phased variants and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants; (b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the plurality of phased variants; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an elevated risk of a genetic abnormality of a fetus of the pregnant subject.

[0145] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the elevated risk of the genetic abnormality based at least in part on the identified one or more indels.

[0146] In one aspect, the present disclosure provides a method comprising: (a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a pregnant subject, wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising a plurality of phased variants relative to a reference genomic sequence, and wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the plurality of phased variants and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants; (b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the plurality of phased variants, wherein a limit of detection of the identification step is less than about 1 out of 50,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an elevated risk of a genetic abnormality of a fetus of the pregnant subject.

[0147] In some embodiments, the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules. In some embodiments, a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide. In some embodiments, the activatable reporter agent is activated upon hybridization of the individual nucleic acid probe to the plurality of phased variants. In some embodiments, the activatable reporter agent is activated upon dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants. In some embodiments, the method further comprises mixing (1) the set of nucleic acid probes and (2) the plurality of cell-free nucleic acid molecules. In some embodiments, the activatable reporter agent is a fluorophore. In some embodiments, analyzing the identified one or more cell-free nucleic acid molecules comprises analyzing (i) the identified one or more cell-free nucleic acid molecules and (ii) other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants as different variables. In some embodiments, the analyzing of the identified one or more cell-free nucleic acid molecules is not based on other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants. In some embodiments, a number of the plurality of phased variants from the identified one or more cell-free nucleic acid molecules is indicative of the genetic abnormality. In some embodiments, a ratio of (i) the number of the plurality of phased variants from the one or more cell-free nucleic acid molecules and (ii) a number of single nucleotide variants (SNVs) from the one or more cell-free nucleic acid molecules is indicative of the genetic abnormality. In some embodiments, a frequency of the plurality of phased variants in the identified one or more cell-free nucleic acid molecules is indicative of the genetic abnormality. In some embodiments, genomic origin of the identified one or more cell-free nucleic acid molecules is indicative of the genetic abnormality. In some embodiments, the first and second phased variants are separated by at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 nucleotides. In some embodiments, the first and second phased variants are separated by at most about 180, at most about 170, at most about 160, at most about 150, or at most about 140 nucleotides.

[0148] In some embodiments, at least about 10%, at least about 20%, at least about 30%, at least about 40%, or at least about 50% of the one or more cell-free nucleic acid molecules comprising a plurality of phased variants comprises a single nucleotide variant (SNV) that is

at least 2 nucleotides away from an adjacent SNV. In some embodiments, the plurality of phased variants comprises at least 3, at least 4, at least 5, at least 10, at least 15, at least 20, or at least 25 phased variants within the same cell-free nucleic acid molecule. In some embodiments, the one or more cell-free nucleic acid molecules identified comprises at least 2, at least 3, at least 4, at least 5, at least 10, at least 50, at least 100, at least 500, or at least 1,000 cell-free nucleic acid molecules. In some embodiments, the reference genomic sequence is derived from a reference cohort. In some embodiments, the reference genomic sequence comprises a consensus sequence from the reference cohort. In some embodiments, the reference genomic sequence comprises at least a portion of hg19 human genome, hg18 genome, hg17 genome, hg16 genome, or hg38 genome. In some embodiments, the reference genomic sequence is derived from a sample of the pregnant subject. In some embodiments, the sample is a healthy sample. In some embodiments, the sample comprises a healthy cell. In some embodiments, the sample is a diseased sample. In some embodiments, the diseased sample comprises a diseased cell. In some embodiments, the healthy cell is from the pregnant subject. In some embodiments, the healthy cell is from the healthy cohort. In some embodiments, the set of nucleic acid probes are designed to hybridize to at least a portion of sequences of genomic loci associated with the genetic abnormality.

[0149] In some embodiments, the set of nucleic acid probes are designed to hybridize to at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3. In some embodiments, each nucleic acid probe of the set of nucleic acid probes has at least about 70%, at least about 80%, at least about 90% sequence identity, at least about 95% sequence identity, or about 100% sequence identity to a probe sequence selected from Table 6. In some embodiments, the set of nucleic acid probes comprises at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90% of probe sequences in Table 6. In some embodiments, the method further comprises determining the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject, based on the identified one or more cell-free nucleic acid molecules comprising the plurality of phased variants. In some embodiments, the method further comprises determining that the one or more cell-free nucleic acid molecules are derived from a sample associated with the presence, the absence, or the elevated risk of the genetic

abnormality of the fetus of the pregnant subject, based on performing a statistical model analysis of the identified one or more cell-free nucleic acid molecules. In some embodiments, the statistical model analysis comprises a Monte Carlo statistical analysis. In some embodiments, the method further comprises monitoring a progress of the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based on the identified one or more cell-free nucleic acid molecules. In some embodiments, the method further comprises performing a different procedure to confirm the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject. In some embodiments, the different procedure comprises a blood test, genetic test, medical imaging, physical exam, or tissue biopsy. In some embodiments, the plurality of cell-free nucleic acid molecules comprise a plurality of cell-free deoxyribonucleic acid (DNA) molecules. In some embodiments, the plurality of cell-free nucleic acid molecules are derived from a bodily sample of the pregnant subject. In some embodiments, the bodily sample comprises plasma, serum, blood, cerebrospinal fluid, lymph fluid, saliva, urine, or stool. In some embodiments, the pregnant subject is a mammal. In some embodiments, the pregnant subject is a human. In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based at least in part on the identified one or more indels.

[0150] In one aspect, the present disclosure provides a method comprising adding a set of nucleic acid probes to a sample comprising a plurality of nucleic acid molecules that have been obtained or derived from a subject, wherein each nucleic acid probe of the set of nucleic acid probes is configured to hybridize to a target nucleic acid molecule comprising a plurality of phased variants such that the nucleic acid probe is complementary to at least a region of the target nucleic acid molecule that extends from a first phased variant of the plurality of phased variants to a second phased variant of the plurality of phased variants. (For clarity, the region includes both the first phased variant and the second phased variant.)

[0151] This method, and embodiments of it described herein, may involve the use of hybrid capture probes/baits, such as biotinylated oligonucleotides, that may be used in a hybrid capture enrichment step such that the hybrid capture probes bind to and preferentially capture nucleic acid molecules that contain phased variants. Such hybrid capture approaches may increase the capture sensitivity of circulating tumor DNA or circulating DNA from a transplanted organ. The hybrid capture probes can be synthesized to specifically target molecules containing phased variants by designing the hybrid capture probe to (1) contain a sequence that is

complementary to the molecule that includes the phased variant (as opposed to the corresponding region of the reference genomic sequence) and (2) have a length that optimizes the nucleic acid binding kinetics/thermodynamics (ΔG or binding energy) such that the hybrid capture probe preferentially binds to a nucleic acid molecule that contains the phased variants of interest as compared to corresponding molecules without the phased variants. Such hybrid capture probes can lead to improved enrichment of relevant nucleic acid sequences, thereby requiring less sequencing as a result. For instance, in some cases (such as in assessing minimal residual disease, disease state, or state of transplant rejection), a cancerous sample or a sample from the transplanted organ may be obtained and sequenced to identify phased variants in such samples relative to a reference genomic sequence, such as a sequence from corresponding healthy cell(s) of the subject, and the hybrid capture probes can be designed to preferentially bind to nucleic acid sequences containing the phased variants identified from the cancerous and/or transplanted organ samples. In some circumstances, such hybrid capture probes can be used for single strand recovery of nucleic acid molecules that contain phased variants. The nucleic acid molecules captured by such probe sets can include DNA or RNA (e.g., single stranded RNA), such as cell-free DNA or cell-free DNA. Probes as described in this particular method can be used on combination with other methods described herein.

[0152] In some embodiments, each nucleic acid probe of the set of nucleic acid probes comprises a pull-down tag, such as biotin. In some embodiments, the method further comprises separation of target nucleic acid molecules that hybridize to the nucleic acid probes from nucleic acid molecules that do not hybridize to the nucleic acid probes to thereby capture target nucleic acid molecules. In some embodiments, the nucleic acid molecules are cell-free nucleic acid molecules. In some embodiments, the first phased variant is selected from the group consisting of a somatic single nucleotide variant, a somatic indel, a somatic translocation breakpoint, a somatic amplification or deletion breakpoint, a germline SNV, a germline indel, a germline translocation breakpoint, a germline amplification or deletion breakpoint, and a region of localized hypermutation, and the second phased variant is selected from the group consisting of a somatic single nucleotide variant, a somatic indel, a somatic translocation breakpoint, a somatic amplification or deletion breakpoint, a germline SNV, a germline indel, a germline translocation breakpoint, a germline amplification or deletion breakpoint, and a region of localized hypermutation. In some embodiments, the first phased variant of the plurality of phased variants and the second phased variant of the plurality of phased variants are separated by at least 1, 2, 3, 4, 5, 10, or 20 nucleotides. In some embodiments, each nucleic acid probe of the set of nucleic acid probes is either (1) less than 40 nucleotides, less than 30

nucleotides, or less than 20 nucleotides in length or (2) no more than 5 nucleotides, nor more than 10 nucleotides, no more than 20 nucleotides, or no more than 30 nucleotides longer than the distance between the first phased variant of the plurality of phased variants and the second phased variant of the plurality of phased variants, wherein the first phased variant and the second phased variant are the most separated phased variants (i.e., have the most number of intervening nucleotides) of the plurality of phased variants.

[0153] In some embodiments, the target nucleic acid molecule is a molecule that is derived from a pre-identified portion of a genome of a cancer cell or a transplanted cell from the subject that differs in sequence from a reference genomic sequence, wherein the preidentified portion of the genome is less than 200, less than 180, or less than 150 nucleotides in length. In some embodiments, each nucleic acid probe of the plurality of nucleic acid probes has a lower ΔG of binding to the target nucleic acid molecule than to a corresponding molecule that is identical in length and sequence to the target nucleic acid molecule except that the corresponding molecule has a sequence that corresponds with a reference genomic sequence. In some embodiments, the reference genomic sequence comprises a portion of either (1) a reference cohort, such as a portion of the hg19 human genome, hg18 genome, hg17 genome, hg16 genome, or hg38 genome or (2) a healthy sample from the subject. In some embodiments, the method involves the capture of the target nucleic acid derived from either the Watson strand or the Crick strand of a chromosome, but does not involve the capture of the corresponding complementary nucleic acid of the other strand. In some embodiments, the method comprises capture of at least 10, at least 100, at least 1000, or at least 10,000 target nucleic acid molecules. In some embodiments, the method further comprises sequencing the captured target nucleic acids to obtain sequencing data derived from the plurality of nucleic acid molecules. In some embodiments, the sequencing does not involve use of molecular barcodes. In some embodiments, the sequencing does not comprise duplex sequencing.

[0154] In one aspect, the present disclosure provides a method for determining a condition of a subject (e.g., assessing minimal residual disease, disease progression, or transplant rejection status), the method comprising obtaining, by a computer system, sequence information obtained by any method described herein involving the use of hybrid capture probes that are designed to bind preferentially to molecules that contain phased variants as compared to corresponding molecules that lack phased variants; processing, by the computer system, the sequencing data to identify one or more nucleic acid molecules of the plurality of nucleic acid molecules, wherein each of the one or more nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence; and

analyzing, by the computer system, the identified one or more nucleic acid molecules to determine a condition of the subject. In some embodiments, such methods do not comprise duplex-mediated error suppression or barcode-mediated error suppression. Individuals may be treated (e.g., with anti-cancer agents, anti-rejection agents, or surgical procedures) based on the identification of a condition (e.g., state) of the subject.

[0155] In one aspect, the present disclosure provides a method comprising: (a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject; (b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence, wherein at least about 10% of the one or more cell-free nucleic acid molecules comprises a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants that are separated by at least one nucleotide; and (c) analyzing, by the computer system, the identified one or more cell-free nucleic acid molecules to determine a condition of the subject. In some embodiments, cellular DNA is used instead of cell-free DNA (e.g., for detection of leukemia or other hematological cancers).

[0156] In some embodiments of any one of the methods disclosed herein, the at least about 10% of the cell-free nucleic acid molecules comprise at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of the one or more cell-free nucleic acid molecules.

[0157] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and (c) further comprises determining the condition of the subject based at least in part on the identified one or more indels.

[0158] In some embodiments, the method further comprises determining the start position (i.e., the 5'-most nucleotide) and the end position (i.e., the 3'-most nucleotide) in a molecule. In some cases, tumor-derived nucleic acids, such as tumor-derived cfDNA molecules can have stereotyped start/end positions, which may reflect cleavage by tissue-specific nucleases. The start and end positions can be used—in connection with phased variants—to identify a condition of a subject.

[0159] In one aspect, the present disclosure provides a method comprising: (a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject; (b) processing, by the computer system,

the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide; and (c) analyzing, by the computer system, the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

[0160] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and (c) further comprises determining the condition of the subject based at least in part on the identified one or more indels.

[0161] In one aspect, the present disclosure provides a method comprising: (a) obtaining sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject; (b) processing the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules with a limit of detection of less than about 1 out of 50,000 observations from the sequencing data; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

[0162] In some embodiments of any one of the methods disclosed herein, the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 observations from the sequencing data.

[0163] In some embodiments of any one of the methods disclosed herein, each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence. In some embodiments of any one of the methods disclosed herein, a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide.

[0164] In some embodiments of any one of the methods disclosed herein, the processes (a) to (c) are performed by a computer system.

[0165] In some embodiments of any one of the methods disclosed herein, the sequencing data is generated based on nucleic acid amplification. In some embodiments of any one of the methods disclosed herein, the sequencing data is generated based on polymerase chain reaction. In some embodiments of any one of the methods disclosed herein, the sequencing data is generated based on amplicon sequencing.

[0166] In some embodiments of any one of the methods disclosed herein, the sequencing data is generated based on next-generation sequencing (NGS). Alternatively, in some embodiments of any one of the methods disclosed herein, the sequencing data is generated based on non-hybridization-based NGS.

[0167] In some embodiments of any one of the methods disclosed herein, the sequencing data is generated without use of molecular barcoding of at least a portion of the plurality of cell-free nucleic acid molecules. In some embodiments of any one of the methods disclosed herein, the sequencing data is obtained without use of sample barcoding of at least a portion of the plurality of cell-free nucleic acid molecules.

[0168] In some embodiments of any one of the methods disclosed herein, the sequencing data is obtained without in silico removal or suppression of (i) background error or (ii) sequencing error.

[0169] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and (c) further comprises determining the condition of the subject based at least in part on the identified one or more indels.

[0170] In one aspect, the present disclosure provides a method of treating a condition of a subject, the method comprising: (a) identifying the subject for treatment of the condition, wherein the subject has been determined to have the condition based on identification of one or more cell-free nucleic acid molecules from a plurality of cell-free nucleic acid molecules that is obtained or derived from the subject, wherein each of the one or more cell-free nucleic acid molecules identified comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide, and wherein a presence of the plurality of phased variants is indicative of the condition of the subject; and (b) subjecting the subject to the treatment based on the identification in (a).

[0171] In some embodiments, the subject has been determined to have the condition based at least in part on one or more insertions or deletions (indels) identified in the one or more cell-free nucleic acid molecules.

[0172] In one aspect, the present disclosure provides a method of monitoring a progress of a condition of a subject, the method comprising: (a) determining a first state of the condition of the subject based on identification of a first set of one or more cell-free nucleic acid molecules from a first plurality of cell-free nucleic acid molecules that is obtained or derived from the subject; (b) determining a second state of the condition of the subject based on identification of a second set of one or more cell-free nucleic acid molecules from a second

plurality of cell-free nucleic acid molecules that is obtained or derived from the subject, wherein the second plurality of cell-free nucleic acid molecules are obtained from the subject subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject; and (c) determining the progress of the condition based on the first state of the condition and the second state of the condition, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide.

[0173] In some embodiments of any one of the methods disclosed herein, the progress of the condition is worsening of the condition.

[0174] In some embodiments of any one of the methods disclosed herein, the progress of the condition is at least a partial remission of the condition.

[0175] In some embodiments of any one of the methods disclosed herein, a presence of the plurality of phased variants is indicative of the first state or the second state of the condition of the subject.

[0176] In some embodiments of any one of the methods disclosed herein, the second plurality of cell-free nucleic acid molecules is obtained from the subject at least about 1 week, at least about 2 weeks, at least about 3 weeks, at least about 4 weeks, at least about 2 months, or at least about 3 months subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject.

[0177] In some embodiments of any one of the methods disclosed herein, the subject is subjected to a treatment for the condition (i) prior to obtaining the second plurality of cell-free nucleic acid molecules from the subject and (ii) subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject.

[0178] In some embodiments of any one of the methods disclosed herein, the progress of the condition is indicative of minimal residual disease of the condition of the subject. In some embodiments of any one of the methods disclosed herein, the progress of the condition is indicative of tumor burden or cancer burden of the subject.

[0179] In some embodiments of any one of the methods disclosed herein, the one or more cell-free nucleic acid molecules are captured from among the plurality of cell-free nucleic acid molecules with a set of nucleic acid probes, wherein the set of nucleic acid probes is configured to hybridize to at least a portion of cell-free nucleic acid molecules comprising one or more genomic regions associated with the condition.

[0180] In some embodiments, the subject has been determined to have the condition based at least in part on one or more insertions or deletions (indels) identified in the one or more cell-free nucleic acid molecules.

[0181] In one aspect, the present disclosure provides a method comprising: (a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject, wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide, and wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the plurality of phased variants and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants; (b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the plurality of phased variants; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

[0182] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and (c) further comprises determining the condition of the subject based at least in part on the identified one or more indels.

[0183] In one aspect, the present disclosure provides a method comprising: (a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject, wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising a plurality of phased variants relative to a reference genomic sequence, and wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the plurality of phased variants and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants; (b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid

molecules comprises the plurality of phased variants, wherein a limit of detection of the identification step is less than about 1 out of 50,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

[0184] In some embodiments of any one of the methods disclosed herein, the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules.

[0185] In some embodiments of any one of the methods disclosed herein, a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide.

[0186] In some embodiments of any one of the methods disclosed herein, the activatable reporter agent is activated upon hybridization of the individual nucleic acid probe to the plurality of phased variants.

[0187] In some embodiments of any one of the methods disclosed herein, the activatable reporter agent is activated upon dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants.

[0188] In some embodiments of any one of the methods disclosed herein, the method further comprises mixing (1) the set of nucleic acid probes and (2) the plurality of cell-free nucleic acid molecules.

[0189] In some embodiments of any one of the methods disclosed herein, the activatable reporter agent is a fluorophore.

[0190] In some embodiments of any one of the methods disclosed herein, analyzing the identified one or more cell-free nucleic acid molecules comprises analyzing (i) the identified one or more cell-free nucleic acid molecules and (ii) other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants as different variables.

[0191] In some embodiments of any one of the methods disclosed herein, the analyzing of the identified one or more cell-free nucleic acid molecules is not based on other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants.

[0192] In some embodiments of any one of the methods disclosed herein, a number of the plurality of phased variants from the identified one or more cell-free nucleic acid molecules is indicative of the condition of the subject. In some embodiments, a ratio of (i) the number of the plurality of phased variants from the one or more cell-free nucleic acid molecules and (ii) a number of single nucleotide variants (SNVs) from the one or more cell-free nucleic acid molecules is indicative of the condition of the subject.

[0193] In some embodiments of any one of the methods disclosed herein, a frequency of the plurality of phased variants in the identified one or more cell-free nucleic acid molecules is indicative of the condition of the subject. In some embodiments, the frequency is indicative of a diseased cell associated with the condition. In some embodiments, the condition is diffuse large B-cell lymphoma, and wherein the frequency is indicative of whether the one or more cell-free nucleic acid molecules are derived from germinal center B-cell (GCB) or activated B-cell (ABC).

[0194] In some embodiments of any one of the methods disclosed herein, genomic origin of the identified one or more cell-free nucleic acid molecules is indicative of the condition of the subject.

[0195] In some embodiments of any one of the methods disclosed herein, the first and second phased variants are separated by at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 nucleotides. In some embodiments of any one of the methods disclosed herein, the first and second phased variants are separated by at most about 180, at most about 170, at most about 160, at most about 150, or at most about 140 nucleotides.

[0196] In some embodiments of any one of the methods disclosed herein, at least about 10%, at least about 20%, at least about 30%, at least about 40%, or at least about 50% of the one or more cell-free nucleic acid molecules comprising a plurality of phased variants comprises a single nucleotide variant (SNV) that is at least 2 nucleotides away from an adjacent SNV.

[0197] In some embodiments of any one of the methods disclosed herein, the plurality of phased variants comprises at least 3, at least 4, at least 5, at least 10, at least 15, at least 20, or at least 25 phased variants within the same cell-free nucleic acid molecule.

[0198] In some embodiments of any one of the methods disclosed herein, the one or more cell-free nucleic acid molecules identified comprises at least 2, at least 3, at least 4, at least 5, at least 10, at least 50, at least 100, at least 500, or at least 1,000 cell-free nucleic acid molecules.

[0199] In some embodiments of any one of the methods disclosed herein, the reference genomic sequence is derived from a reference cohort. In some embodiments, the reference genomic sequence comprises a consensus sequence from the reference cohort. In some embodiments, the reference genomic sequence comprises at least a portion of hg19 human genome, hg18 genome, hg17 genome, hg16 genome, or hg38 genome.

[0200] In some embodiments of any one of the methods disclosed herein, the reference genomic sequence is derived from a sample of the subject.

[0201] In some embodiments of any one of the methods disclosed herein, the sample is a healthy sample. In some embodiments, the sample comprises a healthy cell. In some embodiments, the healthy cell comprises a healthy leukocyte.

[0202] In some embodiments of any one of the methods disclosed herein, the sample is a diseased sample. In some embodiments, the diseased sample comprises a diseased cell. In some embodiments, the diseased cell comprises a tumor cell. In some embodiments, the diseased sample comprises a solid tumor.

[0203] In some embodiments of any one of the methods disclosed herein, the set of nucleic acid probes is designed based on the plurality of phased variants that are identified by comparing (i) sequencing data from a solid tumor, lymphoma, or blood tumor of the subject and (ii) sequencing data from a healthy cell of the subject or a healthy cohort. In some embodiments, the healthy cell is from the subject. In some embodiments, the healthy cell is from the healthy cohort.

[0204] In some embodiments of any one of the methods disclosed herein, the set of nucleic acid probes are designed to hybridize to at least a portion of sequences of genomic loci associated with the condition. In some embodiments, the genomic loci associated with the condition are known to exhibit aberrant somatic hypermutation when the subject has the condition.

[0205] In some embodiments of any one of the methods disclosed herein, the set of nucleic acid probes are designed to hybridize to at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3.

[0206] In some embodiments of any one of the methods disclosed herein, each nucleic acid probe of the set of nucleic acid probes has at least about 70%, at least about 80%, at least about 90% sequence identity, at least about 95% sequence identity, or about 100% sequence identity to a probe sequence selected from Table 6.

[0207] In some embodiments of any one of the methods disclosed herein, the set of nucleic acid probes comprises at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90% of probe sequences in Table 6.

[0208] In some embodiments of any one of the methods disclosed herein, the method further comprises determining that the subject has the condition or determining a degree or status of the condition of the subject, based on the identified one or more cell-free nucleic acid molecules comprising the plurality of phased variants. In some embodiments, the method further comprises determining that the one or more cell-free nucleic acid molecules are derived from a sample associated with the condition, based on performing a statistical model analysis of the identified one or more cell-free nucleic acid molecules. In some embodiments, the statistical model analysis comprises a Monte Carlo statistical analysis.

[0209] In some embodiments of any one of the methods disclosed herein, the method further comprises monitoring a progress of the condition of the subject based on the identified one or more cell-free nucleic acid molecules.

[0210] In some embodiments of any one of the methods disclosed herein, the method further comprises performing a different procedure to confirm the condition of the subject. In some embodiments, the different procedure comprises a blood test, genetic test, medical imaging, physical exam, or tissue biopsy.

[0211] In some embodiments of any one of the methods disclosed herein, the method further comprises determining a treatment for the condition of the subject based on the identified one or more cell-free nucleic acid molecules.

[0212] In some embodiments of any one of the methods disclosed herein, the subject has been subjected to a treatment for the condition prior to (a).

[0213] In some embodiments of any one of the methods disclosed herein, the treatment comprises chemotherapy, radiotherapy, chemoradiotherapy, immunotherapy, adoptive cell therapy, hormone therapy, targeted drug therapy, surgery, transplant, transfusion, or medical surveillance.

[0214] In some embodiments of any one of the methods disclosed herein, the plurality of cell-free nucleic acid molecules comprises a plurality of cell-free deoxyribonucleic acid (DNA) molecules.

[0215] In some embodiments of any one of the methods disclosed herein, condition comprises a disease.

[0216] In some embodiments of any one of the methods disclosed herein, the plurality of cell-free nucleic acid molecules are derived from a bodily sample of the subject. In some embodiments, the bodily sample comprises plasma, serum, blood, cerebrospinal fluid, lymph fluid, saliva, urine, or stool.

[0217] In some embodiments of any one of the methods disclosed herein, the subject is a mammal. In some embodiments of any one of the methods disclosed herein, the subject is a human.

[0218] In some embodiments of any one of the methods disclosed herein, the condition comprises neoplasm, cancer, or tumor. In some embodiments, the condition comprises a solid tumor. In some embodiments, the condition comprises a lymphoma. In some embodiments, the condition comprises a B-cell lymphoma. In some embodiments, the condition comprises a sub-type of B-cell lymphoma selected from the group consisting of diffuse large B-cell lymphoma, follicular lymphoma, Burkitt lymphoma, and B-cell chronic lymphocytic leukemia. In some embodiments of any one of the methods disclosed herein, the condition comprises transplant rejection of or a chromosomal abnormality.

[0219] In some embodiments of any one of the methods disclosed herein, the plurality of phased variants have been previously identified as tumor-derived from sequencing a prior tumor sample or cell-free nucleic acid sample.

[0220] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and (c) further comprises determining the condition of the subject based at least in part on the identified one or more indels.

[0221] In one aspect, the present disclosure provides a composition comprising a bait set comprising a set of nucleic acid probes designed to capture cell-free DNA molecules derived from at least about 5% of genomic regions set forth in (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3.

[0222] In some embodiments of any of the compositions disclosed herein, the set of nucleic acid probes are designed to pull down cell-free DNA molecules derived from at least about

10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of the genomic regions set forth in (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3.

[0223] In some embodiments of any of the compositions disclosed herein, the set of nucleic acid probes are designed to capture the one or more cell-free DNA molecules derived from at most about 10%, at most about 20%, at most about 30%, at most about 40%, at most about 50%, at most about 60%, at most about 70%, at most about 80%, at most about 90%, or about 100% of the genomic regions set forth in (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3.

[0224] In some embodiments of any of the compositions disclosed herein, the bait set comprises at most 5, at most 10, at most 50, at most 100, at most 500, at most 1000, or at most 2000 nucleic acid probes.

[0225] In some embodiments of any of the compositions disclosed herein, an individual nucleic acid probe of the set of nucleic acid probes comprises a pull-down tag.

[0226] In some embodiments of any of the compositions disclosed herein, the pull-down tag comprises a nucleic acid barcode.

[0227] In some embodiments of any of the compositions disclosed herein, the pull-down tag comprises biotin.

[0228] In some embodiments of any of the compositions disclosed herein, each of the cell-free DNA molecules is between about 100 nucleotides and about 180 nucleotides in length.

[0229] In some embodiments of any of the compositions disclosed herein, the genomic regions are associated with a condition.

[0230] In some embodiments of any of the compositions disclosed herein, the genomic regions exhibit aberrant somatic hypermutation when a subject has the condition.

[0231] In some embodiments of any of the compositions disclosed herein, the condition comprises a B-cell lymphoma. In some embodiments, the condition comprises a sub-type of B-cell lymphoma selected from the group consisting of diffuse large B-cell lymphoma, follicular lymphoma, Burkitt lymphoma, and B-cell chronic lymphocytic leukemia.

[0232] In some embodiments of any of the compositions disclosed herein, the composition further comprises a plurality of cell-free DNA molecules obtained or derived from a subject.

[0233] In one aspect, the present disclosure provides a method to perform a clinical procedure on an individual, the method comprising: (a) obtaining or having obtained a targeted sequencing result of a collection of cell-free nucleic acid molecules, wherein the collection of cell-free nucleic acid molecules are sourced from a liquid or waste biopsy of an individual, and wherein the targeting sequencing is performed utilizing nucleic acid probes to pull down sequences of genomic loci known to experience aberrant somatic hypermutation in a B-cell cancer; (b) identifying or having identified a plurality of variants in phase within the cell-free nucleic acid sequencing result; (c) determining or having determined, utilizing a statistical model and the identified phased variants, that the cell-free nucleic acid sequencing result contains nucleotides derived from a neoplasm; and (d) performing a clinical procedure on the individual to confirm the presence of the B-cell cancer, based upon determining that the cell-free nucleic acid sequencing result contains nucleic acid sequences likely derived from the B-cell cancer.

[0234] In some embodiments of any of the compositions disclosed herein, the biopsy is one of blood, serum, cerebrospinal fluid, lymph fluid, urine, or stool.

[0235] In some embodiments of any of the compositions disclosed herein, the genomic loci are selected from (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3.

[0236] In some embodiments of any of the compositions disclosed herein, the sequences of the nucleic acid probes are selected from Table 6.

[0237] In some embodiments of any of the compositions disclosed herein, the clinical is procedure is a blood test, medical imaging, or a physical exam.

[0238] In some embodiments, the method further comprises identifying or having identified one or more insertions or deletions (indels) within the cell-free nucleic acid sequencing result, and determining or having determined, based least in part on the identified one or more indels, that the cell-free nucleic acid sequencing result contains the nucleotides derived from the neoplasm.

[0239] In one aspect, the present disclosure provides a method to treat an individual for a B-cell cancer, the method comprising: (a) obtaining or having obtained a targeted sequencing result of a collection of cell-free nucleic acid molecules, wherein the collection of cell-free nucleic acid molecules are sourced from a liquid or waste biopsy of an individual, and wherein the targeting sequencing is performed utilizing nucleic acid probes to pull down sequences of genomic loci known to experience aberrant somatic hypermutation in a B-cell cancer; (b)

identifying or having identified a plurality of variants in phase within the cell-free nucleic acid sequencing result; (c) determining or having determined, utilizing a statistical model and the identified phased variants, that the cell-free nucleic acid sequencing result contains nucleotides derived from a neoplasm; and (d) treating the individual to curtail the B-cell cancer, based upon determining that the cell-free nucleic acid sequencing result contains nucleic acid sequences derived from the B-cell cancer.

[0240] In some embodiments of any of the compositions disclosed herein, the biopsy is one of blood, serum, cerebrospinal fluid, lymph fluid, urine or stool.

[0241] In some embodiments of any of the compositions disclosed herein, the genomic loci are selected from (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3.

[0242] In some embodiments of any of the compositions disclosed herein, the sequences of the nucleic acid probes are selected from Table 6.

[0243] In some embodiments of any of the compositions disclosed herein, the treatment is chemotherapy, radiotherapy, immunotherapy, hormone therapy, targeted drug therapy, or medical surveillance.

[0244] In some embodiments, the method further comprises identifying or having identified one or more insertions or deletions (indels) within the cell-free nucleic acid sequencing result, and determining or having determined, based least in part on the identified one or more indels, that the cell-free nucleic acid sequencing result contains the nucleotides derived from the neoplasm.

[0245] In one aspect, the present disclosure provides a method to detect cancerous minimal residual disease in an individual and to treat the individual for a cancer, the method comprising: (a) obtaining or having obtained a targeted sequencing result of a collection of cell-free nucleic acid molecules, wherein the collection of cell-free nucleic acid molecules are sourced from a liquid or waste biopsy of an individual, wherein the liquid or waste biopsy is sourced after a series of treatments in order to detect minimal residual disease, and wherein the targeting sequencing is performed utilizing nucleic acid probes to pull down sequences of genomic loci determined to contain a plurality of variants in phase, as determined by a prior sequencing result on a prior biopsy derived from the cancer; (b) identifying or having identified at least one set of the plurality of variants in phase within the cell-free nucleic acid sequencing result; and (c) treating the individual to curtail the cancer, based upon determining that the cell-free nucleic acid sequencing result contains nucleic acid sequences derived from the cancer.

[0246] In some embodiments of any of the compositions disclosed herein, the liquid or waste biopsy is one of blood, serum, cerebrospinal fluid, lymph fluid, urine or stool.

[0247] In some embodiments of any of the compositions disclosed herein, the treatment is chemotherapy, radiotherapy, immunotherapy, hormone therapy, targeted drug therapy, or medical surveillance.

[0248] In some embodiments, the method further comprises identifying or having identified one or more insertions or deletions (indels) within the cell-free nucleic acid sequencing result, and treating the individual to curtail the cancer, based least in part on the identified one or more indels.

[0249] In one aspect, the present disclosure provides a method comprising: (a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject; (b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises one or more insertions or deletions (indels) relative to a reference genomic sequence; and (c) analyzing, by the computer system, the one or more indels to determine a condition of the subject.

[0250] In one aspect, the present disclosure provides a method comprising: (a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject; (b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises one or more insertions or deletions (indels) relative to a reference genomic sequence; and (c) analyzing, by the computer system, the one or more insertions or deletions (indels) to determine a condition of the subject.

[0251] In one aspect, the present disclosure provides a method comprising: (a) obtaining sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject; (b) processing the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules with a limit of detection of less than about 1 out of 50,000 observations from the sequencing data, wherein each of the one or more cell-free nucleic acid molecules comprises one or more insertions or deletions (indels) relative to a reference genomic sequence; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

[0252] In some embodiments, the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 observations from the sequencing data. In some embodiments, (a) to (c) are performed by a computer system. In some embodiments, the sequencing data is generated based on nucleic acid amplification. In some embodiments, the sequencing data is generated based on polymerase chain reaction. In some embodiments, the sequencing data is generated based on amplicon sequencing. In some embodiments, the sequencing data is generated based on next-generation sequencing (NGS). In some embodiments, the sequencing data is generated based on non-hybridization-based NGS. In some embodiments, the sequencing data is generated without use of molecular barcoding of at least a portion of the plurality of cell-free nucleic acid molecules. In some embodiments, the sequencing data is obtained without use of sample barcoding of at least a portion of the plurality of cell-free nucleic acid molecules. In some embodiments, the sequencing data is obtained without in silico removal or suppression of (i) background error or (ii) sequencing error.

[0253] In one aspect, the present disclosure provides a method of treating a condition of a subject, the method comprising: (a) identifying the subject for treatment of the condition, wherein the subject has been determined to have the condition based on identification of one or more cell-free nucleic acid molecules from a plurality of cell-free nucleic acid molecules that is obtained or derived from the subject, wherein each of the one or more cell-free nucleic acid molecules comprises one or more insertions or deletions (indels) relative to a reference genomic sequence, and wherein a presence of the one or more indels is indicative of the condition of the subject; and (b) subjecting the subject to the treatment based on the identification in (a).

[0254] In one aspect, the present disclosure provides a method of monitoring a progress of a condition of a subject, the method comprising: (a) determining a first state of the condition of the subject based on identification of a first set of one or more cell-free nucleic acid molecules from a first plurality of cell-free nucleic acid molecules that is obtained or derived from the subject; (b) determining a second state of the condition of the subject based on identification of a second set of one or more cell-free nucleic acid molecules from a second plurality of cell-free nucleic acid molecules that is obtained or derived from the subject, wherein the second plurality of cell-free nucleic acid molecules are obtained from the subject subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject; and (c) determining the progress of the condition based on the first state of the condition and

the second state of the condition, wherein each of the one or more cell-free nucleic acid molecules comprises one or more insertions or deletions (indels) relative to a reference genomic sequence.

[0255] In some embodiments, the progress of the condition is worsening of the condition. In some embodiments, the progress of the condition is at least a partial remission of the condition. In some embodiments, a presence of the one or more indels is indicative of the first state or the second state of the condition of the subject. In some embodiments, the second plurality of cell-free nucleic acid molecules is obtained from the subject at least about 1 week, at least about 2 weeks, at least about 3 weeks, at least about 4 weeks, at least about 2 months, or at least about 3 months subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject. In some embodiments, the subject is subjected to a treatment for the condition (i) prior to obtaining the second plurality of cell-free nucleic acid molecules from the subject and (ii) subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject. In some embodiments, the progress of the condition is indicative of minimal residual disease of the condition of the subject. In some embodiments, the progress of the condition is indicative of tumor burden or cancer burden of the subject. In some embodiments, the one or more cell-free nucleic acid molecules are captured from among the plurality of cell-free nucleic acid molecules with a set of nucleic acid probes, wherein the set of nucleic acid probes is configured to hybridize to at least a portion of cell-free nucleic acid molecules comprising one or more genomic regions associated with the condition.

[0256] In one aspect, the present disclosure provides a method comprising: (a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject, wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising one or more insertions or deletions (indels) relative to a reference genomic sequence, and wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the one or more indels and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the one or more indels; (b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the one or more indels; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

[0257] In one aspect, the present disclosure provides a method comprising: (a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject, wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising one or more insertions or deletions (indels) relative to a reference genomic sequence, and wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the one or more indels and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the one or more indels; (b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the one or more indels, wherein a limit of detection of the identification step is less than about 1 out of 50,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

[0258] In some embodiments, the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules. In some embodiments, the activatable reporter agent is activated upon hybridization of the individual nucleic acid probe to the one or more indels. In some embodiments, the activatable reporter agent is activated upon dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the one or more indels. In some embodiments, the method further comprises mixing (1) the set of nucleic acid probes and (2) the plurality of cell-free nucleic acid molecules. In some embodiments, the activatable reporter agent is a fluorophore. In some embodiments, analyzing the identified one or more cell-free nucleic acid molecules comprises analyzing (i) the identified one or more cell-free nucleic acid molecules and (ii) other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the one or more indels as different variables. In some embodiments, the analyzing of the identified one or more cell-free nucleic acid molecules is not based on other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the one or more indels. In some embodiments, a number of the one or more indels from the identified one or more cell-free nucleic acid molecules is indicative of the condition of the subject. In

some embodiments, a ratio of (i) the number of the one or more indels from the one or more cell-free nucleic acid molecules and (ii) a number of single nucleotide variants (SNVs) from the one or more cell-free nucleic acid molecules is indicative of the condition of the subject. In some embodiments, a frequency of the one or more indels in the identified one or more cell-free nucleic acid molecules is indicative of the condition of the subject. In some embodiments, the frequency is indicative of a diseased cell associated with the condition. In some embodiments, the condition is diffuse large B-cell lymphoma, and wherein the frequency is indicative of whether the one or more cell-free nucleic acid molecules are derived from germinal center B-cell (GCB) or activated B-cell (ABC). In some embodiments, genomic origin of the identified one or more cell-free nucleic acid molecules is indicative of the condition of the subject.

[0259] In some embodiments, the one or more indels comprises at least 3, at least 4, at least 5, at least 10, at least 15, at least 20, or at least 25 indels within the same cell-free nucleic acid molecule. In some embodiments, the one or more cell-free nucleic acid molecules identified comprises at least 2, at least 3, at least 4, at least 5, at least 10, at least 50, at least 100, at least 500, or at least 1,000 cell-free nucleic acid molecules. In some embodiments, the reference genomic sequence is derived from a reference cohort. In some embodiments, the reference genomic sequence comprises a consensus sequence from the reference cohort. In some embodiments, the reference genomic sequence comprises at least a portion of hg19 human genome, hg18 genome, hg17 genome, hg16 genome, or hg38 genome. In some embodiments, the reference genomic sequence is derived from a sample of the subject. In some embodiments, the sample is a healthy sample. In some embodiments, the sample comprises a healthy cell. In some embodiments, the healthy cell comprises a healthy leukocyte. In some embodiments, the sample is a diseased sample. In some embodiments, the diseased sample comprises a diseased cell. In some embodiments, the diseased cell comprises a tumor cell. In some embodiments, the diseased sample comprises a solid tumor. In some embodiments, the set of nucleic acid probes is designed based on the one or more indels that are identified by comparing (i) sequencing data from a solid tumor, lymphoma, or blood tumor of the subject and (ii) sequencing data from a healthy cell of the subject or a healthy cohort. In some embodiments, the healthy cell is from the subject. In some embodiments, the healthy cell is from the healthy cohort. In some embodiments, the set of nucleic acid probes are designed to hybridize to at least a portion of sequences of genomic loci associated with the condition. In some embodiments, the genomic loci associated with the condition are known to exhibit aberrant somatic hypermutation when the subject has the condition.

[0260] In some embodiments, the set of nucleic acid probes are designed to hybridize to at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of (i) the genomic regions identified in Table 1, or (ii) the genomic regions identified in Table 3. In some embodiments, each nucleic acid probe of the set of nucleic acid probes has at least about 70%, at least about 80%, at least about 90% sequence identity, at least about 95% sequence identity, or about 100% sequence identity to a probe sequence selected from Table 6. In some embodiments, the set of nucleic acid probes comprises at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90% of probe sequences in Table 6.

[0261] In some embodiments, the method further comprises determining that the subject has the condition or determining a degree or status of the condition of the subject, based on the identified one or more cell-free nucleic acid molecules comprising the one or more indels. In some embodiments, the method further comprises determining that the one or more cell-free nucleic acid molecules are derived from a sample associated with the condition, based on performing a statistical model analysis of the identified one or more cell-free nucleic acid molecules. In some embodiments, the statistical model analysis comprises a Monte Carlo statistical analysis. In some embodiments, the method further comprises monitoring a progress of the condition of the subject based on the identified one or more cell-free nucleic acid molecules. In some embodiments, the method further comprises performing a different procedure to confirm the condition of the subject. In some embodiments, the different procedure comprises a blood test, genetic test, medical imaging, physical exam, or tissue biopsy. In some embodiments, the method further comprises determining a treatment for the condition of the subject based on the identified one or more cell-free nucleic acid molecules. In some embodiments, the subject has been subjected to a treatment for the condition prior to (a). In some embodiments, the treatment comprises chemotherapy, radiotherapy, chemoradiotherapy, immunotherapy, adoptive cell therapy, hormone therapy, targeted drug therapy, surgery, transplant, transfusion, or medical surveillance. In some embodiments, the plurality of cell-free nucleic acid molecules comprise a plurality of cell-free deoxyribonucleic acid (DNA) molecules. In some embodiments, the condition comprises a disease. In some embodiments, the plurality of cell-free nucleic acid molecules are derived from a bodily sample of the subject. In some embodiments, the bodily sample comprises plasma, serum, blood, cerebrospinal fluid, lymph fluid, saliva, urine, or stool. In some embodiments, the subject is a

mammal. In some embodiments, the subject is a human. In some embodiments, the condition comprises neoplasm, cancer, or tumor. In some embodiments, the condition comprises a solid tumor. In some embodiments, the condition comprises a lymphoma. In some embodiments, the condition comprises a B-cell lymphoma. In some embodiments, the condition comprises a sub-type of B-cell lymphoma selected from the group consisting of diffuse large B-cell lymphoma, follicular lymphoma, Burkitt lymphoma, and B-cell chronic lymphocytic leukemia. In some embodiments, the one or more indels have been previously identified as tumor-derived from sequencing a prior tumor sample or cell-free nucleic acid sample.

[0262] In one aspect, the present disclosure provides a method to perform a clinical procedure on an individual, the method comprising: obtaining or having obtained a targeted sequencing result of a collection of cell-free nucleic acid molecules, wherein the collection of cell-free nucleic acid molecules are sourced from a liquid or waste biopsy of an individual, and wherein the targeting sequencing is performed utilizing nucleic acid probes to pull down sequences of genomic loci known to experience aberrant somatic hypermutation in a B-cell cancer; identifying or having identified one or more insertions or deletions (indels) within the cell-free nucleic acid sequencing result; determining or having determined, utilizing a statistical model and the identified one or more indels, that the cell-free nucleic acid sequencing result contains nucleotides derived from a neoplasm; and performing a clinical procedure on the individual to confirm the presence of the B-cell cancer, based upon determining that the cell-free nucleic acid sequencing result contains nucleic acid sequences likely derived from the B-cell cancer.

[0263] In some embodiments, the biopsy is one of blood, serum, cerebrospinal fluid, lymph fluid, urine, or stool. In some embodiments, the genomic loci are selected from (i) the genomic regions identified in Table 1, or (ii) the genomic regions identified in Table 3. In some embodiments, the sequences of the nucleic acid probes are selected from Table 6. In some embodiments, the clinical is procedure is a blood test, medical imaging, or a physical exam.

[0264] In one aspect, the present disclosure provides a method to treat an individual for a B-cell cancer, the method comprising: obtaining or having obtained a targeted sequencing result of a collection of cell-free nucleic acid molecules, wherein the collection of cell-free nucleic acid molecules are sourced from a liquid or waste biopsy of an individual, and wherein the targeting sequencing is performed utilizing nucleic acid probes to pull down sequences of genomic loci known to experience aberrant somatic hypermutation in a B-cell cancer; identifying or having identified one or more insertions or deletions (indels) within the cell-free nucleic acid sequencing result; determining or having determined, utilizing a statistical model

and the identified one or more indels, that the cell-free nucleic acid sequencing result contains nucleotides derived from a neoplasm; and treating the individual to curtail the B-cell cancer, based upon determining that the cell-free nucleic acid sequencing result contains nucleic acid sequences derived from the B-cell cancer.

[0265] In some embodiments, the biopsy is one of blood, serum, cerebrospinal fluid, lymph fluid, urine or stool. In some embodiments, the genomic loci are selected from (i) the genomic regions identified in Table 1, or (ii) the genomic regions identified in Table 3. In some embodiments, the sequences of the nucleic acid probes are selected from Table 6. In some embodiments, the treatment is chemotherapy, radiotherapy, immunotherapy, hormone therapy, targeted drug therapy, or medical surveillance.

[0266] In one aspect, the present disclosure provides a method to detect cancerous minimal residual disease in an individual and to treat the individual for a cancer, the method comprising: obtaining or having obtained a targeted sequencing result of a collection of cell-free nucleic acid molecules, wherein the collection of cell-free nucleic acid molecules are sourced from a liquid or waste biopsy of an individual, wherein the liquid or waste biopsy is sourced after a series of treatments in order to detect minimal residual disease, and wherein the targeting sequencing is performed utilizing nucleic acid probes to pull down sequences of genomic loci determined to contain one or more insertions or deletions (indels), as determined by a prior sequencing result on a prior biopsy derived from the cancer; identifying or having identified at least one set of the one or more indels within the cell-free nucleic acid sequencing result; and treating the individual to curtail the cancer, based upon determining that the cell-free nucleic acid sequencing result contains nucleic acid sequences derived from the cancer.

[0267] In some embodiments, the liquid or waste biopsy is one of blood, serum, cerebrospinal fluid, lymph fluid, urine or stool. In some embodiments, the treatment is chemotherapy, radiotherapy, immunotherapy, hormone therapy, targeted drug therapy, or medical surveillance.

[0268] In one aspect, the present disclosure provides a method comprising: (a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject who has received an organ or tissue transplant; (b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence, wherein at least about 10% of the one or more cell-free nucleic acid molecules comprises a first phased variant of the plurality of phased

variants and a second phased variant of the plurality of phased variants that are separated by at least one nucleotide; and (c) analyzing, by the computer system, the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an extent of transplant rejection of the subject.

[0269] In some embodiments, the at least about 10% of the cell-free nucleic acid molecules comprise at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of the one or more cell-free nucleic acid molecules. In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the extent of transplant rejection of the subject based at least in part on the identified one or more indels.

[0270] In one aspect, the present disclosure provides a method comprising: (a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject who has received an organ or tissue transplant; (b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide; and (c) analyzing, by the computer system, the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an extent of transplant rejection of the subject.

[0271] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the extent of transplant rejection of the subject based at least in part on the identified one or more indels.

[0272] In one aspect, the present disclosure provides a method comprising: (a) obtaining sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject who has received an organ or tissue transplant; (b) processing the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules with a limit of detection of less than about 1 out of 50,000 observations from the sequencing data; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an extent of transplant rejection of the subject.

[0273] In some embodiments, the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 observations from the sequencing data. In some embodiments, each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence. In some embodiments, a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide. In some embodiments, (a) to (c) are performed by a computer system. In some embodiments, the sequencing data is generated based on nucleic acid amplification. In some embodiments, the sequencing data is generated based on polymerase chain reaction. In some embodiments, the sequencing data is generated based on amplicon sequencing. In some embodiments, the sequencing data is generated based on next-generation sequencing (NGS). In some embodiments, the sequencing data is generated based on non-hybridization-based NGS. In some embodiments, the sequencing data is generated without use of molecular barcoding of at least a portion of the plurality of cell-free nucleic acid molecules. In some embodiments, the sequencing data is obtained without use of sample barcoding of at least a portion of the plurality of cell-free nucleic acid molecules. In some embodiments, the sequencing data is obtained without in silico removal or suppression of (i) background error or (ii) sequencing error. In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence or the absence of the transplant rejection of the subject based at least in part on the identified one or more indels.

[0274] In one aspect, the present disclosure provides a method of treating a transplant rejection of a subject who has received an organ or tissue transplant, the method comprising: (a) identifying the subject for treatment of the transplant rejection, wherein the subject has been determined to have the transplant rejection based on identification of one or more cell-free nucleic acid molecules from a plurality of cell-free nucleic acid molecules that is obtained or derived from the subject, wherein each of the one or more cell-free nucleic acid molecules identified comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide, and wherein a presence of the plurality of phased variants is indicative of the transplant rejection of the subject; and (b) subjecting the subject to the treatment based on the identification in (a).

[0275] In some embodiments, the subject has been determined to have the transplant rejection based at least in part on one or more insertions or deletions (indels) identified in the one or more cell-free nucleic acid molecules.

[0276] In one aspect, the present disclosure provides a method of monitoring a subject who has received an organ or tissue transplant for a presence, an absence, or an extent of transplant rejection, the method comprising: (a) determining a first state of the presence, the absence, or the extent of transplant rejection of the subject based on identification of a first set of one or more cell-free nucleic acid molecules from a first plurality of cell-free nucleic acid molecules that is obtained or derived from the subject; (b) determining a second state of the presence, the absence, or the extent of transplant rejection of the subject based on identification of a second set of one or more cell-free nucleic acid molecules from a second plurality of cell-free nucleic acid molecules that is obtained or derived from the subject, wherein the second plurality of cell-free nucleic acid molecules are obtained from the subject subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject; and (c) determining a transplant rejection status of the subject based on the first state and the second state, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide.

[0277] In some embodiments, the transplant rejection status is at least a partial transplant rejection. In some embodiments, a presence of the plurality of phased variants is indicative of the first state or the second state. In some embodiments, the second plurality of cell-free nucleic acid molecules is obtained from the subject at least about 1 week, at least about 2 weeks, at least about 3 weeks, at least about 4 weeks, at least about 2 months, or at least about 3 months subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject. In some embodiments, the subject is subjected to a treatment for the transplant rejection (i) prior to obtaining the second plurality of cell-free nucleic acid molecules from the subject and (ii) subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject. In some embodiments, the one or more cell-free nucleic acid molecules are captured from among the plurality of cell-free nucleic acid molecules with a set of nucleic acid probes, wherein the set of nucleic acid probes is configured to hybridize to at least a portion of cell-free nucleic acid molecules comprising one or more genomic regions associated with the transplant rejection. In some embodiments, the subject has been determined to have the presence or the absence of the transplant rejection based at least in part on one or more insertions or deletions (indels) identified in the one or more cell-free nucleic acid molecules.

[0278] In one aspect, the present disclosure provides a method comprising: (a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject who has received an organ or tissue transplant, wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide, and wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the plurality of phased variants and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants; (b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the plurality of phased variants; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an extent of transplant rejection of the subject.

[0279] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence or the absence of the transplant rejection of the subject based at least in part on the identified one or more indels.

[0280] In one aspect, the present disclosure provides a method comprising: (a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject who has received an organ or tissue transplant, wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising a plurality of phased variants relative to a reference genomic sequence, and wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the plurality of phased variants and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants; (b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the plurality of phased variants, wherein a limit of detection of the identification step is less than about 1 out

of 50,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an extent of transplant rejection of the subject.

[0281] In some embodiments, the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules. In some embodiments, a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide. In some embodiments, the activatable reporter agent is activated upon hybridization of the individual nucleic acid probe to the plurality of phased variants. In some embodiments, the activatable reporter agent is activated upon dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants. In some embodiments, the method further comprises mixing (1) the set of nucleic acid probes and (2) the plurality of cell-free nucleic acid molecules. In some embodiments, the activatable reporter agent is a fluorophore. In some embodiments, analyzing the identified one or more cell-free nucleic acid molecules comprises analyzing (i) the identified one or more cell-free nucleic acid molecules and (ii) other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants as different variables. In some embodiments, the analyzing of the identified one or more cell-free nucleic acid molecules is not based on other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants. In some embodiments, a number of the plurality of phased variants from the identified one or more cell-free nucleic acid molecules is indicative of the presence, the absence, or the extent of transplant rejection of the subject. In some embodiments, a ratio of (i) the number of the plurality of phased variants from the one or more cell-free nucleic acid molecules and (ii) a number of single nucleotide variants (SNVs) from the one or more cell-free nucleic acid molecules is indicative of the presence, the absence, or the extent of transplant rejection of the subject. In some embodiments, a frequency of the plurality of phased variants in the identified one or more cell-free nucleic acid molecules is indicative of the presence or the absence of the transplant rejection of the subject. In some embodiments, the frequency is indicative of a diseased cell associated with the presence, the absence, or the extent of transplant rejection. In some embodiments, genomic origin of the identified one or more cell-free nucleic acid molecules is indicative of the presence or the absence of the transplant rejection of the subject. In some embodiments, the first and second phased variants

are separated by at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 nucleotides. In some embodiments, the first and second phased variants are separated by at most about 180, at most about 170, at most about 160, at most about 150, or at most about 140 nucleotides.

[0282] In some embodiments, at least about 10%, at least about 20%, at least about 30%, at least about 40%, or at least about 50% of the one or more cell-free nucleic acid molecules comprising a plurality of phased variants comprises a single nucleotide variant (SNV) that is at least 2 nucleotides away from an adjacent SNV. In some embodiments, the plurality of phased variants comprises at least 3, at least 4, at least 5, at least 10, at least 15, at least 20, or at least 25 phased variants within the same cell-free nucleic acid molecule. In some embodiments, the one or more cell-free nucleic acid molecules identified comprises at least 2, at least 3, at least 4, at least 5, at least 10, at least 50, at least 100, at least 500, or at least 1,000 cell-free nucleic acid molecules. In some embodiments, the reference genomic sequence is derived from a reference cohort. In some embodiments, the reference genomic sequence comprises a consensus sequence from the reference cohort. In some embodiments, the reference genomic sequence comprises at least a portion of hg19 human genome, hg18 genome, hg17 genome, hg16 genome, or hg38 genome. In some embodiments, the reference genomic sequence is derived from a sample of the subject. In some embodiments, the sample is a healthy sample. In some embodiments, the sample comprises a healthy cell. In some embodiments, the healthy cell comprises a healthy leukocyte. In some embodiments, the sample is a diseased sample. In some embodiments, the diseased sample comprises a diseased cell. In some embodiments, the healthy cell is from the subject. In some embodiments, the healthy cell is from the healthy cohort. In some embodiments, the set of nucleic acid probes are designed to hybridize to at least a portion of sequences of genomic loci associated with the presence or the absence of the transplant rejection. In some embodiments, the genomic loci associated with the presence, the absence, or the extent of transplant rejection are known to exhibit aberrant somatic hypermutation when the subject has the transplant rejection.

[0283] In some embodiments, the set of nucleic acid probes are designed to hybridize to at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3. In some embodiments, each nucleic acid probe of the set of nucleic acid probes has at least about 70%, at least about 80%, at least about 90% sequence identity, at least

about 95% sequence identity, or about 100% sequence identity to a probe sequence selected from Table 6. In some embodiments, the set of nucleic acid probes comprises at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90% of probe sequences in Table 6. In some embodiments, the method further comprises determining the presence or the absence of the transplant rejection or determining a degree or status thereof, based on the identified one or more cell-free nucleic acid molecules comprising the plurality of phased variants. In some embodiments, the method further comprises determining that the one or more cell-free nucleic acid molecules are derived from a sample associated with the presence or the absence of the transplant rejection, based on performing a statistical model analysis of the identified one or more cell-free nucleic acid molecules. In some embodiments, the statistical model analysis comprises a Monte Carlo statistical analysis. In some embodiments, the method further comprises monitoring a progress of the presence, the absence, or the extent of transplant rejection of the subject based on the identified one or more cell-free nucleic acid molecules. In some embodiments, the method further comprises performing a different procedure to confirm the presence, the absence, or the extent of transplant rejection of the subject. In some embodiments, the different procedure comprises a blood test, genetic test, medical imaging, physical exam, or tissue biopsy. In some embodiments, the method further comprises determining a treatment for the transplant rejection of the subject based on the identified one or more cell-free nucleic acid molecules. In some embodiments, the subject has been subjected to a treatment for the transplant rejection prior to (a). In some embodiments, the plurality of cell-free nucleic acid molecules comprises a plurality of cell-free deoxyribonucleic acid (DNA) molecules. In some embodiments, the plurality of cell-free nucleic acid molecules are derived from a bodily sample of the subject. In some embodiments, the bodily sample comprises plasma, serum, blood, cerebrospinal fluid, lymph fluid, saliva, urine, or stool. In some embodiments, the subject is a mammal. In some embodiments, the subject is a human. In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the extent of transplant rejection of the subject based at least in part on the identified one or more indels.

[0284] In one aspect, the present disclosure provides a method comprising: (a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a pregnant subject; (b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the

plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence, wherein at least about 10% of the one or more cell-free nucleic acid molecules comprises a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants that are separated by at least one nucleotide; and (c) analyzing, by the computer system, the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an elevated risk of a genetic abnormality of a fetus of the pregnant subject.

[0285] In some embodiments, the at least about 10% of the cell-free nucleic acid molecules comprise at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of the one or more cell-free nucleic acid molecules. In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based at least in part on the identified one or more indels. In some embodiments, the genetic abnormality is a chromosomal aneuploidy. In some embodiments, the chromosomal aneuploidy is in chromosome 13, 18, 21, X, or Y.

[0286] In one aspect, the present disclosure provides a method comprising: (a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a pregnant subject; (b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide; and (c) analyzing, by the computer system, the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an elevated risk of a genetic abnormality of a fetus of the pregnant subject.

[0287] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based at least in part on the identified one or more indels. In some embodiments, the genetic abnormality is a chromosomal aneuploidy. In some embodiments, the chromosomal aneuploidy is in chromosome 13, 18, 21, X, or Y.

[0288] In one aspect, the present disclosure provides a method comprising: (a) obtaining sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a pregnant subject; (b) processing the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules with a limit of detection of less than about 1 out of 50,000 observations from the sequencing data; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an elevated risk of a genetic abnormality of a fetus of the pregnant subject.

[0289] In some embodiments, the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 observations from the sequencing data. In some embodiments, each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence. In some embodiments, a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide. In some embodiments, (a) to (c) are performed by a computer system. In some embodiments, he method of any one of claims 309-313, wherein the sequencing data is generated based on nucleic acid amplification. In some embodiments, the sequencing data is generated based on polymerase chain reaction. In some embodiments, the sequencing data is generated based on amplicon sequencing. In some embodiments, the sequencing data is generated based on next-generation sequencing (NGS). In some embodiments, the sequencing data is generated based on non-hybridization-based NGS. In some embodiments, the sequencing data is generated without use of molecular barcoding of at least a portion of the plurality of cell-free nucleic acid molecules. In some embodiments, the sequencing data is obtained without use of sample barcoding of at least a portion of the plurality of cell-free nucleic acid molecules. In some embodiments, the sequencing data is obtained without in silico removal or suppression of (i) background error or (ii) sequencing error. In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based at least in part on the identified one or more indels. In some embodiments, the genetic abnormality is a chromosomal aneuploidy. In some embodiments, the chromosomal aneuploidy is in chromosome 13, 18, 21, X, or Y.

[0290] In one aspect, the present disclosure provides a method of monitoring a pregnant subject for a presence, an absence, or an elevated risk of a genetic abnormality of a fetus of the pregnant subject, the method comprising: (a) determining a first state of the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based on identification of a first set of one or more cell-free nucleic acid molecules from a first plurality of cell-free nucleic acid molecules that is obtained or derived from the pregnant subject; (b) determining a second state of the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based on identification of a second set of one or more cell-free nucleic acid molecules from a second plurality of cell-free nucleic acid molecules that is obtained or derived from the pregnant subject, wherein the second plurality of cell-free nucleic acid molecules are obtained from the pregnant subject subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the pregnant subject; and (c) determining the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based on the first state and the second state, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide.

[0291] In some embodiments, the transplant rejection status is at least a partial transplant rejection. In some embodiments, a presence of the plurality of phased variants is indicative of the first state or the second state. In some embodiments, the second plurality of cell-free nucleic acid molecules is obtained from the pregnant subject at least about 1 week, at least about 2 weeks, at least about 3 weeks, at least about 4 weeks, at least about 2 months, or at least about 3 months subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the pregnant subject. In some embodiments, the one or more cell-free nucleic acid molecules are captured from among the plurality of cell-free nucleic acid molecules with a set of nucleic acid probes, wherein the set of nucleic acid probes is configured to hybridize to at least a portion of cell-free nucleic acid molecules comprising one or more genomic regions associated with the genetic abnormality. In some embodiments, the fetus has been determined to have the presence, the absence, or the elevated risk of the genetic abnormality based at least in part on one or more insertions or deletions (indels) identified in the one or more cell-free nucleic acid molecules.

[0292] In one aspect, the present disclosure provides a method comprising: (a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a pregnant subject, wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising a plurality of phased variants relative to a

reference genomic sequence that are separated by at least one nucleotide, and wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the plurality of phased variants and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants; (b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the plurality of phased variants; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an elevated risk of a genetic abnormality of a fetus of the pregnant subject.

[0293] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the elevated risk of the genetic abnormality based at least in part on the identified one or more indels.

[0294] In one aspect, the present disclosure provides a method comprising: (a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a pregnant subject, wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising a plurality of phased variants relative to a reference genomic sequence, and wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the plurality of phased variants and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants; (b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the plurality of phased variants, wherein a limit of detection of the identification step is less than about 1 out of 50,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an elevated risk of a genetic abnormality of a fetus of the pregnant subject.

[0295] In some embodiments, the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000,

less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules. In some embodiments, a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide. In some embodiments, the activatable reporter agent is activated upon hybridization of the individual nucleic acid probe to the plurality of phased variants. In some embodiments, the activatable reporter agent is activated upon dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants. In some embodiments, the method further comprises mixing (1) the set of nucleic acid probes and (2) the plurality of cell-free nucleic acid molecules. In some embodiments, the activatable reporter agent is a fluorophore. In some embodiments, analyzing the identified one or more cell-free nucleic acid molecules comprises analyzing (i) the identified one or more cell-free nucleic acid molecules and (ii) other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants as different variables. In some embodiments, the analyzing of the identified one or more cell-free nucleic acid molecules is not based on other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants. In some embodiments, a number of the plurality of phased variants from the identified one or more cell-free nucleic acid molecules is indicative of the genetic abnormality. In some embodiments, a ratio of (i) the number of the plurality of phased variants from the one or more cell-free nucleic acid molecules and (ii) a number of single nucleotide variants (SNVs) from the one or more cell-free nucleic acid molecules is indicative of the genetic abnormality. In some embodiments, a frequency of the plurality of phased variants in the identified one or more cell-free nucleic acid molecules is indicative of the genetic abnormality. In some embodiments, genomic origin of the identified one or more cell-free nucleic acid molecules is indicative of the genetic abnormality. In some embodiments, the first and second phased variants are separated by at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 nucleotides. In some embodiments, the first and second phased variants are separated by at most about 180, at most about 170, at most about 160, at most about 150, or at most about 140 nucleotides.

[0296] In some embodiments, at least about 10%, at least about 20%, at least about 30%, at least about 40%, or at least about 50% of the one or more cell-free nucleic acid molecules comprising a plurality of phased variants comprises a single nucleotide variant (SNV) that is at least 2 nucleotides away from an adjacent SNV. In some embodiments, the plurality of phased variants comprises at least 3, at least 4, at least 5, at least 10, at least 15, at least 20, or

at least 25 phased variants within the same cell-free nucleic acid molecule. In some embodiments, the one or more cell-free nucleic acid molecules identified comprises at least 2, at least 3, at least 4, at least 5, at least 10, at least 50, at least 100, at least 500, or at least 1,000 cell-free nucleic acid molecules. In some embodiments, the reference genomic sequence is derived from a reference cohort. In some embodiments, the reference genomic sequence comprises a consensus sequence from the reference cohort. In some embodiments, the reference genomic sequence comprises at least a portion of hg19 human genome, hg18 genome, hg17 genome, hg16 genome, or hg38 genome. In some embodiments, the reference genomic sequence is derived from a sample of the pregnant subject. In some embodiments, the sample is a healthy sample. In some embodiments, the sample comprises a healthy cell. In some embodiments, the sample is a diseased sample. In some embodiments, the diseased sample comprises a diseased cell. In some embodiments, the healthy cell is from the pregnant subject. In some embodiments, the healthy cell is from the healthy cohort. In some embodiments, the set of nucleic acid probes are designed to hybridize to at least a portion of sequences of genomic loci associated with the genetic abnormality.

[0297] In some embodiments, the set of nucleic acid probes are designed to hybridize to at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3. In some embodiments, each nucleic acid probe of the set of nucleic acid probes has at least about 70%, at least about 80%, at least about 90% sequence identity, at least about 95% sequence identity, or about 100% sequence identity to a probe sequence selected from Table 6. In some embodiments, the set of nucleic acid probes comprises at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90% of probe sequences in Table 6. In some embodiments, the method further comprises determining the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject, based on the identified one or more cell-free nucleic acid molecules comprising the plurality of phased variants. In some embodiments, the method further comprises determining that the one or more cell-free nucleic acid molecules are derived from a sample associated with the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject, based on performing a statistical model analysis of the identified one or more cell-free nucleic acid molecules. In some embodiments,

the statistical model analysis comprises a Monte Carlo statistical analysis. In some embodiments, the method further comprises monitoring a progress of the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based on the identified one or more cell-free nucleic acid molecules. In some embodiments, the method further comprises performing a different procedure to confirm the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject. In some embodiments, the different procedure comprises a blood test, genetic test, medical imaging, physical exam, or tissue biopsy. In some embodiments, the plurality of cell-free nucleic acid molecules comprise a plurality of cell-free deoxyribonucleic acid (DNA) molecules. In some embodiments, the plurality of cell-free nucleic acid molecules are derived from a bodily sample of the pregnant subject. In some embodiments, the bodily sample comprises plasma, serum, blood, cerebrospinal fluid, lymph fluid, saliva, urine, or stool. In some embodiments, the pregnant subject is a mammal. In some embodiments, the pregnant subject is a human. In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based at least in part on the identified one or more indels.

[0298] In one aspect, the present disclosure provides a method comprising adding a set of nucleic acid probes to a sample comprising a plurality of nucleic acid molecules that have been obtained or derived from a subject, wherein each nucleic acid probe of the set of nucleic acid probes is configured to hybridize to a target nucleic acid molecule comprising a plurality of phased variants such that the nucleic acid probe is complementary to at least a region of the target nucleic acid molecule that extends from a first phased variant of the plurality of phased variants to a second phased variant of the plurality of phased variants. (For clarity, the region includes both the first phased variant and the second phased variant.)

[0299] This method, and embodiments of it described herein, may involve the use of hybrid capture probes/baits, such as biotinylated oligonucleotides, that may be used in a hybrid capture enrichment step such that the hybrid capture probes bind to and preferentially capture nucleic acid molecules that contain phased variants. Such hybrid capture approaches may increase the capture sensitivity of circulating tumor DNA or circulating DNA from a transplanted organ. The hybrid capture probes can be synthesized to specifically target molecules containing phased variants by designing the hybrid capture probe to (1) contain a sequence that is complementary to the molecule that includes the phased variant (as opposed to the corresponding region of the reference genomic sequence) and (2) have a length that optimizes

the nucleic acid binding kinetics/thermodynamics (ΔG or binding energy) such that the hybrid capture probe preferentially binds to a nucleic acid molecule that contains the phased variants of interest as compared to corresponding molecules without the phased variants. Such hybrid capture probes can lead to improved enrichment of relevant nucleic acid sequences, thereby requiring less sequencing as a result. For instance, in some cases (such as in assessing minimal residual disease, disease state, or state of transplant rejection), a cancerous sample or a sample from the transplanted organ may be obtained and sequenced to identify phased variants in such samples relative to a reference genomic sequence, such as a sequence from corresponding healthy cell(s) of the subject, and the hybrid capture probes can be designed to preferentially bind to nucleic acid sequences containing the phased variants identified from the cancerous and/or transplanted organ samples. In some circumstances, such hybrid capture probes can be used for single strand recovery of nucleic acid molecules that contain phased variants. The nucleic acid molecules captured by such probe sets can include DNA or RNA (e.g., single stranded RNA), such as cell-free DNA or cell-free DNA. Probes as described in this particular method can be used on combination with other methods described herein.

[0300] In some embodiments, each nucleic acid probe of the set of nucleic acid probes comprises a pull-down tag, such as biotin. In some embodiments, the method further comprises separation of target nucleic acid molecules that hybridize to the nucleic acid probes from nucleic acid molecules that do not hybridize to the nucleic acid probes to thereby capture target nucleic acid molecules. In some embodiments, the nucleic acid molecules are cell-free nucleic acid molecules. In some embodiments, the first phased variant is selected from the group consisting of a somatic single nucleotide variant, a somatic indel, a somatic translocation breakpoint, a somatic amplification or deletion breakpoint, a germline SNV, a germline indel, a germline translocation breakpoint, a germline amplification or deletion breakpoint, and a region of localized hypermutation, and the second phased variant is selected from the group consisting of a somatic single nucleotide variant, a somatic indel, a somatic translocation breakpoint, a somatic amplification or deletion breakpoint, a germline SNV, a germline indel, a germline translocation breakpoint, a germline amplification or deletion breakpoint, and a region of localized hypermutation. In some embodiments, the first phased variant of the plurality of phased variants and the second phased variant of the plurality of phased variants are separated by at least 1, 2, 3, 4, 5, 10, or 20 nucleotides. In some embodiments, each nucleic acid probe of the set of nucleic acid probes is either (1) less than 40 nucleotides, less than 30 nucleotides, or less than 20 nucleotides in length or (2) no more than 5 nucleotides, nor more than 10 nucleotides, no more than 20 nucleotides, or no more than 30 nucleotides longer than

the distance between the first phased variant of the plurality of phased variants and the second phased variant of the plurality of phased variants, wherein the first phased variant and the second phased variant are the most separated phased variants (i.e., have the most number of intervening nucleotides) of the plurality of phased variants.

[0301] In some embodiments, the target nucleic acid molecule is a molecule that is derived from a pre-identified portion of a genome of a cancer cell or a transplanted cell from the subject that differs in sequence from a reference genomic sequence, wherein the preidentified portion of the genome is less than 200, less than 180, or less than 150 nucleotides in length. In some embodiments, each nucleic acid probe of the plurality of nucleic acid probes has a lower ΔG of binding to the target nucleic acid molecule than to a corresponding molecule that is identical in length and sequence to the target nucleic acid molecule except that the corresponding molecule has a sequence that corresponds with a reference genomic sequence. In some embodiments, the reference genomic sequence comprises a portion of either (1) a reference cohort, such as a portion of the hg19 human genome, hg18 genome, hg17 genome, hg16 genome, or hg38 genome or (2) a healthy sample from the subject. In some embodiments, the method involves the capture of the target nucleic acid derived from either the Watson strand or the Crick strand of a chromosome, but does not involve the capture of the corresponding complementary nucleic acid of the other strand. In some embodiments, the method comprises capture of at least 10, at least 100, at least 1000, or at least 10,000 target nucleic acid molecules. In some embodiments, the method further comprises sequencing the captured target nucleic acids to obtain sequencing data derived from the plurality of nucleic acid molecules. In some embodiments, the sequencing does not involve use of molecular barcodes. In some embodiments, the sequencing does not comprise duplex sequencing.

[0302] In one aspect, the present disclosure provides a method for determining a condition of a subject (e.g., assessing minimal residual disease, disease progression, or transplant rejection status), the method comprising obtaining, by a computer system, sequence information obtained by any method described herein involving the use of hybrid capture probes that are designed to bind preferentially to molecules that contain phased variants as compared to corresponding molecules that lack phased variants; processing, by the computer system, the sequencing data to identify one or more nucleic acid molecules of the plurality of nucleic acid molecules, wherein each of the one or more nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence; and analyzing, by the computer system, the identified one or more nucleic acid molecules to determine a condition of the subject. In some embodiments, such methods do not comprise

duplex-mediated error suppression or barcode-mediated error suppression. Individuals may be treated (e.g., with anti-cancer agents, anti-rejection agents, or surgical procedures) based on the identification of a condition (e.g., state) of the subject.

[0303] In one aspect, the present disclosure provides a method comprising: (a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject; (b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence, wherein at least about 10% of the one or more cell-free nucleic acid molecules comprises a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants that are separated by at least one nucleotide; and (c) analyzing, by the computer system, the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

[0304] In some embodiments of any one of the methods disclosed herein, the at least about 10% of the cell-free nucleic acid molecules comprise at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of the one or more cell-free nucleic acid molecules.

[0305] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and (c) further comprises determining the condition of the subject based at least in part on the identified one or more indels.

[0306] In one aspect, the present disclosure provides a method comprising: (a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject; (b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide; and (c) analyzing, by the computer system, the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

[0307] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and (c) further comprises determining the condition of the subject based at least in part on the identified one or more indels.

[0308] In one aspect, the present disclosure provides a method comprising: (a) obtaining sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject; (b) processing the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules with a limit of detection of less than about 1 out of 50,000 observations from the sequencing data; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

[0309] In some embodiments of any one of the methods disclosed herein, the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 observations from the sequencing data.

[0310] In some embodiments of any one of the methods disclosed herein, each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence. In some embodiments of any one of the methods disclosed herein, a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide.

[0311] In some embodiments of any one of the methods disclosed herein, the processes (a) to (c) are performed by a computer system.

[0312] In some embodiments of any one of the methods disclosed herein, the sequencing data is generated based on nucleic acid amplification. In some embodiments of any one of the methods disclosed herein, the sequencing data is generated based on polymerase chain reaction. In some embodiments of any one of the methods disclosed herein, the sequencing data is generated based on amplicon sequencing.

[0313] In some embodiments of any one of the methods disclosed herein, the sequencing data is generated based on next-generation sequencing (NGS). Alternatively, in some embodiments of any one of the methods disclosed herein, the sequencing data is generated based on non-hybridization-based NGS.

[0314] In some embodiments of any one of the methods disclosed herein, the sequencing data is generated without use of molecular barcoding of at least a portion of the plurality of cell-free nucleic acid molecules. In some embodiments of any one of the methods disclosed herein, the sequencing data is obtained without use of sample barcoding of at least a portion of the plurality of cell-free nucleic acid molecules.

[0315] In some embodiments of any one of the methods disclosed herein, the sequencing data is obtained without in silico removal or suppression of (i) background error or (ii) sequencing error.

[0316] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and (c) further comprises determining the condition of the subject based at least in part on the identified one or more indels.

[0317] In one aspect, the present disclosure provides a method of treating a condition of a subject, the method comprising: (a) identifying the subject for treatment of the condition, wherein the subject has been determined to have the condition based on identification of one or more cell-free nucleic acid molecules from a plurality of cell-free nucleic acid molecules that is obtained or derived from the subject, wherein each of the one or more cell-free nucleic acid molecules identified comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide, and wherein a presence of the plurality of phased variants is indicative of the condition of the subject; and (b) subjecting the subject to the treatment based on the identification in (a).

[0318] In some embodiments, the subject has been determined to have the condition based at least in part on one or more insertions or deletions (indels) identified in the one or more cell-free nucleic acid molecules.

[0319] In one aspect, the present disclosure provides a method of monitoring a progress of a condition of a subject, the method comprising: (a) determining a first state of the condition of the subject based on identification of a first set of one or more cell-free nucleic acid molecules from a first plurality of cell-free nucleic acid molecules that is obtained or derived from the subject; (b) determining a second state of the condition of the subject based on identification of a second set of one or more cell-free nucleic acid molecules from a second plurality of cell-free nucleic acid molecules that is obtained or derived from the subject, wherein the second plurality of cell-free nucleic acid molecules are obtained from the subject subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject; and (c) determining the progress of the condition based on the first state of the condition and the second state of the condition, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide.

[0320] In some embodiments of any one of the methods disclosed herein, the progress of the condition is worsening of the condition.

[0321] In some embodiments of any one of the methods disclosed herein, the progress of the condition is at least a partial remission of the condition.

[0322] In some embodiments of any one of the methods disclosed herein, a presence of the plurality of phased variants is indicative of the first state or the second state of the condition of the subject.

[0323] In some embodiments of any one of the methods disclosed herein, the second plurality of cell-free nucleic acid molecules is obtained from the subject at least about 1 week, at least about 2 weeks, at least about 3 weeks, at least about 4 weeks, at least about 2 months, or at least about 3 months subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject.

[0324] In some embodiments of any one of the methods disclosed herein, the subject is subjected to a treatment for the condition (i) prior to obtaining the second plurality of cell-free nucleic acid molecules from the subject and (ii) subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject.

[0325] In some embodiments of any one of the methods disclosed herein, the progress of the condition is indicative of minimal residual disease of the condition of the subject. In some embodiments of any one of the methods disclosed herein, the progress of the condition is indicative of tumor burden or cancer burden of the subject.

[0326] In some embodiments of any one of the methods disclosed herein, the one or more cell-free nucleic acid molecules are captured from among the plurality of cell-free nucleic acid molecules with a set of nucleic acid probes, wherein the set of nucleic acid probes is configured to hybridize to at least a portion of cell-free nucleic acid molecules comprising one or more genomic regions associated with the condition.

[0327] In some embodiments, the subject has been determined to have the condition based at least in part on one or more insertions or deletions (indels) identified in the one or more cell-free nucleic acid molecules.

[0328] In one aspect, the present disclosure provides a method comprising: (a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject, wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide, and wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic

acid probe to the plurality of phased variants and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants; (b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the plurality of phased variants; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

[0329] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and (c) further comprises determining the condition of the subject based at least in part on the identified one or more indels.

[0330] In one aspect, the present disclosure provides a method comprising: (a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject, wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising a plurality of phased variants relative to a reference genomic sequence, and wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the plurality of phased variants and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants; (b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the plurality of phased variants, wherein a limit of detection of the identification step is less than about 1 out of 50,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

[0331] In some embodiments of any one of the methods disclosed herein, the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules.

[0332] In some embodiments of any one of the methods disclosed herein, a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide.

[0333] In some embodiments of any one of the methods disclosed herein, the activatable reporter agent is activated upon hybridization of the individual nucleic acid probe to the plurality of phased variants.

[0334] In some embodiments of any one of the methods disclosed herein, the activatable reporter agent is activated upon dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants.

[0335] In some embodiments of any one of the methods disclosed herein, the method further comprises mixing (1) the set of nucleic acid probes and (2) the plurality of cell-free nucleic acid molecules.

[0336] In some embodiments of any one of the methods disclosed herein, the activatable reporter agent is a fluorophore.

[0337] In some embodiments of any one of the methods disclosed herein, analyzing the identified one or more cell-free nucleic acid molecules comprises analyzing (i) the identified one or more cell-free nucleic acid molecules and (ii) other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants as different variables.

[0338] In some embodiments of any one of the methods disclosed herein, the analyzing of the identified one or more cell-free nucleic acid molecules is not based on other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants.

[0339] In some embodiments of any one of the methods disclosed herein, a number of the plurality of phased variants from the identified one or more cell-free nucleic acid molecules is indicative of the condition of the subject. In some embodiments, a ratio of (i) the number of the plurality of phased variants from the one or more cell-free nucleic acid molecules and (ii) a number of single nucleotide variants (SNVs) from the one or more cell-free nucleic acid molecules is indicative of the condition of the subject.

[0340] In some embodiments of any one of the methods disclosed herein, a frequency of the plurality of phased variants in the identified one or more cell-free nucleic acid molecules is indicative of the condition of the subject. In some embodiments, the frequency is indicative of a diseased cell associated with the condition. In some embodiments, the condition is diffuse large B-cell lymphoma, and wherein the frequency is indicative of whether the one or more

cell-free nucleic acid molecules are derived from germinal center B-cell (GCB) or activated B-cell (ABC).

[0341] In some embodiments of any one of the methods disclosed herein, genomic origin of the identified one or more cell-free nucleic acid molecules is indicative of the condition of the subject.

[0342] In some embodiments of any one of the methods disclosed herein, the first and second phased variants are separated by at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 nucleotides. In some embodiments of any one of the methods disclosed herein, the first and second phased variants are separated by at most about 180, at most about 170, at most about 160, at most about 150, or at most about 140 nucleotides.

[0343] In some embodiments of any one of the methods disclosed herein, at least about 10%, at least about 20%, at least about 30%, at least about 40%, or at least about 50% of the one or more cell-free nucleic acid molecules comprising a plurality of phased variants comprises a single nucleotide variant (SNV) that is at least 2 nucleotides away from an adjacent SNV.

[0344] In some embodiments of any one of the methods disclosed herein, the plurality of phased variants comprises at least 3, at least 4, at least 5, at least 10, at least 15, at least 20, or at least 25 phased variants within the same cell-free nucleic acid molecule.

[0345] In some embodiments of any one of the methods disclosed herein, the one or more cell-free nucleic acid molecules identified comprises at least 2, at least 3, at least 4, at least 5, at least 10, at least 50, at least 100, at least 500, or at least 1,000 cell-free nucleic acid molecules.

[0346] In some embodiments of any one of the methods disclosed herein, the reference genomic sequence is derived from a reference cohort. In some embodiments, the reference genomic sequence comprises a consensus sequence from the reference cohort. In some embodiments, the reference genomic sequence comprises at least a portion of hg19 human genome, hg18 genome, hg17 genome, hg16 genome, or hg38 genome.

[0347] In some embodiments of any one of the methods disclosed herein, the reference genomic sequence is derived from a sample of the subject.

[0348] In some embodiments of any one of the methods disclosed herein, the sample is a healthy sample. In some embodiments, the sample comprises a healthy cell. In some embodiments, the healthy cell comprises a healthy leukocyte.

[0349] In some embodiments of any one of the methods disclosed herein, the sample is a diseased sample. In some embodiments, the diseased sample comprises a diseased cell. In some embodiments, the diseased cell comprises a tumor cell. In some embodiments, the

diseased sample comprises a solid tumor.

[0350] In some embodiments of any one of the methods disclosed herein, the set of nucleic acid probes is designed based on the plurality of phased variants that are identified by comparing (i) sequencing data from a solid tumor, lymphoma, or blood tumor of the subject and (ii) sequencing data from a healthy cell of the subject or a healthy cohort. In some embodiments, the healthy cell is from the subject. In some embodiments, the healthy cell is from the healthy cohort.

[0351] In some embodiments of any one of the methods disclosed herein, the set of nucleic acid probes are designed to hybridize to at least a portion of sequences of genomic loci associated with the condition. In some embodiments, the genomic loci associated with the condition are known to exhibit aberrant somatic hypermutation when the subject has the condition.

[0352] In some embodiments of any one of the methods disclosed herein, the set of nucleic acid probes are designed to hybridize to at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3.

[0353] In some embodiments of any one of the methods disclosed herein, each nucleic acid probe of the set of nucleic acid probes has at least about 70%, at least about 80%, at least about 90% sequence identity, at least about 95% sequence identity, or about 100% sequence identity to a probe sequence selected from Table 6.

[0354] In some embodiments of any one of the methods disclosed herein, the set of nucleic acid probes comprises at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90% of probe sequences in Table 6.

[0355] In some embodiments of any one of the methods disclosed herein, the method further comprises determining that the subject has the condition or determining a degree or status of the condition of the subject, based on the identified one or more cell-free nucleic acid molecules comprising the plurality of phased variants. In some embodiments, the method further comprises determining that the one or more cell-free nucleic acid molecules are derived from a sample associated with the condition, based on performing a statistical model analysis of the identified one or more cell-free nucleic acid molecules. In some embodiments, the statistical model analysis comprises a Monte Carlo statistical analysis.

[0356] In some embodiments of any one of the methods disclosed herein, the method further comprises monitoring a progress of the condition of the subject based on the identified one or more cell-free nucleic acid molecules.

[0357] In some embodiments of any one of the methods disclosed herein, the method further comprises performing a different procedure to confirm the condition of the subject. In some embodiments, the different procedure comprises a blood test, genetic test, medical imaging, physical exam, or tissue biopsy.

[0358] In some embodiments of any one of the methods disclosed herein, the method further comprises determining a treatment for the condition of the subject based on the identified one or more cell-free nucleic acid molecules.

[0359] In some embodiments of any one of the methods disclosed herein, the subject has been subjected to a treatment for the condition prior to (a).

[0360] In some embodiments of any one of the methods disclosed herein, the treatment comprises chemotherapy, radiotherapy, chemoradiotherapy, immunotherapy, adoptive cell therapy, hormone therapy, targeted drug therapy, surgery, transplant, transfusion, or medical surveillance.

[0361] In some embodiments of any one of the methods disclosed herein, the plurality of cell-free nucleic acid molecules comprises a plurality of cell-free deoxyribonucleic acid (DNA) molecules.

[0362] In some embodiments of any one of the methods disclosed herein, condition comprises a disease.

[0363] In some embodiments of any one of the methods disclosed herein, the plurality of cell-free nucleic acid molecules are derived from a bodily sample of the subject. In some embodiments, the bodily sample comprises plasma, serum, blood, cerebrospinal fluid, lymph fluid, saliva, urine, or stool.

[0364] In some embodiments of any one of the methods disclosed herein, the subject is a mammal. In some embodiments of any one of the methods disclosed herein, the subject is a human.

[0365] In some embodiments of any one of the methods disclosed herein, the condition comprises neoplasm, cancer, or tumor. In some embodiments, the condition comprises a solid tumor. In some embodiments, the condition comprises a lymphoma. In some embodiments, the condition comprises a B-cell lymphoma. In some embodiments, the condition comprises a sub-type of B-cell lymphoma selected from the group consisting of diffuse large B-cell lymphoma, follicular lymphoma, Burkitt lymphoma, and B-cell chronic lymphocytic leukemia.

In some embodiments of any one of the methods disclosed herein, the condition comprises transplant rejection of or a chromosomal abnormality.

[0366] In some embodiments of any one of the methods disclosed herein, the plurality of phased variants have been previously identified as tumor-derived from sequencing a prior tumor sample or cell-free nucleic acid sample.

[0367] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and (c) further comprises determining the condition of the subject based at least in part on the identified one or more indels.

[0368] In one aspect, the present disclosure provides a composition comprising a bait set comprising a set of nucleic acid probes designed to capture cell-free DNA molecules derived from at least about 5% of genomic regions set forth in (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3.

[0369] In some embodiments of any of the compositions disclosed herein, the set of nucleic acid probes are designed to pull down cell-free DNA molecules derived from at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of the genomic regions set forth in (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3.

[0370] In some embodiments of any of the compositions disclosed herein, the set of nucleic acid probes are designed to capture the one or more cell-free DNA molecules derived from at most about 10%, at most about 20%, at most about 30%, at most about 40%, at most about 50%, at most about 60%, at most about 70%, at most about 80%, at most about 90%, or about 100% of the genomic regions set forth in (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3.

[0371] In some embodiments of any of the compositions disclosed herein, the bait set comprises at most 5, at most 10, at most 50, at most 100, at most 500, at most 1000, or at most 2000 nucleic acid probes.

[0372] In some embodiments of any of the compositions disclosed herein, an individual nucleic acid probe of the set of nucleic acid probes comprises a pull-down tag.

[0373] In some embodiments of any of the compositions disclosed herein, the pull-down tag comprises a nucleic acid barcode.

[0374] In some embodiments of any of the compositions disclosed herein, the pull-down tag comprises biotin.

[0375] In some embodiments of any of the compositions disclosed herein, each of the cell-free DNA molecules is between about 100 nucleotides and about 180 nucleotides in length.

[0376] In some embodiments of any of the compositions disclosed herein, the genomic regions are associated with a condition.

[0377] In some embodiments of any of the compositions disclosed herein, the genomic regions exhibit aberrant somatic hypermutation when a subject has the condition.

[0378] In some embodiments of any of the compositions disclosed herein, the condition comprises a B-cell lymphoma. In some embodiments, the condition comprises a sub-type of B-cell lymphoma selected from the group consisting of diffuse large B-cell lymphoma, follicular lymphoma, Burkitt lymphoma, and B-cell chronic lymphocytic leukemia.

[0379] In some embodiments of any of the compositions disclosed herein, the composition further comprises a plurality of cell-free DNA molecules obtained or derived from a subject.

[0380] In one aspect, the present disclosure provides a method to perform a clinical procedure on an individual, the method comprising: (a) obtaining or having obtained a targeted sequencing result of a collection of cell-free nucleic acid molecules, wherein the collection of cell-free nucleic acid molecules are sourced from a liquid or waste biopsy of an individual, and wherein the targeting sequencing is performed utilizing nucleic acid probes to pull down sequences of genomic loci known to experience aberrant somatic hypermutation in a B-cell cancer; (b) identifying or having identified a plurality of variants in phase within the cell-free nucleic acid sequencing result; (c) determining or having determined, utilizing a statistical model and the identified phased variants, that the cell-free nucleic acid sequencing result contains nucleotides derived from a neoplasm; and (d) performing a clinical procedure on the individual to confirm the presence of the B-cell cancer, based upon determining that the cell-free nucleic acid sequencing result contains nucleic acid sequences likely derived from the B-cell cancer.

[0381] In some embodiments of any of the compositions disclosed herein, the biopsy is one of blood, serum, cerebrospinal fluid, lymph fluid, urine, or stool.

[0382] In some embodiments of any of the compositions disclosed herein, the genomic loci are selected from (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased

variants in Table 3.

[0383] In some embodiments of any of the compositions disclosed herein, the sequences of the nucleic acid probes are selected from Table 6.

[0384] In some embodiments of any of the compositions disclosed herein, the clinical is procedure is a blood test, medical imaging, or a physical exam.

[0385] In some embodiments, the method further comprises identifying or having identified one or more insertions or deletions (indels) within the cell-free nucleic acid sequencing result, and determining or having determined, based least in part on the identified one or more indels, that the cell-free nucleic acid sequencing result contains the nucleotides derived from the neoplasm.

[0386] In one aspect, the present disclosure provides a method to treat an individual for a B-cell cancer, the method comprising: (a) obtaining or having obtained a targeted sequencing result of a collection of cell-free nucleic acid molecules, wherein the collection of cell-free nucleic acid molecules are sourced from a liquid or waste biopsy of an individual, and wherein the targeting sequencing is performed utilizing nucleic acid probes to pull down sequences of genomic loci known to experience aberrant somatic hypermutation in a B-cell cancer; (b) identifying or having identified a plurality of variants in phase within the cell-free nucleic acid sequencing result; (c) determining or having determined, utilizing a statistical model and the identified phased variants, that the cell-free nucleic acid sequencing result contains nucleotides derived from a neoplasm; and (d) treating the individual to curtail the B-cell cancer, based upon determining that the cell-free nucleic acid sequencing result contains nucleic acid sequences derived from the B-cell cancer.

[0387] In some embodiments of any of the compositions disclosed herein, the biopsy is one of blood, serum, cerebrospinal fluid, lymph fluid, urine or stool.

[0388] In some embodiments of any of the compositions disclosed herein, the genomic loci are selected from (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3.

[0389] In some embodiments of any of the compositions disclosed herein, the sequences of the nucleic acid probes are selected from Table 6.

[0390] In some embodiments of any of the compositions disclosed herein, the treatment is chemotherapy, radiotherapy, immunotherapy, hormone therapy, targeted drug therapy, or medical surveillance.

[0391] In some embodiments, the method further comprises identifying or having identified one or more insertions or deletions (indels) within the cell-free nucleic acid sequencing result, and determining or having determined, based least in part on the identified one or more indels, that the cell-free nucleic acid sequencing result contains the nucleotides derived from the neoplasm.

[0392] In one aspect, the present disclosure provides a method to detect cancerous minimal residual disease in an individual and to treat the individual for a cancer, the method comprising: (a) obtaining or having obtained a targeted sequencing result of a collection of cell-free nucleic acid molecules, wherein the collection of cell-free nucleic acid molecules are sourced from a liquid or waste biopsy of an individual, wherein the liquid or waste biopsy is sourced after a series of treatments in order to detect minimal residual disease, and wherein the targeting sequencing is performed utilizing nucleic acid probes to pull down sequences of genomic loci determined to contain a plurality of variants in phase, as determined by a prior sequencing result on a prior biopsy derived from the cancer; (b) identifying or having identified at least one set of the plurality of variants in phase within the cell-free nucleic acid sequencing result; and (c) treating the individual to curtail the cancer, based upon determining that the cell-free nucleic acid sequencing result contains nucleic acid sequences derived from the cancer.

[0393] In some embodiments of any of the compositions disclosed herein, the liquid or waste biopsy is one of blood, serum, cerebrospinal fluid, lymph fluid, urine or stool.

[0394] In some embodiments of any of the compositions disclosed herein, the treatment is chemotherapy, radiotherapy, immunotherapy, hormone therapy, targeted drug therapy, or medical surveillance.

[0395] In some embodiments, the method further comprises identifying or having identified one or more insertions or deletions (indels) within the cell-free nucleic acid sequencing result, and treating the individual to curtail the cancer, based least in part on the identified one or more indels.

[0396] In one aspect, the present disclosure provides a method comprising: (a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject; (b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises one or more insertions or deletions (indels) relative to a reference genomic sequence; and (c) analyzing, by the computer system, the one or more indels to determine a condition of the subject.

[0397] In one aspect, the present disclosure provides a method comprising: (a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject; (b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises one or more insertions or deletions (indels) relative to a reference genomic sequence; and (c) analyzing, by the computer system, the one or more insertions or deletions (indels) to determine a condition of the subject.

[0398] In one aspect, the present disclosure provides a method comprising: (a) obtaining sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject; (b) processing the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules with a limit of detection of less than about 1 out of 50,000 observations from the sequencing data, wherein each of the one or more cell-free nucleic acid molecules comprises one or more insertions or deletions (indels) relative to a reference genomic sequence; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

[0399] In some embodiments, the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 observations from the sequencing data. In some embodiments, (a) to (c) are performed by a computer system. In some embodiments, the sequencing data is generated based on nucleic acid amplification. In some embodiments, the sequencing data is generated based on polymerase chain reaction. In some embodiments, the sequencing data is generated based on amplicon sequencing. In some embodiments, the sequencing data is generated based on next-generation sequencing (NGS). In some embodiments, the sequencing data is generated based on non-hybridization-based NGS. In some embodiments, the sequencing data is generated without use of molecular barcoding of at least a portion of the plurality of cell-free nucleic acid molecules. In some embodiments, the sequencing data is obtained without use of sample barcoding of at least a portion of the plurality of cell-free nucleic acid molecules. In some embodiments, the sequencing data is obtained without in silico removal or suppression of (i) background error or (ii) sequencing error.

[0400] In one aspect, the present disclosure provides a method of treating a condition of a subject, the method comprising: (a) identifying the subject for treatment of the condition, wherein the subject has been determined to have the condition based on identification of one

or more cell-free nucleic acid molecules from a plurality of cell-free nucleic acid molecules that is obtained or derived from the subject, wherein each of the one or more cell-free nucleic acid molecules comprises one or more insertions or deletions (indels) relative to a reference genomic sequence, and wherein a presence of the one or more indels is indicative of the condition of the subject; and (b) subjecting the subject to the treatment based on the identification in (a).

[0401] In one aspect, the present disclosure provides a method of monitoring a progress of a condition of a subject, the method comprising: (a) determining a first state of the condition of the subject based on identification of a first set of one or more cell-free nucleic acid molecules from a first plurality of cell-free nucleic acid molecules that is obtained or derived from the subject; (b) determining a second state of the condition of the subject based on identification of a second set of one or more cell-free nucleic acid molecules from a second plurality of cell-free nucleic acid molecules that is obtained or derived from the subject, wherein the second plurality of cell-free nucleic acid molecules are obtained from the subject subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject; and (c) determining the progress of the condition based on the first state of the condition and the second state of the condition, wherein each of the one or more cell-free nucleic acid molecules comprises one or more insertions or deletions (indels) relative to a reference genomic sequence.

[0402] In some embodiments, the progress of the condition is worsening of the condition. In some embodiments, the progress of the condition is at least a partial remission of the condition. In some embodiments, a presence of the one or more indels is indicative of the first state or the second state of the condition of the subject. In some embodiments, the second plurality of cell-free nucleic acid molecules is obtained from the subject at least about 1 week, at least about 2 weeks, at least about 3 weeks, at least about 4 weeks, at least about 2 months, or at least about 3 months subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject. In some embodiments, the subject is subjected to a treatment for the condition (i) prior to obtaining the second plurality of cell-free nucleic acid molecules from the subject and (ii) subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject. In some embodiments, the progress of the condition is indicative of minimal residual disease of the condition of the subject. In some embodiments, the progress of the condition is indicative of tumor burden or cancer burden of the subject. In some embodiments, the one or more cell-free nucleic acid molecules are captured from among the plurality of cell-free nucleic acid molecules with a set of nucleic acid probes, wherein the set of nucleic acid

probes is configured to hybridize to at least a portion of cell-free nucleic acid molecules comprising one or more genomic regions associated with the condition.

[0403] In one aspect, the present disclosure provides a method comprising: (a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject, wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising one or more insertions or deletions (indels) relative to a reference genomic sequence, and wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the one or more indels and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the one or more indels; (b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the one or more indels; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

[0404] In one aspect, the present disclosure provides a method comprising: (a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject, wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising one or more insertions or deletions (indels) relative to a reference genomic sequence, and wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the one or more indels and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the one or more indels; (b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the one or more indels, wherein a limit of detection of the identification step is less than about 1 out of 50,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

[0405] In some embodiments, the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000,

less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules. In some embodiments, the activatable reporter agent is activated upon hybridization of the individual nucleic acid probe to the one or more indels. In some embodiments, the activatable reporter agent is activated upon dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the one or more indels. In some embodiments, the method further comprises mixing (1) the set of nucleic acid probes and (2) the plurality of cell-free nucleic acid molecules. In some embodiments, the activatable reporter agent is a fluorophore. In some embodiments, analyzing the identified one or more cell-free nucleic acid molecules comprises analyzing (i) the identified one or more cell-free nucleic acid molecules and (ii) other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the one or more indels as different variables. In some embodiments, the analyzing of the identified one or more cell-free nucleic acid molecules is not based on other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the one or more indels. In some embodiments, a number of the one or more indels from the identified one or more cell-free nucleic acid molecules is indicative of the condition of the subject. In some embodiments, a ratio of (i) the number of the one or more indels from the one or more cell-free nucleic acid molecules and (ii) a number of single nucleotide variants (SNVs) from the one or more cell-free nucleic acid molecules is indicative of the condition of the subject. In some embodiments, a frequency of the one or more indels in the identified one or more cell-free nucleic acid molecules is indicative of the condition of the subject. In some embodiments, the frequency is indicative of a diseased cell associated with the condition. In some embodiments, the condition is diffuse large B-cell lymphoma, and wherein the frequency is indicative of whether the one or more cell-free nucleic acid molecules are derived from germinal center B-cell (GCB) or activated B-cell (ABC). In some embodiments, genomic origin of the identified one or more cell-free nucleic acid molecules is indicative of the condition of the subject.

[0406] In some embodiments, the one or more indels comprises at least 3, at least 4, at least 5, at least 10, at least 15, at least 20, or at least 25 indels within the same cell-free nucleic acid molecule. In some embodiments, the one or more cell-free nucleic acid molecules identified comprises at least 2, at least 3, at least 4, at least 5, at least 10, at least 50, at least 100, at least 500, or at least 1,000 cell-free nucleic acid molecules. In some embodiments, the reference genomic sequence is derived from a reference cohort. In some embodiments, the reference genomic sequence comprises a consensus sequence from the reference cohort. In some

embodiments, the reference genomic sequence comprises at least a portion of hg19 human genome, hg18 genome, hg17 genome, hg16 genome, or hg38 genome. In some embodiments, the reference genomic sequence is derived from a sample of the subject. In some embodiments, the sample is a healthy sample. In some embodiments, the sample comprises a healthy cell. In some embodiments, the healthy cell comprises a healthy leukocyte. In some embodiments, the sample is a diseased sample. In some embodiments, the diseased sample comprises a diseased cell. In some embodiments, the diseased cell comprises a tumor cell. In some embodiments, the diseased sample comprises a solid tumor. In some embodiments, the set of nucleic acid probes is designed based on the one or more indels that are identified by comparing (i) sequencing data from a solid tumor, lymphoma, or blood tumor of the subject and (ii) sequencing data from a healthy cell of the subject or a healthy cohort. In some embodiments, the healthy cell is from the subject. In some embodiments, the healthy cell is from the healthy cohort. In some embodiments, the set of nucleic acid probes are designed to hybridize to at least a portion of sequences of genomic loci associated with the condition. In some embodiments, the genomic loci associated with the condition are known to exhibit aberrant somatic hypermutation when the subject has the condition.

[0407] In some embodiments, the set of nucleic acid probes are designed to hybridize to at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of (i) the genomic regions identified in Table 1, or (ii) the genomic regions identified in Table 3. In some embodiments, each nucleic acid probe of the set of nucleic acid probes has at least about 70%, at least about 80%, at least about 90% sequence identity, at least about 95% sequence identity, or about 100% sequence identity to a probe sequence selected from Table 6. In some embodiments, the set of nucleic acid probes comprises at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90% of probe sequences in Table 6.

[0408] In some embodiments, the method further comprises determining that the subject has the condition or determining a degree or status of the condition of the subject, based on the identified one or more cell-free nucleic acid molecules comprising the one or more indels. In some embodiments, the method further comprises determining that the one or more cell-free nucleic acid molecules are derived from a sample associated with the condition, based on performing a statistical model analysis of the identified one or more cell-free nucleic acid molecules. In some embodiments, the statistical model analysis comprises a Monte Carlo

statistical analysis. In some embodiments, the method further comprises monitoring a progress of the condition of the subject based on the identified one or more cell-free nucleic acid molecules. In some embodiments, the method further comprises performing a different procedure to confirm the condition of the subject. In some embodiments, the different procedure comprises a blood test, genetic test, medical imaging, physical exam, or tissue biopsy. In some embodiments, the method further comprises determining a treatment for the condition of the subject based on the identified one or more cell-free nucleic acid molecules. In some embodiments, the subject has been subjected to a treatment for the condition prior to (a). In some embodiments, the treatment comprises chemotherapy, radiotherapy, chemoradiotherapy, immunotherapy, adoptive cell therapy, hormone therapy, targeted drug therapy, surgery, transplant, transfusion, or medical surveillance. In some embodiments, the plurality of cell-free nucleic acid molecules comprises a plurality of cell-free deoxyribonucleic acid (DNA) molecules. In some embodiments, the condition comprises a disease. In some embodiments, the plurality of cell-free nucleic acid molecules are derived from a bodily sample of the subject. In some embodiments, the bodily sample comprises plasma, serum, blood, cerebrospinal fluid, lymph fluid, saliva, urine, or stool. In some embodiments, the subject is a mammal. In some embodiments, the subject is a human. In some embodiments, the condition comprises neoplasm, cancer, or tumor. In some embodiments, the condition comprises a solid tumor. In some embodiments, the condition comprises a lymphoma. In some embodiments, the condition comprises a B-cell lymphoma. In some embodiments, the condition comprises a sub-type of B-cell lymphoma selected from the group consisting of diffuse large B-cell lymphoma, follicular lymphoma, Burkitt lymphoma, and B-cell chronic lymphocytic leukemia. In some embodiments, the one or more indels have been previously identified as tumor-derived from sequencing a prior tumor sample or cell-free nucleic acid sample.

[0409] In one aspect, the present disclosure provides a method to perform a clinical procedure on an individual, the method comprising: obtaining or having obtained a targeted sequencing result of a collection of cell-free nucleic acid molecules, wherein the collection of cell-free nucleic acid molecules are sourced from a liquid or waste biopsy of an individual, and wherein the targeting sequencing is performed utilizing nucleic acid probes to pull down sequences of genomic loci known to experience aberrant somatic hypermutation in a B-cell cancer; identifying or having identified one or more insertions or deletions (indels) within the cell-free nucleic acid sequencing result; determining or having determined, utilizing a statistical model and the identified one or more indels, that the cell-free nucleic acid sequencing result contains nucleotides derived from a neoplasm; and performing a clinical procedure on

the individual to confirm the presence of the B-cell cancer, based upon determining that the cell-free nucleic acid sequencing result contains nucleic acid sequences likely derived from the B-cell cancer.

[0410] In some embodiments, the biopsy is one of blood, serum, cerebrospinal fluid, lymph fluid, urine, or stool. In some embodiments, the genomic loci are selected from (i) the genomic regions identified in Table 1, or (ii) the genomic regions identified in Table 3. In some embodiments, the sequences of the nucleic acid probes are selected from Table 6. In some embodiments, the clinical is procedure is a blood test, medical imaging, or a physical exam.

[0411] In one aspect, the present disclosure provides a method to treat an individual for a B-cell cancer, the method comprising: obtaining or having obtained a targeted sequencing result of a collection of cell-free nucleic acid molecules, wherein the collection of cell-free nucleic acid molecules are sourced from a liquid or waste biopsy of an individual, and wherein the targeting sequencing is performed utilizing nucleic acid probes to pull down sequences of genomic loci known to experience aberrant somatic hypermutation in a B-cell cancer; identifying or having identified one or more insertions or deletions (indels) within the cell-free nucleic acid sequencing result; determining or having determined, utilizing a statistical model and the identified one or more indels, that the cell-free nucleic acid sequencing result contains nucleotides derived from a neoplasm; and treating the individual to curtail the B-cell cancer, based upon determining that the cell-free nucleic acid sequencing result contains nucleic acid sequences derived from the B-cell cancer.

[0412] In some embodiments, the biopsy is one of blood, serum, cerebrospinal fluid, lymph fluid, urine or stool. In some embodiments, the genomic loci are selected from (i) the genomic regions identified in Table 1, or (ii) the genomic regions identified in Table 3. In some embodiments, the sequences of the nucleic acid probes are selected from Table 6. In some embodiments, the treatment is chemotherapy, radiotherapy, immunotherapy, hormone therapy, targeted drug therapy, or medical surveillance.

[0413] In one aspect, the present disclosure provides a method to detect cancerous minimal residual disease in an individual and to treat the individual for a cancer, the method comprising: obtaining or having obtained a targeted sequencing result of a collection of cell-free nucleic acid molecules, wherein the collection of cell-free nucleic acid molecules are sourced from a liquid or waste biopsy of an individual, wherein the liquid or waste biopsy is sourced after a series of treatments in order to detect minimal residual disease, and wherein the targeting sequencing is performed utilizing nucleic acid probes to pull down sequences of genomic loci determined to contain one or more insertions or deletions (indels), as determined by a prior

sequencing result on a prior biopsy derived from the cancer; identifying or having identified at least one set of the one or more indels within the cell-free nucleic acid sequencing result; and treating the individual to curtail the cancer, based upon determining that the cell-free nucleic acid sequencing result contains nucleic acid sequences derived from the cancer.

[0414] In some embodiments, the liquid or waste biopsy is one of blood, serum, cerebrospinal fluid, lymph fluid, urine or stool. In some embodiments, the treatment is chemotherapy, radiotherapy, immunotherapy, hormone therapy, targeted drug therapy, or medical surveillance.

[0415] In one aspect, the present disclosure provides a method comprising: (a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject who has received an organ or tissue transplant; (b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence, wherein at least about 10% of the one or more cell-free nucleic acid molecules comprises a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants that are separated by at least one nucleotide; and (c) analyzing, by the computer system, the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an extent of transplant rejection of the subject.

[0416] In some embodiments, the at least about 10% of the cell-free nucleic acid molecules comprise at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of the one or more cell-free nucleic acid molecules. In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the extent of transplant rejection of the subject based at least in part on the identified one or more indels.

[0417] In one aspect, the present disclosure provides a method comprising: (a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject who has received an organ or tissue transplant; (b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased

variants relative to a reference genomic sequence that are separated by at least one nucleotide; and (c) analyzing, by the computer system, the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an extent of transplant rejection of the subject.

[0418] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the extent of transplant rejection of the subject based at least in part on the identified one or more indels.

[0419] In one aspect, the present disclosure provides a method comprising: (a) obtaining sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject who has received an organ or tissue transplant; (b) processing the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules with a limit of detection of less than about 1 out of 50,000 observations from the sequencing data; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an extent of transplant rejection of the subject.

[0420] In some embodiments, the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 observations from the sequencing data. In some embodiments, each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence. In some embodiments, a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide. In some embodiments, (a) to (c) are performed by a computer system. In some embodiments, the sequencing data is generated based on nucleic acid amplification. In some embodiments, the sequencing data is generated based on polymerase chain reaction. In some embodiments, the sequencing data is generated based on amplicon sequencing. In some embodiments, the sequencing data is generated based on next-generation sequencing (NGS). In some embodiments, the sequencing data is generated based on non-hybridization-based NGS. In some embodiments, the sequencing data is generated without use of molecular barcoding of at least a portion of the plurality of cell-free nucleic acid molecules. In some embodiments, the sequencing data is obtained without use of sample barcoding of at least a portion of the plurality of cell-free nucleic acid molecules. In some embodiments, the sequencing data is obtained without in silico removal or suppression of (i) background error or (ii) sequencing error. In

some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence or the absence of the transplant rejection of the subject based at least in part on the identified one or more indels.

[0421] In one aspect, the present disclosure provides a method of treating a transplant rejection of a subject who has received an organ or tissue transplant, the method comprising: (a) identifying the subject for treatment of the transplant rejection, wherein the subject has been determined to have the transplant rejection based on identification of one or more cell-free nucleic acid molecules from a plurality of cell-free nucleic acid molecules that is obtained or derived from the subject, wherein each of the one or more cell-free nucleic acid molecules identified comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide, and wherein a presence of the plurality of phased variants is indicative of the transplant rejection of the subject; and (b) subjecting the subject to the treatment based on the identification in (a).

[0422] In some embodiments, the subject has been determined to have the transplant rejection based at least in part on one or more insertions or deletions (indels) identified in the one or more cell-free nucleic acid molecules.

[0423] In one aspect, the present disclosure provides a method of monitoring a subject who has received an organ or tissue transplant for a presence, an absence, or an extent of transplant rejection, the method comprising: (a) determining a first state of the presence, the absence, or the extent of transplant rejection of the subject based on identification of a first set of one or more cell-free nucleic acid molecules from a first plurality of cell-free nucleic acid molecules that is obtained or derived from the subject; (b) determining a second state of the presence, the absence, or the extent of transplant rejection of the subject based on identification of a second set of one or more cell-free nucleic acid molecules from a second plurality of cell-free nucleic acid molecules that is obtained or derived from the subject, wherein the second plurality of cell-free nucleic acid molecules are obtained from the subject subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject; and (c) determining a transplant rejection status of the subject based on the first state and the second state, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide.

[0424] In some embodiments, the transplant rejection status is at least a partial transplant rejection. In some embodiments, a presence of the plurality of phased variants is indicative of the first state or the second state. In some embodiments, the second plurality of cell-free nucleic

acid molecules is obtained from the subject at least about 1 week, at least about 2 weeks, at least about 3 weeks, at least about 4 weeks, at least about 2 months, or at least about 3 months subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject. In some embodiments, the subject is subjected to a treatment for the transplant rejection (i) prior to obtaining the second plurality of cell-free nucleic acid molecules from the subject and (ii) subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject. In some embodiments, the one or more cell-free nucleic acid molecules are captured from among the plurality of cell-free nucleic acid molecules with a set of nucleic acid probes, wherein the set of nucleic acid probes is configured to hybridize to at least a portion of cell-free nucleic acid molecules comprising one or more genomic regions associated with the transplant rejection. In some embodiments, the subject has been determined to have the presence or the absence of the transplant rejection based at least in part on one or more insertions or deletions (indels) identified in the one or more cell-free nucleic acid molecules.

[0425] In one aspect, the present disclosure provides a method comprising: (a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject who has received an organ or tissue transplant, wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide, and wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the plurality of phased variants and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants; (b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the plurality of phased variants; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an extent of transplant rejection of the subject.

[0426] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence or the absence of the transplant rejection of the subject based at least in part on the identified one or more indels.

[0427] In one aspect, the present disclosure provides a method comprising: (a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject who has received an organ or tissue transplant, wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising a plurality of phased variants relative to a reference genomic sequence, and wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the plurality of phased variants and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants; (b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the plurality of phased variants, wherein a limit of detection of the identification step is less than about 1 out of 50,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an extent of transplant rejection of the subject.

[0428] In some embodiments, the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules. In some embodiments, a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide. In some embodiments, the activatable reporter agent is activated upon hybridization of the individual nucleic acid probe to the plurality of phased variants. In some embodiments, the activatable reporter agent is activated upon dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants. In some embodiments, the method further comprises mixing (1) the set of nucleic acid probes and (2) the plurality of cell-free nucleic acid molecules. In some embodiments, the activatable reporter agent is a fluorophore. In some embodiments, analyzing the identified one or more cell-free nucleic acid molecules comprises analyzing (i) the identified one or more cell-free nucleic acid molecules and (ii) other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants as different variables. In some embodiments, the analyzing of the identified one or more cell-free nucleic acid molecules is not based on other cell-free

nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants. In some embodiments, a number of the plurality of phased variants from the identified one or more cell-free nucleic acid molecules is indicative of the presence, the absence, or the extent of transplant rejection of the subject. In some embodiments, a ratio of (i) the number of the plurality of phased variants from the one or more cell-free nucleic acid molecules and (ii) a number of single nucleotide variants (SNVs) from the one or more cell-free nucleic acid molecules is indicative of the presence, the absence, or the extent of transplant rejection of the subject. In some embodiments, a frequency of the plurality of phased variants in the identified one or more cell-free nucleic acid molecules is indicative of the presence or the absence of the transplant rejection of the subject. In some embodiments, the frequency is indicative of a diseased cell associated with the presence, the absence, or the extent of transplant rejection. In some embodiments, genomic origin of the identified one or more cell-free nucleic acid molecules is indicative of the presence or the absence of the transplant rejection of the subject. In some embodiments, the first and second phased variants are separated by at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 nucleotides. In some embodiments, the first and second phased variants are separated by at most about 180, at most about 170, at most about 160, at most about 150, or at most about 140 nucleotides.

[0429] In some embodiments, at least about 10%, at least about 20%, at least about 30%, at least about 40%, or at least about 50% of the one or more cell-free nucleic acid molecules comprising a plurality of phased variants comprises a single nucleotide variant (SNV) that is at least 2 nucleotides away from an adjacent SNV. In some embodiments, the plurality of phased variants comprises at least 3, at least 4, at least 5, at least 10, at least 15, at least 20, or at least 25 phased variants within the same cell-free nucleic acid molecule. In some embodiments, the one or more cell-free nucleic acid molecules identified comprises at least 2, at least 3, at least 4, at least 5, at least 10, at least 50, at least 100, at least 500, or at least 1,000 cell-free nucleic acid molecules. In some embodiments, the reference genomic sequence is derived from a reference cohort. In some embodiments, the reference genomic sequence comprises a consensus sequence from the reference cohort. In some embodiments, the reference genomic sequence comprises at least a portion of hg19 human genome, hg18 genome, hg17 genome, hg16 genome, or hg38 genome. In some embodiments, the reference genomic sequence is derived from a sample of the subject. In some embodiments, the sample is a healthy sample. In some embodiments, the sample comprises a healthy cell. In some embodiments, the healthy cell comprises a healthy leukocyte. In some embodiments, the sample is a diseased

sample. In some embodiments, the diseased sample comprises a diseased cell. In some embodiments, the healthy cell is from the subject. In some embodiments, the healthy cell is from the healthy cohort. In some embodiments, the set of nucleic acid probes are designed to hybridize to at least a portion of sequences of genomic loci associated with the presence or the absence of the transplant rejection. In some embodiments, the genomic loci associated with the presence, the absence, or the extent of transplant rejection are known to exhibit aberrant somatic hypermutation when the subject has the transplant rejection.

[0430] In some embodiments, the set of nucleic acid probes are designed to hybridize to at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3. In some embodiments, each nucleic acid probe of the set of nucleic acid probes has at least about 70%, at least about 80%, at least about 90% sequence identity, at least about 95% sequence identity, or about 100% sequence identity to a probe sequence selected from Table 6. In some embodiments, the set of nucleic acid probes comprises at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90% of probe sequences in Table 6. In some embodiments, the method further comprises determining the presence or the absence of the transplant rejection or determining a degree or status thereof, based on the identified one or more cell-free nucleic acid molecules comprising the plurality of phased variants. In some embodiments, the method further comprises determining that the one or more cell-free nucleic acid molecules are derived from a sample associated with the presence or the absence of the transplant rejection, based on performing a statistical model analysis of the identified one or more cell-free nucleic acid molecules. In some embodiments, the statistical model analysis comprises a Monte Carlo statistical analysis. In some embodiments, the method further comprises monitoring a progress of the presence, the absence, or the extent of transplant rejection of the subject based on the identified one or more cell-free nucleic acid molecules. In some embodiments, the method further comprises performing a different procedure to confirm the presence, the absence, or the extent of transplant rejection of the subject. In some embodiments, the different procedure comprises a blood test, genetic test, medical imaging, physical exam, or tissue biopsy. In some embodiments, the method further comprises determining a treatment for the transplant rejection of the subject based on the identified one or more cell-free nucleic acid molecules. In some embodiments, the subject

has been subjected to a treatment for the transplant rejection prior to (a). In some embodiments, the plurality of cell-free nucleic acid molecules comprise a plurality of cell-free deoxyribonucleic acid (DNA) molecules. In some embodiments, the plurality of cell-free nucleic acid molecules are derived from a bodily sample of the subject. In some embodiments, the bodily sample comprises plasma, serum, blood, cerebrospinal fluid, lymph fluid, saliva, urine, or stool. In some embodiments, the subject is a mammal. In some embodiments, the subject is a human. In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the extent of transplant rejection of the subject based at least in part on the identified one or more indels.

[0431] In one aspect, the present disclosure provides a method comprising: (a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a pregnant subject; (b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence, wherein at least about 10% of the one or more cell-free nucleic acid molecules comprises a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants that are separated by at least one nucleotide; and (c) analyzing, by the computer system, the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an elevated risk of a genetic abnormality of a fetus of the pregnant subject.

[0432] In some embodiments, the at least about 10% of the cell-free nucleic acid molecules comprise at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of the one or more cell-free nucleic acid molecules. In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based at least in part on the identified one or more indels. In some embodiments, the genetic abnormality is a chromosomal aneuploidy. In some embodiments, the chromosomal aneuploidy is in chromosome 13, 18, 21, X, or Y.

[0433] In one aspect, the present disclosure provides a method comprising: (a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a pregnant subject; (b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide; and (c) analyzing, by the computer system, the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an elevated risk of a genetic abnormality of a fetus of the pregnant subject.

[0434] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based at least in part on the identified one or more indels. In some embodiments, the genetic abnormality is a chromosomal aneuploidy. In some embodiments, the chromosomal aneuploidy is in chromosome 13, 18, 21, X, or Y.

[0435] In one aspect, the present disclosure provides a method comprising: (a) obtaining sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a pregnant subject; (b) processing the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules with a limit of detection of less than about 1 out of 50,000 observations from the sequencing data; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an elevated risk of a genetic abnormality of a fetus of the pregnant subject.

[0436] In some embodiments, the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 observations from the sequencing data. In some embodiments, each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence. In some embodiments, a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide. In some embodiments, (a) to (c) are performed by a computer system. In some embodiments, he method of any one of claims 309-313, wherein the sequencing data is generated based on nucleic acid amplification. In some embodiments, the sequencing data is generated based on polymerase chain reaction. In some embodiments, the sequencing data is generated based on amplicon sequencing. In some embodiments, the sequencing data is generated based on next-

generation sequencing (NGS). In some embodiments, the sequencing data is generated based on non-hybridization-based NGS. In some embodiments, the sequencing data is generated without use of molecular barcoding of at least a portion of the plurality of cell-free nucleic acid molecules. In some embodiments, the sequencing data is obtained without use of sample barcoding of at least a portion of the plurality of cell-free nucleic acid molecules. In some embodiments, the sequencing data is obtained without in silico removal or suppression of (i) background error or (ii) sequencing error. In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based at least in part on the identified one or more indels. In some embodiments, the genetic abnormality is a chromosomal aneuploidy. In some embodiments, the chromosomal aneuploidy is in chromosome 13, 18, 21, X, or Y.

[0437] In one aspect, the present disclosure provides a method of monitoring a pregnant subject for a presence, an absence, or an elevated risk of a genetic abnormality of a fetus of the pregnant subject, the method comprising: (a) determining a first state of the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based on identification of a first set of one or more cell-free nucleic acid molecules from a first plurality of cell-free nucleic acid molecules that is obtained or derived from the pregnant subject; (b) determining a second state of the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based on identification of a second set of one or more cell-free nucleic acid molecules from a second plurality of cell-free nucleic acid molecules that is obtained or derived from the pregnant subject, wherein the second plurality of cell-free nucleic acid molecules are obtained from the pregnant subject subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the pregnant subject; and (c) determining the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based on the first state and the second state, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide.

[0438] In some embodiments, the transplant rejection status is at least a partial transplant rejection. In some embodiments, a presence of the plurality of phased variants is indicative of the first state or the second state. In some embodiments, the second plurality of cell-free nucleic acid molecules is obtained from the pregnant subject at least about 1 week, at least about 2 weeks, at least about 3 weeks, at least about 4 weeks, at least about 2 months, or at least about

3 months subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the pregnant subject. In some embodiments, the one or more cell-free nucleic acid molecules are captured from among the plurality of cell-free nucleic acid molecules with a set of nucleic acid probes, wherein the set of nucleic acid probes is configured to hybridize to at least a portion of cell-free nucleic acid molecules comprising one or more genomic regions associated with the genetic abnormality. In some embodiments, the fetus has been determined to have the presence, the absence, or the elevated risk of the genetic abnormality based at least in part on one or more insertions or deletions (indels) identified in the one or more cell-free nucleic acid molecules.

[0439] In one aspect, the present disclosure provides a method comprising: (a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a pregnant subject, wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide, and wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the plurality of phased variants and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants; (b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the plurality of phased variants; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an elevated risk of a genetic abnormality of a fetus of the pregnant subject.

[0440] In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the elevated risk of the genetic abnormality based at least in part on the identified one or more indels.

[0441] In one aspect, the present disclosure provides a method comprising: (a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a pregnant subject, wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising a plurality of phased variants relative to a reference genomic sequence, and wherein the individual nucleic acid probe comprises an

activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the plurality of phased variants and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants; (b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the plurality of phased variants, wherein a limit of detection of the identification step is less than about 1 out of 50,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules; and (c) analyzing the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an elevated risk of a genetic abnormality of a fetus of the pregnant subject.

[0442] In some embodiments, the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules. In some embodiments, a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide. In some embodiments, the activatable reporter agent is activated upon hybridization of the individual nucleic acid probe to the plurality of phased variants. In some embodiments, the activatable reporter agent is activated upon dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants. In some embodiments, the method further comprises mixing (1) the set of nucleic acid probes and (2) the plurality of cell-free nucleic acid molecules. In some embodiments, the activatable reporter agent is a fluorophore. In some embodiments, analyzing the identified one or more cell-free nucleic acid molecules comprises analyzing (i) the identified one or more cell-free nucleic acid molecules and (ii) other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants as different variables. In some embodiments, the analyzing of the identified one or more cell-free nucleic acid molecules is not based on other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants. In some embodiments, a number of the plurality of phased variants from the identified one or more cell-free nucleic acid molecules is indicative of the genetic abnormality. In some embodiments, a ratio of (i) the number of the plurality of phased variants from the one or more cell-free nucleic acid molecules and (ii) a number of single nucleotide variants (SNVs) from the one or more cell-free nucleic acid molecules is indicative

of the genetic abnormality. In some embodiments, a frequency of the plurality of phased variants in the identified one or more cell-free nucleic acid molecules is indicative of the genetic abnormality. In some embodiments, genomic origin of the identified one or more cell-free nucleic acid molecules is indicative of the genetic abnormality. In some embodiments, the first and second phased variants are separated by at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 nucleotides. In some embodiments, the first and second phased variants are separated by at most about 180, at most about 170, at most about 160, at most about 150, or at most about 140 nucleotides.

[0443] In some embodiments, at least about 10%, at least about 20%, at least about 30%, at least about 40%, or at least about 50% of the one or more cell-free nucleic acid molecules comprising a plurality of phased variants comprises a single nucleotide variant (SNV) that is at least 2 nucleotides away from an adjacent SNV. In some embodiments, the plurality of phased variants comprises at least 3, at least 4, at least 5, at least 10, at least 15, at least 20, or at least 25 phased variants within the same cell-free nucleic acid molecule. In some embodiments, the one or more cell-free nucleic acid molecules identified comprises at least 2, at least 3, at least 4, at least 5, at least 10, at least 50, at least 100, at least 500, or at least 1,000 cell-free nucleic acid molecules. In some embodiments, the reference genomic sequence is derived from a reference cohort. In some embodiments, the reference genomic sequence comprises a consensus sequence from the reference cohort. In some embodiments, the reference genomic sequence comprises at least a portion of hg19 human genome, hg18 genome, hg17 genome, hg16 genome, or hg38 genome. In some embodiments, the reference genomic sequence is derived from a sample of the pregnant subject. In some embodiments, the sample is a healthy sample. In some embodiments, the sample comprises a healthy cell. In some embodiments, the sample is a diseased sample. In some embodiments, the diseased sample comprises a diseased cell. In some embodiments, the healthy cell is from the pregnant subject. In some embodiments, the healthy cell is from the healthy cohort. In some embodiments, the set of nucleic acid probes are designed to hybridize to at least a portion of sequences of genomic loci associated with the genetic abnormality.

[0444] In some embodiments, the set of nucleic acid probes are designed to hybridize to at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3. In some embodiments, each nucleic acid probe of the set of nucleic acid

probes has at least about 70%, at least about 80%, at least about 90% sequence identity, at least about 95% sequence identity, or about 100% sequence identity to a probe sequence selected from Table 6. In some embodiments, the set of nucleic acid probes comprises at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90% of probe sequences in Table 6. In some embodiments, the method further comprises determining the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject, based on the identified one or more cell-free nucleic acid molecules comprising the plurality of phased variants. In some embodiments, the method further comprises determining that the one or more cell-free nucleic acid molecules are derived from a sample associated with the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject, based on performing a statistical model analysis of the identified one or more cell-free nucleic acid molecules. In some embodiments, the statistical model analysis comprises a Monte Carlo statistical analysis. In some embodiments, the method further comprises monitoring a progress of the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based on the identified one or more cell-free nucleic acid molecules. In some embodiments, the method further comprises performing a different procedure to confirm the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject. In some embodiments, the different procedure comprises a blood test, genetic test, medical imaging, physical exam, or tissue biopsy. In some embodiments, the plurality of cell-free nucleic acid molecules comprise a plurality of cell-free deoxyribonucleic acid (DNA) molecules. In some embodiments, the plurality of cell-free nucleic acid molecules are derived from a bodily sample of the pregnant subject. In some embodiments, the bodily sample comprises plasma, serum, blood, cerebrospinal fluid, lymph fluid, saliva, urine, or stool. In some embodiments, the pregnant subject is a mammal. In some embodiments, the pregnant subject is a human. In some embodiments, (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based at least in part on the identified one or more indels.

[0445] In one aspect, the present disclosure provides a computer program product comprising a non-transitory computer-readable medium having computer-executable code encoded therein, the computer-executable code adapted to be executed to implement any one of the methods disclosed herein.

[0446] In one aspect, the present disclosure provides a system comprising one or more computer processors and computer memory coupled thereto, wherein the computer memory comprises machine executable code that, upon execution by the one or more computer processors, implements any one of the methods disclosed herein.

[0447] Additional aspects and advantages of the present disclosure will become readily apparent to those skilled in this art from the following detailed description, wherein only illustrative embodiments of the present disclosure are shown and described. As will be realized, the present disclosure is capable of other and different embodiments, and its several details are capable of modifications in various obvious respects, all without departing from the disclosure. Accordingly, the drawings and description are to be regarded as illustrative in nature, and not as restrictive.

INCORPORATION BY REFERENCE

[0448] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference. To the extent publications and patents or patent applications incorporated by reference contradict the disclosure contained in the specification, the specification is intended to supersede and/or take precedence over any such contradictory material.

BRIEF DESCRIPTION OF THE DRAWINGS

[0449] Various features of the invention are set forth with particularity in the appended claims. A better understanding of the features and advantages of the present invention will be obtained by reference to the following detailed description that sets forth illustrative embodiments, in which the principles of the invention are utilized, and the accompanying drawings (also "Figure" and "FIG." herein), of which:

[0450] **FIGs. 1A-1E** illustrate discovery of phased variants and their mutational signatures via analysis of whole-genome sequencing data. **FIG. 1A**. is a cartoon depicting the difference between detection of a single nucleotide variant (SNV) (top) and multiple variants 'in-phase' (phased variants, PVs; bottom) on individual cell-free DNA molecules. In theory, detection of a PV is a more specific event than detection of an isolated SNV. While a phased variants are shown in this figure as SNVs, other changes relative to reference genomic sequence could also be considered as phased variants. **FIG. 1B**. is a scatter plot showing the distribution of the number of PVs from WGS data for 24 different histologies of cancer, normalized by the total

number of SNVs. Bars show the median value and interquartile range. (FL-NHL, follicular lymphoma; DLBCL-NHL, diffuse large B-cell lymphoma; Burkitt-NHL, Burkitt lymphoma; Lung-SCC, squamous cell lung cancer; Lung-Adeno, lung adenocarcinoma; Kidney-RCC, renal cell carcinoma; Bone-Osteosarc, osteosarcoma; Liver-HCC, hepatocellular carcinoma; Breast-Adeno, breast adenocarcinoma; Panc-Adeno, pancreatic adenocarcinoma; Head-SCC, head and neck squamous cell carcinoma; Ovary-Adeno, ovarian adenocarcinoma; Eso-Adeno, esophageal adenocarcinoma; Uterus-Adeno, uterine adenocarcinoma; Stomach-Adeno, stomach adenocarcinoma; CLL, chronic lymphocytic leukemia; ColoRect-Adeno, colorectal adenocarcinoma; Prost-Adeno, prostate adenocarcinoma; CNS-GBM, glioblastoma multiforme; Panc-Endocrine, pancreatic neuroendocrine tumor; Thy-Adeno, thyroid adenocarcinoma; CNS-PiloAstro, piloastrocytoma; CNS-Medullo, medulloblastoma.) **FIG. 1C**. is a heatmap demonstrating the enrichment in single base substitution (SBS) mutational signatures for PVs versus single SNVs across multiple cancer types. Blue represents signatures which are enriched in PVs in specific histologies; darker gray represents signatures where un-phased, single SNVs are enriched; and red represents SNVs occurring in isolation. Only signatures which have a significant difference between PVs and unphased SNVs after correcting for multiple hypotheses are shown; other signatures are grey. Signatures associated with smoking, AID/AICDA, and APOBEC are indicated. **FIG. 1D**. demonstrate bar plots showing the distribution of PVs occurring in stereotyped regions across the genome in B-lymphoid malignancies and lung adenocarcinoma. In this plot, the genome was divided into 1000bp bins, and the fraction of samples of a given histology with a PV in each 1000bp bin was calculated. Only bins that have at least a 2 percent recurrence frequency in any cancer subtype are shown. Key genomic loci are also labeled. **FIG. 1E**. is a comparison of duplex sequencing to phased variant sequencing. A schema comparing error-suppressed sequencing by duplex sequencing vs. recovery of phased variants. In duplex sequencing, recovery of a single SNV observed on both strands of an original DNA double-helix (i.e., in trans) is required. This requires independent recovery of two molecules by sequencing as the plus and minus strands of the original DNA molecule go through library preparation and PCR independently. In contrast, recovery of PVs requires multiple SNVs observed on the same single strand of DNA (i.e., in cis). Thus, recovery of only the plus or the minus strand (rather than both) is sufficient for identification of PVs.

[0451] **FIGs. 2A-2F** illustrate design, validation, and application of phased variant enrichment sequencing. **FIG. 2A** is a schematic of the design for PhasED-Seq. WGS data from DLBCL tumor samples were aggregated (*left*), and areas of recurrent putative PVs were

identified (*middle*). An assay capturing the genomic regions most recurrently containing PVs was then designed (*right*), resulting in an ~7500x enrichment in PVs compared to WGS. The *top right panel* shows the *in silico* expected number of PVs per case per kilobase of panel size (y-axis) for increasing panel sizes (x-axis). The dashed line shows the selected regions in the PhasED-Seq panel. The *bottom right panel* shows the total number of expected PVs per case (y-axis, assessed *in silico* from WGS data, for increasing panel sizes (y-axis). The dark area shows the selected regions in the PhasED-Seq panel. **FIG. 2B** illustrate two panels showing the yield of SNVs (left) and PVs (right) for sequencing tumor DNA and matched germline by a previously established lymphoma CAPP-Seq panel or PhasED-Seq; values are assessed in silico by limiting WGS to the targeted space of interest. PVs reported in the right panel include doublet, triplet, and quadruplet phased events. **FIG. 2C** shows the yield of SNVs (left) and PVs (right) from experimental sequencing of tumor and/or cell-free DNA from CAPP-Seq versus PhasED-Seq, similar to **FIG. 2B**. **FIG. 2D** is a scatterplot showing the frequency of PVs by genomic location (in 1000bp bins) for patients with DLBCL, identified either by WGS or identified by PhasED-Seq. PVs in *IGH*, *BCL2*, *MYC*, and *BCL6* are highlighted. **FIG. 2E** illustrate scatterplots comparing the frequency of PVs by genomic location (in 50bp bins) for patients with different types of lymphomas. The colored circles show the relative frequency of PVs in 50bp bins from a specific gene of interest; the other (gray) circles show the relative frequency of PVs in 50bp bins from the remainder of the PhasED-Seq sequencing panel. **FIG. 2F** illustrate volcano plots summarizing the difference in relative frequency of PVs in specific genetic loci between types of lymphoma, including ABC-DLBCL vs. GCB-DLBCL (dark Gray, left); PMBCL vs DLBCL (dark gray, middle); and HL vs. DLBCL (dark gray, right). The x-axis demonstrates the relative enrichment in PVs in a specific locus, while the y-axis demonstrates the statistical significance of this association. (**Example 10**).

[0452] **FIGs. 3A-3I** illustrate technical performance of PhasED-Seq for disease detection. **FIG. 3A** illustrates bar plot showing the performance of hybrid capture sequencing for recovery of synthetic 150bp oligonucleotides from two loci (*MYC* and *BCL6*) with increasing degree of mutation / non-reference bases. Error bars represent the 95% confidence interval (n=3 replicates of each condition in distinct samples). **FIG. 3B** illustrates plot demonstrating the background error-rate (**Example 10**) for different types of error-suppression from 12 healthy control cell-free DNA samples sequenced on the PhasED-Seq panel. 'PhasED-Seq 2x' or 'doublets' represents detection of two mutations in-phase on the same DNA molecule; 'PhasED-Seq 3x' or 'triplets' represents detection of three mutations in-phase on the same DNA molecule. **FIG. 3C** illustrates bar plot showing the depth of unique molecular recovery

(e.g., depth after barcode-mediated PCR duplicate removal) from sequencing data from 12 cell-free DNA samples for different types of error-suppression, including barcode deduplication, duplex sequencing, and recovery of PVs of increasing maximal distance between SNVs in-phase. **FIG. 3D** illustrates bar plot showing the cumulative fraction of PVs that have a maximal distance between SNVs less than the number of base-pairs shown on the x-axis. **FIG. 3E** illustrates a plot demonstrating the results of a limiting dilution series simulating cell-free DNA samples containing patient-specific tumor fractions of $1x10^{-3}$ to $0.5x10^{-6}$; cfDNA from 3 independent patients samples were used in each dilution. The same sequencing data was analyzed using a variety of error-suppression methods for recovery of expected tumor fractions, including iDES, duplex sequencing, and PhasED-Seq (both for recovery of doublet and triplet molecules). Points and error-bars represent the mean, minimum, and maximum across the three patient-specific tumor mutations considered. The difference between observed and expected tumor fractions for sample < 1:10,000 were compared via paired t-test. *, $P<0.05$, **, $P<0.005$, ***, $P<0.0005$. **FIG. 3F** illustrates plot demonstrating the background signal for detection of tumor-specific alleles in 12 unrelated, healthy cell-free DNA samples, and the healthy cfDNA sample used for limiting dilution series (n=13 total samples). In each sample, tumor-specific SNVs or PVs from the 3 patient samples utilized in the limiting dilution experiment shown in **FIG. 3E**, for a total of 39 assessments were assessed. Bars represent the arithmetic mean across all 39 assessments; statistical comparison performed by Wilcoxon rank-sum test. *, $P<0.05$, **, $P<0.005$, ***, $P<0.0005$. **FIG. 3G** illustrates plot showing the theoretical rate of detection for a sample with a given number of PV-containing regions, according to simple binomial sampling. This plot is produced by assuming a unique sequencing depth of 5000x (line), along with a varying number of independent 150bp PV-containing regions, from 3 regions (blue) to 67 regions (purple). Confidence envelopes consider depth from 4000-6000x; a 5% false-positive rate is also assumed. **FIG. 3H** illustrates plot showing the observed rate of detection (y-axis) for sample of a given true tumor fraction (x-axis), with varying numbers of PV-containing regions. For each number of tumor-reporter regions ranging from 3 to 67, this number of 150bp windows was randomly sampled from each of 3 patient-specific PV reporter lists 25 times and used to assess tumor-detection at each dilution. Filled-in points represent 'wet' dilution series experiments, while open points represent *in silico* dilution experiments. Points and error-bars represent the mean, minimum, and maximum across the three patient-specific PV reporter lists used in the original sampling. **FIG. 3I** illustrates scatter plot compares the predicted vs observed rate of detection for samples from the dilution series shown in panels **FIG. 3G** and **FIG. 3H**. Additional details of this experiment are provided in **Example 10**.

[0453] **FIGs. 4A-4G** illustrate clinical application of PhasED-Seq for ultra-sensitive disease detection and response monitoring in DLBCL. **FIG. 4A** illustrates plot showing ctDNA levels for a patient with DLBCL responding to, and subsequently relapsing after, first-line immuno-chemotherapy. Levels measured by CAPP-Seq are shown in darker gray circles while levels measured by PhasED-Seq are shown in lighter gray circles. Open circles represent undetectable levels by CAPP-Seq. **FIG. 4B** illustrates a univariate scatter plot showing the mean tumor allele fraction measured by PhasED-Seq for clinical samples at time-points of minimal disease (i.e., after 1 or 2 cycles of therapy). The plot is divided by samples detected vs undetected by standard CAPP-Seq; P-value from Wilcoxon rank-sum test. **FIG. 4C** illustrates bar plot showing the fraction of DLBCL patients who have detectable ctDNA by CAPP-Seq after 1 or 2 cycles of treatment (dark gray bars), as well as the fraction of additional patients with detectable disease when adding PhasED-Seq to standard CAPP-Seq (medium gray bars). P-value represents a Fisher's Exact Test for detection by CAPP-Seq alone versus the combination of PhasED-Seq and CAPP-Seq in 171 samples after 1 or 2 cycles of treatment. **FIG. 4D** illustrates a waterfall plot showing the change in ctDNA levels measured by CAPP-Seq after 2 cycles of first-line therapy in patients with DLBCL. Patients with undetectable ctDNA by CAPP-Seq are shown as "ND" ("not detected"), in darker colors. The colors of the bars also indicate the eventual clinical outcomes for these patients. **FIG. 4E** illustrates a Kaplan-Meier plot showing the event-free survival for 52 DLBCL patients with undetectable ctDNA measured by CAPP-Seq after 2 cycles. **FIG. 4F** illustrates a Kaplan-Meier plot showing the event-free survival of 52 patients shown in **FIG. 4E** (undetectable ctDNA by CAPP-Seq) stratified by ctDNA detection via PhasED-Seq at this same time-point (cycle 3, day 1). **FIG. 4G** illustrates a Kaplan-Meier plot showing the event-free survival for 89 patients with DLBCL stratified by ctDNA at cycle 3, day 1 separated into 3 strata – patients failing to achieve a major molecular response (dark gray), patients with a major molecular response who still have detectable ctDNA by PhasED-Seq and/or CAPP-Seq (light grey), and patients who have a stringent molecular remission (undetectable ctDNA by PhasED-Seq and CAPP-Seq; medium gray).

[0454] **FIGs. 5A-5C** illustrate enumeration of SNVs and PVs in diverse cancers from WGS. **FIG. 5A-C** illustrate Univariate scatter plots showing the number of SNVs (**FIG. 5A**), PVs (**FIG. 5B**), and PVs, controlling for total number of SNVs (**FIG. 5C**), from WGS data for 24 different histologies of cancer. Bars show the median value and interquartile range. (FL-NHL, follicular lymphoma; DLBCL-NHL, diffuse large B cell lymphoma; Burkitt-NHL, Burkitt lymphoma; Lung-SCC, squamous cell lung cancer; Lung-Adeno, lung

adenocarcinoma; Kidney-RCC, renal cell carcinoma; Bone-Osteosarc, osteosarcoma; Liver-HCC, hepatocellular carcinoma; Breast-Adeno, breast adenocarcinoma; Panc-Adeno, pancreatic adenocarcinoma; Head-SCC, head and neck squamous cell carcinoma; Ovary-Adeno, ovarian adenocarcinoma; Eso-Adeno, esophageal adenocarcinoma; Uterus-Adeno, uterine adenocarcinoma; Stomach-Adeno, stomach adenocarcinoma; CLL, chronic lymphocytic leukemia; ColoRect-Adeno, colorectal adenocarcinoma; Prost-Adeno, prostate adenocarcinoma; CNS-GBM, glioblastoma multiforme; Panc-Endocrine, pancreatic neuroendocrine tumor; Thy-Adeno, thyroid adenocarcinoma; CNS-PiloAstro, piloastrocytoma; CNS-Medullo, medulloblastoma).

[0455] **FIGs. 6A-6WW** illustrate contribution of mutational signatures in phased and un-phased SNVs in WGS (**FIGs. 6A-6WW**.) Scatterplots showing the contribution of established single base substitution (SBS) mutational signatures to SNVs seen in PVs, shown in dark colors, and SNVs seen outside of possible phased relationships, shown in light colors, from WGS. This is presented for 49 SBS mutational signatures across 24 subtypes of cancer. Mutational signatures that show a significant difference in contribution between phased and un-phased SNVs after multiple hypothesis testing correction are indicated with a *. These figures represent the raw data summarized in FIG. 1C.

[0456] **FIG. 7** illustrates distribution of PVs in stereotyped regions across the genome. Bar plots show the distribution of PVs occurring in stereotyped regions across the genome of multiple cancer types. In this plot, the genome was divided into 1000bp bins, and the fraction of samples of a given histology with a PV in each 1000bp bin was calculated. Only bins that have at least a 2 percent recurrence frequency in any cancer subtype are shown. Histologies shown are as in **FIG. 1E**; activated B-cell (ABC) and germinal center B-cell (GCB) subtypes of DLBCL are also shown.

[0457] **FIGs. 8A-8E** illustrate quantity and genomic location of PVs from WGS in lymphoid malignancies. **FIG. 8A**. illustrates bar plot showing the number of independent 1000bp regions across the genome that recurrently contain PVs for DLBCL, FL, BL, and CLL (n=68, 74, 36, and 151 respectively). **FIG. 8B-D** illustrate plots showing the frequency of PVs for multiple lymphoid malignancies with relationships to specific genetic loci, including **FIG. 8B**: *BCL2*, **FIG. 8C**: *MYC*, and **FIG. 8D**: *ID3*. The location of the transcript for a given gene is shown below the plot in grey; exons are shown in darker gray. * indicates a region with significantly more PVs in a given cancer histology compared to all other histologies by Fisher's Exact Test ($P<0.05$). **FIG. 8E**, similar to **FIG. 8B-D**, these plots show the frequency of PVs across lymphoma subtypes. Here, it is shown the *IGH* locus, consisting of *IGHV*, *IGHD*, and

IGHJ parts, for ABC and GCB subtype DLBCLs (n=25 and 25, respectively). Coding regions for Ig parts, including Ig-constant regions and V-genes, are shown. (DLBCL, diffuse large B-cell lymphoma; FL, follicular lymphoma; BL, Burkitt lymphoma, CLL, chronic lymphocytic leukemia).

[0458] **FIGs. 9A-9K** illustrate performance of PhasED-Seq for recovery of PVs across lymphomas**. FIG. 9A** illustrates univariate scatter plot showing the fraction of all PVs across the genome identified by WGS (n=79) that were recovered by previously reported lymphoma CAPP-Seq panel[8] (left) compared to PhasED-Seq (right). **FIG. 9B** illustrates the expected yield of SNVs per case identified from WGS using a previously established lymphoma CAPP-Seq panel or the PhasED-Seq panel. **FIG. 9C** illustrates the expected yield of PVs per case identified from WGS using a previously established lymphoma CAPP-Seq panel or the PhasED-Seq panel. Data from three independent publicly available cohorts are shown in **FIGs. 9A-9C**. **FIGs. 9D-9F** illustrate plots showing the improvement in recovery of PVs by PhasED-Seq compared to CAPP-Seq in 16 patients sequenced by both assays. This includes improvement in d) two SNVs in phase (e.g., 2x or 'doublet PVs'), e) three SNVs in phase (3x or 'triplet PVs') and f) four SNVs in phase (e.g., 4x or 'quadruplet PVs'). **FIGs. 9G-9K**. illustrate panels showing the number of SNVs and PVs identified for patients with different types of lymphomas. These panels show the number of g) SNVs, h) doublet PVs, i) triplet PVs, j) quadruplet PVs, and k) all PVs. *, $P<0.05$; **, $P<0.01$, ***, $P<0.001$. (DLBCL, diffuse large B-cell lymphoma; GCB, germinal center B-cell like DLBCL; ABC, activated B-cell like DLBCL; PMBCL, primary mediastinal B-cell lymphoma; HL, Hodgkin lymphoma).

[0459] **FIGs. 10A-10Y** illustrate location-specific differences in PVs between ABC-DLBCL and GCB-DLBC (**FIGs. 10A-10Y**.) Similar to **FIG. 2D**, these scatterplots compare the frequency of PVs by genomic location (in 50bp bins) for patients with different types of lymphomas; in this figure, the difference between ABC-DLBCL and GCB-DLBCL is shown. The red circles show the relative frequency of PVs in 50bp bins from a specific gene of interest; the other (grey) circles show the relative frequency of PVs in 50bp bins from the remainder of the PhasED-Seq sequencing panel. Only genes with a statistically significant difference in PVs between ABC-DLBCL and GCB-DLBCL are shown. P-values represent a Wilcoxon rank-sum test of 50bp bins from a given gene against all other 50bp bins; see **Example 10**.

[0460] **FIGs. 11A-11X** illustrate Location-specific differences in PVs between DLBCL and PMBCL (**FIGs. 11A-11X**). Similar to **FIG. 2D**, these scatterplots compare the frequency of PVs by genomic location (in 50bp bins) for patients with different types of lymphomas; in this figure, the difference between DLBCL and PMBCL is shown. The blue circles show the

relative frequency of PVs in 50bp bins from a specific gene of interest; the other (gray) circles show the relative frequency of PVs in 50bp bins from the remainder of the PhasED-Seq sequencing panel. Only genes with a statistically significant difference in PVs between DLBCL and PMBCL are shown. P-values represent a Wilcoxon rank-sum test of 50bp bins from a given gene against all other 50bp bins; see **Example 10**.

[0461] **FIGs. 12A-12NN** illustrate Location-specific differences in PVs between DLBCL and HL. Similar to **Fig. 2D**, scatterplots of **FIGs. 12A-12NN** compare the frequency of PVs by genomic location (in 50bp bins) for patients with different types of lymphomas; in this figure, the difference between DLBCL and HL is shown. The green circles show the relative frequency of PVs in 50bp bins from a specific gene of interest; the other (grey) circles show the relative frequency of PVs in 50bp bins from the remainder of the PhasED-Seq sequencing panel. Only genes with a statistically significant difference in PVs between DLBCL and HL are shown. P-values represent a Wilcoxon rank sum test of 50bp bins from a given gene against all other 50bp bins; see **Example 10**.

[0462] **FIG. 13** illustrates differences in PVs between lymphoma types in mutations in the *IGH* locus. This figure shows the frequency of PVs from PhasED-Seq across the *@IGH* locus for different types of B-cell lymphomas. The bottom track shows the structure of the *@IGH* locus and gene-parts, including Ig-constant genes and V-genes. The next (outlined) track shows the frequency of PVs in this genomic region from WGS data (ICGC cohort). The remainder of the tracks show the frequency of PVs from PhasED-Seq targeted sequencing data, including 1) DLBCL, GCB-DLBCL , ABC-DLBCL, PMBCL, and HL. The regions targeted by the PhasED-Seq panel are shown at the top. Selected immunoglobulin parts with PVs enriched in specific histologies are labeled (i.e., *IGHV4-34*, *Sε*, *Sγ3* and *Sγ1*).

[0463] **FIGs. 14A-14E** illustrate Technical aspects of PhasED-Seq by hybrid-capture sequencing. **FIG. 14A** shows a plot of the theoretical energy of binding for typical 150-mers across the genome with increasing fraction of bases mutated from the reference genome. Mutations were spread throughout the 150-mer either clustered to one end of the sequence, clustered in the middle of the sequence, or randomly throughout the sequence. Point and error-bars represent the median and interquartile ranges from 10,000 *in silico* simulations. **FIG. 14B** illustrates a plot showing two histograms of summary metrics of the mutation rate of 151-bp windows across the PhasED-Seq panel across all patients in this study. The light gray histogram shows the maximum percent mutated in any 151-bp window for all patients in this study; the dark gray histogram shows the 95th percentile mutation rate across all mutated 151-bp

windows. **FIG. 14C** is a plot showing the percentile of mutation rate across all mutated 151-bp windows across all patients in this study. **FIG. 14D** illustrates heatmaps showing the relative error rate (as log10(error rate)) for single SNVs (left, "RED"), doublet PVs (middle, "YELLOW"), and triplet PVs (right, "BLUE"). FIG. 14D demonstrates that analysis based on the plurality of phased variants (e.g., double or triplet PVs) yields a lower error rate than analysis based on single SNVs. In addition, FIG. 14D demonstrates that analysis using a higher number of phased variant sets (e.g., triplet PVs labeled as "BLUE") yields a lower error rate than analysis based on a lower number of phased variant sets (e.g., doublet PVs labeled as "YELLOW"). The error rate of single SNVs from sequencing with multiple error suppression methods is shown, including barcode deduplication, iDES, and duplex sequencing. Error rates are summarized by the type of mutation. In the case of triplet PVs, the x and y-axis of the heatmap represent the first and second type of base alteration in the PV; the third alteration is averaged over all 12 possible base changes. **FIG. 14E** illustrates a plot showing the error rate for doublet / 2x PVs as a function of the genomic distance between the component SNVs.

[0464] **FIGs. 15** and **16A-16B** illustrate comparison of ctDNA quantitation by PhasED-Seq to CAPP-Seq and clinical applications. **FIG. 15** illustrates the detection-rate of ctDNA from pretreatment samples across 107 patients with large-B cell lymphomas by standard CAPP-Seq (green), as well as PhasED-Seq using doublets (light blue), triplets (medium blue), and quadruplets (dark blue). The specificity of ctDNA detection is also shown. In the lower two plots, the false-detection rate in 40 withheld healthy control cfDNA samples is shown. The size of each bar in these two plots shows the detection-rate for patient-specific cfDNA mutations in these 40-withheld controls, across all 107 cases. **FIG. 16A** illustrates table summarizing the sensitivity and specificity for ctDNA detection in pretreatment samples by CAPP-Seq and PhasED-Seq using doublets, triplets, and quadruplets, shown in panel A. Sensitivity is calculated across all 107 cases, while specificity is calculated across the 40 withheld control samples, assessing for each of the 107 independent patient-specific mutation lists, for a total of 4280 independent tests. **FIG. 16B** illustrates a scatterplot showing the quantity of ctDNA (measured as log10(haploid genome equivalents/mL)) as measured by CAPP-Seq vs. PhasED-Seq in individual samples. Samples taken prior to cycle 1 of RCHOP therapy (i.e., pretreatment), prior to cycle 2, and prior to cycle 3, are shown in independent colors (blue, green, and red respectively; 278 total samples). Undetectable levels fall on the axes. Spearman correlation and P-value are shown.

[0465] **FIGs. 17A-17D** illustrate detection of ctDNA after two cycles of systemic therapy. **FIG. 17A** illustrates a scatter plot showing the log-fold change in ctDNA after 2 cycles of therapy (i.e., the Major Molecular Response or MMR) measured by CAPP-Seq or PhasED-Seq for patients receiving RCHOP therapy. Dotted lines show the previously established threshold of a 2.5-log reduction in ctDNA for MMR. Undetectable samples fall on the axes; the correlation coefficient represents a Spearman rho for the 33 samples detected by both CAPP-Seq and PhasED-Seq. **FIG. 17B** illustrates 2 by 2 tables summarizing the detection rate of ctDNA samples after 2 cycles of therapy by PhasED-Seq vs CAPP-Seq. Patients with eventual disease progression are shown in bottom panel, while patients without eventual disease progression are shown in upper panel. **FIG. 17C** illustrates bar-plots showing the area under the receiver operator curve (AUC) for classification of patients for event-free survival at 24 months based on CAPP-Seq (light colors) or PhasED-Seq (dark colors) after 2 cycles of therapy. Classification of all patient (n=89, left) and only patients achieving a MMR (n=69, right) are both shown. **FIG. 17D** illustrates Kaplan-Meier plots showing the event-free survival of 69 patients achieving a MMR stratified by ctDNA detection with CAPP-Seq (top) or PhasED-Seq (bottom).

[0466] **FIGs. 18A-18H** illustrate detection of ctDNA after one cycle of systemic therapy. **FIG. 18A** illustrates scatterplot showing the log-fold change in ctDNA after 1 cycle of therapy (i.e., the Early Molecular Response or EMR) measured by CAPP-Seq or PhasED-Seq for patients receiving RCHOP therapy. Dotted lines show the previously established threshold of a 2-log reduction in ctDNA for EMR. Undetectable samples fall on the axes; the correlation coefficient represents a Spearman rho for the 45 samples detected by both CAPP-Seq and PhasED-Seq. **FIG. 18B** illustrates 2 by 2 tables summarizing the detection rate of ctDNA samples after 1 cycle of therapy by PhasED-Seq vs CAPP-Ceq. Patients with eventual disease progression are shown in red, while patients without eventual disease progression are shown in blue. **FIG. 18C** illustrates bar-plots showing the area under the receiver operator curve (AUC) for classification of patients for event-free survival at 24 months based on CAPP-Seq (light colors) or PhasED-Seq (dark colors) after 1 cycle of therapy. Classification of all patient (n=82, left) and only patients achieving an EMR (n=63, right) are both shown. **FIG. 18D** illustrates Kaplan-Meier plots showing the event-free survival of 63 patients achieving an EMR stratified by ctDNA detection with CAPP-Seq (top) or PhasED-Seq (bottom). **FIG. 18E** illustrates waterfall plot showing the change in ctDNA levels measured by CAPP-Seq after 1 cycle of first-line therapy in patients with DLBCL. Patients with undetectable ctDNA by CAPP-Seq are shown as “ND” (“not detected”), in darker colors. The colors of the bars also

indicate the eventual clinical outcomes for these patients. **FIG. 18F** illustrates a Kaplan-Meier plot showing the event-free survival for 33 DLBCL patients with undetectable ctDNA measured by CAPP-Seq after 1 cycle of therapy. **FIG. 18G** illustrates a Kaplan-Meier plot showing the event-free survival of 33 patients shown in **FIG. 18F** (undetectable ctDNA by CAPP-Seq) stratified by ctDNA detection via PhasED-Seq at this same time-point (cycle 2, day 1). **FIG. 18H** illustrates a Kaplan-Meier plot showing the event-free survival for 82 patients with DLBCL stratified by ctDNA at cycle 2, day 1 separated into 3 strata – patients failing to achieve an early molecular response, patients with an early molecular response who still have detectable ctDNA by PhasED-Seq and/or CAPP-Seq, and patients who have a stringent molecular remission (undetectable ctDNA by PhasED-Seq and CAPP-Seq;).

[0467] **FIG. 19** illustrates a fraction of patients where PhasED-Seq would achieve a lower LOD than duplex sequencing tracking SNVs based on PCAWG data (whole genome sequencing) from which the number of SNVs and phased variants (PVs) in different tumor types was quantified.

[0468] **FIG. 20** illustrates improved LODs achieved in lung cancers (adenocarcinoma, abbreviated 'A', and squamous cell carcinoma, abbreviated 'S'), compared to duplex sequencing of whole genome sequencing data.

[0469] **FIG. 21A** illustrates empiric data from an experiment where WGS was performed on tumor tissue and custom panels were designed for 5 patients with solid tumors (5 lung cancers) to examine and compare the LODs of custom CAPP-Seq vs PhasED-Seq, showing a ~10X lower LOD using PhasED-Seq in 5/5 patients.

[0470] **FIG. 21B** shows the background signal for detecting patient and tumor-specific DNA in control cell-free DNA samples with and without a reanalysis involving targeted resequencing of the original patient's tumor and germline DNA.

[0471] **FIG. 22A** illustrates proof of principle example patient vignette comparing using custom CAPP-Seq and PhasED-Seq for disease surveillance in lung cancer showing earlier detection of relapse using PhasED-Seq.

[0472] **FIG. 22B** illustrates proof of principle example patient vignette comparing using custom CAPP-Seq and PhasED-Seq for early detection of disease in breast cancer, showing earlier detection of disease with PhasED-Seq.

[0473] **FIG. 22C** shows a process for selection of validated phased variants from whole genome sequencing data.

[0474] **FIG. 22D** shows the performance metrics of personalized PhasED-seq across six patients, including background signal and limit of detection. Top, the background rate of SNVs

(squares), duplex SNVs (triangles) or PVs (circles); bars represent the median and IQR. Bottom, the lowest detectable tumor fraction for each sample. The background rate for SNVs is shown at 2×10^{-5} and for PVs at 5×10^{-7}.

[0475] **FIG. 22E** shows a comparison between the recovered tumor fraction by CAPP-seq (x axis) and PhasED-seq (y axis) for all samples from the six patients with solid tumors.

[0476] **FIG. 22F** shows detection of ctDNA for 6 cases of patients with solid tumors, including lung cancer (n = 5) and breast cancer (n = 1) using SNV-based detection (that is, CAPP-Seq) or PhasED-Seq with a personalized panel. Detection of ctDNA in patient plasma samples are shown in blue; samples detectable with PhasED-Seq but not SNV based approaches are in light blue. Specificity of the assay was assessed using 24 healthy control samples; detection of evidence of ctDNA by PhasED-Seq in these are shown on the right in pink across all 6 personalized panels, indicating 97% (139/144) specificity; CAPP-Seq on the same samples showed 95% (137/144) specificity.

[0477] **FIG. 22G** shows the ctDNA profile of a patient with stage 3 lung adenocarcinoma (LUP831) undergoing combined chemo-radiotherapy (CRT) and immunotherapy, measured by both CAPP-Seq and PhasED-Seq. The left panel shows the measured tumor fraction in the tumor biopsy sample using both methods. The right panel shows the tumor fraction from plasma DNA, including a sample detected by PhasED-Seq that is undetected by CAPP-Seq. ND: not detected.

[0478] **FIGs. 23A-23B** illustrate that detection methods describe herein (e.g. method depicted yielding **FIG. 3E** and **FIG. 3F**) does not require barcode meditated error suppression.

[0479] **FIG. 24** illustrates a flow diagram of a process to perform a clinical intervention and/or treatment on an individual based on detecting circulating-tumor nucleic acid sequences in a sequencing result in accordance with an embodiment.

[0480] **FIGs. 25A-25C** show example flowcharts of methods for determining a condition of a subject based on one or more cell-free nucleic acid molecules comprising a plurality of variants.

[0481] **FIG. 25D** shows an example flowchart of a method for treating a condition of a subject based on one or more cell-free nucleic acid molecules comprising a plurality of variants.

[0482] **FIG. 25E** shows an example flowchart of a method for determining a progress (e.g., progression or regression) of a condition of a subject based on one or more cell-free nucleic acid molecules comprising a plurality of variants.

[0483] **FIGs. 25F** and **25G** show example flowcharts of methods for determining a condition of a subject based on one or more cell-free nucleic acid molecules comprising a plurality of variants.

[0484] **FIGs. 26A** and **26B** schematically illustrate different fluorescent probes for identifying one or more cell-free nucleic acid molecules comprising a plurality of phased variants.

[0485] **FIG. 27** shows a computer system that is programmed or otherwise configured to implement methods provided herein.

[0486] **FIG. 28** shows the low error rate of larger indels in comparison to duplex sequencing.

DETAILED DESCRIPTION

[0487] While various embodiments of the invention have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions may occur to those skilled in the art without departing from the invention. It should be understood that various alternatives to the embodiments of the invention described herein may be employed.

[0488] The term "about" or "approximately" generally means within an acceptable error range for the particular value, which may depend in part on how the value is measured or determined, e.g., 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 can mean within an order of magnitude, preferably 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 may be assumed.

[0489] The terms "phased variants," "variants in phase," or "PV," as used interchangeably herein, generally refer to (1) two or more changes in nucleic acid sequence relative to a reference genomic sequence (e.g., SNVs, indel, translocation, amplification, etc.), or (2) one or more changes in nucleic acid sequence relative to a reference sequence and one or more changes in methylation status relative to a reference methylation status, so long as such changes occur within 170 bp of each other as determined by reference to the genomic reference sequence. Examples of changes in nucleic acid sequence relative to a reference genomic

sequence (e.g., a sequence derived from one of more healthy cells or a consensus sequence from a cohort) can include: a somatic single nucleotide variant (SNV), a somatic indel, a somatic translocation breakpoint, a somatic amplification or deletion breakpoint (e.g., the boundary of a large genomic copy number alteration, such as a large-scale deletion or a large-scale amplification), a germline SNV, a germline indel, a germline translocation breakpoint, a germline amplification or deletion breakpoint, or a region of localized hypermutation (kataegis). In some cases, phased variants may occur in *cis* (i.e., on the same strand of a nucleic acid molecule) within a single molecule, such as a single cell-free nucleic acid molecule. In some cases, a cell-free nucleic acid molecule can be a cell-free deoxyribonucleic acid (cfDNA) molecule. In some cases, a cfDNA molecule can be derived from a diseased tissue, such as a tumor (e.g., a circulating tumor DNA (ctDNA) molecule). In some cases, the cell-free nucleic acid molecule can be a cell-free ribonucleic acid molecule. The term "phased variant" can refer to one of the plurality of variants that are required to occur in proximity to one another to constitute phased variants, while the term "set of phased variants," as used in the claims, can refer to the plurality of variants that together form phased variants (i.e., the variants that are within 170 bp of each other with respect to the reference genome, occurring on the same strand of DNA).

[0490] The term "biological sample" or "bodily sample," as used interchangeably herein, generally refers to a tissue or fluid sample derived from a subject. A biological sample can be directly obtained from the subject. Alternatively, a biological sample can be derived from the subject (e.g., by processing an initial biological sample obtained from the subject). The biological sample can be or can include one or more nucleic acid molecules, such as DNA or ribonucleic acid (RNA) molecules. The biological sample can be derived from any organ, tissue or biological fluid. A biological sample can comprise, for example, a bodily fluid or a solid tissue sample. An example of a solid tissue sample is a tumor sample, e.g., from a solid tumor biopsy. Non-limiting examples of bodily fluids include blood, serum, plasma, tumor cells, saliva, urine, cerebrospinal fluid, lymphatic fluid, prostatic fluid, seminal fluid, milk, sputum, stool, tears, and derivatives of these. In some cases, one or more cell-free nucleic acid molecules as disclosed herein can be derived from a biological sample.

[0491] The term "subject," as used herein, generally refers to any animal, mammal, or human. A subject can have, potentially have, or be suspected of having one or more conditions, such as a disease. In some cases, a condition of the subject can be cancer, a symptom(s) associated with cancer, or asymptomatic with respect to cancer or undiagnosed (e.g., not diagnosed for cancer). In some cases, the subject can have cancer, the subject can show a

symptom(s) associated with cancer, the subject can be free from symptoms associated with cancer, or the subject may not be diagnosed with cancer. In some examples, the subject is a human.

[0492] The term "cell-free DNA" or "cfDNA," as used interchangeably herein, generally refers to DNA fragments circulating freely in a blood stream of a subject. Cell-free DNA fragments can have dinucleosomal protection (e.g., a fragment size of at least 240 base pairs ("bp")). These cfDNA fragments with dinucleosomal protection were likely not cut between the nucleosome, resulting in a longer fragment length (e.g., with a typical size distribution centered around 334 bp). Cell-free DNA fragments can have mononucleosomal protection (e.g., a fragment size of less than 240 base pairs ("bp")). These cfDNA fragments with mononucleosomal protection were likely cut between the nucleosome, resulting in a shorter fragment length (e.g., with a typical size distribution centered around 167 bp).

[0493] The term "sequencing data," as used herein, generally refers to "raw sequence reads" and/or "consensus sequences" of nucleic acids, such as cell-free nucleic acids or derivatives thereof. Raw sequence reads are the output of a DNA sequencer, and typically include redundant sequences of the same parent molecule, for example after amplification. "Consensus sequences" are sequences derived from redundant sequences of a parent molecule intended to represent the sequence of the original parent molecule. Consensus sequences can be produced by voting (wherein each majority nucleotide, e.g., the most commonly observed nucleotide at a given base position, among the sequences is the consensus nucleotide) or other approaches such as comparing to a reference genome. In some cases, consensus sequences can be produced by tagging original parent molecules with unique or non-unique molecular tags, which allow tracking of the progeny sequences (e.g., after amplification) by tracking of the tag and/or use of sequence read internal information.

[0494] The term "reference genomic sequence," as used herein, generally refers to a nucleotide sequence against which a subject's nucleotide sequences are compared.

[0495] The term "genomic region," as used herein, generally refers to any region (e.g., range of base pair locations) of a genome, e.g., an entire genome, a chromosome, a gene, or an exon. A genomic region can be a contiguous or a non-contiguous region. A "genetic locus" (or "locus") can be a portion or entirety of a genomic region (e.g., a gene, a portion of a gene, or a single nucleotide of a gene).

[0496] The term "likelihood," as used herein, generally refers to a probability, a relative probability, a presence or an absence, or a degree.

[0497] The term "liquid biopsy," as used herein, generally refers to a non-invasive or minimally invasive laboratory test or assay (e.g., of a biological sample or cell-free nucleic acids). The "liquid biopsy" assays can report detections or measurements (e.g., minor allele frequencies, gene expression, or protein expression) of one or more marker genes associated with a condition of a subject (e.g., cancer or tumor-associated marker genes).

A. Introduction

[0498] Modifications (e.g., mutations) of genomic DNA can be manifested in a formation and/or progression of one or more conditions (e.g., a disease, such as cancer or tumor) of a subject. The present disclosure provides methods and systems for analyzing cell-free nucleic acid molecules, such as cfDNA, from a subject to determine the presence or absence of a condition of the subject, prognosis of a diagnosed condition of the subject, progress of the condition of the subject over time, therapeutic treatment of a diagnosed condition of the subject, or predicted treatment outcome for a condition of the subject.

[0499] Analysis of cell-free nucleic acids, such as cfDNA, have been developed with broad applications in, e.g., prenatal testing, organ or tissue transplantation, infectious disease, and oncology. In the context of detecting or monitoring a disease of a subject, such as cancer, circulating tumor DNA (ctDNA) can be a sensitive and specific biomarker in numerous cancer types. In some cases, ctDNA can be used to detect the presence of minimal residual disease (MRD) or tumor burden after treatment, such as chemotherapies or surgical resection of solid tumors. However, the limit of detection (LOD) for ctDNA analysis can be restricted by a number of factors including (i) low input DNA amounts from a typical blood collection and (ii) background error rates from sequencing.

[0500] In some cases, ctDNA-based cancer detection can be improved by tracking multiple somatic mutations with error-suppressed sequencing, e.g., with LOD of about 2 parts in 100,000 from cfDNA input while using off-the-shelf panels or personalized assays. However, in some cases, current LOD of ctDNA of interest can be insufficient to universally detect MRD in patients destined for disease relapse or progression. For example, such 'loss of detection' can be exemplified in diffuse large B-cell lymphoma (DLBCL). For DLBCL, interim ctDNA detection after only two cycles of curative-intent therapy can represent a major molecular response (MMR), and can be a strong prognostic marker for ultimate clinical outcomes. Despite this, nearly one-third of patients ultimately experiencing disease progression do not have detectable ctDNA at this interim landmark using available techniques (e.g., Cancer Personalized Profiling by Deep Sequencing (CAPP-Seq)), thus representing 'false-negative'

measurements. Such high false-negative rates have also been observed in DLBCL patients by alternative methods, such as monitoring ctDNA through immunoglobulin gene rearrangements. Therefore, there exists a need for improved methods of ctDNA-based cancer detection with greater sensitivity.

[0501] Somatic variants detected on both of the complementary strands of parental DNA duplexes can be used to lower the LOD of ctDNA detection, thereby advantageously increasing the sensitivity of ctDNA detection. Such 'duplex sequencing' can reduce background error profile due to the requirement of two concordant events for detection of a single nucleotide variant (SNV). However, the duplex sequencing approach alone can be limited by inefficient recovery of DNA duplexes as recovery of both original strands can occur in a minority of all recovered molecules. Thus, duplex sequencing may be suboptimal and inefficient for real-world ctDNA detection with limited amount of starting sample, where input DNA from practical blood volumes (e.g., between about 4,000 to about 8,000 genomes per standard 10 milliliter (mL) blood collection tube) is limited and maximal recovery of genomes is essential.

[0502] Thus, there remains a significant unmet need for detection and analysis of ctDNA with low LOD (e.g., thereby yielding high sensitivity) for determining, for example, presence or absence of a disease of a subject, prognosis of the disease, treatment for the disease, and/or predicted outcome of the treatment.

B. Methods and systems for determining or monitoring a condition

[0503] The present disclosure describes methods and systems for detecting and analyzing cell free nucleic acids with a plurality of phased variants as a characteristic of a condition of a subject. In some aspects, the cell-free nucleic acid molecules can comprise cfDNA molecules, such as ctDNA molecules. The methods and systems disclosed herein can utilize sequencing data derived from a plurality of cell-free nucleic acid molecules of the subject to identify a subset of the plurality of cell-free nucleic acid molecules having the plurality of phased variants, thereby to determine the condition of the subject. The methods and systems disclosed herein can directly detect and, in some cases, pull down (or capture) such subset of the plurality of cell-free nucleic acid molecules that exhibit the plurality of phased variants, thereby to determine the condition of the subject with or without sequencing. The methods and systems disclosed herein can reduce background error rate often involved during detection and analysis of cell-free nucleic acid molecules, such as cfDNA.

[0504] In some aspects, methods and systems for cell-free nucleic acid sequencing and detection of cancer are provided. In some embodiments, cell-free nucleic acids (e.g., cfDNA

or cfRNA) can be extracted from a liquid biopsy of an individual and prepared for sequencing. Sequencing results of the cell-free nucleic acids can be analyzed to detect somatic variants in phase (i.e., phased variants, as disclosed herein) as an indication of circulating-tumor nucleic acid (ctDNA or ctRNA) sequences (i.e., sequences that derived or are originated from nucleic acids of a cancer cell). Accordingly, in some cases, cancer can be detected in the individual by extracting a liquid biopsy from the individual and sequencing the cell-free nucleic acids derived from that liquid biopsy to detect circulating-tumor nucleic acid sequences, and the presence of circulating-tumor nucleic acid sequences can indicate that the individual has a cancer (e.g., a specific type of cancer). In some cases, a clinical intervention and/or treatment can be determined and/or performed on the individual based on the detection of the cancer.

[0505] As disclosed herein, a presence of somatic variants in phase can be a strong indication that the nucleic acids containing such phased variants are derived from a bodily sample with a condition, such as a cancerous cell (or alternatively, that the nucleic acids are from derived from a bodily sample obtained or derived from a subject with a condition, such as cancer). Detection of phased somatic variants can enhance the signal-to-noise ratio of cell-free nucleic acid detection methods (e.g., by reducing or eliminating spurious "noise" signals) as it may be unlikely that phased mutations would occur within a small genetic window that is approximately the size of a typical cell-free nucleic acid molecule (e.g., about 170 bp or less).

[0506] In some aspects, a number of genomic regions can be used as hotspots for detection of phased variants, especially in various cancers, e.g., lymphomas. In some cases, enzymes (e.g., AID, Apobec3a) can stereotypically mutagenize DNA in specific genes and locations, leading to development of particular cancers. Accordingly, cell-free nucleic acids derived from such hotspot genomic regions can be captured or targeted (e.g., with or without deep sequencing) for cancer detection and/or monitoring. Alternatively, capture or targeted sequencing can be performed on regions in which phased variants have been previously detected from a cancerous source (e.g., tumor) of a particular individual in order to detect cancer in that individual.

[0507] In some aspects, capture sequencing on cell-free nucleic acids can be performed as a screening diagnostic (e.g., in subjects that have not been previously diagnosed and/or previously suspected or having a condition, such as cancer). In some cases, a screening diagnostic can be developed and used to detect circulating-tumor nucleic acids for cancers that have stereotypical regions of phased variants. In some cases, capture sequencing on cell-free nucleic acids is performed as a diagnostic to detect MRD or tumor burden to determine if a particular disease is present during or after treatment. In some cases, capture sequencing on

cell-free nucleic acids can be performed as a diagnostic to determine progress (e.g., progression or regression) of a treatment.

[0508] In some aspects, cell-free nucleic acid sequencing results can be analyzed to detect whether phased somatic single nucleotide variants (SNVs) or other mutations or variants (e.g., indels) exist within the cell-free nucleic acid sample. In some cases, the presence of particular somatic SNVs or other variants can be indicative of circulating-tumor nucleic acid sequences, and thus indicative of a tumor present in the subject. In some cases, a minimum of two variants can be detected in phase on a cell-free nucleic acid molecule. In some cases, a minimum of three variants can be detected in phase on a cell-free nucleic acid molecule. In some cases, a minimum of four variants can be detected in phase on a cell-free nucleic acid molecule. In some cases, a minimum of five or more variants can be detected in phase on a cell-free nucleic acid molecule. In some cases, the greater number of phased variants detected on a cell-free nucleic acid molecule, the greater the likelihood that the cell-free nucleic acid molecule is derived from cancer, as opposed to detecting an innocuous sequence of somatic variants that arise from molecular preparation of the sequence library or random biological errors. Accordingly, the likelihood of false-positive detection can decrease with detection of more variants in phase within a molecule (e.g., thereby increasing specificity of detection).

[0509] In some aspects, a cell-free nucleic acid sequencing result can be analyzed to detect whether an insertion or deletion of one or more nucleobases (i.e., indel) exist within the cell-free nucleic acid sample, e.g., relative to a reference genomic sequence. Without wishing to be bound by theory, in some cases, presence of indels in a cell-free nucleic acid molecule (e.g., cfDNA) can be indicative of a condition of a subject, e.g., a disease such as cancer. In some cases, a genetic variation as a result of an indel can be treated as a variant or mutation, and thus two indels can be treated as two phased variants, as disclosed herein. In some examples, within a cell-free nucleic acid molecule, a first genetic variation from a first indel (a first phase variant) and a second genetic variation from a second indel (a second phase variant) can be separated from each other by at least 1 nucleotide.

[0510] Within a single cell-free nucleic acid molecule (e.g., a single cfDNA molecule), as disclosed herein, a first phased variant can be a SNV and a second phased variant can be a part of a different small nucleotide polymorphism, e.g., another SNV or a part of a multi-nucleotide variant (MNV). A multi-nucleotide variant can be a cluster of two or more (e.g., at least 2, 3, 4, 5, or more) adjacent variants existing within the same stand of nucleic acid molecule. In some cases, the first phased variant and the second phased variant can be parts of the same MNV within the single cell-free nucleic acid molecule. In some cases, the first phased variant

and the second phased variant can be from two different MNVs within the single cell-free nucleic acid molecule.

[0511] In some aspects, a statistical method can be utilized to calculate the likelihood that detected phased variants are from a cancer and not random or artificial (e.g., from sample prep or sequencing error). In some cases, a Monte Carlo sampling method can be utilized to determine the likelihood that detected phased variants are from a cancer and not random or artificial.

[0512] Aspects of the present disclosure provide identification or detection of cell-free nucleic acids (e.g., cfDNA molecule) with a plurality of phased variants, e.g., from a liquid biopsy of a subject. In some cases, a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants can be directly adjacent to each other (e.g., neighboring SNVs). In some cases, a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants can be separated by at least one nucleotide. The spacing between the first phased variant and the second phased variant can be limited by the length of the cell-free nucleic acid molecule.

[0513] Within a single cell-free nucleic acid molecule (e.g., a single cfDNA molecule), as disclosed herein, a first phased variant and a second phased variant can be separated from each other by at least or up to about 1 nucleotide, at least or up to about 2 nucleotides, at least or up to about 3 nucleotides, at least or up to about 4 nucleotides, at least or up to about 5 nucleotides, at least or up to about 6 nucleotides, at least or up to about 7 nucleotides, at least or up to about 8 nucleotides, at least or up to about 9 nucleotides, at least or up to about 10 nucleotides, at least or up to about 11 nucleotides, at least or up to about 12 nucleotides, at least or up to about 13 nucleotides, at least or up to about 14 nucleotides, at least or up to about 15 nucleotides, at least or up to about 20 nucleotides, at least or up to about 25 nucleotides, at least or up to about 30 nucleotides, at least or up to about 35 nucleotides, at least or up to about 40 nucleotides, at least or up to about 45 nucleotides, at least or up to about 50 nucleotides, at least or up to about 60 nucleotides, at least or up to about 70 nucleotides, at least or up to about 80 nucleotides, at least or up to about 90 nucleotides, at least or up to about 100 nucleotides, at least or up to about 110 nucleotides, at least or up to about 120 nucleotides, at least or up to about 130 nucleotides, at least or up to about 140 nucleotides, at least or up to about 150 nucleotides, at least or up to about 160 nucleotides, at least or up to about 170 nucleotides, or at least or up to about 180 nucleotides. Alternatively, or in addition to, within a single cell-free nucleic acid molecule, a first phased variant and a second phased variant may not or need not be separated by one or more nucleotides and thus can be directly adjacent to one another.

[0514] A single cell-free nucleic acid molecule (e.g., a single cfDNA molecule), as disclosed herein, can comprise at least or up to about 2 phased variants, at least or up to about 3 phased variants, at least or up to about 4 phased variants, at least or up to about 5 phased variants, at least or up to about 6 phased variants, at least or up to about 7 phased variants, at least or up to about 8 phased variants, at least or up to about 9 phased variants, at least or up to about 10 phased variants, at least or up to about 12 phased variants, at least or up to about 12 phased variants, at least or up to about 13 phased variants, at least or up to about 14 phased variants, at least or up to about 15 phased variants, at least or up to about 20 phased variants, or at least or up to about 25 phased variants within the same molecule.

[0515] From a plurality of cell-free nucleic acid molecules obtained (e.g., from a liquid biopsy of a subject), two or more (e.g., 10 or more, 1,000 or more, 10,000 or more) cell-free nucleic acid molecules can be identified to have an average of at least or up to about 2 phased variants, at least or up to about 3 phased variants, at least or up to about 4 phased variants, at least or up to about 5 phased variants, at least or up to about 6 phased variants, at least or up to about 7 phased variants, at least or up to about 8 phased variants, at least or up to about 9 phased variants, at least or up to about 10 phased variants, at least or up to about 12 phased variants, at least or up to about 12 phased variants, at least or up to about 13 phased variants, at least or up to about 14 phased variants, at least or up to about 15 phased variants, at least or up to about 20 phased variants, or at least or up to about 25 phased variants per each cell-free nucleic acid molecule identified to comprise a plurality of phased variants.

[0516] In some cases, a plurality of cell-free nucleic acid molecules (e.g., cfDNA molecules) can be obtained from a biological sample of a subject (e.g., solid tumor or liquid biopsy). Out of the plurality of cell-free nucleic acid molecules, at least or up to 1, at least or up to 2, at least or up to 3, at least or up to 4, at least or up to 5, at least or up to 6, at least or up to 7, at least or up to 8, at least or up to 9, at least or up to 10, at least or up to 15, at least or up to 20, at least or up to 25, at least or up to 30, at least or up to 35, at least or up to 40, at least or up to 45, at least or up to 50, at least or up to 60, at least or up to 70, at least or up to 80, at least or up to 90, at least or up to 100, at least or up to 150, at least or up to 200, at least or up to 300, at least or up to 400, at least or up to 500, at least or up to 600, at least or up to 700, at least or up to 800, at least or up to 900, at least or up to 1,000, at least or up to 5,000, at least or up to, 10,000, at least or up to 50,000, or at least or up to 100,000 cell-free nucleic acid molecules can be identified, such that each identified cell-free nucleic acid molecule comprises the plurality of phased variants, as disclosed herein.

[0517] In some cases, a plurality of cell-free nucleic acid molecules (e.g., cfDNA molecules) can be obtained from a biological sample of a subject (e.g., solid tumor or liquid biopsy). Out of the plurality of cell-free nucleic acid molecules, at least or up to 1, at least or up to 2, at least or up to 3, at least or up to 4, at least or up to 5, at least or up to 6, at least or up to 7, at least or up to 8, at least or up to 9, at least or up to 10, at least or up to 15, at least or up to 20, at least or up to 25, at least or up to 30, at least or up to 35, at least or up to 40, at least or up to 45, at least or up to 50, at least or up to 60, at least or up to 70, at least or up to 80, at least or up to 90, at least or up to 100, at least or up to 150, at least or up to 200, at least or up to 300, at least or up to 400, at least or up to 500, at least or up to 600, at least or up to 700, at least or up to 800, at least or up to 900, or at least or up to 1,000 cell-free nucleic acid molecules can be identified from a target genomic region (e.g., a target genomic locus), such that each identified cell-free nucleic acid molecule comprises the plurality of phased variants, as disclosed herein.

[0518] **FIGs. 1A** and **1E** schematically illustrate examples of (i) a cfDNA molecule comprising a SNV and (ii) another cfDNA molecule comprising a plurality of phased variants. Each variant identified within the cfDNA can indicate a presence of one more genetic mutations in the cell that the cfNDA is originated from. In alternative embodiments, one or more of the phased variants may be an insertion or deletion (indel) or other genomic alteration instead of an SNV.

[0519] In one aspect, the present disclosure provides a method for determining a condition of a subject, as shown by flowchart 2510 in **FIG. 25A**. The method can comprise (a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from the subject (process 2512). The method can further comprise (b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules identified comprises a plurality of phased variants relative to a reference genomic sequence (process 2514). In some cases, at least a portion of the one or more cell-free nucleic acid molecules can comprise a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants that are separated by at least one nucleotide, as disclosed herein. The method can optionally comprise (c) analyzing, by the computer system, at least a portion of the identified one or more cell-free nucleic acid molecules to determine the condition of the subject (process 2516).

[0520] In some cases, at least or up to about 5%, at least or up to about 10%, at least or up to about 15%, at least or up to about 20%, at least or up to about 25%, at least or up to about 30%, at least or up to about 35%, at least or up to about 40%, at least or up to about 45%, at least or up to about 50%, at least or up to about 60%, at least or up to about 70%, at least or up to about 80%, at least or up to about 90%, at least or up to about 95%, at least or up to about 99%, or about 100% of the one or more cell-free nucleic acid molecules can comprise a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants that are separated by at least one nucleotide, as disclosed herein. In some examples, a plurality of phased variants within a single cfDNA molecule can comprise (i) a first plurality of phased variants that are separated by at least one nucleotide from one another and (ii) a second plurality of phased variants that are adjacent to one another (e.g., two phased variants within a MNV). In some examples, a plurality of phased variants within a single cfDNA molecule can consist of phased variants that are separate by at least one nucleotide from one another.

[0521] In one aspect, the present disclosure provides a method for determining a condition of the subject, as shown by flowchart 2520 in **FIG. 25B**. The method can comprise (a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject (process 2522). The method can further comprise (b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence (process 2524). In some cases, a first phased variant of the plurality of phased variant and a second phased variant of the plurality of phased variant can be separated by at least one nucleotide, as disclosed herein. The method can optionally comprise (c) analyzing, by the computer system, at least a portion of the identified one or more cell-free nucleic acid molecules to determine the condition of the subject (process 2526).

[0522] In one aspect, the present disclosure provides a method for determining a condition of a subject, as shown by flowchart 2530 in **FIG. 25C**. The method can comprise (a) obtaining sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from the subject (process 2532). The method can further comprise (b) processing the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules with a LOD being less than about 1 out of 50,000 observations (or cell-free nucleic acid molecules) from the sequencing data (process 2534). In some cases, each

of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence. The method can optionally comprise (c) analyzing at least a portion of the identified one or more cell-free nucleic acid molecules to determine the condition of the subject (process 2536).

[0523] In some cases, the LOD of the operation of identifying the one or more cell-free nucleic acid molecules, as disclosed herein, can be less than about 1 out of 60,000, less than 1 out of 70,000, less than 10 out of 80,000, less than 1 out of 90,000, less than 1 out of 100,000, less than 1 out of 150,000, less than 1 out of 200,000, less than 1 out of 300,000, less than 1 out of 400,000, less than 1 out of 500,000, less than 1 out of 600,000, less than 1 out of 700,000, less than 1 out of 800,000, less than 1 out of 900,000, less than 1 out of 1,000,000, less than 1 out of 1,000,000, less than 1 out of 1,100,000, less than 1 out of 1,200,000, less than 1 out of 1,300,000, less than 1 out of 1,400,000, less than 1 out of 1,500,000, or less than 1 out of 2,000,000 observations from the sequencing data.

[0524] In some cases, at least one cell-free nucleic acid molecule of the identified one or more cell-free nucleic acid molecules can comprise a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants that are separated by at least one nucleotide, as disclosed herein.

[0525] In some cases, one or more of the operations (a) through (c) of the subject method can be performed by a computer system. In an example, all of the operations (a) through (c) of the subject method can be performed by the computer system.

[0526] The sequencing data, as disclosed herein, can be obtained from one or more sequencing methods. A sequencing method can be a first-generation sequencing method (e.g., Maxam-Gilbert sequencing, Sanger sequencing). A sequencing method can be a high-throughput sequencing method, such as next-generation sequencing (NGS) (e.g., sequencing by synthesis). A high-throughput sequencing method can sequence simultaneously (or substantially simultaneously) at least about 10,000, at least about 100,000, at least about 1 million, at least about 10 million, at least about 100 million, at least about 1 billion, or more polynucleotide molecules (e.g., cell-free nucleic acid molecules or derivatives thereof). NGS can be any generation number of sequencing technologies (e.g., second-generation sequencing technologies, third-generation sequencing technologies, fourth-generation sequencing technologies, etc.). Non-limiting examples of high-throughput sequencing methods include massively parallel signature sequencing, polony sequencing, pyrosequencing, sequencing-by-synthesis, combinatorial probe anchor synthesis (cPAS), sequencing-by-ligation (e.g., sequencing by oligonucleotide ligation and detection (SOLiD) sequencing), semiconductor

sequencing (e.g., Ion Torrent semiconductor sequencing), DNA nanoball sequencing, and single-molecule sequencing, sequencing-by-hybridization.

[0527] In some embodiments of any one of the methods disclosed herein, the sequencing data can be obtained based on any of the disclosed sequencing methods that utilizes nucleic acid amplification (e.g., polymerase chain reaction (PCR)). Non-limiting examples of such sequencing methods can include 454 pyrosequencing, polony sequencing, and SoLiD sequencing. In some cases, amplicons (e.g., derivatives of the plurality of cell-free nucleic acid molecules that is obtained or derived from the subject, as disclosed herein) that correspond to a genomic region of interest (e.g., a genomic region associated with a disease) can be generated by PCR, optionally pooled, and subsequently sequenced to generating sequencing data. In some examples, because the regions of interest are amplified into amplicons by PCR before being sequenced, the nucleic acid sample is already enriched for the region of interest, and thus any additional pooling (e.g., hybridization) may not and need not be needed prior to sequencing (e.g., non-hybridization based NGS). Alternatively, pooling via hybridization can further be performed for additional enrichment prior to sequencing. Alternatively, the sequencing data can be obtained without generating PCR copies, e.g., via cPAS sequencing.

[0528] A number of embodiments utilize capture hybridization techniques to perform targeted sequencing. When performing sequencing on cell-free nucleic acids, in order to enhance resolution on particular genomic loci, library products can be captured by hybridization prior to sequencing. Capture hybridization can be particularly useful when trying to detect rare and/or somatic phased variants from a sample at particular genomic loci. In some situations, detection of rare and/or somatic phased variants is indicative of the source of nucleic acids, including nucleic acids derived from a cancer source. Accordingly, capture hybridization is a tool that can enhance detection of circulating-tumor nucleic acids within cell-free nucleic acids.

[0529] Various types of cancers repeatedly experience aberrant somatic hypermutation in particular genomic loci. For instance, the enzyme activation-induced deaminase induces aberrant somatic hypermutation in B-cells, which leads to various B-cell lymphomas, including (but not limited to) diffuse large B-cell lymphoma (DLBCL), follicular lymphoma (FL), Burkitt lymphoma (BL), and B-cell chronic lymphocytic leukemia (CLL). Accordingly, in numerous embodiments, probes are designed to pull down (or capture) genomic loci known to experience aberrant somatic hypermutation in a lymphoma. **FIG. 1D** and **Table 1** describe a number of regions that experience aberrant somatic hypermutation in DLBCL, FL, BL and CLL. Provided in **Table 6** is list of nucleic acid probes that can be utilized to pull down (or

capture) genomic loci to detect aberrant somatic hypermutation in B-cell cancers.

[0530] Capture sequencing can also be performed utilizing personalized nucleic acid probes designed to detect the existence of an individual's cancer. An individual having a cancer can have their cancer biopsied and sequenced to detect somatic phased variants that have accumulated in the cancer. Based on the sequencing result, in accordance with a number of embodiments, nucleic acid probes are designed and synthesized capable of pulling down the genomic loci inclusive of the positions of where the phased variants. These personalized designed and synthesized nucleic acid probes can be utilized to detect circulating-tumor nucleic acids from a liquid biopsy of that individual. Accordingly, the personalized nucleic acid probes can be useful for determining treatment response and/or detecting MRD after treatment.

[0531] In some embodiments of any one of the methods disclosed herein, the sequencing data can be obtained based on any sequencing method that utilizes adapters. Nucleic acid samples (e.g., the plurality of cell-free nucleic acid molecules from the subject, as disclosed herein) can be conjugated with one or more adapters (or adapter sequences) for recognizing (e.g., via hybridization) of the sample or any derivatives thereof (e.g., amplicons). In some examples, the nucleic acid samples can be tagged with a molecular barcode, e.g., such that each cell-free nucleic acid molecule of the plurality of cell-free nucleic acid molecules can have a unique barcode. Alternatively, or in addition to, the nucleic acid samples can be tagged with a sample barcode, e.g., such that the plurality of cell-free nucleic acid molecules from the subject (e.g., a plurality of cell-free nucleic acid molecules obtained from a specific bodily tissue of the subject) can have the same barcode.

[0532] In alternative embodiments, the methods of identifying one or more cell-free nucleic acid molecules comprising the plurality of phased variants, as disclosed herein, can be performed without molecular barcoding, without sample barcoding, or without molecular barcoding and sample barcoding, at least in part due to high specificity and low LOD achieved by relying on identifying the phased variants as opposed to, e.g., a single SNV.

[0533] In some embodiments of any one of the methods disclosed herein, the sequencing data can be obtained and analyzed without in silico removal or suppression of (i) background error and/or (ii) sequencing error, at least in part due to high specificity and low LOD achieved by relying on identifying the phased variants as opposed to, e.g., a single SNV or indel.

[0534] In some embodiments of any one of the methods disclosed herein, using the plurality of variants as a condition to identify target cell-free nucleic acid molecules with specific mutations of interest without in silico methods of error suppression can yield a background error-rate that is lower than that of (i) barcode-deduplication, (ii) integrated digital

error suppression, or (iii) duplex sequencing by at least about 5-fold, at least about 10-fold, at least about 20-fold, at least about 30-fold, at least about 40-fold, at least about 50-fold, at least about 60-fold, at least about 70-fold, at least about 80-fold, at least about 90-fold, at least about 100-fold, at least about 200-fold, at least about 400-fold, at least about 600-fold, at least about 800-fold, or at least about 1,000-fold. This approach may advantageously increase signal-to-noise ratio (thereby increasing sensitivity and/or specificity) of identifying target cell-free nucleic acid molecules with specific mutations of interest.

[0535] In some embodiments of any one of the methods disclosed herein, increasing a minimum number of phased variants (e.g., increasing from at least two phased variants to at least three phased variants) per cell-free nucleic acid molecule required as a condition to identify target cell-free nucleic acid molecules with specific mutations of interest can reduce the background error-rate by at least about 5-fold, at least about 10-fold, at least about 20-fold, at least about 30-fold, at least about 40-fold, at least about 50-fold, at least about 60-fold, at least about 70-fold, at least about 80-fold, at least about 90-fold, or at least about 100-fold. This approach may advantageously increase signal-to-noise ratio (thereby increasing sensitivity and/or specificity) of identifying target cell-free nucleic acid molecules with specific mutations of interest.

[0536] In one aspect, the present disclosure provides a method of treating a condition of a subject, as shown in flowchart 2540 in **FIG. 25D**. The method can comprise (a) identifying the subject for treatment of the condition, wherein the subject has been determined to have the condition based on identification of one or more cell-free nucleic acid molecules from a plurality of cell-free nucleic acid molecules that is obtained or derived from the subject (Process 2542). Each of the identified one or more cell-free nucleic acid molecules can comprise a plurality of phased variants relative to a reference genomic sequence. At least a portion (e.g., partial or all) of the plurality of phased variants can be separated by at least one nucleotide, such that a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide, as disclosed herein. In some cases, a presence of the plurality of phased variants is indicative of the condition (e.g., a disease, such as cancer) of the subject. The method can further comprise (b) subjecting the subject to the treatment based on the step (a) (process 2544). Examples of such treatment of the condition of the subject are disclosed elsewhere in the present disclosure.

[0537] In one aspect, the present disclosure provides a method of monitoring a progress (e.g., progression or regression) of a condition of a subject, as shown in flowchart 2550 in **FIG. 25E**. The method can comprise (a) determining a first state of the condition of the subject

based on identification of a first set of one or more cell-free nucleic acid molecules from a first plurality of cell-free nucleic acid molecules that is obtained or derived from the subject (process 2552). The method can further comprise (b) determining a second state of the condition of the subject based on identification of a second set of one or more cell-free nucleic acid molecules from a second plurality of cell-free nucleic acid molecules that is obtained or derived from the subject (process 2554). The second plurality of cell-free nucleic acid molecules can be obtained from the subject subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject. The method can optionally comprise (c) determining the progress (e.g., progression or regression) of the condition based at least in part on the first state of the condition and the second state of the condition (process 2556). In some cases, each of the one or more cell-free nucleic acid molecules identified (e.g., each of the first set of one or more cell-free nucleic acid molecules identified, each of the second set of one or more cell-free nucleic acid molecules identified) can comprise a plurality of phased variants relative to a reference genomic sequence. At least a portion (e.g., partial or all) of the one or more cell-free nucleic acid molecules identified can be separated by at least one nucleotide, as disclosed herein. In some cases, presence of the plurality of phased variants can be indicative of a state of the condition of the subject.

[0538] In some cases, the first plurality of cell-free nucleic acid molecules from the subject can be obtained (e.g., via blood biopsy) and analyzed to determine (e.g., diagnose) a first state of the condition (e.g., a disease, such as cancer) of the subject. The first plurality of cell-free nucleic acid molecules can be analyzed via any of the methods disclosed herein (e.g., with or without sequencing) to identify the first set of one or more cell-free nucleic acid molecules comprising the plurality of phased variants, and the presence or characteristics of the first set of one or more cell-free nucleic acid molecules can be used to determine the first state of the condition (e.g., an initial diagnosis) of the subject. Based on the determined first state of the condition, the subject can be subjected to one or more treatments (e.g., chemotherapy) as disclosed herein. Subsequent to the one or more treatments, he second plurality of cell-free nucleic acid molecules can be obtained from the subject.

[0539] In some cases, the subject can be subjected to at least or up to about 1 treatment, at least or up to about 2 treatments, at least or up to about 3 treatments, at least or up to about 4 treatments, at least or up to about 5 treatments, at least or up to about 6 treatments, at least or up to about 7 treatments, at least or up to about 8 treatments, at least or up to about 9 treatments, or at least or up to about 10 treatments based on the determined first state of the condition. In some cases, the subject can be subjected to a plurality of treatments based on the determined

first state of the condition, and a first treatment of the plurality of treatments and a second treatment of the plurality of treatments can be separated by at least or up to about 1 day, at least or up to about 7 days, at least or up to about 2 weeks, at least or up to about 3 weeks, at least or up to about 4 weeks, at least or up to about 2 months, at least or up to about 3 months, at least or up to about 4 months, at least or up to about 5 months, at least or up to about 6 months, at least or up to about 12 months, at least or up to about 2 years, at least or up to about 3 years, at least or up to about 4 years, at least or up to about 5 years, or at least or up to about 10 years. The plurality of treatments for the subject can be the same. Alternatively, the plurality of treatments can be different by drug type (e.g., different chemotherapeutic drugs), drug dosage (e.g., increasing dosage, decreasing dosage), presence or absence of a co-therapeutic agent (e.g., chemotherapy and immunotherapy), modes of administration (e.g., intravenous vs oral administrations), frequency of administration (e.g., daily, weekly, monthly), etc.

[0540] In some cases, the subject may not and need not be treated for the condition between determination of the first state of the condition and determination of the second state of the condition. For example, without any intervening treatment, the second plurality of cell-free nucleic acid molecules may be contained (e.g., via liquid biopsy) from the subject to confirm whether the subject still exhibits indications of the first state of the condition.

[0541] In some cases, the second plurality of cell-free nucleic acid molecules from the subject can be obtained (e.g., via blood biopsy) at least or up to about 1 day, at least or up to about 7 days, at least or up to about 2 weeks, at least or up to about 3 weeks, at least or up to about 4 weeks, at least or up to about 2 months, at least or up to about 3 months, at least or up to about 4 months, at least or up to about 5 months, at least or up to about 6 months, at least or up to about 12 months, at least or up to about 2 years, at least or up to about 3 years, at least or up to about 4 years, at least or up to about 5 years, or at least or up to about 10 years after obtaining the first plurality of cell-free nucleic acid molecules from the subject.

[0542] In some cases, at least or up to about 2, at least or up to about 3, at least or up to about 4, at least or up to about 5, at least or up to about 6, at least or up to about 7, at least or up to about 8, at least or up to about 9, or at least or up to about 10 different samples comprising a plurality of nucleic acid molecules (e.g., at least the first plurality of cell-free nucleic acid molecules and the second plurality of cell-free nucleic acid molecules) can be obtained over time (e.g., once every month for 6 months, once every two months for a year, once every three months for a year, once every 6 months for one or more years, etc.) to monitor the progress of the condition of the subject, as disclosed herein.

[0543] In some cases, the step of determining the progress of the condition based on the first state of the condition and the second state of the condition can comprise comparing one or more characteristics of the first state and the second state of the condition, such as, for example, (i) a total number of cell-free nucleic acid molecules identified to comprise the plurality of phased variants in each state (e.g., per equal weight or volume of the biological sample of origin, per equal number of initial cell-free nucleic acid molecules analyzed, etc.), (ii) an average number of the plurality of phased variants per each cell-free nucleic acid molecule identified to comprise a plurality of phased variants (i.e., two or more phased variants), or (iii) a number of cell-free nucleic acid molecules identified to comprise the plurality of phased variants divided by a total number of cell-free nucleic acid molecules that comprise a mutation that overlaps with some of the plurality of phased variants (i.e., phased variant allele frequency). Based on such comparison, MRD of the condition (e.g., cancer or tumor) of the subject can be determined. For example, tumor burden or cancer burden of the subject can be determined based on such comparison.

[0544] In some cases, the progress of the condition can be progression or worsening of the condition. In an example, the worsening of the condition can comprise developing of a cancer from an earlier stage to a later stage, such as from stage I cancer to stage III cancer. In another example, the worsening of the condition can comprise increasing size (e.g., volume) of a solid tumor. Yet in a different example, the worsening of the condition can comprise cancer metastasis from once location to another location within the subject's body.

[0545] In some examples, (i) a total number of cell-free nucleic acid molecules identified to comprise the plurality of phased variants from the second state of the condition of the subject can be higher than (ii) a total number of cell-free nucleic acid molecules identified to comprise the plurality of phased variants from the first state of the condition of the subject by at least or up to about 0.1-fold, at least or up to about 0.2-fold, at least or up to about 0.3-fold, at least or up to about 0.4-fold, at least or up to about 0.5-fold, at least or up to about 0.6-fold, at least or up to about 0.7-fold, at least or up to about 0.8-fold, at least or up to about 0.9-fold, at least or up to about 1-fold, at least or up to about 2-fold, at least or up to about 3-fold, at least or up to about 4-fold, at least or up to about 5-fold, at least or up to about 6-fold, at least or up to about 7-fold, at least or up to about 8-fold, at least or up to about 9-fold, at least or up to about 10-fold, at least or up to about 15-fold, at least or up to about 20-fold, at least or up to about 30-fold, at least or up to about 40-fold, at least or up to about 50-fold, at least or up to about 60-fold, at least or up to about 70-fold, at least or up to about 80-fold, at least or up to about 90-fold, at least or up to about 100-fold, at least or up to about 200-fold, at least or up to about

300-fold, at least or up to about 400-fold, or at least or up to about 500-fold.

[0546] In some examples, (i) an average number of the plurality of phased variants per each cell-free nucleic acid molecule identified to comprise a plurality of phased variants from the second state of the condition of the subject can be higher than (ii) an average number of the plurality of phased variants per each cell-free nucleic acid molecule identified to comprise a plurality of phased variants from the first state of the condition of the subject by at least or up to about 0.1-fold, at least or up to about 0.2-fold, at least or up to about 0.3-fold, at least or up to about 0.4-fold, at least or up to about 0.5-fold, at least or up to about 0.6-fold, at least or up to about 0.7-fold, at least or up to about 0.8-fold, at least or up to about 0.9-fold, at least or up to about 1-fold, at least or up to about 2-fold, at least or up to about 3-fold, at least or up to about 4-fold, at least or up to about 5-fold, at least or up to about 6-fold, at least or up to about 7-fold, at least or up to about 8-fold, at least or up to about 9-fold, at least or up to about 10-fold, at least or up to about 15-fold, at least or up to about 20-fold, at least or up to about 30-fold, at least or up to about 40-fold, at least or up to about 50-fold, at least or up to about 60-fold, at least or up to about 70-fold, at least or up to about 80-fold, at least or up to about 90-fold, at least or up to about 100-fold, at least or up to about 200-fold, at least or up to about 300-fold, at least or up to about 400-fold, or at least or up to about 500-fold.

[0547] In some cases, the progress of the condition can be regression or at least a partial remission of the condition. In an example, the at least the partial remission of the condition can comprise downstaging of a cancer from a later stage to an earlier stage, such as from stage IV cancer to stage II cancer. Alternatively, the at least the partial remission of the condition can be full remission from cancer. In another example, the at least the partial remission of the condition can comprise decreasing size (e.g., volume) of a solid tumor.

[0548] In some examples, (i) a total number of cell-free nucleic acid molecules identified to comprise the plurality of phased variants from the second state of the condition of the subject can be lower than (ii) a total number of cell-free nucleic acid molecules identified to comprise the plurality of phased variants from the first state of the condition of the subject by at least or up to about 0.1-fold, at least or up to about 0.2-fold, at least or up to about 0.3-fold, at least or up to about 0.4-fold, at least or up to about 0.5-fold, at least or up to about 0.6-fold, at least or up to about 0.7-fold, at least or up to about 0.8-fold, at least or up to about 0.9-fold, at least or up to about 1-fold, at least or up to about 2-fold, at least or up to about 3-fold, at least or up to about 4-fold, at least or up to about 5-fold, at least or up to about 6-fold, at least or up to about 7-fold, at least or up to about 8-fold, at least or up to about 9-fold, at least or up to about 10-fold, at least or up to about 15-fold, at least or up to about 20-fold, at least or up to about 30-

fold, at least or up to about 40-fold, at least or up to about 50-fold, at least or up to about 60-fold, at least or up to about 70-fold, at least or up to about 80-fold, at least or up to about 90-fold, at least or up to about 100-fold, at least or up to about 200-fold, at least or up to about 300-fold, at least or up to about 400-fold, or at least or up to about 500-fold.

[0549] In some examples, (i) an average number of the plurality of phased variants per each cell-free nucleic acid molecule identified to comprise a plurality of phased variants from the second state of the condition of the subject can be lower than (ii) an average number of the plurality of phased variants per each cell-free nucleic acid molecule identified to comprise a plurality of phased variants from the first state of the condition of the subject by at least or up to about 0.1-fold, at least or up to about 0.2-fold, at least or up to about 0.3-fold, at least or up to about 0.4-fold, at least or up to about 0.5-fold, at least or up to about 0.6-fold, at least or up to about 0.7-fold, at least or up to about 0.8-fold, at least or up to about 0.9-fold, at least or up to about 1-fold, at least or up to about 2-fold, at least or up to about 3-fold, at least or up to about 4-fold, at least or up to about 5-fold, at least or up to about 6-fold, at least or up to about 7-fold, at least or up to about 8-fold, at least or up to about 9-fold, at least or up to about 10-fold, at least or up to about 15-fold, at least or up to about 20-fold, at least or up to about 30-fold, at least or up to about 40-fold, at least or up to about 50-fold, at least or up to about 60-fold, at least or up to about 70-fold, at least or up to about 80-fold, at least or up to about 90-fold, at least or up to about 100-fold, at least or up to about 200-fold, at least or up to about 300-fold, at least or up to about 400-fold, or at least or up to about 500-fold.

[0550] In some cases, the progress of the condition can remain substantially the same between the two states of the condition of the subject. In some examples, (i) a total number of cell-free nucleic acid molecules identified to comprise the plurality of phased variants from the second state of the condition of the subject can be about the same as (ii) a total number of cell-free nucleic acid molecules identified to comprise the plurality of phased variants from the first state of the condition of the subject. In some examples, (i) an average number of the plurality of phased variants per each cell-free nucleic acid molecule identified to comprise a plurality of phased variants from the second state of the condition of the subject can about the same as (ii) an average number of the plurality of phased variants per each cell-free nucleic acid molecule identified to comprise a plurality of phased variants from the first state of the condition of the subject.

[0551] In some embodiments of any one of the methods disclosed herein, the one or more cell-free nucleic acid molecules comprising the plurality of phased variants can be identified from the plurality of cell-free nucleic acid molecules by one or more sequencing methods.

Alternatively, or in addition to, the one or more cell-free nucleic acid molecules comprising the plurality of phased variants can be identified by being pulled down from (or captured from among) the plurality of cell-free nucleic acid molecules with a set of nucleic acid probes. The pull down (or capture) method via the set of nucleic acid probes can be sufficient to identify the one or more cell-free nucleic acid molecules of interest without sequencing. In some cases, the set of nucleic acid probes can be configured to hybridize to at least a portion of cell-free nucleic acid (e.g., cfDNA) molecules from one or more genomic regions associated with the condition of the subject. As such, a presence of one or more cell-free nucleic acid molecules that have been pulled down by the set of nucleic acid probes can be an indication that the one or more cell-free nucleic acid molecules are derived from the condition (e.g., ctDNA or ctRNA). Additional details of the set of nucleic probes are disclosed elsewhere the present disclosure.

[0552] In some embodiments of any one of the methods disclosed herein, based the sequencing data derived from the plurality of cell-free nucleic acid molecules (e.g., cfDNA) that is obtained or derived from the subject, (i) the one or more cell-free nucleic acid molecules identified to comprise the plurality of phased variants can be separated, in silico, from (ii) one or more other cell-free nucleic acid molecules that are not identified to comprise the plurality of phased variants (or one or more other cell-free nucleic acid molecules that do not comprise the plurality of phased variants). In some cases, the method can further comprise generating an additional data comprising sequencing information of only (i) the one or more cell-free nucleic acid molecules identified to comprise the plurality of phased variants. In some cases, the method can further comprise generating a different data comprising sequencing information of only (ii) the one or more other cell-free nucleic acid molecules that are not identified to comprise the plurality of phased variants (or the one or more other cell-free nucleic acid molecules that do not comprise the plurality of phased variants).

[0553] In one aspect, the present disclosure provides a method for determining a condition of the subject, as shown by flowchart 2560 in **FIG. 25F**. The method can comprise (a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules obtained or derived from the subject (process 2562). In some cases, an individual nucleic acid probe of the set of nucleic acid probes can be designed to hybridize to a target cell-free nucleic acid molecule comprising a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide. As such, a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants can be separated by at least one nucleotide, as disclosed herein. In some

cases, the individual nucleic acid probe can comprise an activatable reporter agent. The activatable reporter agent can be activated by either one of (i) hybridization of the individual nucleic acid probe to the plurality of phased variants and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants. The method can further comprise (b) detecting the reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules (process 2564). Each of the one or more cell-free nucleic acid molecules can comprise the plurality of phased variants. The method can optionally comprise (c) analyzing at least a portion of the identified one or more cell-free nucleic acid molecules to determine the condition of the subject (process 2566).

[0554] In one aspect, the present disclosure provides a method for determining a condition of the subject, as shown by flowchart 2570 in **FIG. 25G**. The method can comprise (a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules obtained or derived from the subject (process 2572). In some cases, an individual nucleic acid probe of the set of nucleic acid probes can be designed to hybridize to a target cell-free nucleic acid molecule comprising a plurality of phased variants relative to a reference genomic sequence. In some cases, the individual nucleic acid probe can comprise an activatable reporter agent. The activatable reporter agent can be activated by either one of (i) hybridization of the individual nucleic acid probe to the plurality of phased variants and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants. The method can further comprise (b) detecting the reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules (process 2574). Each of the one or more cell-free nucleic acid molecules can comprise the plurality of phased variants, and a LOD of the identification step can be less than about 1 out of 50,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, as disclosed herein. The method can optionally comprise (c) analyzing at least a portion of the identified one or more cell-free nucleic acid molecules to determine the condition of the subject (process 2576).

[0555] In some cases, a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide, as disclosed herein.

[0556] In some cases, the LOD of the step of identifying the one or more cell-free nucleic acid molecules, as disclosed herein, can be less than about 1 out of 60,000, less than 1 out of 70,000, less than 10 out of 80,000, less than 1 out of 90,000, less than 1 out of 100,000, less

than 1 out of 150,000, less than 1 out of 200,000, less than 1 out of 300,000, less than 1 out of 400,000, less than 1 out of 500,000, less than 1 out of 600,000, less than 1 out of 700,000, less than 1 out of 800,000, less than 1 out of 900,000, less than 1 out of 1,000,000, less than 1 out of 1,000,000, less than 1 out of 1,100,000, less than 1 out of 1,200,000, less than 1 out of 1,300,000, less than 1 out of 1,400,000, less than 1 out of 1,500,000, less than 1 out of 2,000,000, less than 1 out of 2,500,000, less than 1 out of 3,000,000, less than 1 out of 4,000,000, or less than 1 out of 5,000,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules. Generally, a detection method with a lower LOD has a greater sensitivity of such detection.

[0557] In some embodiments of any one of the methods disclosed herein, the method can further comprise mixing (1) the set of nucleic acid probes and (2) the plurality of cell-free nucleic acid molecules.

[0558] In some embodiments of any one of the methods disclosed herein, the activatable reporter agent of a nucleic acid probe can be activated upon hybridization of the individual nucleic acid probe to the plurality of phased variants. Non-limiting examples of such nucleic acid probe can include a molecular beacon, eclipse probe, amplifluor probe, scorpions PCR primer, and light upon extension fluorogenic PCR primer (LUX primer).

[0559] For example, the nucleic acid probe can be a molecular beacon, as shown in **FIG. 26A**. The molecular beacon can be fluorescently labeled (e.g., dye-labeled) oligonucleotide probe that comprises complementarity to a target cell-free nucleic acid molecule 2603 in a region that comprises the plurality of phased variants. The molecular beacon can have a length between about 25 nucleotides to about 50 nucleotides. The molecular beacon can also be designed to be partially self-complimentary, such that it form a hairpin structure with a stem 2601a and a loop 2601b. The 5' and 3' ends of the molecular beacon probe can have complementary sequences (e.g., about 5–6 nucleotides) that form the stem structure 2601a. The loop portion 2601b of the hairpin can be designed to specifically hybridize to a portion (e.g., about 15–30 nucleotides) of the target sequence comprising two or more phased variants. The hairpin can be designed to hybridize to a portion that comprises at least 2, 3, 4, 5, or more phased variants. A fluorescent reporter molecule can be attached to the 5' end of the molecular beacon probe, and a quencher that quenches fluorescence of the fluorescent reporter can be attached to the 3' end of the molecular beacon probe. Formation of the hairpin therefore can bring the fluorescent reporter and quencher together, such that no fluorescence is emitted. However, during annealing operation of amplification reaction of the plurality of cell-free nucleic acid molecules that is obtained or derived from the subject, the loop portion of the

molecular beacon can bind to its target sequence, causing the stem to denature. Thus, the reporter and quencher can be separated, abolishing quenching, and the fluorescent reporter is activated and detectable. Because fluorescence of the fluorescent reporter is emitted from the molecular beacon probe only when the probe is bound to the target sequence, the amount or level of fluorescence detected can be proportional to the amount of target in the reaction (e.g., (i) a total number of cell-free nucleic acid molecules identified to comprise the plurality of phased variants in each state or (ii) an average number of the plurality of phased variants per each cell-free nucleic acid molecule identified to comprise a plurality of phased variants, as disclosed herein).

[0560] In some embodiments of any one of the methods disclosed herein, the activatable reporter agent can be activated upon dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants. In other words, once the individual nucleic acid probe is hybridized to target cell-free nucleic acid molecule's portion that comprises the plurality of phased variants, dehybridization of at least a portion of the individual nucleic acid prob and the target cell-free nucleic acid can activate the activatable reporter agent. Non-limiting examples of such nucleic acid probe can include a hydrolysis probe (e.g., TaqMan prob), dual hybridization probes, and QZyme PCR primer.

[0561] For example, the nucleic acid probe can be a hydrolysis probe, as shown in **FIG. 26B**. The hydrolysis probe 2611 can be a fluorescently labeled oligonucleotide probe that can specifically hybridize to a portion (e.g., between about 10 and about 25 nucleotides) of the target cell-free nucleic acid molecule 2613, wherein the hybridized portion comprises two or more phased variants. The hydrolysis probe 2611 can be labeled with a fluorescent reporter at the 5' end and a quencher at the 3' end. When the hydrolysis probe is intact (e.g., not cleaved), the fluorescence of the reporter is quenched due to its proximity to the quencher (**FIG. 26B**). During annealing operation of amplification reaction of the plurality of cell-free nucleic acid molecules obtained or derived from the subject, 5' → 3' exonuclease activity of certain thermostable polymerases (e.g., Taq or Tth) The amplification reaction of the plurality of cell-free nucleic acid molecules obtained or derived from the subject can include a combined annealing/extension operation during which the hydrolysis probe hybridizes to the target cell-free nucleic acid molecule, and the dsDNA-specific 5' → 3' exonuclease activity of a thermostable polymerase (e.g., Taq or Tth) cleaves off the fluorescent reporter from the hydrolysis probe. As a result, the fluorescent reporter is separated from the quencher, resulting in a fluorescence signal that is proportional to the amount of target in the sample (e.g., (i) a total number of cell-free nucleic acid molecules identified to comprise the plurality of phased

variants in each state or (ii) an average number of the plurality of phased variants per each cell-free nucleic acid molecule identified to comprise a plurality of phased variants, as disclosed herein).

[0562] In some embodiments of any one of the methods disclosed herein, the reporter agent can comprise a fluorescent reporter. Non-limiting examples of a fluorescent reporter include fluorescein amidite (FAM, 2-[3-(dimethylamino)-6-dimethyliminio-xanthen-9-yl]benzoate TAMRA, (2E)-2-[(2E,4E)-5-(2-tert-butyl-9-ethyl-6,8,8-trimethyl-pyrano[3,2-g]quinolin-1-ium-4-yl)penta-2,4-dienylidene]-1-(6-hydroxy-6-oxo-hexyl)-3,3-dimethyl-indoline-5-sulfonate Dy 750, 6-carboxy-2′,4,4′,5′,7,7′-hexachlorofluorescein, 4,5,6,7-Tetrachlorofluorescein TET™, sulforhodamine 101 acid chloride succinimidyl ester Texas Red-X, ALEXA Dyes, Bodipy Dyes, cyanine Dyes, Rhodamine 123 (hydrochloride), Well RED Dyes, MAX, and TEX 613. In some cases, the reporter agent further comprises a quencher, as disclosed herein. Non-limiting examples of a quencher can include Black Hole Quencher, Iowa Black Quencher, and 4-dimethylaminoazobenzene-4'-sulfonyl chloride (DABCYL).

[0563] In some embodiments of any one of the methods disclosed herein, any PCR reaction utilizing the set of nucleic acid probes can be performed using real-time PCR (qPCR). Alternatively, the PCR reaction utilizing the set of nucleic acid probes can be performed using digital PCR (dPCR).

[0564] Provided in **FIG. 24** is an example flowchart of a process to perform a clinical intervention and/or treatment based on detecting circulating-tumor nucleic acids in an individual's biological sample. In several embodiments, detection of circulating-tumor nucleic acids is determined by the detection of somatic variants in phase in a cell-free nucleic acid sample. In many embodiments, detection of circulating-tumor nucleic acids indicates cancer is present, and thus appropriate clinical intervention and/or treatment can be performed.

[0565] Referring to **FIG. 24**, process 2400 can begin with obtaining, preparing, and sequencing (2401) cell-free nucleic acids obtained from a non-invasive biopsy (e.g., liquid or waste biopsy), utilizing a capture sequencing approach across regions shown to harbor a plurality of genetic mutations or variants occurring in phase. In several embodiments, cfDNA and/or cfRNA is extracted from plasma, blood, lymph, saliva, urine, stool, and/or other appropriate bodily fluid. Cell-free nucleic acids can be isolated and purified by any appropriate means. In some embodiments, column purification is utilized (e.g., QIAamp Circulating Nucleic Acid Kit from Qiagen, Hilden, Germany). In some embodiments, isolated RNA fragments can be converted into complementary DNA for further downstream analysis.

[0566] In some embodiments, a biopsy (e.g., a liquid biopsy) is extracted prior to any indication of cancer. In some embodiments, a biopsy is extracted to provide an early screen in order to detect a cancer. In some embodiments, a biopsy is extracted to detect if residual cancer exists after a treatment. In some embodiments, a biopsy is extracted during treatment to determine whether the treatment is providing the desired response. Screening of any particular cancer can be performed. In some embodiments, screening is performed to detect a cancer that develops somatic phased variants in stereotypical regions in the genome, such as (for example) lymphoma. In some embodiments, screening is performed to detect a cancer in which somatic phased variants were discovered utilizing a prior extracted cancer biopsy.

[0567] In some embodiments, a biopsy is extracted from an individual with a determined risk of developing cancer, such as those with a familial history of the disorder or have determined risk factors (e.g., exposure to carcinogens). In many embodiments, a biopsy is extracted from any individual within the general population. In some embodiments, a biopsy is extracted from individuals within a particular age group with higher risk of cancer, such as, for example, aging individuals above the age of 50. In some embodiments, a biopsy is extracted from an individual diagnosed with and treated for a cancer.

[0568] In some embodiments, extracted cell-free nucleic acids are prepared for sequencing. Accordingly, cell-free nucleic acids are converted into a molecular library for sequencing. In some embodiments, adapters and/or primers are attached onto cell-free nucleic acids to facilitate sequencing. In some embodiments, targeted sequencing of particular genomic loci is to be performed, and thus particular sequences corresponding to the particular loci are captured via hybridization prior to sequencing (e.g., capture sequencing). In some embodiments, capture sequencing is performed utilizing a set of probes that pull down (or capture) regions that have been discovered to commonly harbor phased variants for a particular cancer (e.g., lymphoma). In some embodiments, capture sequencing is performed utilizing a set of probes that pull down (or capture) regions that have been discovered to harbor phased variants as determined prior by sequencing a biopsy of the cancer. More detailed discussion of capture sequencing and probes is provided in the section entitled "Capture Sequencing."

[0569] In some embodiments, any appropriate sequencing technique can be utilized that can detect phased variants indicative of circulating-tumor nucleic acids. Sequencing techniques include (but are not limited to) 454 sequencing, Illumina sequencing, SOLiD sequencing, Ion Torrent sequencing, single-read sequencing, paired-end sequencing, etc.

[0570] Process 2400 analyzes (2403) the cell-free nucleic acid sequencing result to detect circulating-tumor nucleic acid sequences, as determined by detection of somatic variants

occurring in phase. Because cancers are actively growing and expanding, neoplastic cells are often releasing biomolecules (especially nucleic acids) into the vasculature, lymph, and/or waste systems. In addition, due to biophysical constraints in their local environment, neoplastic cells are often rupturing, releasing their inner cell contents into the vasculature, lymph, and/or waste systems. Accordingly, it is possible to detect distal primary tumors and/or metastases from a liquid or waste biopsy.

[0571] Detection of circulating-tumor nucleic acid sequences indicates that a cancer is present in the individual being examined. Accordingly, based on detection of circulating-tumor nucleic acids, a clinical intervention and/or treatment may be performed (2405). In a number of embodiments, a clinical procedure is performed, such as (for example) a blood test, genetic test, medical imaging, physical exam, a tumor biopsy, or any combination thereof. In several embodiments, diagnostics are preformed to determine the particular stage of cancer. In a number of embodiments, a treatment is performed, such as (for example) chemotherapy, radiotherapy, chemoradiotherapy, immunotherapy, hormone therapy, targeted drug therapy, surgery, transplant, transfusion, medical surveillance, or any combination thereof. In some embodiments, an individual is assessed and/or treated by medical professional, such as a doctor, physician, physician's assistant, nurse practitioner, nurse, caretaker, dietician, or similar.

[0572] Various embodiments of the present disclosure are directed towards utilizing detection of cancer to perform clinical interventions. In a number of embodiments, an individual has a liquid or waste biopsy screened and processed by methods described herein to indicate that the individual has cancer and thus an intervention is to be performed. Clinical interventions include clinical procedures and treatments. Clinical procedures include (but are not limited to) blood tests, genetic test, medical imaging, physical exams, and tumor biopsies. Treatments include (but are not limited to) chemotherapy, radiotherapy, chemoradiotherapy, immunotherapy, hormone therapy, targeted drug therapy, surgery, transplant, transfusion, and medical surveillance. In several embodiments, diagnostics are performed to determine the particular stage of cancer. In some embodiments, an individual is assessed and/or treated by medical professional, such as a doctor, physician, physician's assistant, nurse practitioner, nurse, caretaker, dietician, or similar.

[0573] In several embodiments as described herein a cancer can be detected utilizing a sequencing result of cell-free nucleic acids derived from blood, serum, cerebrospinal fluid, lymph fluid, urine or stool. In many embodiments, cancer is detected when a sequencing result has one or more somatic variants present in phase within a short genetic window, such as the

length of a cell-free molecule (e.g., about 170 bp). In numerous embodiments, a statistical method is utilized to determine whether the presence of phased variants is derived from a cancerous source (as opposed to molecular artifact or other biological source). Various embodiments utilize a Monte Carlo sampling method as the statistical method to determine whether a sequencing result of cell-free nucleic acids includes sequences of circulating-tumor nucleic acids based on a score as determined by the presence of phased variants. Accordingly, in a number of embodiments, cell-free nucleic acids are extracted, processed, and sequenced, and the sequencing result is analyzed to detect cancer. This process is especially useful in a clinical setting to provide a diagnostic scan.

[0574] An exemplary procedure for a diagnostic scan of an individual for a B-cell cancer is as follows:

(a) extract liquid or waste biopsy from individual,

(b) prepare and perform targeted sequencing of cell-free nucleic acids from biopsy utilizing nucleic acid probes specific for the B-cell cancer,

(c) detect phased variants in a sequencing result that are indicative of circulating-tumor nucleic acid sequences, and

(d) perform clinical intervention based on detection of circulating-tumor nucleic acid sequences.

[0575] An exemplary procedure for a personalized diagnostic scan of an individual for a cancer that has been previously sequenced to detect phased variants in particular genomic loci is as follows:

(a) design and synthesize nucleic acid probes for genomic loci that include the positions of the detected phased variants,

(b) extract liquid or waste biopsy from individual,

(c) prepare and perform targeted sequencing of cell-free nucleic acids from biopsy utilizing the designed and synthesized nucleic acid probes,

(d) detect phased variants in a sequencing result that are indicative of circulating-tumor nucleic acid sequences, and

(e) perform clinical intervention based on detection of circulating-tumor nucleic acid sequences.

[0576] In some embodiments of any one of the methods disclosed herein, at least a portion of the identified one or more cell-free nucleic acid molecules comprising the plurality of phased variants can be further analyzed for determining the condition of the subject. In such analysis, (i) the identified one or more cell-free nucleic acid molecules and (ii) other cell-free nucleic

acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants can be analyzed as different variables. In some cases, a ratio of (i) a number the identified one or more cell-free nucleic acid molecules and (ii) a number of the other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants can be used a factor to determine the condition of the subject. In some cases, comparison of (i) a position(s) of the identified one or more cell-free nucleic acid molecules relative to the reference genomic sequence and (ii) a position(s) of the other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants relative to the reference genomic sequence can be used a factor to determine the condition of the subject.

[0577] Alternatively, in some cases, the analysis of the identified one or more cell-free nucleic acid molecules comprising the plurality of phased variants for determining the condition of the subject may not and need not be based on the other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants. As disclosed herein, non-limiting examples of information or characteristics of the one or more cell-free nucleic acid molecules comprising the plurality of phased variants can include (i) a total number of such cell-free nucleic acid molecules and (ii) an average number of the plurality of phased variations per each nucleic acid molecule in the population of identified cell-free nucleic acid molecules.

[0578] Thus, in some embodiments of any one of the methods disclosed herein, a number of the plurality of phased variants from the one or more cell-free nucleic acid molecules that have been identified to have the plurality of phased variants can be indicative of the condition of the subject. In some cases, a ratio of (i) the number of the plurality of phased variants from the one or more cell-free nucleic acid molecules and (ii) a number of single nucleotide variants from the one or more cell-free nucleic acid molecules can be indicative of the condition of the subject. For instance, a particular condition (e.g., follicular lymphoma) can exhibit a signature ratio that is different than that of another condition (e.g., breast cancer). In some examples, for cancer or solid tumor, the ratio as disclosed herein can be between about 0.01 and about 0.20. In some examples, for cancer or solid tumor, the ratio as disclosed herein can be about 0.01, about 0.02, about 0.03, about 0.04, about 0.05, about 0.06, about 0.07, about 0.08, about 0.09, about 0.10, about 0.11, about 0.12, about 0.13, about 0.14, about 0.15, about 0.16, about 0.17, about 0.18, about 0.19, or about 0.20. In some examples, for cancer or solid tumor, the ratio as disclosed herein can be at least or up to about 0.01, at least or up to about 0.02, at least or up to about 0.03, at least or up to about 0.04, at least or up to about 0.05, at least or up to about

0.06, at least or up to about 0.07, at least or up to about 0.08, at least or up to about 0.09, at least or up to about 0.10, at least or up to about 0.11, at least or up to about 0.12, at least or up to about 0.13, at least or up to about 0.14, at least or up to about 0.15, at least or up to about 0.16, at least or up to about 0.17, at least or up to about 0.18, at least or up to about 0.19, or at least or up to about 0.20.

[0579] In some embodiments of any one of the methods disclosed herein, a frequency of the plurality of phased variants in the one or more cell-free nucleic acid molecules that have been identified can be indicative of the condition of the subject. In some cases, based on the sequencing data disclosed herein, an average frequency of the plurality of phased variant per a predetermined bin length (e.g., a bin of about 50 base pairs) within each of the identified cell-free nucleic acid molecule can be indicative of the condition of the subject. In some cases, based on the sequencing data disclosed herein, an average frequency of the plurality of phased variant per a predetermined bin length (e.g., a bin of about 50 base pairs) within each of the identified cell-free nucleic acid molecule that is associated with a particular gene (e.g., BCL2, PIM1) can be indicative of the condition of the subject. The size of the bin can be about 30, about 40, about 50, about 60, about 70, or about 80.

[0580] In some examples, a first condition (e.g., Hodgkin lymphoma or HL) can exhibit a first average frequency and a second condition (e.g., DLBCL) can exhibit a different average frequency, thereby allowing identification and/or determination of whether the subject has or is suspected of having a particular condition. In some examples, a first sub-type of a disease can exhibit a first average frequency and a second sub-type of the same disease can exhibit a different average frequency, thereby allowing identification and/or determination of whether the subject has or is suspected of having a particular sub-type of the disease. For example, the subject can have DLBCL, and one or more cell-free nucleic acid molecules derived from germinal center B-cell (GCB) DLBCL or activated B-cell (ABC) DLBCL can have different average frequency of the plurality of phased variant per a predetermined bin length, as disclosed herein.

[0581] In some example, a condition of the subject may have a predetermined number of phased variants spanning predetermined genomic loci (i.e., a predetermined frequency of phased variants). When the predetermined frequency of phased variants match a frequency of the plurality of phased variants in the one or more cell-free nucleic acid molecules that have been identified from a plurality of cell-free nucleic acid molecules from the subject, it may indicate that the subject has such condition.

[0582] In some embodiments of any one of the methods disclosed herein, the one or more cell-free nucleic acid molecules identified to comprise the plurality of phased variants can be analyzed to determine their genomic origin (e.g., which gene locus they are from). The genomic origin of the one or more cell-free nucleic acid molecules that have been identified can be indicative of the condition of the subject, as different disease can have the plurality of phased variants in different signature genes. For example, a subject can have GCB DLBCL, and one or more cell-free nucleic acid molecules originated from GCBs of the subject can have the phased variants prevalent in BCL2 gene, while one or more cell-free nucleic acid molecules originated from ABCs of the same subject may not comprise as many phased variants in the BCL2 gene as those from GCBs. On the other hand, a subject can have ABC DLBCL, and one or more cell-free nucleic acid molecules originated from ABCs of the subject can have the phased variants prevalent in PIM1 gene, while one or more cell-free nucleic acid molecules originated from GCBs of the same subject may not comprise as many phased variants in the PIM1 gene as those from ABCs.

[0583] In some embodiments of any one of the methods disclosed herein, at least or up to about 10%, at least or up to about 15%, at least or up to about 20%, at least or up to about 25%, at least or up to about 30%, at least or up to about 35%, at least or up to about 40%, at least or up to about 45%, at least or up to about 50%, at least or up to about 55%, at least or up to about 60%, at least or up to about 65%, at least or up to about 70%, at least or up to about 75%, at least or up to about 80%, at least or up to about 85%, at least or up to about 90%, at least or up to about 95%, at least or up to about 99%, or about 100% of the one or more cell-free nucleic acid molecules comprising the plurality of phased variants can comprise a single nucleotide variant (SNV) that is at least 2 nucleotides away from an adjacent SNV.

[0584] In some embodiments of any one of the methods disclosed herein, at least or up to about 5%, at least or up to about 10%, at least or up to about 15%, at least or up to about 20%, at least or up to about 25%, at least or up to about 30%, at least or up to about 35%, at least or up to about 40%, at least or up to about 45%, or at least or up to about 50% of the one or more cell-free nucleic acid molecules comprising the plurality of phased variants can comprise a single nucleotide variant (SNV) that is at least 3 nucleotides away from an adjacent SNV.

[0585] In some embodiments of any one of the methods disclosed herein, at least or up to about 5%, at least or up to about 10%, at least or up to about 15%, at least or up to about 20%, at least or up to about 25%, at least or up to about 30%, at least or up to about 35%, at least or up to about 40%, at least or up to about 45%, or at least or up to about 50% of the one or more cell-free nucleic acid molecules comprising the plurality of phased variants can comprise a

single nucleotide variant (SNV) that is at least 4 nucleotides away from an adjacent SNV.

[0586] In some embodiments of any one of the methods disclosed herein, at least or up to about 5%, at least or up to about 10%, at least or up to about 15%, at least or up to about 20%, at least or up to about 25%, at least or up to about 30%, at least or up to about 35%, at least or up to about 40%, at least or up to about 45%, or at least or up to about 50% of the one or more cell-free nucleic acid molecules comprising the plurality of phased variants can comprise a single nucleotide variant (SNV) that is at least 5 nucleotides away from an adjacent SNV.

[0587] In some embodiments of any one of the methods disclosed herein, at least or up to about 5%, at least or up to about 10%, at least or up to about 15%, at least or up to about 20%, at least or up to about 25%, at least or up to about 30%, at least or up to about 35%, at least or up to about 40%, at least or up to about 45%, or at least or up to about 50% of the one or more cell-free nucleic acid molecules comprising the plurality of phased variants can comprise a single nucleotide variant (SNV) that is at least 6 nucleotides away from an adjacent SNV.

[0588] In some embodiments of any one of the methods disclosed herein, at least or up to about 5%, at least or up to about 10%, at least or up to about 15%, at least or up to about 20%, at least or up to about 25%, at least or up to about 30%, at least or up to about 35%, at least or up to about 40%, at least or up to about 45%, or at least or up to about 50% of the one or more cell-free nucleic acid molecules comprising the plurality of phased variants can comprise a single nucleotide variant (SNV) that is at least 7 nucleotides away from an adjacent SNV.

[0589] In some embodiments of any one of the methods disclosed herein, at least or up to about 5%, at least or up to about 10%, at least or up to about 15%, at least or up to about 20%, at least or up to about 25%, at least or up to about 30%, at least or up to about 35%, at least or up to about 40%, at least or up to about 45%, or at least or up to about 50% of the one or more cell-free nucleic acid molecules comprising the plurality of phased variants can comprise a single nucleotide variant (SNV) that is at least 8 nucleotides away from an adjacent SNV.

[0590] In some embodiments of any one of the methods disclosed herein, at least or up to about 5%, at least or up to about 10%, at least or up to about 15%, at least or up to about 20%, at least or up to about 25%, at least or up to about 30%, at least or up to about 35%, at least or up to about 40%, at least or up to about 45%, or at least or up to about 50% of the one or more cell-free nucleic acid molecules comprising the plurality of phased variants can comprise a single nucleotide variant (SNV) that is at least 9 nucleotides away from an adjacent SNV.

[0591] In some embodiments of any one of the methods disclosed herein, at least or up to about 5%, at least or up to about 10%, at least or up to about 15%, at least or up to about 20%, at least or up to about 25%, at least or up to about 30%, at least or up to about 35%, at least or

up to about 40%, at least or up to about 45%, or at least or up to about 50% of the one or more cell-free nucleic acid molecules comprising the plurality of phased variants can comprise a single nucleotide variant (SNV) that is at least 10 nucleotides away from an adjacent SNV.

C. Reference genomic sequence

[0592] In some embodiments of any one of the methods disclosed herein, the reference genomic sequence can be at least a portion of a nucleic acid sequence database (i.e., a reference genome), which database is assembled from genetic data and intended to represent the genome of a reference cohort. In some cases, a reference cohort can be a collection of individuals from a specific or varying genotype, haplotype, demographics, sex, nationality, age, ethnicity, relatives, physical condition (e.g., healthy or having been diagnosed to have the same or different condition, such as a specific type of cancer), or other groupings. A reference genomic sequence as disclosed herein can be a mosaic (or a consensus sequence) of the genomes of two or more individuals. The reference genomic sequence can comprise at least a portion of a publicly available reference genome or a private reference genome. Non-limiting examples of a human reference genome include hgl9, hg18, hg17, hg16, and hg38.

[0593] In some examples, the reference genomic sequence can comprise at least or up to about 500 nucleobases, at least or up to about 1 kilobase (kb), at least or up to about 2 kb, at least or up to about 3 kb, at least or up to about 4 kb, at least or up to about 5 kb, at least or up to about 6 kb, at least or up to about 7 kb, at least or up to about 8 kb, at least or up to about 9 kb, at least or up to about 10 kb, at least or up to about 20 kb, at least or up to about 30 kb, at least or up to about 40 kb, at least or up to about 50 kb, at least or up to about 60 kb, at least or up to about 70 kb, at least or up to about 80 kb, at least or up to about 90 kb, at least or up to about 100 kb, at least or up to about 200 kb, at least or up to about 300 kb, at least or up to about 400 kb, at least or up to about 500 kb, at least or up to about 600 kb, at least or up to about 700 kb, at least or up to about 800 kb, at least or up to about 900 kb, at least or up to about 1,000 kb, at least or up to about 2,000 kb, at least or up to about 3,000 kb, at least or up to about 4,000 kb, at least or up to about 5,000 kb, at least or up to about 6,000 kb, at least or up to about 7,000 kb, at least or up to about 8,000 kb, at least or up to about 9,000 kb, at least or up to about 10,000 kb, at least or up to about 20,000 kb, at least or up to about 30,000 kb, at least or up to about 40,000 kb, at least or up to about 50,000 kb, at least or up to about 60,000 kb, at least or up to about 70,000 kb, at least or up to about 80,000 kb, at least or up to about 90,000 kb, or at least or up to about 100,000 kb.

[0594] In some cases, the reference genomic sequence can be whole reference genome or a portion (e.g., a portion relevant to the condition of interest) of the genome. For example, the reference genomic sequence can consist of at least 1, 2, 3, 4, 5, or more genes that experience aberrant somatic hypermutation under certain types of cancer. In some cases, the reference genomic sequence can be a whole chromosomal sequence, or a fragment thereof. In some cases, the reference genomic sequence can comprise two or more (e.g., at least 2, 3, 4, 5, or more) different portions of the reference genome that are not adjacent to one another (e.g., within the same chromosome or from different chromosomes).

[0595] In some embodiments of any one of the methods disclosed herein, the reference genomic sequence can be at least a portion of a reference genome of a selected individual, such as a healthy individual or the subject of any of the methods as disclosed herein.

[0596] In some cases, the reference genomic sequence can be derived from an individual who is not the subject (e.g., a healthy control individual). Alternatively, in some cases, the reference genomic sequence can be derived from a sample of the subject. In some examples, the sample can be a healthy sample of the subject. The healthy sample of the subject can be any subject cell that is healthy, e.g., a healthy leukocyte. By comparing sequencing data of the plurality of cell-free nucleic acid molecules (e.g., cfDNA molecules) of the subject against at least a portion of the genomic sequence of a healthy cell of the same subject, one or more cell-free nucleic acid molecules that comprise the plurality of phased variants can be identified and analyzed, as disclosed herein. In some examples, the sample can be a diseased sample of the subject, such as a diseased cell (e.g., a tumor cell) or a solid tumor. The reference genomic sequence can be obtained from sequencing at least a portion of a diseased cell of the subject or from sequencing a plurality of cell-free nucleic acid molecules obtained from the solid tumor of the subject. Once the subject is diagnosed to have a particular condition (e.g., a disease), the reference genomic sequence of the subject that comprises the plurality of phased variants can be used to determine whether the subject still exhibits the same phased variants at future time points. In this context, any new phased variants identified between the "diseased" reference genomic sequence of the subject and new cell-free nucleic acid molecules obtained or derived from the subject can indicate a reduced degree of aberrant somatic hypermutation in particular genomic loci (e.g., at least a partial remission).

[0597] In various embodiments, diagnostic scans can be performed for any neoplasm type, including (but not limited to) acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), anal cancer, astrocytomas, basal cell carcinoma, bile duct cancer, bladder cancer, breast cancer, Burkitt's lymphoma, cervical cancer, chronic lymphocytic leukemia (CLL)

chronic myelogenous leukemia (CML), chronic myeloproliferative neoplasms, colorectal cancer, diffuse large B-cell lymphoma, endometrial cancer, ependymoma, esophageal cancer, esthesioneuroblastoma, Ewing sarcoma, fallopian tube cancer, follicular lymphoma, gallbladder cancer, gastric cancer, gastrointestinal carcinoid tumor, hairy cell leukemia, hepatocellular cancer, Hodgkin lymphoma, hypopharyngeal cancer, Kaposi sarcoma, Kidney cancer, Langerhans cell histiocytosis, laryngeal cancer, leukemia, liver cancer, lung cancer, lymphoma, melanoma, Merkel cell cancer, mesothelioma, mouth cancer, neuroblastoma, non-Hodgkin lymphoma, non-small cell lung cancer, osteosarcoma, ovarian cancer, pancreatic cancer, pancreatic neuroendocrine tumors, pharyngeal cancer, pituitary tumor, prostate cancer, rectal cancer, renal cell cancer, retinoblastoma, skin cancer, small cell lung cancer, small intestine cancer, squamous neck cancer, T-cell lymphoma, testicular cancer, thymoma, thyroid cancer, uterine cancer, vaginal cancer, and vascular tumors.

[0598] In a number of embodiments, a diagnostic scan is utilized to provide an early detection of cancer. In some embodiments, a diagnostic scan detects cancer in individuals having stage I, II, or III cancer. In some embodiments, a diagnostic scan is utilized to detect MRD or tumor burden. In some embodiments, a diagnostic scan is utilized to determine progress (e.g., progression or regression) of treatment. Based on the diagnostic scan, a clinical procedure and/or treatment may be performed.

D. Nucleic acid probes

[0599] In some embodiments of any one of the methods disclosed herein, the set of nucleic acid probes can be designed based on the any of the subject reference genomic sequences of the present disclosure. In some cases, the set of nucleic acid probes can be designed based on the plurality of phased variants that have been identified by comparing (i) sequencing data from a solid tumor of the subject and (ii) sequencing data from a healthy cell of the subject or a healthy cohort, as disclosed herein. The set of nucleic acid probes can be designed based on the plurality of phased variants that have been identified by comparing (i) sequencing data from a solid tumor of the subject and (ii) sequencing data from a healthy cell of the subject. The set of nucleic acid probes can be designed based on the plurality of phased variants that have been identified by comparing (i) sequencing data from a solid tumor of the subject and (ii) sequencing data from a healthy cell of a healthy cohort.

[0600] In some embodiments of any one of the methods disclosed herein, the set of nucleic acid probes are designed to hybridize to sequences of genomic loci associated with the condition. As disclosed herein, the genomic loci associated with the condition can be

determined to experience or exhibit aberrant somatic hypermutation when the subject has the condition. Alternatively, the set of nucleic acid probes are designed to hybridize to sequences of stereotyped regions.

[0601] In some embodiments of any one of the methods disclosed herein, the set of nucleic acid probes can be designed to hybridize to at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 99%, or about 100% of the genomic regions identified in Table 1.

[0602] In some embodiments of any one of the methods disclosed herein, the set of nucleic acid probes can be designed to hybridize to at least a portion of cell-free nucleic acid (e.g., cfDNA) molecules derived from at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 99%, or about 100% of the genomic regions identified in Table 1.

[0603] In some embodiments of any one of the methods disclosed herein, each nucleic acid probe of the set of nucleic acid probes can have at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90% sequence identity, at least about 95% sequence identity, at least about 99%, or about 100% sequence identity to a probe sequence selected from Table 6.

[0604] In some embodiments of any one of the methods disclosed herein, the set of nucleic acid probes can comprise at least about 1%, at least about 2%, at least about 3%, at least about 4%, at least about 5%, at least about 6%, at least about 7%, at least about 8%, at least about 9%, at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 99%, or about 100% of probe sequences in Table 6.

[0605] In some embodiments of any one of the methods disclosed herein, the set of nucleic acid probes can be designed to cover one or more target genomic regions comprising at least or up to about 500 nucleobases, at least or up to about 1 kilobase (kb), at least or up to about 2 kb, at least or up to about 3 kb, at least or up to about 4 kb, at least or up to about 5 kb, at least or up to about 6 kb, at least or up to about 7 kb, at least or up to about 8 kb, at least or up to about 9 kb, at least or up to about 10 kb, at least or up to about 20 kb, at least or up to about 30 kb, at least or up to about 40 kb, at least or up to about 50 kb, at least or up to about 60 kb, at

least or up to about 70 kb, at least or up to about 80 kb, at least or up to about 90 kb, at least or up to about 100 kb, at least or up to about 200 kb, at least or up to about 300 kb, at least or up to about 400 kb, or at least or up to about 500 kb.

[0606] In some embodiments of any one of the methods disclosed herein, a target genomic region (e.g., a target genomic locus) of the one or more target genomic regions can comprise at most about 200 nucleobases, at most about 300 nucleobases, 400 nucleobases, at most about 500 nucleobases, at most about 600 nucleobases, at most about 700 nucleobases, at most about 800 nucleobases, at most about 900 nucleobases, at most about 1 kb, at most about 2 kb, at most about 3 kb, at most about 4 kb, at most about 5 kb, at most about 6 kb, at most about 7 kb, at most about 8 kb, at most about 9 kb, at most about 10 kb, at most about 11 kb, at most about 12 kb, at most about 13 kb, at most about 14 kb, at most about 15 kb, at most about 16 kb, at most about 17 kb, at most about 18 kb, at most about 19 kb, at most about 20 kb, at most about 25 kb, at most about 30 kb, at most about 35 kb, at most about 40 kb, at most about 45 kb, at most about 50 kb, or at most about 100 kb.

[0607] In some embodiments of any one of the methods disclosed herein, the set of nucleic acid probes can comprise at least or up to about 10, at least or up to about 20, at least or up to about 30, at least or up to about 40, at least or up to about 50, at least or up to about 60, at least or up to about 70, at least or up to about 80, at least or up to about 90, at least or up to about 100, at least or up to about 200, at least or up to about 300, at least or up to about 400, at least or up to about 500, at least or up to about 600, at least or up to about 700, at least or up to about 800, at least or up to about 900, at least or up to about 1,000, at least or up to about 2,000, at least or up to about 3,000, at least or up to about 4,000, or at least or up to about 5,000 different nucleic acid probes designed to hybridize to different target nucleic acid sequences.

[0608] In some embodiments of any one of the methods disclosed herein, the set of nucleic acid probes can have a length of at least or up to about 50, at least or up to about 55, at least or up to about 60, at least or up to about 65, at least or up to about 70, at least or up to about 75, at least or up to about 80, at least or up to about 85, at least or up to about 90, at least or up to about 95, or at least or up to about 100 nucleotides.

[0609] In one aspect, the present disclosure provides a composition comprising a bait set comprising any one of the set of nucleic acid probes disclosed herein. The composition comprising such bait set can be used for any of the methods disclosed herein. In some cases, the set of nucleic acid probes can be designed to pull down (or capture) cfDNA molecules. In some cases, the set of nucleic acid probes can be designed to pull down (or capture) cfRNA molecules.

[0610] In some embodiments, the bait set can comprise a set of nucleic acid probes designed to pull down cell-free nucleic acid (e.g., cfDNA) molecules derived from genomic regions set forth in Table 1. The set of nucleic acid probes can be designed to pull down cell-free nucleic acid molecules derived from at least or up to about 1%, at least or up to about 2%, at least or up to about 3%, at least or up to about 4%, at least or up to about 5%, at least or up to about 6%, at least or up to about 7%, at least or up to about 8%, at least or up to about 9%, at least or up to about 10%, at least or up to about 15%, at least or up to about 20%, at least or up to about 25%, at least or up to about 30%, at least or up to about 35%, at least or up to about 40%, at least or up to about 45%, at least or up to about 50%, at least or up to about 55%, at least or up to about 60%, at least or up to about 65%, at least or up to about 70%, at least or up to about 75%, at least or up to about 80%, at least or up to about 85%, at least or up to about 90%, at least or up to about 95%, at least or up to about 99%, or about 100% of the genomic regions set forth in Table 1. In some cases, the set of nucleic acid probes can be designed to pull down cfDNA molecules. In some cases, the set of nucleic acid probes can be designed to pull down cfRNA molecules.

[0611] In some embodiments of any one of the compositions disclosed herein, an individual nucleic acid probe (or each nucleic acid probe) of the set of nucleic acid probes can comprise a pull-down tag. The pull-down tag can be used to enrich a sample (e.g., a sample comprising the plurality of nucleic acid molecules obtained or derived from the subject) for a specific subset (e.g., for cell-free nucleic acid molecules comprising the plurality of phased variants as disclosed herein).

[0612] In some cases, pull-down tag can comprise a nucleic acid barcode (e.g., on either or both sides of the nucleic acid probe). By utilizing beads or substrates comprising nucleic acid sequences having complementarity to the nucleic acid barcode, the nucleic acid barcode can be used to pull-down and enrich for any nucleic acid probe that is hybridized to a target cell-free nucleic acid molecule. Alternatively, or in addition to, the nucleic acid barcode can be used to identify the target cell-free nucleic acid molecule from any sequencing data (e.g., sequencing by amplification) obtained by using any of the set of nucleic acid probes disclosed herein.

[0613] In some cases, the pull-down tag can comprise an affinity target moiety that can be specifically recognized and bound by an affinity binding moiety. The affinity binding moiety specifically can bind the affinity target moiety to form an affinity pair. In some cases, by utilizing beads or substrates comprising the affinity binding moiety, the affinity target moiety can be used to pull-down and enrich for any nucleic acid probe that is hybridized to a target

cell-free nucleic acid molecule. Alternatively, the pull-down tag can comprise the affinity binding moiety, while the beads/substrates can comprise the affinity target moiety. Non-limiting examples of the affinity pair can include biotin/avidin, antibody/antigen, biotin/streptavidin, metal/chelator, ligand/receptor, nucleic acid and binding protein, and complementary nucleic acids. In an example, the pull-down tag can comprise biotin.

[0614] In some embodiments of any one of the compositions disclosed herein, a length of a target cell-free nucleic acid (e.g., cfDNA) molecule that is to be pulled down by any subject nucleic acid probe can be about 100 nucleotides to about 200 nucleotides. The length of the target cell-free nucleic acid molecule can be at least about 100 nucleotides. The length of the target cell-free nucleic acid molecule can be at most about 200 nucleotides. The length of the target cell-free nucleic acid molecule can be about 100 nucleotides to about 110 nucleotides, about 100 nucleotides to about 120 nucleotides, about 100 nucleotides to about 130 nucleotides, about 100 nucleotides to about 140 nucleotides, about 100 nucleotides to about 150 nucleotides, about 100 nucleotides to about 160 nucleotides, about 100 nucleotides to about 170 nucleotides, about 100 nucleotides to about 180 nucleotides, about 100 nucleotides to about 190 nucleotides, about 100 nucleotides to about 200 nucleotides, about 110 nucleotides to about 120 nucleotides, about 110 nucleotides to about 130 nucleotides, about 110 nucleotides to about 140 nucleotides, about 110 nucleotides to about 150 nucleotides, about 110 nucleotides to about 160 nucleotides, about 110 nucleotides to about 170 nucleotides, about 110 nucleotides to about 180 nucleotides, about 110 nucleotides to about 190 nucleotides, about 110 nucleotides to about 200 nucleotides, about 120 nucleotides to about 130 nucleotides, about 120 nucleotides to about 140 nucleotides, about 120 nucleotides to about 150 nucleotides, about 120 nucleotides to about 160 nucleotides, about 120 nucleotides to about 170 nucleotides, about 120 nucleotides to about 180 nucleotides, about 120 nucleotides to about 190 nucleotides, about 120 nucleotides to about 200 nucleotides, about 130 nucleotides to about 140 nucleotides, about 130 nucleotides to about 150 nucleotides, about 130 nucleotides to about 160 nucleotides, about 130 nucleotides to about 170 nucleotides, about 130 nucleotides to about 180 nucleotides, about 130 nucleotides to about 190 nucleotides, about 130 nucleotides to about 200 nucleotides, about 140 nucleotides to about 150 nucleotides, about 140 nucleotides to about 160 nucleotides, about 140 nucleotides to about 170 nucleotides, about 140 nucleotides to about 180 nucleotides, about 140 nucleotides to about 190 nucleotides, about 140 nucleotides to about 200 nucleotides, about 150 nucleotides to about 160 nucleotides, about 150 nucleotides to about 170 nucleotides, about 150 nucleotides to about 180 nucleotides, about 150 nucleotides to about 190 nucleotides, about 150 nucleotides to about 200 nucleotides, about 160 nucleotides to about 170 nucleotides, about 160 nucleotides to about 180 nucleotides,

about 160 nucleotides to about 190 nucleotides, about 160 nucleotides to about 200 nucleotides, about 170 nucleotides to about 180 nucleotides, about 170 nucleotides to about 190 nucleotides, about 170 nucleotides to about 200 nucleotides, about 180 nucleotides to about 190 nucleotides, about 180 nucleotides to about 200 nucleotides, or about 190 nucleotides to about 200 nucleotides. The length of the target cell-free nucleic acid molecule can be about 100 nucleotides, about 110 nucleotides, about 120 nucleotides, about 130 nucleotides, about 140 nucleotides, about 150 nucleotides, about 160 nucleotides, about 170 nucleotides, about 180 nucleotides, about 190 nucleotides, or about 200 nucleotides. In some examples, the length of the target cell-free nucleic acid molecule can range between about 100 nucleotides and about 180 nucleotides.

[0615] In some embodiments of any one of the compositions disclosed herein, the genomic regions can be associated with a condition. The genomic regions can be determined to exhibit aberrant somatic hypermutation when a subject has the condition. For example, the condition can comprise B-cell lymphoma or a sub-type thereof, such as diffuse large B-cell lymphoma, follicular lymphoma, Burkitt lymphoma, and B-cell chronic lymphocytic leukemia. Additional details of the condition are provided below.

[0616] In some embodiments of any one of the compositions disclosed herein, the composition further comprises the plurality of cell-free nucleic acid (e.g., cfDNA) molecules obtained or derived from the subject.

E. Diagnostic or therapeutic applications

[0617] A number of embodiments are directed towards performing a diagnostic scan on cell-free nucleic acids of an individual and then based on results of the scan indicating cancer, performing further clinical procedures and/or treating the individual. In accordance with various embodiments, numerous types of neoplasms can be detected.

[0618] In some embodiments of any one of the methods disclosed herein, the method can comprise determining that the subject has the condition or determining a degree or status of the condition of the subject, based on the one or more cell-free nucleic acid molecules comprising the plurality of phased variants. In some cases, the method can further comprise determining that the one or more cell-free nucleic acid molecules (each identified to comprise a plurality of phased variants) are derived from a sample associated with the condition (e.g., cancer), based on a statistical model analysis (i.e., molecular analysis). For example, the method can comprise using one or more algorithms (e.g., Monte Carlos simulation) to determine a first probability of a cell-free nucleic acid identified to have a plurality of phased variants being associated with

or originated from a first condition (e.g., 80%) and a second probability of the same cell-free nucleic acid being associated with or originated from a second condition (or from a healthy cell) (e.g., 20%). In some cases, the method can comprise determining a likelihood or probability that the subject has one or more conditions based on analysis of the one or more cell-free nucleic acid molecules each identified to comprise a plurality of phased variants (i.e., macro- or global analysis). For example, the method can comprise using one or more algorithms (e.g., comprising one or more mathematical models as disclosed herein, such as binomial sampling) to analyze a plurality of cell-free nucleic acid molecules each identified to comprise a plurality of phased variants, thereby to determine a first probability of the subject having a first condition (e.g., 80%) and a second probability of the subject having a second condition (or being healthy) (e.g., 20%).

[0619] The statistical model analysis as disclosed herein can be an approximate solution by a numerical approximation such as a binomial model, a ternary model, a Monte Carlo simulation, or a finite difference method. In an example, the statistical model analysis as used herein can be a Monte Carlo statistical analysis. In another example, the statistical model analysis as used herein can be a binomial or ternary model analysis.

[0620] In some embodiments of any one of the methods disclosed herein, the method can comprise monitoring a progress of the condition of the subject based on the one or more cell-free nucleic acid molecules identified, such that each of the identified cell-free nucleic acid molecule comprises a plurality of phased variants. In some cases, the progress of the condition can be worsening of the condition, as described in the present disclosure (e.g., developing from stage I cancer to stage III cancer). In some cases, the progress of the condition can be at least a partial remission of the condition, as described in the present disclosure (e.g., downstaging from stage IV cancer to stage II cancer). Alternatively, in some cases, the progress of the condition can remain substantially the same between two different time points, as described in the present disclosure. In an example, the method can comprise determining likelihoods or probabilities of different progresses of the condition of the subject. For example, the method can comprise using one or more algorithms (e.g., comprising one or more mathematical models as disclosed herein, such as binomial sampling) to determine a first probability of the subject's condition being worse than before (e.g., 20%), a second probability of at least partial remission of the condition (e.g., 70%), and a third probability that the subject's condition is the same as before (e.g., 10%).

[0621] In some embodiments of any one of the methods disclosed herein, the method can comprise comprising performing a different procedure (e.g., follow-up diagnostic procedures) to confirm the condition of the subject, which condition has been determined and/or monitored progress thereof, as provided in the present disclosure. Non-limiting examples of a different procedure can include physical exam, medical imaging, genetic test, mammography, endoscopy, stool sampling, pap test, alpha-fetoprotein blood test, CA-125 test, prostate-specific antigen (PSA) test, biopsy extraction, bone marrow aspiration, and tumor marker detection tests. Medical imaging includes (but is not limited to) X-ray, magnetic resonance imaging (MRI), computed tomography (CT), ultrasound, and positron emission tomography (PET). Endoscopy includes (but is not limited to) bronchoscopy, colonoscopy, colposcopy, cystoscopy, esophagoscopy, gastroscopy, laparoscopy, neuroendoscopy, proctoscopy, and sigmoidoscopy.

[0622] In some embodiments of any one of the methods disclosed herein, the method can comprise determining a treatment for the condition of the subject based on the one or more cell-free nucleic acid molecules identified, each identified cell-free nucleic acid molecule comprising a plurality of phased variants. In some cases, the treatment can be determined based on (i) the determined condition of the subject and/or (ii) the determined progress of the condition of the subject. In addition, the treatment can be determined based on one or more additional factors of the following: sex, nationality, age, ethnicity, and other physical conditions of the subject. In some examples, the treatment can be determined based on one or more features of the plurality of phased variants of the identified cell-free nucleic acid molecules, as disclosed herein.

[0623] In some embodiments of any one of the methods disclosed herein, the subject may not have been subjected to any treatment for the condition, e.g., the subject may not have been diagnosed with the condition (e.g., a lymphoma). In some embodiments of any one of the methods disclosed herein, the subject may been subjected to a treatment for the condition prior to any subject method of the present disclosure. In some cases, the methods disclosed herein can be performed to monitor progress of the condition that the subject has been diagnosed with, thereby to (i) determine efficacy of the previous treatment and (ii) assess whether to keep the treatment, modify the treatment, or cancel the treatment in favor of a new treatment.

[0624] In some embodiments of any one of the methods disclosed herein, non-limiting examples of a treatment (e.g., prior treatment, new treatment to be determined based on the methods of the present disclosure, etc.) can include chemotherapy, radiotherapy, chemoradiotherapy, immunotherapy, adoptive cell therapy (e.g., chimeric antigen receptor

(CAR) T cell therapy, CAR NK cell therapy, modified T cell receptor (TCR) T cell therapy, etc.) hormone therapy, targeted drug therapy, surgery, transplant, transfusion, or medical surveillance.

[0625] In some embodiments of any one of the methods disclosed herein, the condition can comprise a disease. In some embodiments of any one of the methods disclosed herein, the condition can comprise neoplasm, cancer, or tumor. In an example, the condition can comprise a solid tumor. In another example, the condition can comprise a lymphoma, such as B-cell lymphoma (BCL). Non-limiting examples of BCL can include diffuse large B-cell lymphoma (DLBCL), follicular lymphoma (FL), Burkitt lymphoma (BL), B-cell chronic lymphocytic leukemia (CLL), Marginal zone B-cell lymphoma (MZL), and Mantle cell lymphoma (MCL).

[0626] As disclosed herein, a treatment for a condition of subject can comprise administering the subject with one or more therapeutic agents. The one or more therapeutic drugs can be administered to the subject by one or more of the following: orally, intraperitoneally, intravenously, intraarterially, transdermally, intramuscularly, liposomally, via local delivery by catheter or stent, subcutaneously, intraadiposally, and intrathecally.

[0627] Non-limiting examples of the therapeutic drugs can include cytotoxic agents, chemotherapeutic agents, growth inhibitory agents, agents used in radiation therapy, anti-angiogenesis agents, apoptotic agents, anti-tubulin agents, and other agents to treat cancer, for example, anti-CD20 antibodies, anti-PD1 antibodies (e.g., Pembrolizumab) platelet derived growth factor inhibitors (e.g., GLEEVEC™ (imatinib mesylate)), a COX-2 inhibitor (e.g., celecoxib), interferons, cytokines, antagonists (e.g., neutralizing antibodies) that bind to one or more of the following targets PDGFR-β, BlyS, APRIL, BCMA receptor(s), TRAIL/Apo2, other bioactive and organic chemical agents, and the like.

[0628] Non-limiting examples of a cytotoxic agent can include radioactive isotopes (e.g., At211, I131, I125, Y90, Re186, Re188, Sm153, Bi212, P32, and radioactive isotopes of Lu), chemotherapeutic agents, e.g., methotrexate, adriamycin, vinca alkaloids (vincristine, vinblastine, etoposide), doxorubicin, melphalan, mitomycin C, chlorambucil, daunorubicin or other intercalating agents, enzymes and fragments thereof such as nucleolytic enzymes, antibiotics, and toxins such as small molecule toxins or enzymatically active toxins of bacterial, fungal, plant or animal origin.

[0629] Non-limiting examples of a chemotherapeutic agent can include alkylating agents such as thiotepa and CYTOXAN® cyclophosphamide; alkyl sulfonates such as busulfan, improsulfan and piposulfan; aziridines such as benzodopa, carboquone, meturedopa, and uredopa; ethylenimines and methylamelamines including altretamine, triethylenemelamine,

triethylenephosphoramide, triethiylenethiophosphoramide and trimethylolmelamine; acetogenins (especially bullatacin and bullatacinone); delta-9-tetrahydrocannabinol (dronabinol, MARINOL®); beta-lapachone; lapachol; colchicines; betulinic acid; a camptothecin (including the synthetic analogue topotecan (HYCAMTIN®), CPT-11 (irinotecan, CAMPTOSAR®), acetylcamptothecin, scopolectin, and 9-aminocamptothecin); bryostatin; callystatin; CC-1065 (including its adozelesin, carzelesin and bizelesin synthetic analogues); podophyllotoxin; podophyllinic acid; teniposide; cryptophycins (particularly cryptophycin 1 and cryptophycin 8); dolastatin; duocarmycin (including the synthetic analogues, KW-2189 and CB1-TM1); eleutherobin; pancratistatin; a sarcodictyin; spongistatin; nitrogen mustards such as chlorambucil, chlornaphazine, cyclophosphamide, estramustine, ifosfamide, mechlorethamine, mechlorethamine oxide hydrochloride, melphalan, novembichin, phenesterine, prednimustine, trofosfamide, uracil mustard; nitrosoureas such as carmustine, chlorozotocin, fotemustine, lomustine, nimustine, and ranimnustine; antibiotics such as the enediyne antibiotics; dynemicin, including dynemicin A; an espiramicina; as well as neocarzinostatin chromophore and related chromoprotein enediyne antibiotic chromophores), aclacinomycins, actinomycin, anthramycin, azaserine, bleomycins, cactinomycin, carabicin, carminomycin, carzinophilin, chromomycinis, dactinomycin, daunorubicin, detorubicin, 6-diazo-5-oxo-L-norleucine, ADRIAMYCIN® doxorubicin (including morpholino-doxorubicin, cyanomorpholino-doxorubicin, 2-pyrrolino-doxorubicin and deoxydoxorubicin), epirubicin, esorubicin, idarubicin, marcellomycin, mitomycins such as mitomycin C, mycophenolic acid, nogalamycin, olivomycins, peplomycin, potfiromycin, puromycin, quelamycin, rodorubicin, streptonigrin, streptozocin, tubercidin, ubenimex, zinostatin, zorubicin; anti-metabolites such as methotrexate and 5-fluorouracil (5-FU); folic acid analogues such as denopterin, methotrexate, pteropterin, trimetrexate; purine analogs such as fludarabine, 6-mercaptopurine, thiamiprine, thioguanine; pyrimidine analogs such as ancitabine, azacitidine, 6-azauridine, carmofur, cytarabine, dideoxyuridine, doxifluridine, enocitabine, floxuridine; androgens such as calusterone, dromostanolone propionate, epitiostanol, mepitiostane, testolactone; anti-adrenals such as aminoglutethimide, mitotane, trilostane; folic acid replenisher such as folinic acid; aceglatone; aldophosphamide glycoside; aminolevulinic acid; eniluracil; amsacrine; bestrabucil; bisantrene; edatraxate; defofamine; demecolcine; diaziquone; eflornithine; elliptinium acetate; an epothilone; etoglucid; gallium nitrate; hydroxyurea; lentinan; lonidainine; maytansinoids such as maytansine and ansamitocins; mitoguazone; mitoxantrone; mopidanmol; nitraerine; pentostatin; phenamet; pirarubicin; losoxantrone; 2-ethylhydrazide; procarbazine; PSK® polysaccharide complex

(JHS Natural Products, Eugene, Oreg.); razoxane; rhizoxin; sizofiran; spirogermanium; tenuazonic acid; triaziquone; 2,2′,2″-trichlorotriethylamine; trichothecenes (especially T-2 toxin, verrucarin A, roridin A and anguidine); urethan; vindesine (ELDISINE®, FILDESIN®); dacarbazine; mannomustine; mitobronitol; mitolactol; pipobroman; gacytosine; arabinoside ("Ara-C"); thiotepa; taxoids, for example taxanes including TAXOL® paclitaxel (Bristol-Myers Squibb Oncology, Princeton, N.J.), ABRAXANE™ Cremophor-free, albumin-engineered nanoparticle formulation of paclitaxel (American Pharmaceutical Partners, Schaumberg, Ill.), and TAXOTERE® docetaxel (Rhône-Poulenc Rorer, Antony, France); chlorambucil; gemcitabine (GEMZAR®); 6-thioguanine; mercaptopurine; methotrexate; platinum analogs such as cisplatin and carboplatin; vinblastine (VELBAN®); platinum; etoposide (VP-16); ifosfamide; mitoxantrone; vincristine (ONCOVIN®); oxaliplatin; leucovovin; vinorelbine (NAVELBINE®); novantrone; edatrexate; daunomycin; aminopterin; ibandronate; topoisomerase inhibitor RFS 2000; difluoromethylornithine (DMFO); retinoids such as retinoic acid; capecitabine (XELODA®); pharmaceutically acceptable salts, acids or derivatives of any of the above; as well as combinations of two or more of the above such as CHOP, an abbreviation for a combined therapy of cyclophosphamide, doxorubicin, vincristine, and prednisolone, and FOLFOX, an abbreviation for a treatment regimen with oxaliplatin (ELOXATIN™) combined with 5-FU and leucovorin.

[0630] Examples of a chemotherapeutic agent can also include "anti-hormonal agents" or "endocrine therapeutics" that act to regulate, reduce, block, or inhibit the effects of hormones that can promote the growth of cancer, and are often in the form of systemic, or whole-body treatment. They may be hormones themselves. Examples include anti-estrogens and selective estrogen receptor modulators (SERMs), including, for example, tamoxifen (including NOLVADEX® tamoxifen), EVISTA® raloxifene, droloxifene, 4-hydroxytamoxifen, trioxifene, keoxifene, LY117018, onapristone, and FARESTON® toremifene; anti-progesterones; estrogen receptor down-regulators (ERDs); agents that function to suppress or shut down the ovaries, for example, leutinizing hormone-releasing hormone (LHRH) agonists such as LUPRON® and ELIGARD) leuprolide acetate, goserelin acetate, buserelin acetate and tripterelin; other anti-androgens such as flutamide, nilutamide and bicalutamide; and aromatase inhibitors that inhibit the enzyme aromatase, which regulates estrogen production in the adrenal glands, such as, for example, 4(5)-imidazoles, aminoglutethimide, MEGASE® megestrol acetate, AROMASIN® exemestane, formestanie, fadrozole, RIVISOR® vorozole, FEMARA® letrozole, and ARIMIDEX® anastrozole. In addition, such definition of chemotherapeutic agents includes bisphosphonates such as clodronate (for example,

BONEFOS® or OSTAC®), DIDROCAL® etidronate, NE-58095, ZOMETA® zoledronic acid/zoledronate, FOSAMAX® alendronate, AREDIA® pamidronate, SKELID® tiludronate, or ACTONEL® risedronate; as well as troxacitabine (a 1,3-dioxolane nucleoside cytosine analog); antisense oligonucleotides, particularly those that inhibit expression of genes in signaling pathways implicated in abherant cell proliferation, such as, for example, PKC-alpha, Raf, H-Ras, and epidermal growth factor receptor (EGFR); vaccines such as THERATOPE® vaccine and gene therapy vaccines, for example, ALLOVECTIN® vaccine, LEUVECTIN® vaccine, and VAXID® vaccine; LURTOTECAN® topoisomerase 1 inhibitor; ABARELIX® rmRH; lapatinib ditosylate (an ErbB-2 and EGFR dual tyrosine kinase small-molecule inhibitor also known as GW572016); and pharmaceutically acceptable salts, acids or derivatives of any of the above.

[0631] Examples of a chemotherapeutic agent can also include antibodies such as alemtuzumab (Campath), bevacizumab (AVASTIN®, Genentech); cetuximab (ERBITUX®, Imclone); panitumumab (VECTIBIX®, Amgen), rituximab (RITUXAN®, Genentech/Biogen Idec), pertuzumab (OMNITARG®, 2C4, Genentech), trastuzumab (HERCEPTIN®, Genentech), tositumomab (Bexxar, Corixia), and the antibody drug conjugate, gemtuzumab ozogamicin (MYLOTARG®, Wyeth). Additional humanized monoclonal antibodies with therapeutic potential as agents in combination with the compounds of the invention include: apolizumab, aselizumab, atlizumab, bapineuzumab, bivatuzumab mertansine, cantuzumab mertansine, cedelizumab, certolizumab pegol, cidfusituzumab, cidtuzumab, daclizumab, eculizumab, efalizumab, epratuzumab, erlizumab, feMzumab, fontolizumab, gemtuzumab ozogamicin, inotuzumab ozogamicin, ipilimumab, labetuzumab, lintuzumab, matuzumab, mepolizumab, motavizumab, motovizumab, natalizumab, nimotuzumab, nolovizumab, numavizumab, ocrelizumab, omalizumab, palivizumab, pascolizumab, pecfusituzumab, pectuzumab, pexelizumab, ralivizumab, ranibizumab, reslivizumab, reslizumab, resyvizumab, rovelizumab, ruplizumab, sibrotuzumab, siplizumab, sontuzumab, tacatuzumab tetraxetan, tadocizumab, talizumab, tefibazumab, tocilizumab, toralizumab, tucotuzumab celmoleukin, tucusituzumab, umavizumab, urtoxazumab, ustekinumab, visilizumab, and the anti-interleukin-12 (ABT-874/J695, Wyeth Research and Abbott Laboratories) which is a recombinant exclusively human-sequence, full-length IgG1λ antibody genetically modified to recognize interleukin-12 p40 protein.

[0632] Examples of a chemotherapeutic agent can also include "tyrosine kinase inhibitors" such as an EGFR-targeting agent (e.g., small molecule, antibody, etc.); small molecule HER2 tyrosine kinase inhibitor such as TAK165 available from Takeda; CP-724,714, an oral selective

inhibitor of the ErbB2 receptor tyrosine kinase (Pfizer and OSI); dual-HER inhibitors such as EKB-569 (available from Wyeth) which preferentially binds EGFR but inhibits both HER2 and EGFR-overexpressing cells; lapatinib (GSK572016; available from Glaxo-SmithKline), an oral HER2 and EGFR tyrosine kinase inhibitor; PKI-166 (available from Novartis); pan-HER inhibitors such as canertinib (CI-1033; Pharmacia); Raf-1 inhibitors such as antisense agent ISIS-5132 available from ISIS Pharmaceuticals which inhibit Raf-1 signaling; non-HER targeted TK inhibitors such as imatinib mesylate (GLEEVEC®, available from Glaxo SmithKline); multi-targeted tyrosine kinase inhibitors such as sunitinib (SUTENT®, available from Pfizer); VEGF receptor tyrosine kinase inhibitors such as vatalanib (PTK787/ZK222584, available from Novartis/Schering AG); MAPK extracellular regulated kinase I inhibitor CI-1040 (available from Pharmacia); quinazolines, such as PD 153035,4-(3-chloroanilino) quinazoline; pyridopyrimidines; pyrimidopyrimidines; pyrrolopyrimidines, such as CGP 59326, CGP 60261 and CGP 62706; pyrazolopyrimidines, 4-(phenylamino)-7H-pyrrolo[2,3-d] pyrimidines; curcumin (diferuloyl methane, 4,5-bis (4-fluoroanilino)phthalimide); tyrphostines containing nitrothiophene moieties; PD-0183805 (Warner-Lamber); antisense molecules (e.g., those that bind to HER-encoding nucleic acid); quinoxalines (U.S. Pat. No. 5,804,396); tryphostins (U.S. Pat. No. 5,804,396); ZD6474 (Astra Zeneca); PTK-787 (Novartis/Schering AG); pan-HER inhibitors such as CI-1033 (Pfizer); Affinitac (ISIS 3521; Isis/Lilly); imatinib mesylate (GLEEVEC®); PKI 166 (Novartis); GW2016 (Glaxo SmithKline); CI-1033 (Pfizer); EKB-569 (Wyeth); Semaxinib (Pfizer); ZD6474 (AstraZeneca); PTK-787 (Novartis/Schering AG); INC-1C11 (Imclone); and rapamycin (sirolimus, RAPAMUNE®).

[0633] Examples of a chemotherapeutic agent can also include dexamethasone, interferons, colchicine, metoprine, cyclosporine, amphotericin, metronidazole, alemtuzumab, alitretinoin, allopurinol, amifostine, arsenic trioxide, asparaginase, BCG live, bevacuzimab, bexarotene, cladribine, clofarabine, darbepoetin alfa, denileukin, dexrazoxane, epoetin alfa, elotinib, filgrastim, histrelin acetate, ibritumomab, interferon alfa-2a, interferon alfa-2b, lenalidomide, levamisole, mesna, methoxsalen, nandrolone, nelarabine, nofetumomab, oprelvekin, palifermin, pamidronate, pegademase, pegaspargase, pegfilgrastim, pemetrexed disodium, plicamycin, porfimer sodium, quinacrine, rasburicase, sargramostim, temozolomide, VM-26, 6-TG, toremifene, tretinoin, ATRA, valrubicin, zoledronate, and zoledronic acid, and pharmaceutically acceptable salts thereof.

[0634] Examples of a chemotherapeutic agent can also include hydrocortisone, hydrocortisone acetate, cortisone acetate, tixocortol pivalate, triamcinolone acetonide,

triamcinolone alcohol, mometasone, amcinonide, budesonide, desonide, fluocinonide, fluocinolone acetonide, betamethasone, betamethasone sodium phosphate, dexamethasone, dexamethasone sodium phosphate, fluocortolone, hydrocortisone-17-butyrate, hydrocortisone-17-valerate, aclometasone dipropionate, betamethasone valerate, betamethasone dipropionate, prednicarbate, clobetasone-17-butyrate, clobetasol-17-propionate, fluocortolone caproate, fluocortolone pivalate and fluprednidene acetate: immune selective anti-inflammatory peptides (ImSAIDs) such as phenylalanine-glutamine-glycine (FEG) and its D-isomeric form (feG) (IMULAN BioTherapeutics, LLC); anti-rheumatic drugs such as azathioprine, ciclosporin (cyclosporine A), D-penicillamine, gold salts, hydroxychloroquine, leflunomideminocycline, sulfasalazine, tumor necrosis factor alpha (TNFα) blockers such as etanercept (ENBREL®), infliximab (REMICADE®), adalimumab (HUMIRA®), certolizumab pegol (CIMZIA®), golimumab (SIMPONI®), Interleukin 1 (IL-1) blockers such as anakinra (KINERET®), T-cell costimulation blockers such as abatacept (ORENCIA®), Interleukin 6 (IL-6) blockers such as tocilizumab (ACTEMERA®); Interleukin 13 (IL-13) blockers such as lebrikizumab; Interferon alpha (IFN) blockers such as rontalizumab; beta 7 integrin blockers such as rhuMAb Beta7; IgE pathway blockers such as Anti-M1 prime; Secreted homotrimeric LTa3 and membrane bound heterotrimer LTa/β2 blockers such as Anti-lymphotoxin alpha (LTa); miscellaneous investigational agents such as thioplatin, PS-341, phenylbutyrate, ET-18-OCH3, or famesyl transferase inhibitors (L-739749, L-744832); polyphenols such as quercetin, resveratrol, piceatannol, epigallocatechine gallate, theaflavins, flavanols, procyanidins, betulinic acid and derivatives thereof; autophagy inhibitors such as chloroquine; delta-9-tetrahydrocannabinol (dronabinol, MARINOL®); beta-lapachone; lapachol; colchicines; betulinic acid; acetylcamptothecin, scopolectin, and 9-aminocamptothecin); podophyllotoxin; tegafur (UFTORAL®); bexarotene (TARGRETIN®); bisphosphonates such as clodronate (for example, BONEFOS® or OSTAC®), etidronate (DIDROCAL®), NE-58095, zoledronic acid/zoledronate (ZOMETA®), alendronate (FOSAMAX®), pamidronate (AREDIA®), tiludronate (SKELID®), or risedronate (ACTONEL®); and epidermal growth factor receptor (EGF-R); vaccines such as THERATOPE® vaccine; perifosine, COX-2 inhibitor (e.g., celecoxib or etoricoxib), proteosome inhibitor (e.g., PS341); CCI-779; tipifamib (R11577); orafenib, ABT510; Bcl-2 inhibitor such as oblimersen sodium (GENASENSE®); pixantrone; famesyltransferase inhibitors such as lonafamib (SCH 6636, SARASAR™); and pharmaceutically acceptable salts, acids or derivatives of any of the above; as well as combinations of two or more of the above.

[0635] In accordance with many embodiments, once a diagnosis of cancer is indicated, a number of treatments can be performed, including (but not limited to) surgery, resection, chemotherapy, radiation therapy, immunotherapy, targeted therapy, hormone therapy, stem cell transplant, and blood transfusion. In some embodiments, an anti-cancer and/or chemotherapeutic agent is administered, including (but not limited to) alkylating agents, platinum agents, taxanes, vinca agents, anti-estrogen drugs, aromatase inhibitors, ovarian suppression agents, endocrine/hormonal agents, bisphophonate therapy agents and targeted biological therapy agents. Medications include (but are not limited to) cyclophosphamide, fluorouracil (or 5-fluorouracil or 5-FU), methotrexate, thiotepa, carboplatin, cisplatin, taxanes, paclitaxel, protein-bound paclitaxel, docetaxel, vinorelbine, tamoxifen, raloxifene, toremifene, fulvestrant, gemcitabine, irinotecan, ixabepilone, temozolomide, topotecan, vincristine, vinblastine, eribulin, mutamycin, capecitabine, capecitabine, anastrozole, exemestane, letrozole, leuprolide, abarelix, buserelin, goserelin, megestrol acetate, risedronate, pamidronate, ibandronate, alendronate, zoledronate, tykerb, daunorubicin, doxorubicin, epirubicin, idarubicin, valrubicin mitoxantrone, bevacizumab, cetuximab, ipilimumab, ado-trastuzumab emtansine, afatinib, aldesleukin, alectinib, alemtuzumab, atezolizumab, avelumab, axtinib, belimumab, belinostat, bevacizumab, blinatumomab, bortezomib, bosutinib, brentuximab vedotin, brigatinib, cabozantinib, canakinumab, carfilzomib, certinib, cetuximab, cobimetinib, crizotinib, dabrafenib, daratumumab, dasatinib, denosumab, dinutuximab, durvalumab, elotuzumab, enasidenib, erlotinib, everolimus, gefitinib, ibritumomab tiuxetan, ibrutinib, idelalisib, imatinib, ipilimumab, ixazomib, lapatinib, lenvatinib, midostaurin, necitumumab, neratinib, nilotinib, niraparib, nivolumab, obinutuzumab, ofatumumab, olaparib, olaratumab, osimertinib, palbociclib, panitumumab, panobinostat, pembrolizumab, pertuzumab, ponatinib, ramucirumab, regorafenib, ribociclib, rituximab, romidepsin, rucaparib, ruxolitinib, siltuximab, sipuleucel-T, sonidegib, sorafenib, temsi rolimus, tocilizumab, tofacitinib, tositumomab, trametinib, trastuzumab, vandetanib, vemurafenib, venetoclax, vismodegib, vorinostat, and ziv-aflibercept. In accordance with various embodiments, an individual may be treated, by a single medication or a combination of medications described herein. A common treatment combination is cyclophosphamide, methotrexate, and 5-fluorouracil (CMF).

[0636] In some embodiments of any one of the methods disclosed herein, any of the cell-free nucleic acid molecules (e.g., cfDNA, cfRNA) can be derived from a cell. For example, a cell sample or tissue sample may be obtained from a subject and processed to remove all cells from the sample, thereby producing cell-free nucleic acid molecules derived from the sample.

[0637] In some embodiments of any one of the methods disclosed herein, a reference genomic sequence can be derived from a cell of an individual. The individual can be a healthy control or the subject who is being subjected to the methods disclosed herein for determining or monitoring progress of a condition.

[0638] A cell can be a healthy cell. Alternatively, a cell can be a diseased cell. A diseased cell can have altered metabolic, gene expression, and/or morphologic features. A diseased cell can be a cancer cell, a diabetic cell, and an apoptotic cell. A diseased cell can be a cell from a diseased subject. Exemplary diseases can include blood disorders, cancers, metabolic disorders, eye disorders, organ disorders, musculoskeletal disorders, cardiac disease, and the like.

[0639] A cell can be a mammalian cell or derived from a mammalian cell. A cell can be a rodent cell or derived from a rodent cell. A cell can be a human cell or derived from a human cell. A cell can be a prokaryotic cell or derived from a prokaryotic cell. A cell can be a bacterial cell or can be derived from a bacterial cell. A cell can be an archaeal cell or derived from an archaeal cell. A cell can be a eukaryotic cell or derived from a eukaryotic cell. A cell can be a pluripotent stem cell. A cell can be a plant cell or derived from a plant cell. A cell can be an animal cell or derived from an animal cell. A cell can be an invertebrate cell or derived from an invertebrate cell. A cell can be a vertebrate cell or derived from a vertebrate cell. A cell can be a microbe cell or derived from a microbe cell. A cell can be a fungi cell or derived from a fungi cell. A cell can be from a specific organ or tissue.

[0640] Non-limiting examples of a cell(s) can include lymphoid cells, such as B cell, T cell (Cytotoxic T cell, Natural Killer T cell, Regulatory T cell, T helper cell), Natural killer cell, cytokine induced killer (CIK) cells; myeloid cells, such as granulocytes (Basophil granulocyte, Eosinophil granulocyte, Neutrophil granulocyte/Hypersegmented neutrophil), Monocyte/Macrophage, Red blood cell (Reticulocyte), Mast cell, Thrombocyte/Megakaryocyte, Dendritic cell; cells from the endocrine system, including thyroid (Thyroid epithelial cell, Parafollicular cell), parathyroid (Parathyroid chief cell, Oxyphil cell), adrenal (Chromaffin cell), pineal (Pinealocyte) cells; cells of the nervous system, including glial cells (Astrocyte, Microglia), Magnocellular neurosecretory cell, Stellate cell, Boettcher cell, and pituitary (Gonadotrope, Corticotrope, Thyrotrope, Somatotrope, Lactotroph); cells of the Respiratory system, including Pneumocyte (Type I pneumocyte, Type II pneumocyte), Clara cell, Goblet cell, Dust cell; cells of the circulatory system, including Myocardiocyte, Pericyte; cells of the digestive system, including stomach (Gastric chief cell, Parietal cell), Goblet cell, Paneth cell, G cells, D cells, ECL cells, I cells, K cells, S cells;

enteroendocrine cells, including enterochromaffm cell, APUD cell, liver (Hepatocyte, Kupffer cell), Cartilage/bone/muscle; bone cells, including Osteoblast, Osteocyte, Osteoclast, teeth (Cementoblast, Ameloblast); cartilage cells, including Chondroblast, Chondrocyte; skin cells, including Trichocyte, Keratinocyte, Melanocyte (Nevus cell); muscle cells, including Myocyte; urinary system cells, including Podocyte, Juxtaglomerular cell, Intraglomerular mesangial cell/Extraglomerular mesangial cell, Kidney proximal tubule brush border cell, Macula densa cell; reproductive system cells, including Spermatozoon, Sertoli cell, Leydig cell, Ovum; and other cells, including Adipocyte, Fibroblast, Tendon cell, Epidermal keratinocyte (differentiating epidermal cell), Epidermal basal cell (stem cell), Keratinocyte of fingernails and toenails, Nail bed basal cell (stem cell), Medullary hair shaft cell, Cortical hair shaft cell, Cuticular hair shaft cell, Cuticular hair root sheath cell, Hair root sheath cell of Huxley's layer, Hair root sheath cell of Henle's layer, External hair root sheath cell, Hair matrix cell (stem cell), Wet stratified barrier epithelial cells, Surface epithelial cell of stratified squamous epithelium of cornea, tongue, oral cavity, esophagus, anal canal, distal urethra and vagina, basal cell (stem cell) of epithelia of cornea, tongue, oral cavity, esophagus, anal canal, distal urethra and vagina, Urinary epithelium cell (lining urinary bladder and urinary ducts), Exocrine secretory epithelial cells, Salivary gland mucous cell (polysaccharide-rich secretion), Salivary gland serous cell (glycoprotein enzyme-rich secretion), Von Ebner's gland cell in tongue (washes taste buds), Mammary gland cell (milk secretion), Lacrimal gland cell (tear secretion), Ceruminous gland cell in ear (wax secretion), Eccrine sweat gland dark cell (glycoprotein secretion), Eccrine sweat gland clear cell (small molecule secretion). Apocrine sweat gland cell (odoriferous secretion, sex-hormone sensitive), Gland of Moll cell in eyelid (specialized sweat gland), Sebaceous gland cell (lipid-rich sebum secretion), Bowman's gland cell in nose (washes olfactory epithelium), Brunner's gland cell in duodenum (enzymes and alkaline mucus), Seminal vesicle cell (secretes seminal fluid components, including fructose for swimming sperm), Prostate gland cell (secretes seminal fluid components), Bulbourethral gland cell (mucus secretion), Bartholin's gland cell (vaginal lubricant secretion), Gland of Littre cell (mucus secretion), Uterus endometrium cell (carbohydrate secretion), Isolated goblet cell of respiratory and digestive tracts (mucus secretion), Stomach lining mucous cell (mucus secretion), Gastric gland zymogenic cell (pepsinogen secretion), Gastric gland oxyntic cell (hydrochloric acid secretion), Pancreatic acinar cell (bicarbonate and digestive enzyme secretion), Paneth cell of small intestine (lysozyme secretion), Type II pneumocyte of lung (surfactant secretion), Clara cell of lung, Hormone secreting cells, Anterior pituitary cells, Somatotropes, Lactotropes, Thyrotropes, Gonadotropes, Corticotropes, Intermediate pituitary

cell, Magnocellular neurosecretory cells, Gut and respiratory tract cells, Thyroid gland cells, thyroid epithelial cell, parafollicular cell, Parathyroid gland cells, Parathyroid chief cell, Oxyphil cell, Adrenal gland cells, chromaffin cells, Ley dig cell of testes, Theca interna cell of ovarian follicle, Corpus luteum cell of ruptured ovarian follicle, Granulosa lutein cells, Theca lutein cells, Juxtaglomerular cell (renin secretion), Macula densa cell of kidney, Metabolism and storage cells, Barrier function cells (Lung, Gut, Exocrine Glands and Urogenital Tract), Kidney, Type I pneumocyte (lining air space of lung), Pancreatic duct cell (centroacinar cell), Nonstriated duct cell (of sweat gland, salivary gland, mammary gland, etc.), Duct cell (of seminal vesicle, prostate gland, etc.), Epithelial cells lining closed internal body cavities, Ciliated cells with propulsive function, Extracellular matrix secretion cells, Contractile cells; Skeletal muscle cells, stem cell, Heart muscle cells, Blood and immune system cells, Erythrocyte (red blood cell), Megakaryocyte (platelet precursor), Monocyte, Connective tissue macrophage (various types), Epidermal Langerhans cell, Osteoclast (in bone), Dendritic cell (in lymphoid tissues), Microglial cell (in central nervous system), Neutrophil granulocyte, Eosinophil granulocyte, Basophil granulocyte, Mast cell, Helper T cell, Suppressor T cell, Cytotoxic T cell, Natural Killer T cell, B cell, Natural killer cell, Reticulocyte, Stem cells and committed progenitors for the blood and immune system (various types), Pluripotent stem cells, Totipotent stem cells, Induced pluripotent stem cells, adult stem cells, Sensory transducer cells, Autonomic neuron cells, Sense organ and peripheral neuron supporting cells, Central nervous system neurons and glial cells, Lens cells, Pigment cells, Melanocyte, Retinal pigmented epithelial cell, Germ cells, Oogonium/Oocyte, Spermatid, Spermatocyte, Spermatogonium cell (stem cell for spermatocyte), Spermatozoon, Nurse cells, Ovarian follicle cell, Sertoli cell (in testis), Thymus epithelial cell, Interstitial cells, and Interstitial kidney cells.

[0641] In some embodiments of any one of the methods disclosed herein, the condition can be a cancer or tumor. Non-limiting examples of such condition can include Acanthoma, Acinic cell carcinoma, Acoustic neuroma, Acral lentiginous melanoma, Acrospiroma, Acute eosinophilic leukemia, Acute lymphoblastic leukemia, Acute megakaryoblastic leukemia, Acute monocytic leukemia, Acute myeloblastic leukemia with maturation, Acute myeloid dendritic cell leukemia, Acute myeloid leukemia, Acute promyelocytic leukemia, Adamantinoma, Adenocarcinoma, Adenoid cystic carcinoma, Adenoma, Adenomatoid odontogenic tumor, Adrenocortical carcinoma, Adult T-cell leukemia, Aggressive NK-cell leukemia, AIDS-Related Cancers, AIDS-related lymphoma, Alveolar soft part sarcoma, Ameloblastic fibroma, Anal cancer, Anaplastic large cell lymphoma, Anaplastic thyroid cancer, Angioimmunoblastic T-cell lymphoma, Angiomyolipoma, Angiosarcoma, Appendix

cancer, Astrocytoma, Atypical teratoid rhabdoid tumor, Basal cell carcinoma, Basal-like carcinoma, B-cell leukemia, B-cell lymphoma, Bellini duct carcinoma, Biliary tract cancer, Bladder cancer, Blastoma, Bone Cancer, Bone tumor, Brain Stem Glioma, Brain Tumor, Breast Cancer, Brenner tumor, Bronchial Tumor, Bronchioloalveolar carcinoma, Brown tumor, Burkitt's lymphoma, Cancer of Unknown Primary Site, Carcinoid Tumor, Carcinoma, Carcinoma in situ, Carcinoma of the penis, Carcinoma of Unknown Primary Site, Carcinosarcoma, Castleman's Disease, Central Nervous System Embryonal Tumor, Cerebellar Astrocytoma, Cerebral Astrocytoma, Cervical Cancer, Cholangiocarcinoma, Chondroma, Chondrosarcoma, Chordoma, Choriocarcinoma, Choroid plexus papilloma, Chronic Lymphocytic Leukemia, Chronic monocytic leukemia, Chronic myelogenous leukemia, Chronic Myeloproliferative Disorder, Chronic neutrophilic leukemia, Clear-cell tumor, Colon Cancer, Colorectal cancer, Craniopharyngioma, Cutaneous T-cell lymphoma, Degos disease, Dermatofibrosarcoma protuberans, Dermoid cyst, Desmoplastic small round cell tumor, Diffuse large B cell lymphoma, Dysembryoplastic neuroepithelial tumor, Embryonal carcinoma, Endodermal sinus tumor, Endometrial cancer, Endometrial Uterine Cancer, Endometrioid tumor, Enteropathy-associated T-cell lymphoma, Ependymoblastoma, Ependymoma, Epithelioid sarcoma, Erythroleukemia, Esophageal cancer, Esthesioneuroblastoma, Ewing Family of Tumor, Ewing Family Sarcoma, Ewing's sarcoma, Extracranial Germ Cell Tumor, Extragonadal Germ Cell Tumor, Extrahepatic Bile Duct Cancer, Extramammary Paget's disease, Fallopian tube cancer, Fetus in fetu, Fibroma, Fibrosarcoma, Follicular lymphoma, Follicular thyroid cancer, Gallbladder Cancer, Gallbladder cancer, Ganglioglioma, Ganglioneuroma, Gastric Cancer, Gastric lymphoma, Gastrointestinal cancer, Gastrointestinal Carcinoid Tumor, Gastrointestinal Stromal Tumor, Gastrointestinal stromal tumor, Germ cell tumor, Germinoma, Gestational choriocarcinoma, Gestational Trophoblastic Tumor, Giant cell tumor of bone, Glioblastoma multiforme, Glioma, Gliomatosis cerebri, Glomus tumor, Glucagonoma, Gonadoblastoma, Granulosa cell tumor, Hairy Cell Leukemia, Hairy cell leukemia, Head and Neck Cancer, Head and neck cancer, Heart cancer, Hemangioblastoma, Hemangiopericytoma, Hemangiosarcoma, Hematological malignancy, Hepatocellular carcinoma, Hepatosplenic T-cell lymphoma, Hereditary breast-ovarian cancer syndrome, Hodgkin Lymphoma, Hodgkin's lymphoma, Hypopharyngeal Cancer, Hypothalamic Glioma, Inflammatory breast cancer, Intraocular Melanoma, Islet cell carcinoma, Islet Cell Tumor, Juvenile myelomonocytic leukemia, Kaposi Sarcoma, Kaposi's sarcoma, Kidney Cancer, Klatskin tumor, Krukenberg tumor, Laryngeal Cancer, Laryngeal cancer, Lentigo maligna melanoma, Leukemia, Leukemia, Lip and Oral Cavity Cancer,

Liposarcoma, Lung cancer, Luteoma, Lymphangioma, Lymphangiosarcoma, Lymphoepithelioma, Lymphoid leukemia, Lymphoma, Macroglobulinemia, Malignant Fibrous Histiocytoma, Malignant fibrous histiocytoma, Malignant Fibrous Histiocytoma of Bone, Malignant Glioma, Malignant Mesothelioma, Malignant peripheral nerve sheath tumor, Malignant rhabdoid tumor, Malignant triton tumor, MALT lymphoma, Mantle cell lymphoma, Mast cell leukemia, Mediastinal germ cell tumor, Mediastinal tumor, Medullary thyroid cancer, Medulloblastoma, Medulloblastoma, Medulloepithelioma, Melanoma, Melanoma, Meningioma, Merkel Cell Carcinoma, Mesothelioma, Mesothelioma, Metastatic Squamous Neck Cancer with Occult Primary, Metastatic urothelial carcinoma, Mixed Mullerian tumor, Monocytic leukemia, Mouth Cancer, Mucinous tumor, Multiple Endocrine Neoplasia Syndrome, Multiple Myeloma, Multiple myeloma, Mycosis Fungoides, Mycosis fungoides, Myelodysplastic Disease, Myelodysplastic Syndromes, Myeloid leukemia, Myeloid sarcoma, Myeloproliferative Disease, Myxoma, Nasal Cavity Cancer, Nasopharyngeal Cancer, Nasopharyngeal carcinoma, Neoplasm, Neurinoma, Neuroblastoma, Neuroblastoma, Neurofibroma, Neuroma, Nodular melanoma, Non-Hodgkin Lymphoma, Non-Hodgkin lymphoma, Nonmelanoma Skin Cancer, Non-Small Cell Lung Cancer, Ocular oncology, Oligoastrocytoma, Oligodendroglioma, Oncocytoma, Optic nerve sheath meningioma, Oral Cancer, Oral cancer, Oropharyngeal Cancer, Osteosarcoma, Osteosarcoma, Ovarian Cancer, Ovarian cancer, Ovarian Epithelial Cancer, Ovarian Germ Cell Tumor, Ovarian Low Malignant Potential Tumor, Paget's disease of the breast, Pancoast tumor, Pancreatic Cancer, Pancreatic cancer, Papillary thyroid cancer, Papillomatosis, Paraganglioma, Paranasal Sinus Cancer, Parathyroid Cancer, Penile Cancer, Perivascular epithelioid cell tumor, Pharyngeal Cancer, Pheochromocytoma, Pineal Parenchymal Tumor of Intermediate Differentiation, Pineoblastoma, Pituicytoma, Pituitary adenoma, Pituitary tumor, Plasma Cell Neoplasm, Pleuropulmonary blastoma, Polyembryoma, Precursor T-lymphoblastic lymphoma, Primary central nervous system lymphoma, Primary effusion lymphoma, Primary Hepatocellular Cancer, Primary Liver Cancer, Primary peritoneal cancer, Primitive neuroectodermal tumor, Prostate cancer, Pseudomyxoma peritonei, Rectal Cancer, Renal cell carcinoma, Respiratory Tract Carcinoma Involving the NUT Gene on Chromosome 15, Retinoblastoma, Rhabdomyoma, Rhabdomyosarcoma, Richter's transformation, Sacrococcygeal teratoma, Salivary Gland Cancer, Sarcoma, Schwannomatosis, Sebaceous gland carcinoma, Secondary neoplasm, Seminoma, Serous tumor, Sertoli-Leydig cell tumor, Sex cord-stromal tumor, Sezary Syndrome, Signet ring cell carcinoma, Skin Cancer, Small blue round cell tumor, Small cell carcinoma, Small Cell Lung Cancer, Small cell lymphoma, Small intestine cancer, Soft

tissue sarcoma, Somatostatinoma, Soot wart, Spinal Cord Tumor, Spinal tumor, Splenic marginal zone lymphoma, Squamous cell carcinoma, Stomach cancer, Superficial spreading melanoma, Supratentorial Primitive Neuroectodermal Tumor, Surface epithelial-stromal tumor, Synovial sarcoma, T-cell acute lymphoblastic leukemia, T-cell large granular lymphocyte leukemia, T-cell leukemia, T-cell lymphoma, T-cell prolymphocytic leukemia, Teratoma, Terminal lymphatic cancer, Testicular cancer, Thecoma, Throat Cancer, Thymic Carcinoma, Thymoma, Thyroid cancer, Transitional Cell Cancer of Renal Pelvis and Ureter, Transitional cell carcinoma, Urachal cancer, Urethral cancer, Urogenital neoplasm, Uterine sarcoma, Uveal melanoma, Vaginal Cancer, Verner Morrison syndrome, Verrucous carcinoma, Visual Pathway Glioma, Vulvar Cancer, Waldenstrom's macroglobulinemia, Warthin's tumor, and Wilms' tumor.

[0642] In accordance with various embodiments, numerous types of neoplasms can be detected, including (but not limited to) acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), anal cancer, astrocytomas, basal cell carcinoma, bile duct cancer, bladder cancer, breast cancer, Burkitt's lymphoma, cervical cancer, chronic lymphocytic leukemia (CLL) chronic myelogenous leukemia (CML), chronic myeloproliferative neoplasms, colorectal cancer, diffuse large B-cell lymphoma, endometrial cancer, ependymoma, esophageal cancer, esthesioneuroblastoma, Ewing sarcoma, fallopian tube cancer, follicular lymphoma, gallbladder cancer, gastric cancer, gastrointestinal carcinoid tumor, hairy cell leukemia, hepatocellular cancer, Hodgkin lymphoma, hypopharyngeal cancer, Kaposi sarcoma, Kidney cancer, Langerhans cell histiocytosis, laryngeal cancer, leukemia, liver cancer, lung cancer, lymphoma, melanoma, Merkel cell cancer, mesothelioma, mouth cancer, neuroblastoma, non-Hodgkin lymphoma, non-small cell lung cancer, osteosarcoma, ovarian cancer, pancreatic cancer, pancreatic neuroendocrine tumors, pharyngeal cancer, pituitary tumor, prostate cancer, rectal cancer, renal cell cancer, retinoblastoma, skin cancer, small cell lung cancer, small intestine cancer, squamous neck cancer, T-cell lymphoma, testicular cancer, thymoma, thyroid cancer, uterine cancer, vaginal cancer, and vascular tumors.

[0643] Many embodiments are directed to diagnostic or companion diagnostic scans performed during cancer treatment of an individual. When performing diagnostic scans during treatment, the ability of agent to treat the cancer growth can be monitored. Most anti-cancer therapeutic agents result in death and necrosis of neoplastic cells, which should release higher amounts nucleic acids from these cells into the samples being tested. Accordingly, the level of circulating-tumor nucleic acids can be monitored over time, as the level should increase during early treatments and begin to decrease as the number of cancerous cells are decreased. In some

embodiments, treatments are adjusted based on the treatment effect on cancer cells. For instance, if the treatment isn't cytotoxic to neoplastic cells, a dosage amount may be increased or an agent with higher cytotoxicity can be administered. In the alternative, if cytotoxicity of cancer cells is good but unwanted side effects are high, a dosage amount can be decreased or an agent with less side effects can be administered.

[0644] Various embodiments are also directed to diagnostic scans performed after treatment of an individual to detect residual disease and/or recurrence of cancer. If a diagnostic scan indicates residual and/or recurrence of cancer, further diagnostic tests and/or treatments may be performed as described herein. If the cancer and/or individual is susceptible to recurrence, diagnostic scans can be performed frequently to monitor any potential relapse.

F. Computer systems

[0645] In one aspect, the present disclosure provides a computer program product comprising a non-transitory computer-readable medium having computer-executable code encoded therein, the computer-executable code adapted to be executed to implement any one of the preceding methods.

[0646] The present disclosure provides computer systems that are programmed to implement methods of the disclosure. The system can, in some cases, include components such as a processor, an input module for inputting sequencing data or data derived therefrom, a computer-readable medium containing instructions that, when executed by the processor, perform an algorithm on the input regarding one or more cell-free nucleic acids molecules, and an output module providing one or more indicia associated with the condition.

[0647] **FIG. 27** shows a computer system 2701 that is programmed or otherwise configured to implement partial or all of the methods disclosed herein. The computer system 2701 can regulate various aspects of the present disclosure, such as, for example, (i) identify, from sequencing data derived from a plurality of cell-free nucleic acid molecules, one or more cell-free nucleic acid molecules comprising the plurality of phased variants, (ii) analyze any of the identified cell-free nucleic acid molecules, (iii) determine a condition of the subject based at least in part on the identified cell-free nucleic acid molecules, (iv) monitor a progress of the condition of the subject based at least in part on the identified cell-free nucleic acid molecules, (v) identify the subject based at least in part on the identified cell-free nucleic acid molecules, or (vi) determine an appropriate treatment of the condition of the subject based at least in part on the identified cell-free nucleic acid molecules. The computer system 2701 can be an electronic device of a user or a computer system that is remotely located with respect to the

electronic device. The electronic device can be a mobile electronic device.

[0648] The computer system 2701 includes a central processing unit (CPU, also "processor" and "computer processor" herein) 2705, which can be a single core or multi core processor, or a plurality of processors for parallel processing. The computer system 2701 also includes memory or memory location 2710 (e.g., random-access memory, read-only memory, flash memory), electronic storage unit 2715 (e.g., hard disk), communication interface 2720 (e.g., network adapter) for communicating with one or more other systems, and peripheral devices 2725, such as cache, other memory, data storage and/or electronic display adapters. The memory 2710, storage unit 2715, interface 2720 and peripheral devices 2725 are in communication with the CPU 2705 through a communication bus (solid lines), such as a motherboard. The storage unit 2715 can be a data storage unit (or data repository) for storing data. The computer system 2701 can be operatively coupled to a computer network ("network") 2730 with the aid of the communication interface 2720. The network 2730 can be the Internet, an internet and/or extranet, or an intranet and/or extranet that is in communication with the Internet. The network 2730 in some cases is a telecommunication and/or data network. The network 2730 can include one or more computer servers, which can enable distributed computing, such as cloud computing. The network 2730, in some cases with the aid of the computer system 2701, can implement a peer-to-peer network, which may enable devices coupled to the computer system 2701 to behave as a client or a server.

[0649] The CPU 2705 can execute a sequence of machine-readable instructions, which can be embodied in a program or software. The instructions may be stored in a memory location, such as the memory 2710. The instructions can be directed to the CPU 2705, which can subsequently program or otherwise configure the CPU 2705 to implement methods of the present disclosure. Examples of operations performed by the CPU 2705 can include fetch, decode, execute, and writeback.

[0650] The CPU 2705 can be part of a circuit, such as an integrated circuit. One or more other components of the system 2701 can be included in the circuit. In some cases, the circuit is an application specific integrated circuit (ASIC).

[0651] The storage unit 2715 can store files, such as drivers, libraries and saved programs. The storage unit 2715 can store user data, e.g., user preferences and user programs. The computer system 2701 in some cases can include one or more additional data storage units that are external to the computer system 2701, such as located on a remote server that is in communication with the computer system 2701 through an intranet or the Internet.

[0652] The computer system 2701 can communicate with one or more remote computer systems through the network 2730. For instance, the computer system 2701 can communicate with a remote computer system of a user. Examples of remote computer systems include personal computers (e.g., portable PC), slate or tablet PC's (e.g., Apple® iPad, Samsung® Galaxy Tab), telephones, Smart phones (e.g., Apple® iPhone, Android-enabled device, Blackberry®), or personal digital assistants. The user can access the computer system 2701 via the network 2730.

[0653] Methods as described herein can be implemented by way of machine (e.g., computer processor) executable code stored on an electronic storage location of the computer system 2701, such as, for example, on the memory 2710 or electronic storage unit 2715. The machine executable or machine readable code can be provided in the form of software. During use, the code can be executed by the processor 2705. In some cases, the code can be retrieved from the storage unit 2715 and stored on the memory 2710 for ready access by the processor 2705. In some situations, the electronic storage unit 2715 can be precluded, and machine-executable instructions are stored on memory 2710.

[0654] The code can be pre-compiled and configured for use with a machine having a processer adapted to execute the code, or can be compiled during runtime. The code can be supplied in a programming language that can be selected to enable the code to execute in a pre-compiled or as-compiled fashion.

[0655] Aspects of the systems and methods provided herein, such as the computer system 2701, can be embodied in programming. Various aspects of the technology may be thought of as "products" or "articles of manufacture" typically in the form of machine (or processor) executable code and/or associated data that is carried on or embodied in a type of machine readable medium. Machine-executable code can be stored on an electronic storage unit, such as memory (e.g., read-only memory, random-access memory, flash memory) or a hard disk. "Storage" type media can include any or all of the tangible memory of the computers, processors or the like, or associated modules thereof, such as various semiconductor memories, tape drives, disk drives and the like, which may provide non-transitory storage at any time for the software programming. All or portions of the software may at times be communicated through the Internet or various other telecommunication networks. Such communications, for example, may enable loading of the software from one computer or processor into another, for example, from a management server or host computer into the computer platform of an application server. Thus, another type of media that may bear the software elements includes optical, electrical and electromagnetic waves, such as used across physical interfaces between

local devices, through wired and optical landline networks and over various air-links. The physical elements that carry such waves, such as wired or wireless links, optical links or the like, also may be considered as media bearing the software. As used herein, unless restricted to non-transitory, tangible "storage" media, terms such as computer or machine "readable medium" refer to any medium that participates in providing instructions to a processor for execution.

[0656] Hence, a machine readable medium, such as computer-executable code, may take many forms, including but not limited to, a tangible storage medium, a carrier wave medium or physical transmission medium. Non-volatile storage media include, for example, optical or magnetic disks, such as any of the storage devices in any computer(s) or the like, such as may be used to implement the databases, etc. shown in the drawings. Volatile storage media include dynamic memory, such as main memory of such a computer platform. Tangible transmission media include coaxial cables; copper wire and fiber optics, including the wires that comprise a bus within a computer system. Carrier-wave transmission media may take the form of electric or electromagnetic signals, or acoustic or light waves such as those generated during radio frequency (RF) and infrared (IR) data communications. Common forms of computer-readable media therefore include for example: a floppy disk, a flexible disk, hard disk, magnetic tape, any other magnetic medium, a CD-ROM, DVD or DVD-ROM, any other optical medium, punch cards paper tape, any other physical storage medium with patterns of holes, a RAM, a ROM, a PROM and EPROM, a FLASH-EPROM, any other memory chip or cartridge, a carrier wave transporting data or instructions, cables or links transporting such a carrier wave, or any other medium from which a computer may read programming code and/or data. Many of these forms of computer readable media may be involved in carrying one or more sequences of one or more instructions to a processor for execution.

[0657] The computer system 2701 can include or be in communication with an electronic display 2735 that comprises a user interface (UI) 2740 for providing, for example, (i) analysis of any of the identified cell-free nucleic acid molecules, (ii) a determined condition of the subject based at least in part on the identified cell-free nucleic acid molecules, (iii) a determined progress of the condition of the subject based at least in part on the identified cell-free nucleic acid molecules, (iv) the identified subject suspected of having the condition based at least in part on the identified cell-free nucleic acid molecules, or (v) a determined treatment of the condition of the subject based at least in part on the identified cell-free nucleic acid molecules. Examples of UI's include, without limitation, a graphical user interface (GUI) and web-based user interface.

[0658] Methods and systems of the present disclosure can be implemented by way of one or more algorithms. An algorithm can be implemented by way of software upon execution by the central processing unit 2705. The algorithm can, for example, (i) identify, from sequencing data derived from a plurality of cell-free nucleic acid molecules, one or more cell-free nucleic acid molecules comprising the plurality of phased variants, (ii) analyze any of the identified cell-free nucleic acid molecules, (iii) determine a condition of the subject based at least in part on the identified cell-free nucleic acid molecules, (iv) monitor a progress of the condition of the subject based at least in part on the identified cell-free nucleic acid molecules, (v) identify the subject based at least in part on the identified cell-free nucleic acid molecules, or (vi) determine an appropriate treatment of the condition of the subject based at least in part on the identified cell-free nucleic acid molecules.

EXAMPLES

[0659] The following illustrative examples are representative of embodiments of the stimulation, systems, and methods described herein and are not meant to be limiting in any way.

Example 1: Genomic Distribution of Phased Variants

[0660] Described is an alternative to duplex sequencing for reducing the background error rate that involves detection of 'phased variants' (PVs), where two or more mutations occur in cis (i.e., on the same strand of DNA **FIG. 1A** and **FIG. 1E**). Similar to duplex sequencing, this method provides lower error profiles due to the concordant detection of two separate non-reference events in individual molecules. However, unlike duplex sequencing, both events occur on the same sequencing read-pair, thereby increasing the efficiency of genome recovery. Phased mutations are present in diverse cancer types, but occur in stereotyped portions of the genome in B-cell malignancies, likely due to on-target and aberrant somatic hypermutation (aSHM) driven by activation-induced deaminase (AID). The most common regions of aSHM in B-cell non-Hodgkin lymphomas (NHL) are identified. Described herein is phased variant Enrichment and Detection Sequencing (PhasED-Seq), a novel method to detect ctDNA through phased variants to tumor fractions on the order of parts per million. Described herein is demonstration that PhasED-Seq can meaningfully improve detection of ctDNA in clinical samples both during therapy and prior to disease relapse.

[0661] To identify malignancies where PVs may potentially improve disease detection, the frequency of PVs across cancer types were assessed. Publicly available whole-genome

sequencing data was analyzed to identify sets of variants occurring at a distance of <170bp apart, which represents the typical length of a single cfDNA fragment consisting of a single core nucleosome and associated linker. The frequency of these 'putative phased variants," (**Example 10**) controlling for the total number of SNVs, from 2538 tumors across 24 cancer histologies including solid tumors and hematological malignancies (**FIG. 1B**, **FIG. 5**, and **Table 1**) was identified and summarized. PVs were most significantly enriched in two B-cell lymphomas (DLBCL and follicular lymphoma, FL, $P<0.05$ vs all other histologies), a group of diseases with hypermutation driven by AID/AICDA.

Example 2: Mutational Mechanisms Underlying PVs

[0662] To investigate the origin of PVs, the single base substitution (SBS) mutational signatures contributing to SNVs occurring within 170bp of another SNV, and SNVs occurring in isolation (e.g., not having another SNV within 170 bp) (Example 10) were compared. As expected, PVs were highly enriched in several mutational signatures associated with clustered mutations. Signatures of clustered mutations associated with activity of AID (SBS84 and SBS85) were significantly enriched in PVs from B-cell lymphomas and CLL, while signatures associated with activity of APOBEC3B (SBS2 and SBS13) – another mechanism of kataegis hypermutation – were significantly enriched in PVs from multiple solid cancer histologies, including ovarian, pancreatic, prostate, and breast adenocarcinomas (**FIG. 1C** and **FIGs. 6A-6WW**). Signatures of clustered mutations associated with activity of AID (SBS84 and SBS85) were enriched in PVs found in lymphomas and CLL, while signatures associated with activity of APOBEC3B (SBS2 and SBS13) were significantly enriched in breast cancer (**FIG. 1C** and **FIGs. 6A-6WW**). PVs from multiple tumor types were also associated with SBS4, a signature associated with tobacco use. Furthermore, among PVs across multiple tumor histologies, it was observed that novel enrichments in several other signatures without clearly associated mechanisms (e.g., SBS24, SBS37, SBS38, and SBS39). In contrast, aging-associated mutational signatures such as SBS1 and SBS5 were significantly enriched in isolated SNVs.

Example 3: PVs Occur in Stereotyped Genomic Regions in Lymphoid Cancers

[0663] To assess the genomic distribution of putative PVs, these events were first binned into 1-kb regions to visualize their frequency across tumor types. It was observed that a strikingly stereotyped distribution of PVs in individual lymphoid neoplasms (e.g., DLBCL, FL, Burkitt lymphoma (BL), and chronic lymphocytic leukemia (CLL); **FIG. 1D** and **FIG. 7**). In contrast, non-lymphoid cancers generally did not exhibit substantial recurrence of clustered

PVs in stereotyped regions. This lack of stereotype in the position of PVs was true even when considering melanomas and lung cancers, diseases with frequent PVs.

[0664] Notably, the majority of hypermutated regions were shared between all three lymphoma subtypes, with the highest densities seen in known targets of aSHM including BCL2, BCL6, and MYC, as well as the immunoglobulin (Ig) loci encoding the heavy and light chains IGH, IGK, and IGL (**Table 2**). Strikingly, certain regions within Ig loci were densely mutated in nearly all lymphoma patients as well as in patients with CLL (**FIG. 1D**). Among lymphoma subtypes, DLBCL tumors harbored the most 1-kb regions recurrently containing PVs (**FIG. 8A**), consistent with the highest number of recurrently mutated genes being observed in this tumor type. In total, 1639 unique 1-kb regions recurrently containing PVs in B-lymphoid malignancies were identified. Among these lymphoma-associated 1-kb regions, nearly one-third fell into genomic areas previously associated with physiological or aberrant SHM in B-cells. Specifically, 19% (315/1639) were located in Ig regions, while 13% (218/1639) were in portions of 68 previously identified targets of aSHM (**Table 2**). While most PVs fell into noncoding regions of the genome, additional recurrently affected loci not previously described as targets of aSHM, including XBP1, LPP, and AICDA, among others, were also identified.

[0665] The distribution of PVs within each lymphoid malignancy correlated with oncogenic features associated with the distinct pathophysiology of the corresponding disease. For example, cases of FL - where more than 90% of tumors harbor oncogenic BCL2 fusions - were significantly more likely to contain phased variants in BCL2 than other lymphoid malignancies (**FIG. 1D** and **FIG. 8B**). Similarly, significantly more Burkitt lymphomas (BL) harbored PVs in MYC and ID3, two driver genes strongly associated with the BL pathogenesis, than other lymphoid malignancies (**FIG. 1D** and **FIGs. 8C-8D**). DLBCL molecular subtypes associated with distinct cell-of-origin also demonstrated distinct distributions of PVs (**Table 2**). Specifically, while germinal center B-cell like (GCB) and activated B-cell like (ABC) DLBCLs harbored similar frequencies of PVs overall (median 798 vs 516, P = 0.37), significant enrichment for PVs in the telomeric IGH class-switch regions (Sγ1, and Sγ3) in ABC-DLBCLs, consistent with previous reports41 (**FIG. 8E**), was found. Conversely, GCB-DLBCLs harbored more phased haplotypes in centromeric IGH class switch regions (Sα2 and Sε) and in BCL2.

Example 4: Design and Validation of PhasED-Seq Panel for Lymphoma

[0666] To validate these PV-rich regions and assess their utility for disease detection from ctDNA, a sequencing panel targeting putative PVs identified within WGS from three

independent cohorts of patients with DLBCL, as well as in patients with CLL (**FIG. 2A** and **Example 10**) was designed. This final Phased variant Enrichment and Detection Sequencing (PhasED-Seq) panel targeted ~115kb of genomic space focused on PVs, along with an additional ~200kb targeting genes that are recurrently mutated in B-NHLs (**Table 3**). While the 115kb of space dedicated to PV-capture targets only 0.0035% of the human genome, it captures 26% of phased variants observed in mature B-cell neoplasms profiled by WGS (**FIG 9A**), thus yielding a ~7500-fold PV enrichment by PhasED-Seq over WGS.

[0667] Expected SNV and PV recovery was compared to previously reported CAPP-Seq selector designed to maximize SNVs per patient in B-cell lymphomas (**FIG. 9A-C**). When considering diverse B-NHLs with available WGS data, PhasED-Seq recovered 3.0x more SNVs (81 vs. 27) and 2.9x more PVs (50 vs. 17) in the median case than previous CAPP-Seq panel. This observation highlights the importance of including non-coding portions of the genome for maximal mutation recovery. To validate these yield improvements experimentally, 16 pretreatment tumor or plasma DNA samples from patients with DLBCL (**Table 4**) were profiled. Both CAPP-Seq and PhasED-Seq panels were applied to each specimen in parallel and then sequenced them to high unique molecular depths (**FIG. 2B**). Compared to the expected enrichment established from WGS, similar improvements in yield of SNVs by PhasED-Seq compared to CAPP-Seq (2.7x; median 304.5 vs. 114) were observed. However, when enumerating PVs observed in individual sequenced DNA fragments, an improvement in favor of PhasED-Seq beyond the expected improvement from WGS (7.7x; median 5554 vs 719.5 PVs/case) was found. This improvement is potentially due to either 1) the higher sequencing depth in targeted sequencing which leads to improvement in rare allele detection, or 2) enumeration of higher order PVs in targeted sequencing with PhasED-Seq or CAPP-Seq, which was not accounted for in the WGS design (i.e., >2 SNVs per fragment; **FIGs. 9D-9F**). Furthermore, across 1-kb windows in the panel, robust correlation between the frequency of putative PVs in WGS data and PVs from targeted sequencing by PhasED-Seq across 101 DLBCL samples (**FIG. 2C**) was observed, further validating the frequency and distribution of PVs in B-cell malignancies.

Example 5: Differences in Phased Variants between Lymphoma Subtypes

[0668] Having validated the PhasED-Seq panel, the biological differences in PVs between various B-cell malignancies, including DLBCL (n=101), primary mediastinal B-cell lymphoma (PMBCL) (n=16), and classical Hodgkin lymphoma (cHL) (n=23) were examined. The number of SNVs identified per case was not significantly different between lymphoma

subtypes (**FIGs. 9G-9K**). However, when considering mutational haplotypes, cHL had a significantly lower burden of PVs than either DLBCL or PMBCL. In addition to this quantitative disparity, differences in the genomic locations of PVs between different B-cell lymphoma subtypes were also observed (**FIGs. 2D-2E** and **FIGs. 10-12**). This included previously established biological associations in DLBCL subtypes, including more frequent PVs in BCL2 in GCB-type than ABC-type DLBCL, with the opposite association seen for PIM1. More frequent PVs in CIITA in PMBCL compared with DLBCL, a gene in which breakpoints are common in PMBCL, was also observed. Relative enrichments were also observed throughout the IGH locus, with more frequent PVs seen in Sγ3 and Sγ1 regions in ABC-DLBCL (compared with GCB-DLBCL) and interestingly, more frequent PVs in the Sε locus in cHL compared with DLBCL (**FIG. 2E** and **FIG. 13**). In total, after correcting for testing multiple hypotheses, significant relative enrichments in 25 genetic loci between ABC- and GCB-DLBCL, 24 between DLBCL and PMBCL, and 40 between DLBCL and cHL were found (**FIG. 10-12**).

Example 6: Recovery of Phased Variants through PhasED-Seq

[0669] To facilitate detection of ctDNA using PVs, efficient recovery of DNA molecules is desired. Hybrid-capture sequencing is potentially sensitive to DNA mismatches, with increasing mutations decreasing hybridization efficiency. Indeed, AID hotspots can contain a 5-10% local mutation rate, with even higher rates in certain regions of IGH. To empirically assess the effect of mutation rate on capture efficiency, DNA hybridization of 150-mers with varying mutation rates in silico was simulated. As expected, predicted binding energy decreased with an increasing number of mutations (**FIG 14A**). Notably, randomly distributed mutations had a greater effect on binding energy than clustered mutations. To assess the effect of this decreased binding affinity, 150-mer DNA oligonucleotides with 0 to 10% difference from the reference sequence in MYC and BCL6, two loci that are targets of aSHM were synthesized. To assess the worst-case scenario for hybridization, non-reference bases were randomly distributed rather than in clusters (**Example 10**). An equimolar mixture of these oligonucleotides were then captured with PhasED-Seq panel. Concordant with the in silico predictions, increased mutational rates resulted in decreased capture efficiency (**FIG. 3A**). Molecules with a 5% mutation rate were captured with 85% efficiency relative to fully-wildtype counterparts, while molecules with 10% mutation were captured with only 27% relative efficiency. To assess the prevalence of this degree of mutation in human tumors, the distribution of variants in panel in 140 patients with B-cell lymphomas, calculating the fraction

of mutated bases in overlapping 151-bp windows (**Example 10**) was examined. Only 7% (10/140) of patients had any 151-bp window exceeding 10% mutation rate (**FIG. 14B-C**). Indeed, in the experiment with synthetic oligonucleotides, a 5% mutation rate was recovered nearly as efficiently as the wild-type sequence. In over half of all cases considered, no locus had >5% mutation rate at any window, while in all cases >90% of windows had <5% mutations. Overall, these observations indicate that the majority of phased mutations are recoverable by efficient hybrid capture, despite hybridization biases.

Example 7: Error Profile and Limit of Detection for Phased Variant Sequencing

[0670] Previous methods for highly error-suppressed sequencing applied to cfDNA have utilized either a combination of molecular and in silico methods for error suppression (e.g., integrated digital error suppression, iDES) or duplex molecular recovery. However, each of these has limitations, either for detecting events at ultra-low tumor fractions or for efficient recovery of original DNA molecules, which are important considerations for cfDNA analysis where input DNA is limited. The error profile and recovery of input genomes from plasma cfDNA samples form 12 heathy adults by PhasED-Seq were compared with both iDES-CAPP-Seq and duplex sequencing. While iDES-enhanced CAPP-Seq had a lower background error profile than barcode-deduplication alone, duplex sequencing offered the lowest background error rate for non-reference single nucleotide substitutions (**FIG. 3B**, 3.3×10^{-5} vs. 1.2×10^{-5}, $P<0.0001$). However, the rate of phased errors – e.g., multiple non-reference bases occurring on the same sequencing fragment - was significantly lower than the rate of single errors in either iDES-enhanced CAPP-Seq or duplex sequencing data. This was true for the incidence of both two (2x or 'doublet' PVs) or three (3x or 'triplet' PVs) substitutions on the same DNA molecule (**FIG. 3B**, 8.0×10^{-7} and 3.4×10^{-8} respectively, $P<0.0001$). Phased errors containing C to T or T to C transition substitutions were more common than other types of PVs (**FIG. 14D**). Notably, the rate doublet PVs errors in cfDNA was also correlated with distance between positions, with the highest PV error-rate consisting of neighboring SNVs (e.g., DNVs) and decreasing error rate with increasing distance between constituent variants (**FIG. 14E**). When considering unique molecular depth, duplex sequencing recovered only 19% of all unique cfDNA fragments (**FIG. 3C**). In contrast, the unique depth of PVs within a genomic distance of <20bp was nearly identical to the depth of individual positions (e.g., molecules covering individual SNVs). Similarly, PVs up to 80bps in size had depth greater than 50% of the median unique molecular depth for a sample. Importantly, almost half (48%) of all PVs were within 80bp of each other, demonstrating their utility for disease detection from input-limited cfDNA

samples (**FIG. 3D**).

[0671] To quantitatively compare the performance of PhasED-Seq to alternative methods for ctDNA detection, limiting dilutions of ctDNA from 3 lymphoma patients into healthy control cfDNA were generated, resulting in expected tumor fractions between 0.1% and 0.00005% (1 part in 2,000,000; (**Example 10**). The expected tumor fraction was compared to the estimated tumor content in each of these dilutions using PhasED-Seq to track tumor-derived PVs, as well as to error-suppressed detection methods depending on individual SNVs (e.g. iDES-enhanced CAPP-Seq or duplex sequencing; **FIG. 3E**). All methods performed equally well down to tumor fractions of 0.01% (1 part in 10,000). However, below this level (e.g., 0.001%, 0.0002%, 0.0001%, and 0.00005%), both PhasED-Seq and duplex sequencing significantly outperformed iDES-enhanced CAPP-Seq ($P<0.0001$ for duplex, '2x' PhasED-Seq, and '3x' PhasED-Seq; **FIG. 3E**). In addition, when compared to duplex-sequencing, tracking either 2 or 3 variants in-phase (e.g., 2x and 3x PhasED-Seq) more accurately identified expected tumor content, with superior linearity down to 1 part in 2,000,000 ($P = 0.005$ for duplex vs 2x PhasED-Seq, $P=0.002$ for 3x PhasED-Seq) (**Example 10**). Specificity of PVs by looking for evidence of tumor-derived SNVs or PVs in cfDNA samples from 12 unrelated healthy control subjects and the healthy control used for the limiting dilution was assessed. Here again, both 2x- or 3x-PhasED-Seq showed significantly lower background signal levels than did CAPP-Seq and duplex sequencing (**FIG. 3F**). This lower error rate and background from PVs improves the detection limit for ctDNA disease detection. In some instances, the method of sequencing-based cfDNA assays described herein (e.g. the method depicted in **FIG. 3E** and **FIG. 3F**) does not require molecular barcodes to achieve exquisite error-suppression and low limits of detection. Signal assessed by the method without barcode used limiting dilution series from 1 : 1,000 to 5 : 10,000,000, and 'blank' controls (**FIGs. 23A-23B**).

[0672] This dilution series was used to assess the limit of detection for a given number of PVs (**FIGs. 3G-3I**). When considering a set of PVs within 150 base pair (bp) regions, the probability of detection for a given sample may be accurately modelled by binomial sampling, considering both the depth of sequencing and the number of 150bp regions with PVs (**Example 10**).

Example 8: Improvements in Detection of Low-Burden Minimal Residual Disease

[0673] To test the utility of the lower LOD afforded by PhasED-Seq for detection of ultra-low burden MRD from cfDNA, Serial cell-free DNA samples were sequenced from a patient undergoing front-line therapy for DLBCL (**FIG. 4A**). Using CAPP-Seq, this patient had

undetectable ctDNA after only one cycle of therapy, with multiple subsequent samples during and after treatment also remaining undetectable. This patient had subsequent re-emergence of detectable ctDNA >250 days after the start of therapy, with eventual clinical and radiographic disease progression 5 months later, indicating falsely negative serial measurements with CAPP-Seq. Strikingly, all four of the plasma samples that were undetectable by CAPP-Seq during and after treatment had detectable ctDNA levels by PhasED-Seq, with mean allelic fractions as low as 6 parts in 1,000,000. This increased sensitivity improved the lead-time of disease detection by ctDNA compared to radiographic surveillance from 5 with CAPP-Seq to 10 months with PhasED-Seq.

[0674] Next, the performance of PhasED-Seq ctDNA detection in a cohort of 107 patients with large B-cell lymphomas and blood samples available after 1 or 2 cycles of standard immuno-chemotherapy was next assessed. Importantly, ctDNA levels measured by PhasED-Seq were highly correlated with those measured by CAPP-Seq. In total, 443 tumor, germ-line, and cell-free DNA samples, including cfDNA prior to therapy (n=107) and after 1 or 2 cycles of treatment (n=82 and 89), were assessed. Prior to therapy, patient-specific PVs were detectable by PhaseED-Seq in 98% of samples, with 95% specificity in cfDNA from healthy controls (**FIGs. 15** and **16A**). Importantly, ctDNA levels measured by PhasED-Seq were highly correlated with those measured by CAPP-Seq, considering both pretreatment and post treatment samples (Spearman rho=0.91, **FIG. 16B**). Next, quantitative levels of ctDNA measured by PhasED-Seq and CAPP-Seq from cfDNA samples after initiation of therapy were compared. In total, 72% (78/108) of samples with detectable ctDNA by PhasED-Seq after 1 or 2 cycles were also detected by conventional CAPP-Seq (**FIG. 4B**). Among 108 samples detected by PhasED-Seq, disease burden was significantly lower for those with undetectable (28%) vs. detectable (72%) ctDNA levels using conventional CAPP-Seq, with a >10x difference in median ctDNA levels (tumor fraction $2.2x10^{-4}$ vs $1.2x10^{-5}$, $P<0.001$, **FIG. 4B**). In total, an additional 16% (13/82) of samples after 1 cycle of therapy and 19% (17/89) of samples after 2 cycles of therapy had detectable ctDNA when comparing PhasED-Seq with CAPP-Seq (**FIG. 4C**).

[0675] ctDNA molecular response criteria was previously described for DLBCL patients using CAPP-Seq, including Major Molecular Response (MMR), defined as a 2.5-log reduction in ctDNA after 2 cycles of therapy22. While MMR at this time-point is prognostic for outcomes, many patients have undetectable ctDNA by CAPP-Seq at this landmark (**FIGs. 4D-4E**). Importantly, even in patients with undetectable ctDNA by CAPP-Seq, detection of occult ultra-low ctDNA levels by PhasED-Seq was prognostic for outcomes including event-free and

overall survival (**FIG. 4D**). Indeed, in the 89 patients with a sample available from this time-point, 58% (52/89) had undetectable ctDNA by CAPP-Seq at their interim MMR assessment, after completing 2 of 6 planned cycles of therapy. Using PhasED-Seq, 33% (17/52) of samples not detected by CAPP-Seq had evidence of ctDNA as evidenced by PVs, with levels as low as ~3:1,000,000 (**FIGs. 17A-17D**) – these 17 cases additionally detected by PhasED-Seq represent potential false negative tests by CAPP-Seq. Similar results were seen at the Early Molecular Response (EMR) time-point (i.e., after 1 cycle of therapy, **FIGs. 18A-18H**).

[0676] While detection of ctDNA in DLBCL after 1 or 2 cycles of therapy is a known adverse prognostic marker outcome for patients with undetectable ctDNA at these time-points are heterogeneous (**FIG. 4E** and **FIG. 18F**). Importantly, even in patients with undetectable ctDNA by CAPP-Seq after 1 or 2 cycles of therapy, detection of ultra-low ctDNA levels by PhasED-Seq was strongly prognostic for outcomes including event-free survival (**FIG. 4F**, **FIG. 17C-D**, **FIG. 18C-D**, and **FIG. 18G**). When combining detection by PhasED-Seq with previously described MMR threshold, patients could be stratified into three groups – patients not achieving MMR, patients achieving MMR but with persistent ctDNA, and patients with undetectable ctDNA (**FIG. 4G**). Interestingly, while patients not achieving MMR were at especially high risk for early events despite additional planned first line therapy (e.g., within the first year of treatment), patients with persistent low levels of ctDNA appeared to have a higher risk of later relapse or progression events. In contrast, patients with undetectable ctDNA after 2 cycles of therapy by PhasED-Seq had overwhelmingly favorable outcomes, with 95% being event-free and 97% overall survival at 5 years. Similar results were seen at the EMR time-point after 1 cycle of therapy (**FIG. 18H**).

Example 9: Exemplary embodiments of mutation detection using next generation sequencing (NGS) when the mutation is not a single base substation, but rather a pair of mutations

[0677] In many instances, a limitation of cfDNA tracking may be the limitation on the number of molecules available for detection. Additionally, there are multiple potential limitations on tracking tumor molecules from cell-free DNA, including not only the sequencing error profile, but also the number of molecules available for detection. The number of molecules available for detection - here termed the number of "evaluable fragments" - can be thought of as both a function of the number of recovered unique genomes (e.g., unique depth of sequencing) and the number of somatic mutations being tracked. More specifically, the number of evaluable fragments is equal to: EF = d * n.

[0678] Where d = the unique molecular depth considered and n = the number of somatic alterations tracked. For the typical cell-free DNA samples, less than 10,000 unique genomes are often recovered (d), requiring any sensitive method to track multiple alterations (n). Furthermore, as stated above, the major limitation for duplex sequencing is difficulty recovering sufficient unique molecular depth (d); thus, from a typical plasma sample with duplex depth of ~1,500x, even if following 100 somatic alterations, there are only 150,000 evaluable fragments. Thus, in this scenario, sensitivity is limited by the number of molecules available for detection. In contrast, other methods such as iDES-enhanced CAPP-Seq consider all molecules recovered. Here, as many as 5,000-6,000x unique haploid genomes can be recovered. Therefore, the number of evaluable fragments, tracking the same 100 somatic alterations, may be 500,000-600,000x. However, the error profile of single-stranded sequencing, even with error suppression, allows detection to levels of at best 1 part in 50,000. Therefore, methods aiming to improve on the detection limits for ctDNA must overcome both the error-profile of sequencing and the recovery of sufficient evaluable fragments to utilize said lower error-profiles.

[0679] To remedy this apparent deficiency, the method of PhasED-Seq, as described in the instant disclosure, allows for lymphoid malignancies and was applicable to other cancer histologies, (e.g., using a "personalized" approach). For a personalized approach, customized hybrid-capture oligonucleotides (or primers for PCR amplicons) were used to capture personalized somatic mutations identified from whole exome or genome sequencing. The PCAWG dataset assessed for SNVs occurring within 170bp of each other in genomic space was re-analyzed. It was found that in 14 of 24 cancer histologies considered, the median case contained >100 possible phased variants, including in several solid tumors such as Melanoma (median 2072), lung squamous cell carcinoma (1268), lung adenocarcinoma (644.5), and colorectal adenocarcinoma (216.5).

[0680] Next, the expected limit of detection in all cases in the PCAWG dataset using either duplex sequencing or PhasED-Seq was assessed. Again, the limit of detection was defined by the expected number of evaluable fragments, and thus depends on both the number of variants tracked and the expected depth of sequencing. Utilizing the data from optimized hybrid capture conditions, a model to predict the expected deduplicated (single-stranded) and duplex (double-stranded) molecular depth with a given DNA input and number of sequencing reads was constructed. Using this, along with the number of SNVs or possible PVs from the PCAWG dataset, for each case, which method would lead to a greater number of evaluable fragments, and therefore a superior limit of detection was assessed. The results of this exercise, assuming

64 nanograms (ng) of total cfDNA input and a total of 20 million sequencing reads are shown in **FIG. 19**. Notably, in the majority of cancer types (18/24 histologies), PhasED-Seq had a lower limit of detection than duplex sequencing. This importantly included not only B-cell lymphomas, but common solid tumors, including lung squamous cell carcinoma and adenocarcinoma, colorectal adenocarcinoma, esophageal and gastric adenocarcinoma, and breast adenocarcinoma, among others. Indeed, taking lung cancers as a specific example, an almost 10-fold lower limit of detection was found for the median squamous cell and adenocarcinoma lung cancer case using PhasED-Seq compared to duplex sequencing (**FIG. 20**). Both PhasED-Seq and duplex sequencing using a personalized approach had a lower limit of detection than non-personalized approaches (e.g., iDES-enhanced CAPP-Seq).

[0681] To further confirm the applicability of phased variants and PhasED-Seq in diverse solid tumors, WGS (~20-30x depth) was performed on paired tumor and normal DNA to identify PVs from five solid tumor patients predicted to have low ctDNA burden prior to treatment (lung cancer (n=5), along with one patient having breast cancer (n=1)). Sequencing reads were aligned to hg19 and deduplicated with samtools markdup. In accordance with GATK practices, tumor and normal deduplicated BAM files were processed with GATK IndelRealigner and BaseRecalibrator before variant calling, using default parameters (GATK v3.8-1-0-gf15c1c3ef) (Van der Auwera, G. A. et al. From FastQ data to high-confidence variant calls: the Genome Analysis Toolkit best practices pipeline. Curr. Protoc. Bioinformatics 43, 11.10.1–11.10.33 (2013)). Variant calling was performed using three methods: VarScan2 (v2.3.9) (Koboldt, D. C. et al. VarScan 2: somatic mutation and copy number alteration discovery in cancer by exome sequencing. Genome Res. 22, 568–576 (2012)), Mutect (v1.1.7) (Cibulskis, K. et al. Sensitive detection of somatic point mutations in impure and heterogeneous cancer samples. Nat. Biotechnol. 31, 213–219 (2013)), and Strelka2 (v2.9.1) (Kim, S. et al. Strelka2: fast and accurate calling of germline and somatic variants. Nat. Methods 15, 591 594 (2018)). Mutect and VarScan2 VCF files were annotated by annovar (v2018Apr16), and Strelka VCF files were annotated by Oncotator (v1.9.8.0). Variants called by each method were combined and filtered according to the following criteria: (1) pass caller-intrinsic quality filters (for example, base quality, orientation bias and germline risk); (2) depth $\geq 30\times$; (3) AF $\geq 5\%$; and (4) variant identified by ≥ 2 variant callers. SNVs passing all filters were then assessed for possible phased relationships—any pair of SNVs ≤ 170 bp from its nearest neighbor was considered a viable PV. ("Viable PVs" are defined in this example as PVs initially identified by WGS.) We also genotyped PVs directly from WGS reads, considering any viable PVs with at least two supporting reads, $10\times$ depth and 5% tumor fraction. Viable PVs were then assessed

and prioritized for tumor specificity, considering the (1) presence in individual tumor reads as phased relationships, (2) absence of read support in matched normal, (3) presence of other non-reference bases on the supporting reads, (4) base quality, (5) mapping quality and (6) uniqueness of genomic positions. Based on these metrics, candidate PVs were then selected for targeted resequencing below. ("Candidate PVs" are defined as the subset of viable PVs selected for targeted resequencing and validation). As used in this example, "putative PVs" can refer to either or both or viable PVs or candidate PVs.

[0682] After identifying candidate PVs from each of these six tumors, we designed 120-bp biotinylated hybrid-capture oligonucleotides targeting the regions of interest (Integrated DNA Technologies). We then performed hybrid capture resequencing of the tumor–normal pairs to high unique molecular depth (~1000–3000× deduplicated depth) to create a validated list of PVs for tumor monitoring (**FIG. 22C**). The numbers shown in each column of FIG. 22C represent the number of regions of less than 170 bp in length that include a plurality of phased variants. A PV was considered to be validated if it was present in the tumor at higher than 5% AF and had no read support in the matched germline DNA.

[0683] We applied the above personalized hybrid-capture panels targeting PVs to plasma samples from each of these six participants, sequencing to high unique molecular depth (~1000 to 10,000× deduplicated depth). We also sequenced 24 control healthy cfDNA samples with each panel to assess specificity.

[0684] Tumor fraction was defined as the number of reads containing an a priori defined PV over the total number of reads covering a PV position. Most samples had been assessed for ctDNA content using SNV-based CAPP-seq approaches previously, providing comparison to PhasED-seq. The results of these experiments are shown in **FIGS. 22D-22G.**

[0685] Considering the five lung cancer cases, the PhasED-Seq approach achieved a ~10-fold improvement in analytical sensitivity, achieving a median LOD of 0.00018% compared to 0.0019% using customized CAPP-Seq (**FIG. 21A and FIG. 21B**).

[0686] To demonstrate the clinical significance of this improved limit of detection for ctDNA from PhasED-Seq in solid tumors, serial plasma samples from a patient with stage 3 adenocarcinoma of the lung treated with chemoradiotherapy with curative intent (LUP814) were analyzed using both CAPP-Seq and PhasED-Seq. As outlined above, both CAPP-Seq and PhasED-Seq quantified a similar level of ctDNA prior to therapy (~1% tumor fraction). However, 3 subsequent samples after beginning therapy had undetectable ctDNA by standard CAPP-Seq, including samples during and after chemoradiation and during adjuvant immunotherapy with Durvalumab. Despite the lack of detectable disease by CAPP-Seq, the

patient had biopsy-confirmed recurrent disease after an initial radiographic response. However, when analyzing these same samples with PhasED-Seq, molecular residual disease in 3/3 (100%) of samples was detected, with mean tumor fraction as low as 0.00016% (1.6 parts per million). Furthermore, the trend in ctDNA quantitation mirrored the patient's disease course, with an initial response to chemoradiotherapy but disease progression during immunotherapy. Importantly, this patient's disease remained detectable at all timepoints, with detectable disease at the completion of chemoradiotherapy 8 months prior to the patient's biopsy-confirmed disease progression (**FIG. 22**).

Example 10: Methods of phased variant enrichment for enhanced disease detection from cell-free DNA

10(a): Whole-genome sequencing analysis

10(a)(1): Whole-Genome Sequencing Data Putative Phased Variant Identification

[0687] Whole-genome sequencing data were obtained from two sources. Data for lymphoid malignancies (diffuse large B-cell lymphoma, DLBCL; follicular lymphoma, FL; Burkitt lymphoma, BL; chronic lymphocytic leukemia, CLL) were downloaded from the International Cancer Genome Consortium (ICGC) data portal on May 7th, 2018. Data from all other histologies were part of the pan-Cancer analysis of whole genomes (PCAWG) and downloaded on November 11th, 2019. Only cancer histologies with at least 35 available cases were considered; details of the dataset considered are provided in **Table 1**. All samples had somatic mutations called from WGS using matched tumor and normal genotyping. Queries were limited to base substitutions obtained from WGS (single, double, triple, and oligo nucleotide variants; SNVs, DNVs, TNVs, and ONVs). Having thus identified the cases and variants of interest, the number of putative phased variants (PVs) in each tumor was next identified. To function as a PV on a single cell-free DNA (cfDNA) molecule, two variants, such as two single nucleotide variants (SNVs) generally must occur within a genomic distance less than the length of a typical cfDNA molecule (~170bp). Therefore, putative PVs were defined as two variants occurring on the same chromosome within a genomic distance of < 170bp. DNVs, TNVs, and ONVs were considered as the set of their respective component SNVs. The number of SNVs as well as the identity of putative PVs for each case are detailed in **Table 1**. The raw number of SNVs and putative PVs, as well as the number of putative PVs controlling for the number of SNVs, is shown in **FIG. 5A-C**.

10(a)(2): Mutational Signatures of Phased Variants from WGS

[0688] To assess the mutational processes associated with phased and non-phased mutations across different cancer types/subtypes, the mutational signatures of single base substitutions (SBS) were enumerated for each WGS case described above using the R package 'deconstructSigs'. The list of SNVs for each patient was first divided into two groups: 1) SNVs contained within a possible PV; that is, with an adjacent or 'nearest neighbor' SNV <170bp away, and 2) isolated SNVs (i.e., non-phased), defined as those occurring ≥170bp in distance from the closest adjacent SNV. 'DeconstructSigs' was then applied using the 49 SBS signatures described in COSMIC (excluding signatures linked to possible sequencing artefacts) to assess the contribution of each SBS signature to both candidate phased SNVs and un-phased SNVs for each patient. To compare the contribution of each SBS signature to phased and isolated SNVs, a Wilcoxon signed rank test was performed to compare the relative contribution of each SBS signature between these two categories for each cancer type (**FIGs. 6A-6WW**). To account for multiple hypotheses, Bonferroni's correction was applied, by considering any SBS signature that differed in contribution to phased vs. un-phased SNVs to be significant if the Wilcoxon signed rank test resulted in a P-value of <0.05 / 49 or 0.001. The distributions of these comparisons, along with significance testing, are depicted in **FIGs. 6A-6WW**. A summary of this analysis is also shown in **FIG. 1C** using a heat-map display, where the 'heat' represents the difference between the mean contribution of the SBS signature to phased variants to the mean contribution to isolated/un-phased variants.

10(a)(3): Genomic Distribution of Phased Variants from WGS

[0689] The recurrence frequency for PVs was assessed in each cancer type across the genome within each tumor type. Specifically, the human genome (build GRCh37 / hg19) was first divided into 1-kb bins (3,095,689 total bins); then, for each sample, the number of PVs (as defined above) contained in each 1-kb bin was counted. For this analysis, any PV with at least one of its constituent SNVs falling within the 1-kb bin of interest was included. The fraction of patients whose tumors harbored a PV for each cancer type within each genomic bin was then calculated. To identify 1-kb bins recurrently harboring PVs across patients, the fraction of patients containing PVs in each 1-kb bin vs. genomic coordinates (**FIG. 1D** and **FIG. 7**) was plotted; for this analysis, only bins where at least 2% of samples contained a PV in at least one cancer subtype were plotted.

10(a)(4): Identification of Recurrent 1-kb Bins with Phased Variants

[0690] To identify 1-kb bins that recurrently contain PVs in B-lymphoid malignancies, WGS data was utilized from the following diseases: DLBCL, FL, BL, and CLL. Any 1-kb bin

where >1 sample from these tumor types was considered to recurrently contain PVs from B-lymphoid malignancies. The genomic coordinates of 1-kb bins containing recurrent PVs in lymphoid malignancies are enumerated in **Table 2**, and are plotted in **FIG. 8A**.

10(b): Design of PhasED-Seq panel for B-lymphoid malignancies

10(b)(1): Identification of recurrent PVs from WGS data at higher resolution

[0691] Given the prevalence of recurrent putative PVs from WGS data in B-cell malignancies, a targeted sequencing approach was designed for their hybridization-mediated capture – Phased variant Enrichment Sequencing (PhasED-Seq) – to enrich these specific PV events from tumor or cell-free DNA. In addition to the ICGC data described above, WGS data was also utilized from other sources in this design, including both B-cell NHLs as well as CLL.

[0692] Previous experience with targeted sequencing from cfDNA in NHLs was also examined. Pairs of SNVs occurring at a distance of <170bp apart in each B-cell tumor sample were identified. Then, genomic "windows" that contained PVs was identified as follows: for each chromosome, the PVs were sorted by genomic coordinates relative to reference genome. Then, the lowest (i.e., left-most) position was identified for any PV in any patient; this defined the left-hand (5') coordinate seeding a desired window of interest, to be captured from the genome. This window was then extended by growing its 3' end to capture successive PVs until a gap of ≥340bp was reached, with 340-bp chosen as capturing two successive chromatosomal sized fragments of ~170-bp. When such a gap was reached, a new window was started, and this iterative process of adding neighboring PVs was repeated again until the next gap of ≥340bp was reached. This resulted in a BED file of genomic windows containing all possible PVs from all samples considered. Finally, each window was additionally padded by 50bp on each side, to enable efficient capture from flanking sequences in rare scenarios when repetitive or poorly mapping intervening sequences might preclude their direct targeting for enrichment.

[0693] Having identified the regions of interest containing putative PVs, each window was then into 170bp segments (e.g., the approximate size of a chromatosomal cfDNA molecule). Then, the number of cases containing a PV was enumerated in each case. For each 170bp region, the region in final sequencing panel design was included if one or more of the following criteria was met: 1) at least one patient contained a PV in the 170bp region in 3 of 5 independent data-sets, 2) at least one patient contained a PV in the region in 2 of 5 independent data-sets if one dataset was prior CAPP-Seq experience, or 3) at least one patient contained a PV in the region in 2 of 5 independent data-sets, with a total of at least 3 patients containing a PV in the region. This resulted in 691 'tiles', with each tile representing a 170bp genomic region. These

tiles, along with an additional ~200kb of genomic space targeting driver genes recurrently mutated in B-NHL, were combined into a unified targeted sequencing panel as previously described for both tumor and cfDNA genotyping using NimbleDesign (Roche NimbleGen). The final coordinates of this panel are provided in **Table 3**.

10(b)(2): Comparison of PhasED-Seq and CAPP-Seq Performance in PV Yield

[0694] To evaluate the performance of PhasED-Seq for capturing both SNVs and PVs compared to previously reported CAPP-Seq selector for B-cell lymphomas, the predicted number of both SNVs and PVs that may be recovered with each panel by limiting WGS *in silico* to the capture targets of each approach (**FIG. 9A-C**) was quantified. The predicted number of variants was then compared using the Wilcoxon signed rank test. Both CAPP-Seq and PhasED-Seq were also performed on 16 samples from patients with DLBCL. In these samples, tumor or plasma DNA, along with matched germ-line DNA, was sequenced. The resulting number of variants were again compared by the Wilcoxon signed rank text (**FIG. 2B**, and **FIGs. 9D-9E**). The sequencing depth for the samples included in this analysis are provided in **Tables 4**.

10(c): Identification of phased variants from targeted sequencing data

10(c)(1): Patient enrollment and clinical sample collection

[0695] Patients with B-cell lymphomas undergoing front-line therapy were enrolled on this study from six centers across North America and Europe, including Stanford University, MD Anderson Cancer Center, the National Cancer Institute, University of Eastern Piedmont (Italy), Essen University Hospital (Germany), and CHU Dijon (France). In total, 343 cell-free DNA, 73 tumor, and 183 germ-line samples from 183 patients were included in this study. All patient samples were collected with written informed consent for research use and were approved by the corresponding Institutional Review Boards in accordance with the Declaration of Helsinki. Cell-free, tumor, and germ-line DNA were isolated as previously described. All radiographic imaging was performed as part of standard clinical care.

10(c)(2): Library preparation and sequencing

[0696] To generate sequencing libraries and targeted sequencing data, CAPP-Seq was applied as previously described. Briefly, cell-free, tumor, and germ-line DNA were used to construct sequencing libraries through end repair, A-tailing, and adapter ligation following the KAPA Hyper Prep Kit manufacturer's instructions with ligation performed overnight at 4°C. CAPP-Seq adapters with unique molecular identifiers (UMIDs) were used for barcoding of unique DNA duplexes and subsequent deduplication of sequencing read pairs. Hybrid capture

was then performed (SeqCap EZ Choice; NimbleGen) using the PhasED-Seq panel described above. Affinity capture was performed according to the manufacturer's protocol, with all 47 °C hybridizations conducted on an Eppendorf thermal cycler. Following enrichment, libraries were sequenced using an Illumina HiSeq4000 instrument with 2x150bp paired-end (PE) reads.

10(c)(3): Pre-processing and alignment

[0697] FASTQ files were de-multiplexed and UMIDs were extracted using a custom pipeline as previously described. Following demultiplexing, reads were aligned to the human genome (build GRCh37 / hg19) using BWA ALN. Molecular barcode-mediated error suppression and background polishing (i.e., integrated digital error suppression; iDES) were then performed as previously described.

10(c)(4): Identification of phased variants and allelic quantitation

[0698] After generating UMID error-suppressed alignment files (e.g., BAM files), PVs were identified from each sample as follows. First, matched germ-line sequencing of uninvolved peripheral blood mononuclear cells (PBMCs) was performed to identify patient-specific constitutional single nucleotide polymorphisms (SNPs). These were defined as non-reference positions with a variant allele fraction (VAF) above 40% with a depth of at least 10, or a VAF of above 0.25% with a depth of at least 100. Next, PVs were identified from read-level data for a sample of interest. Following UMID-mediated error suppression, each individual paired-end (PE) read and identified all non-reference positions were using 'samtools calmd'. PE data was used rather than single reads to identify variants occurring on the same template DNA molecule, which may subsequently fall into either read 1 or read 2. Any read-pair containing ≥2 non-reference positions was considered to represent a possible somatic PV. For reads with >2 non-reference positions, each permutation of size ≥2 was considered independently: i.e., if 4 non-reference positions were identified in a read-pair, all combinations of 2 SNVs (i.e., 'doublet' phased variants) and all combinations of 3 SNVs (i.e., 'triplet' phased variants) were independently considered. PVs containing putative germ-line SNPs were also removed as follows: if in a given *n*-mer (i.e., *n* SNVs in phase on a given molecule) ≥*n*-1 of the component variants were identified as germ-line SNPs, the PV was redacted. This filtering strategy ensures that for any remaining PV, at least 2 of the component SNVs were not seen in the germ-line, as relevant for both sensitivity and specificity.

[0699] Putative somatic PVs were filtered using a heuristic blacklisting approach in considering sequencing data from 170 germ-line DNA samples serving as controls. In each of these samples, PVs were identified on read-pairs as described above, but without filtering for matched germ-line. Any PV that occurred in one or greater paired-end read, in one or more of

these control samples, was included in the blacklist and removed from patient-specific somatic PV lists.

[0700] To calculate the VAF of each PV, a numerator representing the number of DNA molecules containing a PV of interest was calculated over a denominator representing the total number of DNA molecules that covered the genomic region of interest. That is, the numerator is simply the total number of deduplicated read-pairs that contain a given PV while the denominator is the number of read-pairs that span the genomic locus of a given PV.

10(c)(5): Genotyping phased variants from pretreatment samples

[0701] The above strategy resulted in a list of PVs of ≥1 read-depth in each sample. To identify PVs serving as tumor-specific somatic reporters for disease monitoring, for each case a 'best genotyping' specimen – either DNA from a tumor tissue biopsy (preferred), or pretreatment cell-free DNA was identified. After identifying all possible PVs in the 'best genotyping sample', the list for specificity was further filtered as follows. For any n-mer PV set, if ≥n-1 of the constituent SNVs were present as germ-line SNPs in the 170 control samples described above, the PV was removed. Furthermore, only PVs that meet the following criteria were considered: 1) AF > 1%; 2) depth of the PV locus of ≥100 read-pairs, and 3) at least one component SNV must be in the on-target space. Finally, 4) any PV meeting these criteria was assessed for read-support in a cohort of 12 healthy control cfDNA samples. If any read-support was present in >1 of these 12 samples, the PV was removed. For genotyping from cell-free DNA samples identified as low tumor fraction by SNVs (i.e., < 1% mean AF across all SNVs), the AF threshold for determining PVs was relaxed to >0.2%. This filtering resulted in the PV lists used for disease monitoring and MRD detection.

10(c)(6): Determination of tumor fraction in a sample from phased variants

[0702] For evaluation of a sample for minimal residual disease (MRD) detection with prior knowledge of the tumor genotype, the presence of any PV identified in the best pretreatment genotyping sample in the MRD sample of interest can be assessed. Given a list of k possible tumor-derived PVs observed in the best genotyping sample, all read-pairs covering at least 1 of the k possible PVs were determined. This value, d, can be thought of as the aggregated 'informative depth' across all PVs spanned by cfDNA molecules in a PhasED-Seq experiment. It was then assessed how many of these d read-pairs actually contained 1 or more of the k possible PVs – this value, x, represents the number of tumor-derived molecules containing somatic PVs in a given sample. The number of tumor-derived molecules containing PVs divided by the informative depth – x/d – is therefore the phased-variant tumor fraction (PVAF) in a given sample. For detection of MRD in each sample, PVAF was calculated independently

for doublet, triplet, and quadruplet PVs.

10(c)(7): Monte Carlo simulation for empirical significance of PV detection within a specimen

[0703] To assess the statistical significance of the detection of tumor-derived PVs in any sample, an empiric significance testing approach was implemented. A test statistic *f* was first defined as follows – from a given list of *k* possible tumor-derived PVs observed in the best genotyping sample, the arithmetic mean of allele fractions was calculated across all *k* PVs (allele fraction defined as the number of read-pairs containing an individual PV (x_i) over the number of read-pairs spanning the PV positions (d_i)):

$$\mathrm{f} = \frac{\sum_{i=1}^{k} \frac{x_i}{d_i}}{k} \quad (1)$$

to assess the hypothesis that *f* is not significantly different from the background error-rate of similar PVs assessed from the same sample. A Monte Carlo approach was used to develop a null distribution and perform statistical testing as follows:

1. Given a set of k PVs, $\{pv_1 \ldots pv_i \ldots pv_k\}$, an 'alternate' list of PVs, $\{pv'_1 \ldots pv'_i \ldots pv'_k\}$, was generated such that for each alternate PV had the same type of base change and distance between SNVs as the test PV. For example, if a doublet PV, chr14:106329929 C>T and chr14:106329977 G>A, was identified in the genotyping sample and searched for an alternate two positions at the same genomic distance (here, 48bp) with reference bases C and G, and assessed for read-pairs with the same types of base changes (i.e., C>T and G>A), using the heuristic search scheme below.
2. For each tumor pv_i in the set of k, 50 such alternates were identified. This was performed with a random search algorithm to scan the genomic space and identify alternates. To find these 50 alternates, a random position on the same chromosome as the test pv_i was identified and then searched for the same types of reference bases at the same genomic distance as described above. Synteny of observed/alternate PVs was used to control for regional variation in SHM/aSHM as well as copy number variation, as potential confounders of the null distribution. Alternate positions that were identified as a germ-line SNP, defined as having AF > 5%, were excluded.
3. After identifying 50 such alternates for each pv_i, 10,000 random permutations of 1 alternate were generated for each of the k original PVs and calculated the phased-

variant fraction *f'* for these alternate lists in the sample of interest being evaluated for presence of MRD, as described above.

4. An empiric P-value was calculated, defined as the fraction of times the true phased-variant fraction *f* is observed to be less than or equal to the alternate *f'* across the 10,000 random PV lists as an empirical measure of significance of MRD significance in the blood sample of interest.

[0704] While this resulting comparison is a measure of the significance for PV detection of tumor-reporter list compared to the empirically defined background PV error-rate *within* the sample of interest, its relationship to specificity of detection *across* cases and control samples was also evaluated, as described below.

10(c)(8): Assessment of specificity of PhasED-Seq

[0705] To determine the specificity of disease and MRD detection through PhasED-Seq, patient-specific PVs from 107 patients with DLBCL were first identified using pretreatment tumor or plasma DNA along with paired germ-line samples. 40 independent plasma DNA samples were then assessed from healthy individuals for presence of these patient-specific PVs, using the Monte Carlo approach outlined above. A threshold for P-values was empirically determined from Monte Carlo such that 95% specificity was achieved for disease detection from doublet, triplet, and quadruplet PVs. The P-value threshold yielding ≥95% specificity for each size of PV was as follows: < 0.041 for doublets, <1 for triplets, and <1 for quadruplets. The results of this specificity in control cfDNA analysis is shown in **FIGs. 15 and 16A and 16B**.

10(c)(9): Calculation of error rates

[0706] To assess the error profile of both isolated SNVs and PVs, the non-reference base observation rate of each type of variant was examined across all reads. For isolated SNVs, the error-rate for each possible base change $e_{n1>n1'}$ was calculated as the fraction of on-target bases with reference allele $n1$ that are mutated to alternate allele $n1'$, when considering all possible base-changes of the reference allele. Positions with a non-reference allele rate exceeding 5% were classified as probable germ-line events, and excluded from the error-rate analysis. A global error rate, defined as the rate of mutation from the hg19 reference allele to any alternate allele, was also calculated.

[0707] For phased variants, a similar calculation was performed. For the error-rate of a given type of phased variant composed of k constituent base-changes $\{e_{n1>n1'} \ldots e_{nk>nk'}\}$, the error-rate was calculated by determining both the number of instances of the type of base

change (i.e., the numerator), as well as the number of possible instances for the base change (i.e., the denominator). To calculate the numerator, *N*, the number of occurrences of the PV of interest over all read-pairs was counted in a given sample. For example, to calculate the error-rate of C>T and G>A phased doublets, the number of read-pairs that include *both* a reference C mutated to a T as well as a reference G mutated to an A was first counted.

[0708] To calculate the denominator, *D*, the number of possible instances of this type of phased variant was also calculated; this was performed first for each read-pair *i*, and then summed over all read pairs. A PV with *k* components can be summarized as having certain set of reference bases p_A, p_C, p_G, p_T, where p_N is the number of each reference base in the PV. Similarly, a given read pair contains a certain set of reference bases b_A, b_C, b_G, b_T, where b_N is the number of each reference base in the read pair. Therefore, for each read pair in a given sample, the number of possible occurrences of PV type of interest can be calculated combinatorically as:

$$D_i = \binom{b_A}{p_A}\binom{b_C}{p_C}\binom{b_G}{p_G}\binom{b_T}{p_T} \quad (2)$$

For example, consider a read-pair with 40 reference As, 50 reference Cs, 45 reference Gs, and 35 reference Ts. The number of positions for a C>T and G>A PV is:

$$D_i = \binom{40}{0}\binom{50}{1}\binom{45}{1}\binom{35}{0} = 2250 \quad (3)$$

The aggregated denominator, *D*, for error rate calculation is then simply the sum of this value over all read pairs. The error rate for this type of PV is then simply *N/D*.

10(d): Differences in phased variants between lymphoma subtypes

[0709] To compare the distribution of phased variants in different types of lymphomas, tumor-specific PVs were identified in 101 DLBCL, 16 PMBCL, and 23 cHL patients via sequencing of tumor biopsy specimens and/or pre-treatment cell-free DNA and paired germ-line specimens. After identifying these tumor-specific PVs, their distribution was the assessed across the targeted sequencing panel. The panel was first divided into 50bp bins; for each patient, it was then determined if each patient had evidence of a PV within the 50bp bin, defined as having at least one component of the PV within the bin. The nearest gene to each 50bp bin was further determined, based on GENCODEv19 annotation of the reference genome.

[0710] To assess how the distribution of PVs between subtypes of lymphoma varies at the level of specific genes, the distribution of PVs was examined across the 50bp bins spanning

each gene (or nearest gene). For example, consider a given gene with *n* such 50bp bins represented in targeted sequencing panel. For each bin, it was first determined the fraction of patients, *f*, in each type of lymphoma with a PV falling within the 50bp bin – i.e., determining $\{f_{type1,1}, \cdots f_{type1,n}\}$ and $\{f_{type2,1}, \cdots f_{type2,n}\}$. Then, any two histologies were then compared for the fraction of cases harboring PVs in the set of 50bp bins assigned to each gene. These comparisons are depicted for individual genes on gene-specific plots in **FIG. 2D** and **FIGs. 10-12**.

[0711] The enrichment in PVs was statistically compared in a specific lymphoma type or subtype vs. another by calculating the difference in the fraction of patients which contain a PV in each 50bp bin across all bins assigned to a gene (i.e., overlapping a given gene or with a given nearest gene). Specifically, for any comparison between two lymphoma types ($type_1$ and $type_2$), this set of differences in PV-rate was first identified between histologies $\{f_{type1,1} - f_{type2,1}, \cdots f_{type1,n} - f_{type2,n}\}$. This set of gene-specific differences in frequency of PVs was the compared between types of lymphoma against the distribution of all other 50bp bins in the sequencing panel by the Wilcoxon rank sum test. For this test, the set of *n* 50bp bins assigned to a given gene was compared to all other 50bp bins (i.e., 6755 – n, since there are 6755 50bp bins in sequencing panel). This P-value, along with the mean difference in fraction of patients with a PV in each bin for each gene between histologies, is depicted as a volcano plot in **FIG. 2E**. To account for the global difference in rate of PVs between different histologies, the mean difference in fraction of patients with a PV between histologies was centered on 0 by subtracting the mean difference across all genes.

10(e): Hybridization Bias

[0712] To assess the effect of mutations on hybridization efficiency, the affinity of mutated molecules to wildtype capture baits *in silico* was first estimated by considering DNA fragments harboring 0-30% mutations across the entire fragment. For each mutation condition across this range, 10,000 regions were first randomly sampled, each 150bp in length, from across the whole genome. These 150-mers were then mutated *in silico* to simulate the desired mutation rate in 3 different ways: 1) mutating 'clustered' or contiguous bases starting from the ends of a sequence, 2) mutating clustered bases started from the middle of the sequence, or 3) mutating bases selected at random positions throughout the sequence. The *energy.c* package was then used to calculate the theoretical binding energy (kcal/mol) between the mutated and wild-type sequences, in relying on a nearest-neighbor model employing established thermodynamic

parameters (**FIG. 14A**).

[0713] This *in silico* experiment was then replicated by testing the effects of same mutation rates *in vitro*. Specifically, oligonucleotides (IDT) were synthesized and annealed to form DNA duplexes harboring 0-10% mutations at defined positions relative to the human reference genome sequence. These synthetic DNA molecules were then captured together at equimolar concentrations and quantified the relative capture efficiency of mutated duplexes compared to the wild-type, unmutated species (**FIG. 3A**). Two sets of oligonucleotide sequences were selected from coding regions of *BCL6* and *MYC* to capture AID-mediated aberrant somatic hypermutations associated with each gene (**Table 5**); the preserved mappability of the mutated species was ensured by BWA ALN. These synthetic oligonucleotide duplexes were then subjected to library preparation, then captured and sequenced using PhasED-Seq, performed in triplicate using distinct samples. This allowed assessment of the relative efficiency of hybrid capture and molecular recovery as directly compared to wildtype molecules identical to the reference genome.

10(f): Assessment of limit of detection with limiting dilution series

[0714] To empirically define the analytical sensitivity of PhasED-Seq, a limited dilution series of cell-free DNA from 3 patients that were spiked into healthy control cell-free DNA at defined concentrations was utilized. The dilution series contained samples with an expected mean tumor fraction of 0.1%, 0.01%, 0.001%, 0.0002%, 0.0001%, and 0.00005% or ranging from 1 part in 1,000 to 1 part in 2,000,000. The sequencing characteristics and ctDNA quantification via CAPP-Seq, duplex sequencing, and PhasED-Seq are provided. To compare the performance of each method, the difference was calculated, δ, between the observed and expected tumor fraction for each patient *i* at each dilution concentration *j*:

$$\delta_{i,j} = \widehat{tumorfrac}_{i,j} - tumorfrac_{i,j} \quad (4)$$

This value was calculated for patients $i = \{1,2,3\}$ and concentrations $j = \{0.001\%, 0.0002\%, 0.0001\%, 0.00005\%\}$ for each ctDNA detection method (CAPP-Seq, duplex, doublet PhasED-Seq, and triplet PhasED-Seq). The performance of each method was then compared to each other by paired t-test across this set of patients and concentrations.

10(g): Model to predict the probability of detection for a given set of phased variants

[0715] To build a mathematical model to predict the probability of detection for a given

sample of interest, it began with the common assumption that cfDNA detection can be considered a random process based on binomial sampling. However, unlike SNVs occurring at large genomic distances apart from one another, detection of PVs can be highly inter-dependent, especially when PVs are degenerate (i.e., when two PVs share component SNVs) or occur in close proximity. To account for this, only PVs occurring >150bp apart from each other was considered as independent 'tumor reporters'. The number of 'tumor reporters' to allow for disease detection in a given sample can thus be determined as follows. The PhasED-Seq panel was broken apart into 150bp bins. Each PV in a given patient's reporter list was then turned into a BED coordinate, consisting of the start position (defined as the left-most component SNV) and end position (defined as the right-most component SNV). For each PV, the 150bp bin from the PhasED-Seq selector panel containing the PV was determined; if a PV spanned two or more 150bp bins, it was assigned to both bins. The number of independent tumor reporters was then defined as the number of separate 150bp bins containing a tumor-specific PV.

[0716] A mathematical model was then developed comparing the expected probability of detection for a given sample at a given tumor fraction with a given number of independent tumor reporters (e.g., 150 bp bins). With a given number of tumor reporters r, at a given tumor fraction f, with a given sequencing depth d, the probability of detecting 1 or more cell-free DNA molecule containing a tumor-specific PV containing can be defined as:

$$Pr(detection) = 1 - Pr(nondetection) \tag{5}$$

$$= 1 - \binom{d * r}{0} f^0 (1-f)^{d*r} \tag{6}$$

based on simple binomial sampling. However, as ctDNA detection method was trained to have a 5% false positive rate, this false positive rate term was added to the model as well:

$$Pr(detection) = 1 - Pr(nondetection) + 0.05 * Pr(nondetection) \tag{7}$$

$$Pr(detection) = 1 - 0.95 * Pr(nondetection) \tag{8}$$

$$= 1 - 0.95 * \binom{d * r}{0} f^0 (1-f)^{d*r} \tag{9}$$

FIG. 3G shows the results of this model for a range of tumor reporters r from 3 to 67 at depth d of 5000. The confidence envelope on this plot shows solutions for a range of depth d from 4000 to 6000.

[0717] To empirically validate this model assessing the probability of disease detection, samples from limiting dilution series were utilized. In this dilution series, 3 patient cfDNA samples, each containing patient-specific PVs, were spiked into healthy control cfDNA. For each list of patient specific PVs, 25 random subsamplings of the 150bp bins containing patient-specific PVs were performed to generate reporter lists containing variable numbers of tumor-specific reporters. A maximum bin number of 67 was selected to allow sampling from all 3 patient-specific PV lists, followed by scaling down the number of bins by 2x or 3x per operation. This resulted in reporter lists containing patient-specific PVs from 3, 6, 17, 34, or 67 independent 150bp bins. Disease detection was then assessed using each of these patient-specific PV lists of increasing size in each of 'wet' limiting dilution samples from 1:1,000 to 1:1,000,000 (**FIG. 3H,** closed circles). *In silico* mixtures was further created using sequencing reads from limiting dilution samples with varying expected tumor-content, and again assessed for the probability of disease detection using patient-specific subsampled PV reporter lists of varying lengths (open circles). For this experiment, both the 'wet' and '*in-silico*' dilution bam files were down-sampled to achieve a depth of ~4000-6000x to correspond with modeled depth. The final mean and standard deviation of depth across all down-sampled bam files was 4214x ± 789. The probability of detection was summarized across all tests at a given expected tumor fraction, for a given patient-specific PV list. For each given dilution, multiple independently sampled sets of reads were considered to allow superior estimation of the true probability of detection. Specifically, the following number of replicates at each dilution indicated was considered in **Table 7**.

Table 7. Replicates at each dilution for predicting the probability of detection for a given set of phased variants.

Dilution	**Replicates**	**Number of Tests (Replicates * 25)**	**Wet or *In silico***
1 : 1,000	1	25	Wet
5 : 10,000	3	75	*In silico*
3.5 : 10,000	3	75	*In silico*
2 : 10,000	3	75	*In silico*

1 : 10,000	3	75	Wet
5 : 100,000	3	75	*In silico*
3.5 : 100,000	3	75	*In silico*
2 : 100,000	3	75	*In silico*
1 : 100,000	3	75	Wet
5 : 1,000,000	8	200	*In silico*
3.5 : 1,000,000	8	200	*In silico*
2 : 1,000,000	8	200	Wet
1 : 1,000,000	8	200	Wet

[0718] The total number of tests, for each patient-specific PV list, is therefore the number of randomly subsampled PV lists (e.g., 25) times the number of independently downsampled bam files; this number is provided in the table above. In **FIG. 3H**, the points and error-bars represent the mean, minimum, and maximum across all three patients. The concordance between the predicted probability of disease detection from theoretical mathematical model and wet and *in silico* samples validating this model, is shown in **FIG. 3I**.

10(h): Statistical Analyses & Software Availability

[0719] All P-values reported in this manuscript are 2-sided unless otherwise noted. Comparisons of matched samples and populations were performed using the Wilcoxon signed rank test; comparisons of samples drawn from unrelated populations were performed using the Wilcoxon rank-sum test. Comparisons of paired samples were performed by paired t-test. Survival probabilities were estimated using the Kaplan-Meier method; survival of groups of patients based on ctDNA levels were compared using the log-rank test. Other statistical tests are noted in the manuscript text where utilized. All analyses were performed with the use of MATLAB, version 2018b, R Statistical Software version 3.4.1, and GraphPad Prism, version 8.0.2. The contribution of known mutational processes to phased and isolated SNVs from WGS was assessed with the deconstruct Sigs R package using the COSMIC signature set (v2) as described. Calculation of AUC accounting for survival and censorship was performed using the R 'survivalROC' package version 1.0.3 with default settings. An executable version of the PhasED-Seq software, developed in C++17, is available at phasedseq(dot)stanford(dot)edu.

Example 11

[0720] Using methods and systems of the present disclosure, cell-free nucleic acid molecules may be analyzed to detect insertions and deletions (indels) contained therein, and the detected indels may be applied toward various applications (e.g., determining a presence or absence of a condition in a subject, such as a neoplasm of the subject, a cancer of the subject, a transplant rejection of the subject, or a chromosomal abnormality of a fetus of the subject; and determining whether cell-free nucleic acid molecules are tumor-derived).

[0721] For example, using methods and systems of the present disclosure, cell-free nucleic acid molecules may be analyzed from a subject who has received an organ or tissue transplant to detect phased variants and/or insertions and deletions (indels) contained therein, and the detected PVs and/or indels may be applied toward various applications (e.g., determining a presence or absence of a transplant rejection of a subject.

[0722] As another example, using methods and systems of the present disclosure, cell-free nucleic acid molecules may be analyzed from a pregnant subject to detect phased variants and/or insertions and deletions (indels) contained therein, and the detected PVs and/or indels may be applied toward various applications (e.g., determining a presence, an absence, or an elevated risk of a genetic abnormality of a fetus of the pregnant subject).

[0723] While indels share some factors in common with phased variants (e.g., they contain multiple non-reference bases), indels may also differ from phased variants in various ways (e.g., biological differences, where a biological indel can occur with a single DNA replication error, while a PV may require two separate errors; and technical errors related to mapping, in which an indel may require one mismatch and/or non-templated event, while a phased variant may require two or more such mismatches and/or non-templated events).

[0724] In some embodiments, the indels alone that are detected in cell-free nucleic acid molecules may be applied toward various applications by leveraging their low background or error rates (e.g., determining a presence or absence of a condition in a subject, such as a neoplasm or cancer; and determining whether cell-free nucleic acid molecules are tumor-derived). In some embodiments, the detected indels in combination with detected phased variants in cell-free nucleic acid molecules may be applied toward various applications (e.g., determining a presence or absence of a condition in a subject, such as a neoplasm or cancer; and determining whether cell-free nucleic acid molecules are tumor-derived).

[0725] A set of 12 healthy cfDNA samples used to assess the error or background rate in iDES-enhanced CAPP-Seq, duplex sequencing, and PhasED-Seq, was analyzed to assess for the error-rate of indels as well. This analysis was performed on the same sequencing data,

making the error-rates comparable. The error or background rate was defined for each of these types of alterations as follows. The SNV background rate was defined as the number of non-reference bases over the total number of bases, as described herein. The indel background rate was defined as the total number of indels observed after mapping over the total number of bases, as described herein. The PV background rate was defined as the total number of combinations of non-reference PVs over the total number of possible PVs for a given size, as described herein.

[0726] All events occurring at greater than 5% allele fraction were considered to be germline and were not included here. In addition to the observed background in SNVs and PVs reported, **FIG. 28** shows the background rate of indels of all sizes, greater or equal to 2 base pairs, greater or equal to 3 bps, and greater or equal to 4bps, and across this set of 12 healthy control cfDNA samples.

[0727] As **FIG. 28** demonstrates, the error profile of indels improves when only larger indels are considered. Interestingly, the background rate for indels of length 1 bp or larger was observed to be similar to the background rate for SNVs without in silico error suppression (8.0E-5 vs. 8.0E-5, respectively). However, longer indels (e.g., specifically those greater than or equal to 4bp long) had a lower background rate, comparable with the background rate of SNVs from duplex sequencing (8.9E-6 vs 1.2E-5). However, the background rate of both doublet and triplet PVs was observed to be lower than that of both the duplex and larger indels (background rate of 8.0E-7 and 3.5E-8 respectively for doublet and triplet PVs). Notably, this lower background for PVs was true even without the use of UMIs or molecular barcodes.

[0728] This lower background rate for PVs is likely biological in origin. As discussed herein, there is substantial potential for true biological background in SNVs or indels, which may be greater than for PVs, as each of the SNVs or indels may only require one somatic mutational event, while PVs may require at least two somatic events. Nevertheless, the background rate for PVs supports its utility for improving the limit of detection for low-level tumor burden from cell-free DNA. However, in cases with low numbers of PVs, tracking longer indels (e.g., greater than or equal to 3 bp in length) may provide an alternative source of low error-rate tumor-reporters to enable ultra-sensitive tumor monitoring. Therefore, indel monitoring may be leveraged as a complementary or alternative approach to the detection and analysis of PVs in cell-free DNA.

Example 12

[0729] Using methods and systems of the present disclosure, cell-free nucleic acid molecules may be analyzed from a subject who has received an organ or tissue transplant to detect phased variants and/or insertions and deletions (indels) contained therein, and the detected PVs and/or indels may be applied toward various applications (e.g., determining a presence or absence of a transplant rejection of a subject). In some embodiments, the subject has received a transplant of an organ (e.g., heart, kidney, liver, lung, pancreas, stomach and intestine), a tissue (e.g., cornea, bone, tendon, skin, pancreas islets, heart valves, nerves and veins), cells (e.g., bone marrow and stem cells), or a limb (e.g., a hand, an arm, a foot).

[0730] In some embodiments, upon identifying a subject as having a transplant rejection, the method may further comprise treating the subject for the transplant rejection. In some embodiments, the treatment comprises an immunosuppressive drug, an anti-body based treatment, a blood transfer, a marrow transplant, a gene therapy, a transplant removal, and/or a re-transplant procedure. In some embodiments, the immunosuppressive drug comprises a corticosteroid (e.g., prednisolone, hydrocortisone), a calcineurin inhibitor (e.g., ciclosporin, tacrolimus), an anti-proliferative (e.g., azathioprine, mycophenolic acid), or an mTOR inhibitor (e.g., sirolimus, everolimus). In some embodiments, the antibody-based treatment comprises a monoclonal anti-IL-2Rα receptor antibody (e.g., basiliximab, daclizumab), a polyclonal anti-T-cell antibody (e.g., anti-thymocyte globulin (ATG), anti-lymphocyte globulin (ALG)), or a monoclonal anti-CD20 antibody (e.g., rituximab).

[0731] In some embodiments, the subject may be monitored over time (e.g., by analyzing cell-free nucleic acid molecules to detect PVs and/or indels at a plurality of different time points) to assess the transplant rejection status of the subject and/or to determine a progression of the transplant rejection status of the subject.

[0732] In some embodiments, the detected PVs and/or indels of a subject may be compared to those of a first subject cohort having transplant rejection and/or a second subject cohort not having transplant rejection.

Example 13

[0733] Using methods and systems of the present disclosure, cell-free nucleic acid molecules may be analyzed from a pregnant subject to detect phased variants and/or insertions and deletions (indels) contained therein, and the detected PVs and/or indels may be applied toward various applications (e.g., determining a presence, an absence, or an elevated risk of a genetic abnormality of a fetus of the pregnant subject).

[0734] In some embodiments, upon identifying the fetus of the pregnant subject as having a genetic abnormality, the method may further comprise treating the subject or conducting follow-up clinical procedures (e.g., an invasive or non-invasive diagnostic procedure) for the pregnant subject.

[0735] In some embodiments, the detected PVs and/or indels of a subject may be compared to those of a first subject cohort having a fetus with a genetic abnormality and/or a second subject cohort not having a fetus with a genetic abnormality.

[0736] In some embodiments, the genetic abnormality is a chromosomal aneuploidy. In some embodiments, the chromosomal aneuploidy is in chromosome 13, 18, 21, X, or Y.

Example 14

[0737] Additional details of the tables described throughout the present disclosure are provided herein:

[0738] **TABLE 1**: 1000bp regions of interest throughout the genome containing putative phased variants (PV) in various lymphoid neoplasms. Only regions containing > 1 subject with a PV are shown. Coordinates are in hg19. Regions from genes that were previously identified as targets of activation-induced deaminase (AID) are labeled. Regions that contain PVs in > 5% of subjects in any histology (BL, CLL, DLBCL, FL) are also labeled. BL, Burkitt lymphoma; CLL, chronic lymphocytic leukemia; DLBCL, diffuse large B-cell lymphoma; FL, follcicular lymphoma.

[0739] **TABLE 2**: 1000bp regions of interest throughout the genome containing putative phased variants (PV) in the ABC and GCB subtypes of DLBCL. Only regions containing > 1 subject with a PV are shown. Coordinates are in hg19. Regions from genes that were previously identified as targets of AID are labeled. ABC, activated B-cell subtype; GCB, germinal center B-cell subtype.

[0740] **TABLE 3**: Regions used for the PhasED-Seq capture reagent described in this paper focused on lymphoid malignancies. Coordinates are in hg19. The closest gene and the reason for inclusion (Phased Variants vs general DLBCL genotyping) is also shown.

[0741] **TABLE 4:** Enrichment of PVs at genetic loci throughout the PhasED-Seq targeted sequencing panel for different types of B-cell lymphomas (DLBCL including ABC and GCB subtypes, PMBCL, and cHL). The PhasED-Seq selector was binned into 50bp bins in hg19 coordinates, and each bin was labelled by gene or nearest gene. The mean of the fraction of cases of a given histology with a PV across all 50bp bins is shown. Significance was determined by rank-sum (Mann-Whitney U) test of 50bp bins for a given gene against the remainder of the

sequencing panel. Uncorrected P-values are shown; multiple-hypothesis testing correction was performed by Bonferroni method. DLBCL, diffuse large B-cell lymphoma; PMBCL, primary mediastinal B-cell lymphoma; cHL, classical Hodgkin lymphoma; ABC, activated B-cell DLBCL; GCB, germinal center B-cell DLBCL.

[0742] **TABLE 5:** Sequences of oligonucleotides synthesized to assess hybridization and molecular recovery bias with increasing mutational burden (SEQ ID NOs. 1331-1358).

[0743] **TABLE 6:** Nucleic acid probes for Capture Sequencing of B-cell Cancers (SEQ ID NOs. 0001-1330).

EMBODIMENTS

[0744] The following are illustrative examples of embodiments of the present disclosure and are not meant to be limiting in any way.

1. A method comprising:

(a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject;

(b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence, wherein at least about 10% of the one or more cell-free nucleic acid molecules comprises a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants that are separated by at least one nucleotide; and

(c) analyzing, by the computer system, the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

2. The method of embodiment 1, wherein the at least about 10% of the cell-free nucleic acid molecules comprise at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of the one or more cell-free nucleic acid molecules.

3. The method of embodiment 1 or 2, wherein (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the condition of the subject based at least in part on the identified one or more indels.

4. A method comprising:

(a) obtaining, by a computer system, sequencing data derived from a plurality of cell-

free nucleic acid molecules that is obtained or derived from a subject;

(b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide; and

(c) analyzing, by the computer system, the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

5. The method of embodiment 4, wherein (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the condition of the subject based at least in part on the identified one or more indels.

6. A method comprising:

(a) obtaining sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject;

(b) processing the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules with a limit of detection of less than about 1 out of 50,000 observations from the sequencing data; and

(c) analyzing the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

7. The method of embodiment 6, wherein the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 observations from the sequencing data.

8. The method of any one of embodiments 6-7, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence.

9. The method of embodiment 8, wherein a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide.

10. The method of any one of embodiments 6-9, wherein (a) to (c) are performed by a computer system.

11. The method of any one of the preceding embodiments, wherein the sequencing data is generated based on nucleic acid amplification.

12. The method of any one of the preceding embodiments, wherein the sequencing data is generated based on polymerase chain reaction.

13. The method of any one of the preceding embodiments, wherein the sequencing data is generated based on amplicon sequencing.

14. The method of any one of the preceding embodiments, wherein the sequencing data is generated based on next-generation sequencing (NGS).

15. The method of any one of the preceding embodiments, wherein the sequencing data is generated based on non-hybridization-based NGS.

16. The method of any one of the preceding embodiments, wherein the sequencing data is generated without use of molecular barcoding of at least a portion of the plurality of cell-free nucleic acid molecules.

17. The method of any one of the preceding embodiments, wherein the sequencing data is obtained without use of sample barcoding of at least a portion of the plurality of cell-free nucleic acid molecules.

18. The method of any one of the preceding embodiments, wherein the sequencing data is obtained without in silico removal or suppression of (i) background error or (ii) sequencing error.

19. The method of any one of embodiments 6-18, wherein (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the condition of the subject based at least in part on the identified one or more indels.

20. A method of treating a condition of a subject, the method comprising:

(a) identifying the subject for treatment of the condition, wherein the subject has been determined to have the condition based on identification of one or more cell-free nucleic acid molecules from a plurality of cell-free nucleic acid molecules that is obtained or derived from the subject,

wherein each of the one or more cell-free nucleic acid molecules identified comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide, and

wherein a presence of the plurality of phased variants is indicative of the condition of the subject; and

(b) subjecting the subject to the treatment based on the identification in (a).

21. The method of embodiment 20, wherein the subject has been determined to have the condition based at least in part on one or more insertions or deletions (indels) identified in the

one or more cell-free nucleic acid molecules.

22. A method of monitoring a progress of a condition of a subject, the method comprising:

(a) determining a first state of the condition of the subject based on identification of a first set of one or more cell-free nucleic acid molecules from a first plurality of cell-free nucleic acid molecules that is obtained or derived from the subject;

(b) determining a second state of the condition of the subject based on identification of a second set of one or more cell-free nucleic acid molecules from a second plurality of cell-free nucleic acid molecules that is obtained or derived from the subject,

wherein the second plurality of cell-free nucleic acid molecules are obtained from the subject subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject; and

(c) determining the progress of the condition based on the first state of the condition and the second state of the condition,

wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide.

23. The method of embodiment 22, wherein the progress of the condition is worsening of the condition.

24. The method of embodiment 22, wherein the progress of the condition is at least a partial remission of the condition.

25. The method of any one of embodiments 22-24, wherein a presence of the plurality of phased variants is indicative of the first state or the second state of the condition of the subject.

26. The method of any one of embodiments 22-25, wherein the second plurality of cell-free nucleic acid molecules is obtained from the subject at least about 1 week, at least about 2 weeks, at least about 3 weeks, at least about 4 weeks, at least about 2 months, or at least about 3 months subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject.

27. The method of any one of embodiments 22-26, wherein the subject is subjected to a treatment for the condition (i) prior to obtaining the second plurality of cell-free nucleic acid molecules from the subject and (ii) subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject.

28. The method of any one of embodiments 22-27, wherein the progress of the condition is indicative of minimal residual disease of the condition of the subject.

29. The method of any one of embodiments 22-28, wherein the progress of the condition is indicative of tumor burden or cancer burden of the subject.

30. The method of any one of the preceding embodiments, wherein the one or more cell-free nucleic acid molecules are captured from among the plurality of cell-free nucleic acid molecules with a set of nucleic acid probes, wherein the set of nucleic acid probes is configured to hybridize to at least a portion of cell-free nucleic acid molecules comprising one or more genomic regions associated with the condition.

31. The method of any one of embodiments 22-30, wherein the subject has been determined to have the condition based at least in part on one or more insertions or deletions (indels) identified in the one or more cell-free nucleic acid molecules.

32. The method of any one of embodiments 22-31, wherein the subject has received an organ or tissue transplant, and wherein the condition comprises transplant rejection of the subject.

33. A method comprising:

(a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject,

wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide, and

wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the plurality of phased variants and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants;

(b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the plurality of phased variants; and

(c) analyzing the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

34. The method of embodiment 33, wherein (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the condition of the subject based at least in part on the identified one or more indels.

35. The method of any one of embodiments 33-34, wherein the subject has received an

organ or tissue transplant, and wherein the condition comprises transplant rejection of the subject.

36. A method comprising:

(a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject,

wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising a plurality of phased variants relative to a reference genomic sequence, and

wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the plurality of phased variants and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants;

(b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the plurality of phased variants, wherein a limit of detection of the identification step is less than about 1 out of 50,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules; and

(c) analyzing the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

37. The method of embodiment 36, wherein the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules.

38. The method of embodiment 36 or 37, wherein a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide.

39. The method of any one of embodiments 36-38, wherein the activatable reporter agent is activated upon hybridization of the individual nucleic acid probe to the plurality of phased variants.

40. The method of any one of embodiments 36-38, wherein the activatable reporter agent is activated upon dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants.

41. The method of any one of embodiments 36-40, further comprising mixing (1) the set of

nucleic acid probes and (2) the plurality of cell-free nucleic acid molecules.

42. The method of any one of embodiments 36-41, wherein the activatable reporter agent is a fluorophore.

43. The method of any one of the preceding embodiments, wherein analyzing the identified one or more cell-free nucleic acid molecules comprises analyzing (i) the identified one or more cell-free nucleic acid molecules and (ii) other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants as different variables.

44. The method of any one of the preceding embodiments, wherein the analyzing of the identified one or more cell-free nucleic acid molecules is not based on other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants.

45. The method of any one of the preceding embodiments, wherein a number of the plurality of phased variants from the identified one or more cell-free nucleic acid molecules is indicative of the condition of the subject.

46. The method of embodiment 45, wherein a ratio of (i) the number of the plurality of phased variants from the one or more cell-free nucleic acid molecules and (ii) a number of single nucleotide variants (SNVs) from the one or more cell-free nucleic acid molecules is indicative of the condition of the subject.

47. The method of any one of the preceding embodiments, wherein a frequency of the plurality of phased variants in the identified one or more cell-free nucleic acid molecules is indicative of the condition of the subject.

48. The method of embodiment 47, wherein the frequency is indicative of a diseased cell associated with the condition.

49. The method of embodiment 48, wherein the condition is diffuse large B-cell lymphoma, and wherein the frequency is indicative of whether the one or more cell-free nucleic acid molecules are derived from germinal center B-cell (GCB) or activated B-cell (ABC).

50. The method of any one of the preceding embodiments, wherein genomic origin of the identified one or more cell-free nucleic acid molecules is indicative of the condition of the subject.

51. The method of any one of the preceding embodiments, wherein the first and second phased variants are separated by at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 nucleotides.

52. The method of any one of the preceding embodiments, wherein the first and second

phased variants are separated by at most about 180, at most about 170, at most about 160, at most about 150, or at most about 140 nucleotides.

53. The method of any one of the preceding embodiments, wherein at least about 10%, at least about 20%, at least about 30%, at least about 40%, or at least about 50% of the one or more cell-free nucleic acid molecules comprising a plurality of phased variants comprises a single nucleotide variant (SNV) that is at least 2 nucleotides away from an adjacent SNV.

54. The method of any one of the preceding embodiments, wherein the plurality of phased variants comprises at least 3, at least 4, at least 5, at least 10, at least 15, at least 20, or at least 25 phased variants within the same cell-free nucleic acid molecule.

55. The method of any one of the preceding embodiments, wherein the one or more cell-free nucleic acid molecules identified comprises at least 2, at least 3, at least 4, at least 5, at least 10, at least 50, at least 100, at least 500, or at least 1,000 cell-free nucleic acid molecules.

56. The method of any one of the preceding embodiments, wherein the reference genomic sequence is derived from a reference cohort.

57. The method of embodiment 56, wherein the reference genomic sequence comprises a consensus sequence from the reference cohort.

58. The method of embodiment 56, wherein the reference genomic sequence comprises at least a portion of hg19 human genome, hg18 genome, hg17 genome, hg16 genome, or hg38 genome.

59. The method of any one of the preceding embodiments, wherein the reference genomic sequence is derived from a sample of the subject.

60. The method of embodiment 59, wherein the sample is a healthy sample.

61. The method of embodiment 60, wherein the sample comprises a healthy cell.

62. The method of embodiment 61, wherein the healthy cell comprises a healthy leukocyte.

63. The method of embodiment 59, wherein the sample is a diseased sample.

64. The method of embodiment 63, wherein the diseased sample comprises a diseased cell.

65. The method of embodiment 64, wherein the diseased cell comprises a tumor cell.

66. The method of embodiment 63, wherein the diseased sample comprises a solid tumor.

67. The method of any one of the preceding embodiments, wherein the set of nucleic acid probes is designed based on the plurality of phased variants that are identified by comparing (i) sequencing data from a solid tumor, lymphoma, or blood tumor of the subject and (ii) sequencing data from a healthy cell of the subject or a healthy cohort.

68. The method of embodiment 67, wherein the healthy cell is from the subject.

69. The method of embodiment 67, wherein the healthy cell is from the healthy cohort.

70. The method of any one of the preceding embodiments, wherein the set of nucleic acid probes are designed to hybridize to at least a portion of sequences of genomic loci associated with the condition.

71. The method of embodiment 70, wherein the genomic loci associated with the condition are known to exhibit aberrant somatic hypermutation when the subject has the condition.

72. The method of any one of the preceding embodiments, wherein the set of nucleic acid probes are designed to hybridize to at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3.

73. The method of any one of the preceding embodiments, wherein each nucleic acid probe of the set of nucleic acid probes has at least about 70%, at least about 80%, at least about 90% sequence identity, at least about 95% sequence identity, or about 100% sequence identity to a probe sequence selected from Table 6.

74. The method of any one of the preceding embodiments, wherein the set of nucleic acid probes comprises at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90% of probe sequences in Table 6.

75. The method of any one of the preceding embodiments, further comprising determining that the subject has the condition or determining a degree or status of the condition of the subject, based on the identified one or more cell-free nucleic acid molecules comprising the plurality of phased variants.

76. The method of embodiment 75, further comprising determining that the one or more cell-free nucleic acid molecules are derived from a sample associated with the condition, based on performing a statistical model analysis of the identified one or more cell-free nucleic acid molecules.

77. The method of embodiment 76, wherein the statistical model analysis comprises a Monte Carlo statistical analysis.

78. The method of any one of the preceding embodiments, further comprising monitoring a progress of the condition of the subject based on the identified one or more cell-free nucleic acid molecules.

79. The method of any one of the preceding embodiments, further comprising performing a different procedure to confirm the condition of the subject.

80. The method of embodiment 79, wherein the different procedure comprises a blood test, genetic test, medical imaging, physical exam, or tissue biopsy.

81. The method of any one of the preceding embodiments, further comprising determining a treatment for the condition of the subject based on the identified one or more cell-free nucleic acid molecules.

82. The method of any one of the preceding embodiments, wherein the subject has been subjected to a treatment for the condition prior to (a).

83. The method of any one of the preceding embodiments, wherein the treatment comprises chemotherapy, radiotherapy, chemoradiotherapy, immunotherapy, adoptive cell therapy, hormone therapy, targeted drug therapy, surgery, transplant, transfusion, or medical surveillance.

84. The method of any one of the preceding embodiments, wherein the plurality of cell-free nucleic acid molecules comprise a plurality of cell-free deoxyribonucleic acid (DNA) molecules.

85. The method of any one of the preceding embodiments, wherein the condition comprises a disease.

86. The method of any one of the preceding embodiments, wherein the plurality of cell-free nucleic acid molecules are derived from a bodily sample of the subject.

87. The method of embodiment 86, wherein the bodily sample comprises plasma, serum, blood, cerebrospinal fluid, lymph fluid, saliva, urine, or stool.

88. The method of any one of the preceding embodiments, wherein the subject is a mammal.

89. The method of any one of the preceding embodiments, wherein the subject is a human.

90. The method of any one of the preceding embodiments, wherein the condition comprises neoplasm, cancer, or tumor.

91. The method of embodiment 90, wherein the condition comprises a solid tumor.

92. The method of embodiment 90, wherein the condition comprises a lymphoma.

93. The method of embodiment 92, wherein the condition comprises a B-cell lymphoma.

94. The method of embodiment 93, wherein the condition comprises a sub-type of B-cell lymphoma selected from the group consisting of diffuse large B-cell lymphoma, follicular lymphoma, Burkitt lymphoma, and B-cell chronic lymphocytic leukemia.

95. The method of any one of the preceding embodiments, wherein the plurality of phased variants have been previously identified as tumor-derived from sequencing a prior tumor sample or cell-free nucleic acid sample.

96. The method of any one of embodiments 36-95, wherein (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the condition of the subject based at least in part on the identified one or more indels.

97. The method of any one of embodiments 36-96, wherein the subject has received an organ or tissue transplant, and wherein the condition comprises transplant rejection of the subject.

98. A composition comprising a bait set comprising a set of nucleic acid probes designed to capture cell-free DNA molecules derived from at least about 5% of genomic regions set forth in (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3.

99. The composition of embodiment 98, wherein the set of nucleic acid probes are designed to pull down cell-free DNA molecules derived from at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of the genomic regions set forth in (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3.

100. The composition of any one of embodiments 98-99, wherein the set of nucleic acid probes are designed to capture the one or more cell-free DNA molecules derived from at most about 10%, at most about 20%, at most about 30%, at most about 40%, at most about 50%, at most about 60%, at most about 70%, at most about 80%, at most about 90%, or about 100% of the genomic regions set forth in (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3.

101. The composition of any one of embodiments 98-100, wherein the bait set comprises at most 5, at most 10, at most 50, at most 100, at most 500, at most 1000, or at most 2000 nucleic acid probes.

102. The composition of any one of embodiments 98-101, wherein an individual nucleic acid probe of the set of nucleic acid probes comprises a pull-down tag.

103. The composition of any one of embodiments 98-102, wherein the pull-down tag comprises a nucleic acid barcode.

104. The composition of any one of embodiments 98-103, wherein the pull-down tag comprises biotin.

105. The composition of any one of embodiments 98-104, wherein each of the cell-free DNA

molecules is between about 100 nucleotides and about 180 nucleotides in length.

106. The composition of any one of embodiments 98-105, wherein the genomic regions are associated with a condition.

107. The composition of any one of embodiments 98-106, wherein the genomic regions exhibit aberrant somatic hypermutation when a subject has the condition.

108. The composition of any one of embodiments 98-107, wherein the condition comprises a B-cell lymphoma.

109. The composition of embodiment 108, wherein the condition comprises a sub-type of B-cell lymphoma selected from the group consisting of diffuse large B-cell lymphoma, follicular lymphoma, Burkitt lymphoma, and B-cell chronic lymphocytic leukemia.

110. The composition of any one of embodiments 98-109, further comprising a plurality of cell-free DNA molecules obtained or derived from a subject.

111. A method to perform a clinical procedure on an individual, the method comprising:

obtaining or having obtained a targeted sequencing result of a collection of cell-free nucleic acid molecules,

wherein the collection of cell-free nucleic acid molecules are sourced from a liquid or waste biopsy of an individual, and

wherein the targeting sequencing is performed utilizing nucleic acid probes to pull down sequences of genomic loci known to experience aberrant somatic hypermutation in a B-cell cancer;

identifying or having identified a plurality of variants in phase within the cell-free nucleic acid sequencing result;

determining or having determined, utilizing a statistical model and the identified phased variants, that the cell-free nucleic acid sequencing result contains nucleotides derived from a neoplasm; and

performing a clinical procedure on the individual to confirm the presence of the B-cell cancer, based upon determining that the cell-free nucleic acid sequencing result contains nucleic acid sequences likely derived from the B-cell cancer.

112. The method of embodiment 111, wherein the biopsy is one of blood, serum, cerebrospinal fluid, lymph fluid, urine, or stool.

113. The method of embodiment 111, wherein the genomic loci are selected from (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3.

114. The method of embodiment 111, wherein the sequences of the nucleic acid probes are

selected from Table 6.

115. The method of embodiment 111, wherein the clinical is procedure is a blood test, medical imaging, or a physical exam.

116. The method of any one of embodiments 111-115, further comprising identifying or having identified one or more insertions or deletions (indels) within the cell-free nucleic acid sequencing result, and determining or having determined, based least in part on the identified one or more indels, that the cell-free nucleic acid sequencing result contains the nucleotides derived from the neoplasm.

117. A method to treat an individual for a B-cell cancer, the method comprising:

obtaining or having obtained a targeted sequencing result of a collection of cell-free nucleic acid molecules,

wherein the collection of cell-free nucleic acid molecules are sourced from a liquid or waste biopsy of an individual, and

wherein the targeting sequencing is performed utilizing nucleic acid probes to pull down sequences of genomic loci known to experience aberrant somatic hypermutation in a B-cell cancer;

identifying or having identified a plurality of variants in phase within the cell-free nucleic acid sequencing result;

determining or having determined, utilizing a statistical model and the identified phased variants, that the cell-free nucleic acid sequencing result contains nucleotides derived from a neoplasm; and

treating the individual to curtail the B-cell cancer, based upon determining that the cell-free nucleic acid sequencing result contains nucleic acid sequences derived from the B-cell cancer.

118. The method of embodiment 117, wherein the biopsy is one of blood, serum, cerebrospinal fluid, lymph fluid, urine or stool.

119. The method of embodiment 117, wherein the genomic loci are selected from (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3.

120. The method of embodiment 117, wherein the sequences of the nucleic acid probes are selected from Table 6.

121. The method of embodiment 117, wherein the treatment is chemotherapy, radiotherapy, immunotherapy, hormone therapy, targeted drug therapy, or medical surveillance.

122. The method of any one of embodiments 117-121, further comprising identifying or

having identified one or more insertions or deletions (indels) within the cell-free nucleic acid sequencing result, and determining or having determined, based least in part on the identified one or more indels, that the cell-free nucleic acid sequencing result contains the nucleotides derived from the neoplasm.

123. A method to detect cancerous minimal residual disease in an individual and to treat the individual for a cancer, the method comprising:

obtaining or having obtained a targeted sequencing result of a collection of cell-free nucleic acid molecules,

wherein the collection of cell-free nucleic acid molecules are sourced from a liquid or waste biopsy of an individual,

wherein the liquid or waste biopsy is sourced after a series of treatments in order to detect minimal residual disease, and

wherein the targeting sequencing is performed utilizing nucleic acid probes to pull down sequences of genomic loci determined to contain a plurality of variants in phase, as determined by a prior sequencing result on a prior biopsy derived from the cancer;

identifying or having identified at least one set of the plurality of variants in phase within the cell-free nucleic acid sequencing result; and

treating the individual to curtail the cancer, based upon determining that the cell-free nucleic acid sequencing result contains nucleic acid sequences derived from the cancer.

124. The method of embodiment 123, wherein the liquid or waste biopsy is one of blood, serum, cerebrospinal fluid, lymph fluid, urine or stool.

125. The method of embodiment 123, wherein the treatment is chemotherapy, radiotherapy, immunotherapy, hormone therapy, targeted drug therapy, or medical surveillance.

126. The method of any one of embodiments 123-125, further comprising identifying or having identified one or more insertions or deletions (indels) within the cell-free nucleic acid sequencing result, and treating the individual to curtail the cancer, based least in part on the identified one or more indels.

127. A computer program product comprising a non-transitory computer-readable medium having computer-executable code encoded therein, the computer-executable code adapted to be executed to implement a method according to any one of the preceding embodiments.

128. A system comprising one or more computer processors and computer memory coupled thereto, wherein the computer memory comprises machine executable code that, upon execution by the one or more computer processors, implements a method according to any one of the preceding embodiments.

129. A method comprising:

(a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that are obtained or derived from a subject;

(b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises one or more insertions or deletions (indels) relative to a reference genomic sequence; and

(c) analyzing, by the computer system, the one or more indels to determine a condition of the subject.

130. A method comprising:

(a) obtaining sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject;

(b) processing the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules with a limit of detection of less than about 1 out of 50,000 observations from the sequencing data, wherein each of the one or more cell-free nucleic acid molecules comprises one or more insertions or deletions (indels) relative to a reference genomic sequence; and

(c) analyzing the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

131. The method of embodiment 129 or 130, wherein the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 observations from the sequencing data.

132. The method of any one of embodiments 129-131, wherein (a) to (c) are performed by a computer system.

133. The method of any one of embodiments 129-132, wherein the sequencing data is generated based on nucleic acid amplification.

134. The method of any one of embodiments 129-133, wherein the sequencing data is generated based on polymerase chain reaction.

135. The method of any one of embodiments 129-134, wherein the sequencing data is generated based on amplicon sequencing.

136. The method of any one of embodiments 129-135, wherein the sequencing data is generated based on next-generation sequencing (NGS).

137. The method of any one of embodiments 129-136, wherein the sequencing data is

generated based on non-hybridization-based NGS.

138. The method of any one of embodiments 129-137, wherein the sequencing data is generated without use of molecular barcoding of at least a portion of the plurality of cell-free nucleic acid molecules.

139. The method of any one of embodiments 129-138, wherein the sequencing data is obtained without use of sample barcoding of at least a portion of the plurality of cell-free nucleic acid molecules.

140. The method of any one of embodiments 129-139, wherein the sequencing data is obtained without in silico removal or suppression of (i) background error or (ii) sequencing error.

141. A method of treating a condition of a subject, the method comprising:

(a) identifying the subject for treatment of the condition, wherein the subject has been determined to have the condition based on identification of one or more cell-free nucleic acid molecules from a plurality of cell-free nucleic acid molecules that is obtained or derived from the subject,

wherein each of the one or more cell-free nucleic acid molecules comprises one or more insertions or deletions (indels) relative to a reference genomic sequence, and

wherein a presence of the one or more indels is indicative of the condition of the subject; and

(b) subjecting the subject to the treatment based on the identification in (a).

142. A method of monitoring a progress of a condition of a subject, the method comprising:

(a) determining a first state of the condition of the subject based on identification of a first set of one or more cell-free nucleic acid molecules from a first plurality of cell-free nucleic acid molecules that is obtained or derived from the subject;

(b) determining a second state of the condition of the subject based on identification of a second set of one or more cell-free nucleic acid molecules from a second plurality of cell-free nucleic acid molecules that is obtained or derived from the subject,

wherein the second plurality of cell-free nucleic acid molecules are obtained from the subject subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject; and

(c) determining the progress of the condition based on the first state of the condition and the second state of the condition,

wherein each of the one or more cell-free nucleic acid molecules comprises one or more insertions or deletions (indels) relative to a reference genomic sequence.

143. The method of embodiment 142, wherein the progress of the condition is worsening of the condition.

144. The method of embodiment 142, wherein the progress of the condition is at least a partial remission of the condition.

145. The method of any one of embodiments 142-144, wherein a presence of the one or more indels is indicative of the first state or the second state of the condition of the subject.

146. The method of any one of embodiments 142-145, wherein the second plurality of cell-free nucleic acid molecules is obtained from the subject at least about 1 week, at least about 2 weeks, at least about 3 weeks, at least about 4 weeks, at least about 2 months, or at least about 3 months subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject.

147. The method of any one of embodiments 142-146, wherein the subject is subjected to a treatment for the condition (i) prior to obtaining the second plurality of cell-free nucleic acid molecules from the subject and (ii) subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject.

148. The method of any one of embodiments 142-147, wherein the progress of the condition is indicative of minimal residual disease of the condition of the subject.

149. The method of any one of embodiments 142-148, wherein the progress of the condition is indicative of tumor burden or cancer burden of the subject.

150. The method of any one of embodiments 142-149, wherein the one or more cell-free nucleic acid molecules are captured from among the plurality of cell-free nucleic acid molecules with a set of nucleic acid probes, wherein the set of nucleic acid probes is configured to hybridize to at least a portion of cell-free nucleic acid molecules comprising one or more genomic regions associated with the condition.

151. A method comprising:

(a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject,

wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising one or more insertions or deletions (indels) relative to a reference genomic sequence, and

wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the one or more indels and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been

hybridized to the one or more indels;

(b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the one or more indels; and

(c) analyzing the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

152. A method comprising:

(a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject,

wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising one or more insertions or deletions (indels) relative to a reference genomic sequence, and

wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the one or more indels and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the one or more indels;

(b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the one or more indels, wherein a limit of detection of the identification step is less than about 1 out of 50,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules; and

(c) analyzing the identified one or more cell-free nucleic acid molecules to determine a condition of the subject.

153. The method of embodiment 151 or 152, wherein the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules.

154. The method of any one of embodiments 151-153, wherein the activatable reporter agent is activated upon hybridization of the individual nucleic acid probe to the one or more indels.

155. The method of any one of embodiments 151-154, wherein the activatable reporter agent is activated upon dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the one or more indels.

156. The method of any one of embodiments 151-155, further comprising mixing (1) the set

of nucleic acid probes and (2) the plurality of cell-free nucleic acid molecules.

157. The method of any one of embodiments 151-156, wherein the activatable reporter agent is a fluorophore.

158. The method of any one of embodiments 151-157, wherein analyzing the identified one or more cell-free nucleic acid molecules comprises analyzing (i) the identified one or more cell-free nucleic acid molecules and (ii) other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the one or more indels as different variables.

159. The method of any one of embodiments 151-158, wherein the analyzing of the identified one or more cell-free nucleic acid molecules is not based on other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the one or more indels.

160. The method of any one of embodiments 151-159, wherein a number of the one or more indels from the identified one or more cell-free nucleic acid molecules is indicative of the condition of the subject.

161. The method of any one of embodiments 151-160, wherein a ratio of (i) the number of the one or more indels from the one or more cell-free nucleic acid molecules and (ii) a number of single nucleotide variants (SNVs) from the one or more cell-free nucleic acid molecules is indicative of the condition of the subject.

162. The method of any one of embodiments 151-161, wherein a frequency of the one or more indels in the identified one or more cell-free nucleic acid molecules is indicative of the condition of the subject.

163. The method of embodiment 162, wherein the frequency is indicative of a diseased cell associated with the condition.

164. The method of embodiment 163, wherein the condition is diffuse large B-cell lymphoma, and wherein the frequency is indicative of whether the one or more cell-free nucleic acid molecules are derived from germinal center B-cell (GCB) or activated B-cell (ABC).

165. The method of any one of embodiments 151-164, wherein genomic origin of the identified one or more cell-free nucleic acid molecules is indicative of the condition of the subject.

166. The method of any one of embodiments 151-165, wherein the one or more indels comprises at least 3, at least 4, at least 5, or at least 10 indels within the same cell-free nucleic acid molecule.

167. The method of any one of embodiments 151-166, wherein the one or more cell-free

nucleic acid molecules identified comprises at least 2, at least 3, at least 4, at least 5, at least 10, at least 50, at least 100, at least 500, or at least 1,000 cell-free nucleic acid molecules.

168. The method of any one of embodiments 151-167, wherein the reference genomic sequence is derived from a reference cohort.

169. The method of embodiment 168, wherein the reference genomic sequence comprises a consensus sequence from the reference cohort.

170. The method of embodiment 168, wherein the reference genomic sequence comprises at least a portion of hg19 human genome, hg18 genome, hg17 genome, hg16 genome, or hg38 genome.

171. The method of any one of embodiments 151-170, wherein the reference genomic sequence is derived from a sample of the subject.

172. The method of embodiment 171, wherein the sample is a healthy sample.

173. The method of embodiment 172, wherein the sample comprises a healthy cell.

174. The method of embodiment 173, wherein the healthy cell comprises a healthy leukocyte.

175. The method of embodiment 171, wherein the sample is a diseased sample.

176. The method of embodiment 175, wherein the diseased sample comprises a diseased cell.

177. The method of embodiment 176, wherein the diseased cell comprises a tumor cell.

178. The method of embodiment 175, wherein the diseased sample comprises a solid tumor.

179. The method of any one of embodiments 151-178, wherein the set of nucleic acid probes is designed based on the one or more indels that are identified by comparing (i) sequencing data from a solid tumor, lymphoma, or blood tumor of the subject and (ii) sequencing data from a healthy cell of the subject or a healthy cohort.

180. The method of embodiment 179, wherein the healthy cell is from the subject.

181. The method of embodiment 179, wherein the healthy cell is from the healthy cohort.

182. The method of any one of embodiments 151-181, wherein the set of nucleic acid probes are designed to hybridize to at least a portion of sequences of genomic loci associated with the condition.

183. The method of embodiment 182, wherein the genomic loci associated with the condition are known to exhibit aberrant somatic hypermutation when the subject has the condition.

184. The method of any one of embodiments 151-183, wherein the set of nucleic acid probes

are designed to hybridize to at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of (i) the genomic regions identified in Table 1, or (ii) the genomic regions identified in Table 3.

185. The method of any one of embodiments 151-184, wherein each nucleic acid probe of the set of nucleic acid probes has at least about 70%, at least about 80%, at least about 90% sequence identity, at least about 95% sequence identity, or about 100% sequence identity to a probe sequence selected from Table 6.

186. The method of any one of embodiments 151-185, wherein the set of nucleic acid probes comprises at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90% of probe sequences in Table 6.

187. The method of any one of embodiments 151-186, further comprising determining that the subject has the condition or determining a degree or status of the condition of the subject, based on the identified one or more cell-free nucleic acid molecules comprising the one or more indels.

188. The method of embodiment 187, further comprising determining that the one or more cell-free nucleic acid molecules are derived from a sample associated with the condition, based on performing a statistical model analysis of the identified one or more cell-free nucleic acid molecules.

189. The method of embodiment 188, wherein the statistical model analysis comprises a Monte Carlo statistical analysis.

190. The method of any one of embodiments 151-189, further comprising monitoring a progress of the condition of the subject based on the identified one or more cell-free nucleic acid molecules.

191. The method of any one of embodiments 151-190, further comprising performing a different procedure to confirm the condition of the subject.

192. The method of embodiment 191, wherein the different procedure comprises a blood test, genetic test, medical imaging, physical exam, or tissue biopsy.

193. The method of any one of embodiments 151-192, further comprising determining a treatment for the condition of the subject based on the identified one or more cell-free nucleic acid molecules.

194. The method of any one of embodiments 151-193, wherein the subject has been subjected to a treatment for the condition prior to (a).

195. The method of any one of embodiments 151-194, wherein the treatment comprises chemotherapy, radiotherapy, chemoradiotherapy, immunotherapy, adoptive cell therapy, hormone therapy, targeted drug therapy, surgery, transplant, transfusion, or medical surveillance.

196. The method of any one of embodiments 151-195, wherein the plurality of cell-free nucleic acid molecules comprise a plurality of cell-free deoxyribonucleic acid (DNA) molecules.

197. The method of any one of embodiments 151-196, wherein the condition comprises a disease.

198. The method of any one of embodiments 151-197, wherein the plurality of cell-free nucleic acid molecules are derived from a bodily sample of the subject.

199. The method of embodiment 198, wherein the bodily sample comprises plasma, serum, blood, cerebrospinal fluid, lymph fluid, saliva, urine, or stool.

200. The method of any one of embodiments 151-199, wherein the subject is a mammal.

201. The method of any one of embodiments 151-200, wherein the subject is a human.

202. The method of any one of embodiments 151-201, wherein the condition comprises neoplasm, cancer, or tumor.

203. The method of embodiment 202, wherein the condition comprises a solid tumor.

204. The method of embodiment 202, wherein the condition comprises a lymphoma.

205. The method of embodiment 204, wherein the condition comprises a B-cell lymphoma.

206. The method of embodiment 205, wherein the condition comprises a sub-type of B-cell lymphoma selected from the group consisting of diffuse large B-cell lymphoma, follicular lymphoma, Burkitt lymphoma, and B-cell chronic lymphocytic leukemia.

207. The method of any one of embodiments 151-206, wherein the one or more indels have been previously identified as tumor-derived from sequencing a prior tumor sample or cell-free nucleic acid sample.

208. A method to perform a clinical procedure on an individual, the method comprising:

obtaining or having obtained a targeted sequencing result of a collection of cell-free nucleic acid molecules,

wherein the collection of cell-free nucleic acid molecules are sourced from a liquid or waste biopsy of an individual, and

wherein the targeting sequencing is performed utilizing nucleic acid probes to pull down sequences of genomic loci known to experience aberrant somatic hypermutation in a B-cell cancer;

identifying or having identified one or more insertions or deletions (indels) within the cell-free nucleic acid sequencing result;

determining or having determined, utilizing a statistical model and the identified one or more indels, that the cell-free nucleic acid sequencing result contains nucleotides derived from a neoplasm; and

performing a clinical procedure on the individual to confirm the presence of the B-cell cancer, based upon determining that the cell-free nucleic acid sequencing result contains nucleic acid sequences likely derived from the B-cell cancer.

209. The method of embodiment 208, wherein the biopsy is one of blood, serum, cerebrospinal fluid, lymph fluid, urine, or stool.

210. The method of embodiment 208 or 209, wherein the genomic loci are selected from (i) the genomic regions identified in Table 1, or (ii) the genomic regions identified in Table 3.

211. The method of any one of embodiments 208-210, wherein the sequences of the nucleic acid probes are selected from Table 6.

212. The method of any one of embodiments 208-211, wherein the clinical is procedure is a blood test, medical imaging, or a physical exam.

213. A method to treat an individual for a B-cell cancer, the method comprising:

obtaining or having obtained a targeted sequencing result of a collection of cell-free nucleic acid molecules,

wherein the collection of cell-free nucleic acid molecules are sourced from a liquid or waste biopsy of an individual, and

wherein the targeting sequencing is performed utilizing nucleic acid probes to pull down sequences of genomic loci known to experience aberrant somatic hypermutation in a B-cell cancer;

identifying or having identified one or more insertions or deletions (indels) within the cell-free nucleic acid sequencing result;

determining or having determined, utilizing a statistical model and the identified one or more indels, that the cell-free nucleic acid sequencing result contains nucleotides derived from a neoplasm; and

treating the individual to curtail the B-cell cancer, based upon determining that the cell-free nucleic acid sequencing result contains nucleic acid sequences derived from the B-cell cancer.

214. The method of embodiment 213, wherein the biopsy is one of blood, serum, cerebrospinal fluid, lymph fluid, urine or stool.

215. The method of embodiment 213 or 214, wherein the genomic loci are selected from (i) the genomic regions identified in Table 1, or (ii) the genomic regions identified in Table 3.

216. The method of any one of embodiments 213-215, wherein the sequences of the nucleic acid probes are selected from Table 6.

217. The method of any one of embodiments 213-216, wherein the treatment is chemotherapy, radiotherapy, immunotherapy, hormone therapy, targeted drug therapy, or medical surveillance.

218. A method to detect cancerous minimal residual disease in an individual and to treat the individual for a cancer, the method comprising:

obtaining or having obtained a targeted sequencing result of a collection of cell-free nucleic acid molecules,

wherein the collection of cell-free nucleic acid molecules are sourced from a liquid or waste biopsy of an individual,

wherein the liquid or waste biopsy is sourced after a series of treatments in order to detect minimal residual disease, and

wherein the targeting sequencing is performed utilizing nucleic acid probes to pull down sequences of genomic loci determined to contain one or more insertions or deletions (indels), as determined by a prior sequencing result on a prior biopsy derived from the cancer;

identifying or having identified at least one set of the one or more indels within the cell-free nucleic acid sequencing result; and

treating the individual to curtail the cancer, based upon determining that the cell-free nucleic acid sequencing result contains nucleic acid sequences derived from the cancer.

219. The method of embodiment 218, wherein the liquid or waste biopsy is one of blood, serum, cerebrospinal fluid, lymph fluid, urine or stool.

220. The method of embodiment 218 or 219, wherein the treatment is chemotherapy, radiotherapy, immunotherapy, hormone therapy, targeted drug therapy, or medical surveillance.

221. A computer program product comprising a non-transitory computer-readable medium having computer-executable code encoded therein, the computer-executable code adapted to be executed to implement a method according to any one of the preceding embodiments.

222. A system comprising one or more computer processors and computer memory coupled thereto, wherein the computer memory comprises machine executable code that, upon execution by the one or more computer processors, implements a method according to any one of the preceding embodiments.

223. A method comprising:

(a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject who has received an organ or tissue transplant;

(b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence, wherein at least about 10% of the one or more cell-free nucleic acid molecules comprises a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants that are separated by at least one nucleotide; and

(c) analyzing, by the computer system, the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an extent of transplant rejection of the subject.

224. The method of embodiment 223, wherein the at least about 10% of the cell-free nucleic acid molecules comprise at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of the one or more cell-free nucleic acid molecules.

225. The method of embodiment 223 or 224, wherein (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the extent of transplant rejection of the subject based at least in part on the identified one or more indels.

226. A method comprising:

(a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject who has received an organ or tissue transplant;

(b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide; and

(c) analyzing, by the computer system, the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an extent of transplant rejection of the subject.

227. The method of embodiment 226, wherein (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the extent of transplant rejection of the subject based at least in part on the identified one or more indels.

228. A method comprising:

(a) obtaining sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject who has received an organ or tissue transplant;

(b) processing the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules with a limit of detection of less than about 1 out of 50,000 observations from the sequencing data; and

(c) analyzing the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an extent of transplant rejection of the subject.

229. The method of any one of embodiments 223-228, wherein the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 observations from the sequencing data.

230. The method of any one of embodiments 223-229, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence.

231. The method of embodiment 230, wherein a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide.

232. The method of any one of embodiments 223-231, wherein (a) to (c) are performed by a computer system.

233. The method of any one of embodiments 223-232, wherein the sequencing data is generated based on nucleic acid amplification.

234. The method of any one of embodiments 223-233, wherein the sequencing data is generated based on polymerase chain reaction.

235. The method of any one of embodiments 223-234, wherein the sequencing data is generated based on amplicon sequencing.

236. The method of any one of embodiments 223-235, wherein the sequencing data is generated based on next-generation sequencing (NGS).

237. The method of any one of embodiments 223-236, wherein the sequencing data is

generated based on non-hybridization-based NGS.

238. The method of any one of embodiments 223-237, wherein the sequencing data is generated without use of molecular barcoding of at least a portion of the plurality of cell-free nucleic acid molecules.

239. The method of any one of embodiments 223-238, wherein the sequencing data is obtained without use of sample barcoding of at least a portion of the plurality of cell-free nucleic acid molecules.

240. The method of any one of embodiments 223-239, wherein the sequencing data is obtained without in silico removal or suppression of (i) background error or (ii) sequencing error.

241. The method of any one of embodiments 223-240, wherein (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the extent of the transplant rejection of the subject based at least in part on the identified one or more indels.

242. A method of treating a transplant rejection of a subject who has received an organ or tissue transplant, the method comprising:

(a) identifying the subject for treatment of the transplant rejection, wherein the subject has been determined to have the transplant rejection based on identification of one or more cell-free nucleic acid molecules from a plurality of cell-free nucleic acid molecules that are obtained or derived from the subject,

wherein each of the one or more cell-free nucleic acid molecules identified comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide, and

wherein a presence of the plurality of phased variants is indicative of the transplant rejection of the subject; and

(b) subjecting the subject to the treatment based on the identification in (a).

243. The method of embodiment 242, wherein the subject has been determined to have the transplant rejection based at least in part on one or more insertions or deletions (indels) identified in the one or more cell-free nucleic acid molecules.

244. The method of embodiment 242 or 243, wherein the plurality of cell-free nucleic acid molecules are donor-derived cell-free nucleic acid molecules.

245. The method of any one of embodiments 242-244, wherein the reference genomic sequence comprises at least a portion of hg19 human genome, hg18 genome, hg17 genome,

hg16 genome, or hg38 genome.

246. The method of any one of embodiments 242-245, wherein the treatment is selected from the group consisting of an immunosuppressive drug, an anti-body based treatment, a blood transfer, a marrow transplant, a gene therapy, a transplant removal, and a re-transplant procedure.

247. The method of embodiment 246, wherein the immunosuppressive drug is selected from the group consisting of a corticosteroid, a calcineurin inhibitor, an anti-proliferative, and an mTOR inhibitor.

248. The method of embodiment 246, wherein the antibody-based treatment is selected from the group consisting of a monoclonal anti-IL-2Rα receptor antibody, a polyclonal anti-T-cell, and a monoclonal anti-CD20 antibody.

249. A method of monitoring a subject who has received an organ or tissue transplant for a presence, an absence, or an extent of transplant rejection, the method comprising:

(a) determining a first state of the presence, the absence, or the extent of transplant rejection of the subject based on identification of a first set of one or more cell-free nucleic acid molecules from a first plurality of cell-free nucleic acid molecules that is obtained or derived from the subject;

(b) determining a second state of the presence, the absence, or the extent of transplant rejection of the subject based on identification of a second set of one or more cell-free nucleic acid molecules from a second plurality of cell-free nucleic acid molecules that is obtained or derived from the subject,

wherein the second plurality of cell-free nucleic acid molecules are obtained from the subject subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject; and

(c) determining a transplant rejection status of the subject based on the first state and the second state,

wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide.

250. The method of embodiment 249, wherein the transplant rejection status is at least a partial transplant rejection.

251. The method of any one of embodiments 249-250, wherein a presence of the plurality of phased variants is indicative of the first state or the second state.

252. The method of any one of embodiments 249-251, wherein the second plurality of cell-

free nucleic acid molecules is obtained from the subject at least about 1 week, at least about 2 weeks, at least about 3 weeks, at least about 4 weeks, at least about 2 months, or at least about 3 months subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject.

253. The method of any one of embodiments 249-252, wherein the subject has been determined to have the presence, the absence, or the extent of the transplant rejection based at least in part on one or more insertions or deletions (indels) identified in the one or more cell-free nucleic acid molecules.

254. The method of any one of embodiments 249-253, wherein the plurality of cell-free nucleic acid molecules are donor-derived cell-free nucleic acid molecules.

255. The method of any one of embodiments 249-254, wherein the reference genomic sequence comprises at least a portion of hg19 human genome, hg18 genome, hg17 genome, hg16 genome, or hg38 genome.

256. A method comprising:

(a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that are obtained or derived from a subject who has received an organ or tissue transplant,

wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide, and

wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the plurality of phased variants and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants;

(b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the plurality of phased variants; and

(c) analyzing the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an extent of transplant rejection of the subject.

257. The method of any one of embodiments 253-256, wherein (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid

molecules, and wherein (c) further comprises determining the presence or the absence of the transplant rejection of the subject based at least in part on the identified one or more indels.

258. The method of any one of embodiments 253-257, wherein the plurality of cell-free nucleic acid molecules are donor-derived cell-free nucleic acid molecules.

259. The method of any one of embodiments 253-258, wherein the reference genomic sequence comprises at least a portion of hg19 human genome, hg18 genome, hg17 genome, hg16 genome, or hg38 genome.

260. A method comprising:

(a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a subject who has received an organ or tissue transplant,

wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising a plurality of phased variants relative to a reference genomic sequence, and

wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the plurality of phased variants and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants;

(b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the plurality of phased variants, wherein a limit of detection of the identification step is less than about 1 out of 50,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules; and

(c) analyzing the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an extent of transplant rejection of the subject.

261. The method of any one of embodiments 223-260, wherein the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules.

262. The method of any one of embodiments 223-261, wherein a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide.

263. The method of any one of embodiments 223-262, wherein the activatable reporter agent

is activated upon hybridization of the individual nucleic acid probe to the plurality of phased variants.

264. The method of any one of embodiments 223-263, wherein the activatable reporter agent is activated upon dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants.

265. The method of any one of embodiments 223-264, further comprising mixing (1) the set of nucleic acid probes and (2) the plurality of cell-free nucleic acid molecules.

266. The method of any one of embodiments 223-265, wherein the activatable reporter agent is a fluorophore.

267. The method of any one of embodiments 223-266, wherein analyzing the identified one or more cell-free nucleic acid molecules comprises analyzing (i) the identified one or more cell-free nucleic acid molecules and (ii) other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants as different variables.

268. The method of any one of embodiments 223-267, wherein the analyzing of the identified one or more cell-free nucleic acid molecules is not based on other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants.

269. The method of any one of embodiments 223-268, wherein a number of the plurality of phased variants from the identified one or more cell-free nucleic acid molecules is indicative of the presence, the absence, or the extent of transplant rejection of the subject.

270. The method of embodiment 269, wherein a ratio of (i) the number of the plurality of phased variants from the one or more cell-free nucleic acid molecules and (ii) a number of single nucleotide variants (SNVs) from the one or more cell-free nucleic acid molecules is indicative of the presence, the absence, or the extent of transplant rejection of the subject.

271. The method of any one of embodiments 223-270, wherein a frequency of the plurality of phased variants in the identified one or more cell-free nucleic acid molecules is indicative of the presence or the absence of the transplant rejection of the subject.

272. The method of embodiment 271, wherein the frequency is indicative of a diseased cell associated with the presence, the absence, or the extent of transplant rejection.

273. The method of any one of embodiments 223-272, wherein genomic origin of the identified one or more cell-free nucleic acid molecules is indicative of the presence or the absence of the transplant rejection of the subject.

274. The method of any one of embodiments 223-273, wherein the first and second phased

variants are separated by at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 nucleotides.

275. The method of any one of embodiments 223-274, wherein the first and second phased variants are separated by at most about 180, at most about 170, at most about 160, at most about 150, or at most about 140 nucleotides.

276. The method of any one of embodiments 223-275, wherein at least about 10%, at least about 20%, at least about 30%, at least about 40%, or at least about 50% of the one or more cell-free nucleic acid molecules comprising a plurality of phased variants comprises a single nucleotide variant (SNV) that is at least 2 nucleotides away from an adjacent SNV.

277. The method of any one of embodiments 223-276, wherein the plurality of phased variants comprises at least 3, at least 4, at least 5, at least 10, at least 15, at least 20, or at least 25 phased variants within the same cell-free nucleic acid molecule.

278. The method of any one of embodiments 223-277, wherein the one or more cell-free nucleic acid molecules identified comprises at least 2, at least 3, at least 4, at least 5, at least 10, at least 50, at least 100, at least 500, or at least 1,000 cell-free nucleic acid molecules.

279. The method of any one of embodiments 223-278, wherein the reference genomic sequence comprises at least a portion of hg19 human genome, hg18 genome, hg17 genome, hg16 genome, or hg38 genome.

280. The method of any one of embodiments 223-279, wherein the set of nucleic acid probes are designed to hybridize to at least a portion of sequences of genomic loci.

281. The method of any one of embodiments 223-280, further comprising determining the presence or the absence of the transplant rejection or determining a degree or status thereof, based on the identified one or more cell-free nucleic acid molecules comprising the plurality of phased variants.

282. The method of embodiment 281, further comprising determining that the one or more cell-free nucleic acid molecules are derived from a sample associated with the presence or the absence of the transplant rejection, based on performing a statistical model analysis of the identified one or more cell-free nucleic acid molecules.

283. The method of embodiment 282, wherein the statistical model analysis comprises a Monte Carlo statistical analysis.

284. The method of any one of embodiments 223-283, further comprising monitoring a progress of the presence, the absence, or the extent of transplant rejection of the subject based on the identified one or more cell-free nucleic acid molecules.

285. The method of any one of embodiments 223-284, further comprising performing a

different procedure to confirm the presence, the absence, or the extent of transplant rejection of the subject.

286. The method of embodiment 285, wherein the different procedure comprises a blood test, genetic test, medical imaging, physical exam, or tissue biopsy.

287. The method of any one of embodiments 223-286, further comprising determining a treatment for the transplant rejection of the subject based on the identified one or more cell-free nucleic acid molecules.

288. The method of any one of embodiments 223-287, wherein the plurality of cell-free nucleic acid molecules comprise a plurality of cell-free deoxyribonucleic acid (DNA) molecules.

289. The method of any one of embodiments 223-288, wherein the plurality of cell-free nucleic acid molecules are derived from a bodily sample of the subject.

290. The method of embodiment 289, wherein the bodily sample comprises plasma, serum, blood, cerebrospinal fluid, lymph fluid, saliva, urine, or stool.

291. The method of any one of embodiments 223-290, wherein the subject is a mammal.

292. The method of any one of embodiments 223-291, wherein the subject is a human.

293. The method of any one of embodiments 223-292, wherein (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the extent of transplant rejection of the subject based at least in part on the identified one or more indels.

294. The method of any one of embodiments 257-293, wherein the plurality of cell-free nucleic acid molecules are donor-derived cell-free nucleic acid molecules.

295. A method comprising:

(a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a pregnant subject;

(b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence, wherein at least about 10% of the one or more cell-free nucleic acid molecules comprises a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants that are separated by at least one nucleotide; and

(c) analyzing, by the computer system, the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an elevated risk of a genetic abnormality of a fetus of the pregnant subject.

296. The method of embodiment 295, wherein the at least about 10% of the cell-free nucleic acid molecules comprise at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of the one or more cell-free nucleic acid molecules.

297. The method of embodiment 295 or 296, wherein (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based at least in part on the identified one or more indels.

298. The method of any one of embodiments 295-297, wherein the genetic abnormality is a chromosomal aneuploidy.

299. The method of embodiment 298, wherein the chromosomal aneuploidy is in chromosome 13, 18, 21, X, or Y.

300. The method of any one of embodiments 249-299, wherein the reference genomic sequence comprises at least a portion of hg19 human genome, hg18 genome, hg17 genome, hg16 genome, or hg38 genome.

301. A method comprising:

(a) obtaining, by a computer system, sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a pregnant subject;

(b) processing, by the computer system, the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide; and

(c) analyzing, by the computer system, the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an elevated risk of a genetic abnormality of a fetus of the pregnant subject.

302. The method of embodiment 301, wherein (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based at least in part on the identified one or

more indels.

303. The method of any one of embodiments 301-302, wherein the genetic abnormality is a chromosomal aneuploidy.

304. The method of embodiment 303, wherein the chromosomal aneuploidy is in chromosome 13, 18, 21, X, or Y.

305. A method comprising:

(a) obtaining sequencing data derived from a plurality of cell-free nucleic acid molecules that is obtained or derived from a pregnant subject;

(b) processing the sequencing data to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules with a limit of detection of less than about 1 out of 50,000 observations from the sequencing data; and

(c) analyzing the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an elevated risk of a genetic abnormality of a fetus of the pregnant subject.

306. The method of any one of embodiments 295-305, wherein the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 observations from the sequencing data.

307. The method of any one of embodiments 295-306, wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence.

308. The method of embodiment 307, wherein a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide.

309. The method of any one of embodiments 295-308, wherein (a) to (c) are performed by a computer system.

310. The method of any one of embodiments 295-309, wherein the sequencing data is generated based on nucleic acid amplification.

311. The method of any one of embodiments 295-310, wherein the sequencing data is generated based on polymerase chain reaction.

312. The method of any one of embodiments 295-311, wherein the sequencing data is generated based on amplicon sequencing.

313. The method of any one of embodiments 295-312, wherein the sequencing data is generated based on next-generation sequencing (NGS).

314. The method of any one of embodiments 295-313, wherein the sequencing data is generated based on non-hybridization-based NGS.

315. The method of any one of embodiments 295-314, wherein the sequencing data is generated without use of molecular barcoding of at least a portion of the plurality of cell-free nucleic acid molecules.

316. The method of any one of embodiments 295-315, wherein the sequencing data is obtained without use of sample barcoding of at least a portion of the plurality of cell-free nucleic acid molecules.

317. The method of any one of embodiments 295-316, wherein the sequencing data is obtained without in silico removal or suppression of (i) background error or (ii) sequencing error.

318. The method of any one of embodiments 295-317, wherein (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based at least in part on the identified one or more indels.

319. The method of any one of embodiments 295-318, wherein the genetic abnormality is a chromosomal aneuploidy.

320. The method of embodiment 319, wherein the chromosomal aneuploidy is in chromosome 13, 18, 21, X, or Y.

321. The method of any one of embodiments 295-320, wherein the one or more cell-free nucleic acid molecules are captured from among the plurality of cell-free nucleic acid molecules with a set of nucleic acid probes, wherein the set of nucleic acid probes is configured to hybridize to at least a portion of cell-free nucleic acid molecules comprising one or more genomic regions associated with the genetic abnormality.

322. The method of any one of embodiments 295-321, wherein the fetus has been determined to have the presence, the absence, or the elevated risk of the genetic abnormality based at least in part on one or more insertions or deletions (indels) identified in the one or more cell-free nucleic acid molecules.

323. A method comprising:

(a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a pregnant subject,

wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising

a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide, and

wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the plurality of phased variants and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants;

(b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the plurality of phased variants; and

(c) analyzing the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an elevated risk of a genetic abnormality of a fetus of the pregnant subject.

324. The method of embodiment 323, wherein (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the elevated risk of the genetic abnormality based at least in part on the identified one or more indels.

325. A method comprising:

(a) providing a mixture comprising (1) a set of nucleic acid probes and (2) a plurality of cell-free nucleic acid molecules that is obtained or derived from a pregnant subject,

wherein an individual nucleic acid probe of the set of nucleic acid probes is designed to hybridize to at least a portion of a target cell-free nucleic acid molecule comprising a plurality of phased variants relative to a reference genomic sequence, and

wherein the individual nucleic acid probe comprises an activatable reporter agent, activation of the activatable reporter agent being selected from the group consisting of: (i) hybridization of the individual nucleic acid probe to the plurality of phased variants and (ii) dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants;

(b) detecting the activatable reporter agent that is activated, to identify one or more cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules, wherein each of the one or more cell-free nucleic acid molecules comprises the plurality of phased variants, wherein a limit of detection of the identification step is less than about 1 out of 50,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules; and

(c) analyzing the identified one or more cell-free nucleic acid molecules to determine a presence, an absence, or an elevated risk of a genetic abnormality of a fetus of the pregnant subject.

326. The method of any one of embodiments 295-325, wherein the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules.

327. The method of any one of embodiments 295-326, wherein a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide.

328. The method of any one of embodiments 295-327, wherein the activatable reporter agent is activated upon hybridization of the individual nucleic acid probe to the plurality of phased variants.

329. The method of any one of embodiments 295-328, wherein the activatable reporter agent is activated upon dehybridization of at least a portion of the individual nucleic acid probe that has been hybridized to the plurality of phased variants.

330. The method of any one of embodiments 295-329, further comprising mixing (1) the set of nucleic acid probes and (2) the plurality of cell-free nucleic acid molecules.

331. The method of any one of embodiments 295-330, wherein the activatable reporter agent is a fluorophore.

332. The method of any one of embodiments 295-331, wherein analyzing the identified one or more cell-free nucleic acid molecules comprises analyzing (i) the identified one or more cell-free nucleic acid molecules and (ii) other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants as different variables.

333. The method of any one of embodiments 295-332, wherein the analyzing of the identified one or more cell-free nucleic acid molecules is not based on other cell-free nucleic acid molecules of the plurality of cell-free nucleic acid molecules that do not comprise the plurality of phased variants.

334. The method of any one of embodiments 295-333, wherein a number of the plurality of phased variants from the identified one or more cell-free nucleic acid molecules is indicative of the genetic abnormality.

335. The method of embodiment 334, wherein a ratio of (i) the number of the plurality of phased variants from the one or more cell-free nucleic acid molecules and (ii) a number of

single nucleotide variants (SNVs) from the one or more cell-free nucleic acid molecules is indicative of the genetic abnormality.

336. The method of any one of embodiments 295-335, wherein a frequency of the plurality of phased variants in the identified one or more cell-free nucleic acid molecules is indicative of the genetic abnormality.

337. The method of any one of embodiments 295-336, wherein genomic origin of the identified one or more cell-free nucleic acid molecules is indicative of the genetic abnormality.

338. The method of any one of embodiments 295-337, wherein the first and second phased variants are separated by at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 nucleotides.

339. The method of any one of embodiments 295-338, wherein the first and second phased variants are separated by at most about 180, at most about 170, at most about 160, at most about 150, or at most about 140 nucleotides.

340. The method of any one of embodiments 295-339, wherein at least about 10%, at least about 20%, at least about 30%, at least about 40%, or at least about 50% of the one or more cell-free nucleic acid molecules comprising a plurality of phased variants comprises a single nucleotide variant (SNV) that is at least 2 nucleotides away from an adjacent SNV.

341. The method of any one of embodiments 295-340, wherein the plurality of phased variants comprises at least 3, at least 4, at least 5, at least 10, at least 15, at least 20, or at least 25 phased variants within the same cell-free nucleic acid molecule.

342. The method of any one of embodiments 295-341, wherein the one or more cell-free nucleic acid molecules identified comprises at least 2, at least 3, at least 4, at least 5, at least 10, at least 50, at least 100, at least 500, or at least 1,000 cell-free nucleic acid molecules.

343. The method of any one of embodiments 295-342, wherein the reference genomic sequence comprises at least a portion of hg19 human genome, hg18 genome, hg17 genome, hg16 genome, or hg38 genome.

344. The method of any one of embodiments 295-343, wherein the set of nucleic acid probes are designed to hybridize to at least a portion of sequences of genomic loci.

345. The method of any one of embodiments 295-344, wherein the set of nucleic acid probes are designed to hybridize to at least a portion of sequences of genomic loci associated with the genetic abnormality.

346. The method of any one of embodiments 295-345, further comprising determining the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject, based on the identified one or more cell-free nucleic acid molecules comprising the

plurality of phased variants.

347. The method of embodiment 346, further comprising determining that the one or more cell-free nucleic acid molecules are derived from a sample associated with the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject, based on performing a statistical model analysis of the identified one or more cell-free nucleic acid molecules.

348. The method of embodiment 347, wherein the statistical model analysis comprises a Monte Carlo statistical analysis.

349. The method of any one of embodiments 295-348, further comprising monitoring a progress of the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based on the identified one or more cell-free nucleic acid molecules.

350. The method of any one of embodiments 295-349, further comprising performing a different procedure to confirm the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject.

351. The method of embodiment 350, wherein the different procedure comprises a blood test, genetic test, medical imaging, physical exam, or tissue biopsy.

352. The method of any one of embodiments 295-351, wherein the plurality of cell-free nucleic acid molecules comprise a plurality of cell-free deoxyribonucleic acid (DNA) molecules.

353. The method of any one of embodiments 295-352, wherein the plurality of cell-free nucleic acid molecules are derived from a bodily sample of the pregnant subject.

354. The method of embodiment 353, wherein the bodily sample comprises plasma, serum, blood, cerebrospinal fluid, lymph fluid, saliva, urine, or stool.

355. The method of any one of embodiments 295-354, wherein the pregnant subject is a mammal.

356. The method of any one of embodiments 295-355, wherein the pregnant subject is a human.

357. The method of any one of embodiments 295-356, wherein (b) further comprises identifying one or more insertions or deletions (indels) in the one or more cell-free nucleic acid molecules, and wherein (c) further comprises determining the presence, the absence, or the elevated risk of the genetic abnormality of the fetus of the pregnant subject based at least in part on the identified one or more indels.

358. A method comprising:

(a) obtaining, by a computer system, sequencing data derived from a plurality of nucleic acid molecules that are obtained or derived from a subject;

(b) processing, by the computer system, the sequencing data to identify one or more nucleic acid molecules of the plurality of nucleic acid molecules, wherein each of the one or more nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence, wherein at least about 10% of the one or more nucleic acid molecules comprises a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants that are separated by at least one nucleotide; and

(c) analyzing, by the computer system, the identified one or more nucleic acid molecules to determine a condition of the subject.

359. The method of embodiment 358, wherein the at least about 10% of the nucleic acid molecules comprise at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of the one or more nucleic acid molecules.

360. The method of embodiment 358 or embodiment 359, wherein the plurality of nucleic acid molecules are DNA molecules.

361. The method of embodiment 360, wherein the DNA molecules are cellular DNA molecules.

362. The method of embodiment 360, wherein the cellular DNA molecules are derived from hematological cancer cells or circulating tumor cells.

363. The method of embodiment 360, wherein the nucleic acid molecules are cell-free DNA molecules.

364. The method of embodiment 363, further comprising determining one or both of a start position and an end position of the cfDNA molecules and determining whether the subject has the condition based at least in part on the one or both of the start position and end position of the cfDNA molecules.

365. The method of any one of embodiments 358-359, wherein the nucleic acid molecules are RNA molecules.

366. The method of embodiment 365, wherein the nucleic acid molecules are cell-free RNA molecules.

367. The method of any one of embodiments 358-366, wherein the subject had not been determined to have the condition prior to step (c).

368. The method of any one of embodiments 358-367, wherein analyzing the identified one or more nucleic acid molecules to determine a condition of the subject comprises determining

a cancer of the subject in a patient that had not been previously diagnosed and/or suspected of having the cancer.

369. The method of any one of embodiments 358-368, wherein the phased variants are within 180 bp, within 170 bp, within 160 bp, or within 150 bp of each other as determined by reference to the reference genomic sequence.

370. The method of any one of embodiments 358-369, wherein a first phased variant of the plurality of phased variants is a somatic single nucleotide variant (SNV).

371. The method of any one of embodiments 358-369, wherein a first phased variant of the plurality of phased variants is a somatic indel.

372. The method of any one of embodiments 358-369, wherein a first phased variant of the plurality of phased variants is a somatic translocation breakpoint.

373. The method of any one of embodiments 358-369, wherein a first phased variant of the plurality of phased variants is a somatic amplification or deletion breakpoint.

374. The method of any one of embodiments 358-369, wherein a first phased variant of the plurality of phased variants is a region of localized hypermutation.

375. The method of any one of embodiments 358-369, wherein a first phased variant of the plurality of phased variants is a methylation status change relative to a reference methylation status.

376. The method of any one of embodiments 358-369, wherein a first phased variant of the plurality of phased variants is a germline single nucleotide variant (SNV).

377. The method of any one of embodiments 358-369, wherein a first phased variant of the plurality of phased variants is a germline indel.

378. The method of any one of embodiments 358-369, wherein a first phased variant of the plurality of phased variants is a germline translocation breakpoint.

379. The method of any one of embodiments 358-369, wherein a first phased variant of the plurality of phased variants is a germline amplification or deletion breakpoint.

380. The method of any one of embodiments 370-379, wherein a second phased variant of the plurality of phased variants is a somatic single nucleotide variant (SNV).

381. The method of any one of embodiments 370-379, wherein a second phased variant of the plurality of phased variants is a somatic indel.

382. The method of any one of embodiments 370-379, wherein a second phased variant of the plurality of phased variants is a somatic translocation breakpoint.

383. The method of any one of embodiments 370-379, wherein a second phased variant of the plurality of phased variants is a somatic amplification or deletion breakpoint.

384. The method of any one of embodiments 370-379, wherein a second phased variant of the plurality of phased variants is a region of localized hypermutation.

385. The method of any one of embodiments 370-379, wherein a second phased variant of the plurality of phased variants is a methylation change relative to a reference methylation status.

386. The method of any one of embodiments 370-379, wherein a second phased variant of the plurality of phased variants is a germline single nucleotide variant (SNV).

387. The method of any one of embodiments 370-379, wherein a second phased variant of the plurality of phased variants is a germline indel.

388. The method of any one of embodiments 370-379, wherein a second phased variant of the plurality of phased variants is a germline translocation breakpoint.

389. The method of any one of embodiments 370-379, wherein a second phased variant of the plurality of phased variants is a germline amplification or deletion breakpoint.

390. The method of any one of embodiments 358-389, wherein (b) further comprises identifying one or more insertions or deletions (indels) in the one or more nucleic acid molecules, and wherein (c) further comprises determining the condition of the subject based at least in part on the identified one or more indels.

391. A method comprising:

(a) obtaining, by a computer system, sequencing data derived from a plurality of nucleic acid molecules that is obtained or derived from a subject;

(b) processing, by the computer system, the sequencing data to identify one or more nucleic acid molecules of the plurality of nucleic acid molecules, wherein each of the one or more nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide; and

(c) analyzing, by the computer system, the identified one or more nucleic acid molecules to determine a condition of the subject.

392. The method of embodiment 391, wherein the plurality of nucleic acid molecules are DNA molecules

393. The method of embodiment 392, wherein the DNA molecules are cellular DNA molecules.

394. The method of embodiment 392, wherein the cellular DNA molecules are derived from hematological cancer cells or circulating tumor cells.

395. The method of embodiment 392, wherein the nucleic acid molecules are cell-free DNA molecules.

396. The method of embodiment 395, further comprising determining one or both of a start position and a end position of the cfDNA molecules and determining whether the subject has the condition based at least in part on the one or both of the start position and end position of the cfDNA molecules.

397. The method of any one of embodiments 391-396, wherein the nucleic acid molecules are RNA molecules.

398. The method of embodiment 397, wherein the nucleic acid molecules are cell-free RNA molecules.

399. The method of any one of embodiments 391-398, wherein the subject had not been determined to have the condition prior to step (c).

400. The method of any one of embodiments 391-399, wherein analyzing the identified one or more nucleic acid molecules to determine a condition of the subject comprises determining a cancer of the subject in a patient that had not been previously diagnosed and/or suspected of having the cancer.

401. The method of any one of embodiments 391–400, wherein the phased variants are within 180 bp, within 170 bp, within 160 bp, or within 150 bp of each other as determined by reference to the reference genomic sequence.

402. The method of any one of embodiments 391-401, wherein a first phased variant of the plurality of phased variants is a somatic single nucleotide variant (SNV).

403. The method of any one of embodiments 391-401, wherein a first phased variant of the plurality of phased variants is a somatic indel.

404. The method of any one of embodiments 391-401, wherein a first phased variant of the plurality of phased variants is a somatic translocation breakpoint.

405. The method of any one of embodiments 391-401, wherein a first phased variant of the plurality of phased variants is a somatic amplification or deletion breakpoint.

406. The method of any one of embodiments 391-401, wherein a first phased variant of the plurality of phased variants is a region of localized hypermutation.

407. The method of any one of embodiments 391-401, wherein a first phased variant of the plurality of phased variants is a methylation status change relative to a reference methylation status.

408. The method of any one of embodiments 391-401, wherein a first phased variant of the plurality of phased variants is a germline single nucleotide variant (SNV).

409. The method of any one of embodiments 391-401, wherein a first phased variant of the plurality of phased variants is a germline indel.

410. The method of any one of embodiments 391-401, wherein a first phased variant of the plurality of phased variants is a germline translocation breakpoint.

411. The method of any one of embodiments 391-401, wherein a first phased variant of the plurality of phased variants is a germline amplification or deletion breakpoint.

412. The method of any one of embodiments 402-411, wherein a second phased variant of the plurality of phased variants is a somatic single nucleotide variant (SNV).

413. The method of any one of embodiments 402-411, wherein a second phased variant of the plurality of phased variants is a somatic indel.

414. The method of any one of embodiments 402-411, wherein a second phased variant of the plurality of phased variants is a somatic translocation breakpoint.

415. The method of any one of embodiments 402-411, wherein a second phased variant of the plurality of phased variants is a somatic amplification or deletion breakpoint.

416. The method of any one of embodiments 402-411, wherein a second phased variant of the plurality of phased variants is a region of localized hypermutation.

417. The method of any one of embodiments 402-411, wherein a second phased variant of the plurality of phased variants is a methylation change relative to a reference methylation status.

418. The method of any one of embodiments 402-411, wherein a second phased variant of the plurality of phased variants is a germline single nucleotide variant (SNV).

419. The method of any one of embodiments 402-411, wherein a second phased variant of the plurality of phased variants is a germline indel.

420. The method of any one of embodiments 402-411, wherein a second phased variant of the plurality of phased variants is a germline translocation breakpoint.

421. The method of any one of embodiments 402-411, wherein a second phased variant of the plurality of phased variants is a germline amplification or deletion breakpoint.

422. The method of any one of embodiments 391-421, wherein (b) further comprises identifying one or more insertions or deletions (indels) in the one or more nucleic acid molecules, and wherein (c) further comprises determining the condition of the subject based at least in part on the identified one or more indels.

423. A method comprising:

(a) obtaining sequencing data derived from a plurality of nucleic acid molecules that is obtained or derived from a subject;

(b) processing the sequencing data to identify one or more nucleic acid molecules of the plurality of nucleic acid molecules with a limit of detection of less than about 1 out of

50,000 observations from the sequencing data; and

(c) analyzing the identified one or more nucleic acid molecules to determine a condition of the subject.

424. The method of embodiment 423, wherein the limit of detection of the identification step is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 observations from the sequencing data.

425. The method of any one of embodiments 423-424, wherein each of the one or more nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence.

426. The method of embodiment 425, wherein a first phased variant of the plurality of phased variants and a second phased variant of the plurality of phased variants are separated by at least one nucleotide.

427. The method of any one of embodiments 423-426, wherein (a) to (c) are performed by a computer system.

428. The method of any one of embodiments 423-427, wherein the plurality of nucleic acid molecules are DNA molecules

429. The method of embodiment 428, wherein the DNA molecules are cellular DNA molecules.

430. The method of embodiment 428, wherein the cellular DNA molecules are derived from hematological cancer cells or circulating tumor cells.

431. The method of embodiment 428, wherein the nucleic acid molecules are cell-free DNA molecules.

432. The method of embodiment 431, further comprising determining one or both of a start position and a end position of the cfDNA molecules and determining whether the subject has the condition based at least in part on the one or both of the start position and end position of the cfDNA molecules.

433. The method of any one of embodiments 423-427, wherein the nucleic acid molecules are RNA molecules.

434. The method of embodiment 433, wherein the nucleic acid molecules are cell-free RNA molecules.

435. The method of any one of embodiments 423-434, wherein the subject had not been determined to have the condition prior to step (c).

436. The method of any one of embodiments 423-435, wherein analyzing the identified one

or more nucleic acid molecules to determine a condition of the subject comprises determining a cancer of the subject in a patient that had not been previously diagnosed and/or suspected of having the cancer.

437. The method of any one of embodiments 423-436, wherein the phased variants are within 180 bp, within 170 bp, within 160 bp, or within 150 bp of each other as determined by reference to the reference genomic sequence.

438. The method of any one of embodiments 423-437, wherein a first phased variant of the plurality of phased variants is a somatic single nucleotide variant (SNV).

439. The method of any one of embodiments 423-437, wherein a first phased variant of the plurality of phased variants is a somatic indel.

440. The method of any one of embodiments 423-437, wherein a first phased variant of the plurality of phased variants is a somatic translocation breakpoint.

441. The method of any one of embodiments 423-437, wherein a first phased variant of the plurality of phased variants is a somatic amplification or deletion breakpoint.

442. The method of any one of embodiments 423-437, wherein a first phased variant of the plurality of phased variants is a region of localized hypermutation.

443. The method of any one of embodiments 423-437, wherein a first phased variant of the plurality of phased variants is a methylation status change relative to a reference methylation status.

444. The method of any one of embodiments 423-437, wherein a first phased variant of the plurality of phased variants is a germline single nucleotide variant (SNV).

445. The method of any one of embodiments 423-437, wherein a first phased variant of the plurality of phased variants is a germline indel.

446. The method of any one of embodiments 423-437, wherein a first phased variant of the plurality of phased variants is a germline translocation breakpoint.

447. The method of any one of embodiments 423-437, wherein a first phased variant of the plurality of phased variants is a germline amplification or deletion breakpoint.

448. The method of any one of embodiments 438-447, wherein a second phased variant of the plurality of phased variants is a somatic single nucleotide variant (SNV).

449. The method of any one of embodiments 438-447, wherein a second phased variant of the plurality of phased variants is a somatic indel.

450. The method of any one of embodiments 438-447, wherein a second phased variant of the plurality of phased variants is a somatic translocation breakpoint.

451. The method of any one of embodiments 438-447, wherein a second phased variant of

the plurality of phased variants is a somatic amplification or deletion breakpoint.

452. The method of any one of embodiments 438-447, wherein a second phased variant of the plurality of phased variants is a region of localized hypermutation.

453. The method of any one of embodiments 438-447, wherein a second phased variant of the plurality of phased variants is a methylation change relative to a reference methylation status.

454. The method of any one of embodiments 438-447, wherein a second phased variant of the plurality of phased variants is a germline single nucleotide variant (SNV).

455. The method of any one of embodiments 438-447, wherein a second phased variant of the plurality of phased variants is a germline indel.

456. The method of any one of embodiments 438-447, wherein a second phased variant of the plurality of phased variants is a germline translocation breakpoint.

457. The method of any one of embodiments 438-447, wherein a second phased variant of the plurality of phased variants is a germline amplification or deletion breakpoint.

458. The method of any one of the preceding embodiments, wherein the sequencing data is generated based on nucleic acid amplification.

459. The method of any one of the preceding embodiments, wherein the sequencing data is generated based on polymerase chain reaction.

460. The method of any one of the preceding embodiments, wherein the sequencing data is generated based on amplicon sequencing.

461. The method of any one of the preceding embodiments, wherein the sequencing data is generated based on next-generation sequencing (NGS).

462. The method of any one of the preceding embodiments, wherein the sequencing data is generated based on non-hybridization-based NGS.

463. The method of any one of the preceding embodiments, wherein the sequencing data is generated without use of molecular barcoding of at least a portion of the plurality of nucleic acid molecules.

464. The method of any one of the preceding embodiments, wherein the sequencing data is obtained without use of sample barcoding of at least a portion of the plurality of nucleic acid molecules.

465. The method of any one of the preceding embodiments, wherein the sequencing data is obtained without in silico removal or suppression of (i) background error or (ii) sequencing error.

466. The method of any one of embodiments 423-465, wherein (b) further comprises

identifying one or more insertions or deletions (indels) in the one or more nucleic acid molecules, and wherein (c) further comprises determining the condition of the subject based at least in part on the identified one or more indels.

467. A method of treating a condition of a subject, the method comprising:

(a) identifying the subject for treatment of the condition, wherein the subject has been determined to have the condition based on identification of one or more nucleic acid molecules from a plurality of nucleic acid molecules that is obtained or derived from the subject,

wherein each of the one or more nucleic acid molecules identified comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide, and

wherein a presence of the plurality of phased variants is indicative of the condition of the subject; and

(b) subjecting the subject to the treatment based on the identification in (a).

468. The method of embodiment 467, wherein the plurality of nucleic acid molecules are DNA molecules

469. The method of embodiment 468, wherein the DNA molecules are cellular DNA molecules.

470. The method of embodiment 468, wherein the cellular DNA molecules are derived from hematological cancer cells or circulating tumor cells.

471. The method of embodiment 468, wherein the nucleic acid molecules are cell-free DNA molecules.

472. The method of embodiment 471, further comprising determining one or both of a start position and a end position of the cfDNA molecules and, wherein identifying the subject for treatment for the condition is based at least in part on the one or both of the start position and end position of the cfDNA molecules.

473. The method of embodiment 467, wherein the nucleic acid molecules are RNA molecules.

474. The method of embodiment 473, wherein the nucleic acid molecules are cell-free RNA molecules.

475. The method of any one of embodiments 467-474, wherein the subject had not been predetermined to have the condition.

476. The method of any one of embodiments 467-475, wherein subjecting the subject to the treatment comprising treating the subject for cancer, wherein the subject had not been previously diagnosed and/or suspected of having cancer.

477. The method of any one of embodiments 467-476, wherein the phased variants are within 180 bp, within 170 bp, within 160 bp, or within 150 bp of each other as determined by reference to the reference genomic sequence.

478. The method of any one of embodiments 467-477, wherein a first phased variant of the plurality of phased variants is a somatic single nucleotide variant (SNV).

479. The method of any one of embodiments 467-477, wherein a first phased variant of the plurality of phased variants is a somatic indel.

480. The method of any one of embodiments 467-477, wherein a first phased variant of the plurality of phased variants is a somatic translocation breakpoint.

481. The method of any one of embodiments 467-477, wherein a first phased variant of the plurality of phased variants is a somatic amplification or deletion breakpoint.

482. The method of any one of embodiments 467-477, wherein a first phased variant of the plurality of phased variants is a region of localized hypermutation.

483. The method of any one of embodiments 467-477, wherein a first phased variant of the plurality of phased variants is a methylation status change relative to a reference methylation status.

484. The method of any one of embodiments 467-477, wherein a first phased variant of the plurality of phased variants is a germline single nucleotide variant (SNV).

485. The method of any one of embodiments 467-477, wherein a first phased variant of the plurality of phased variants is a germline indel.

486. The method of any one of embodiments 467-477, wherein a first phased variant of the plurality of phased variants is a germline translocation breakpoint.

487. The method of any one of embodiments 467-477, wherein a first phased variant of the plurality of phased variants is a germline amplification or deletion breakpoint.

488. The method of any one of embodiments 478-487, wherein a second phased variant of the plurality of phased variants is a somatic single nucleotide variant (SNV).

489. The method of any one of embodiments 478-487, wherein a second phased variant of the plurality of phased variants is a somatic indel.

490. The method of any one of embodiments 478-487, wherein a second phased variant of the plurality of phased variants is a somatic translocation breakpoint.

491. The method of any one of embodiments 478-487, wherein a second phased variant of the plurality of phased variants is a somatic amplification or deletion breakpoint.

492. The method of any one of embodiments 478-487, wherein a second phased variant of the plurality of phased variants is a region of localized hypermutation.

493. The method of any one of embodiments 478-487, wherein a second phased variant of the plurality of phased variants is a methylation change relative to a reference methylation status.

494. The method of any one of embodiments 478-487, wherein a second phased variant of the plurality of phased variants is a germline single nucleotide variant (SNV).

495. The method of any one of embodiments 478-487, wherein a second phased variant of the plurality of phased variants is a germline indel.

496. The method of any one of embodiments 478-487, wherein a second phased variant of the plurality of phased variants is a germline translocation breakpoint.

497. The method of any one of embodiments 478-487, wherein a second phased variant of the plurality of phased variants is a germline amplification or deletion breakpoint.

498. The method of any one of embodiments 467-497, wherein the subject has been determined to have the condition based at least in part on one or more insertions or deletions (indels) identified in the one or more nucleic acid molecules.

499. A method of monitoring a progress of a condition of a subject, the method comprising:

(a) determining a first state of the condition of the subject based on identification of a first set of one or more cell-free nucleic acid molecules from a first plurality of cell-free nucleic acid molecules that is obtained or derived from the subject;

(b) determining a second state of the condition of the subject based on identification of a second set of one or more cell-free nucleic acid molecules from a second plurality of cell-free nucleic acid molecules that is obtained or derived from the subject,

wherein the second plurality of cell-free nucleic acid molecules are obtained from the subject subsequent to obtaining the first plurality of cell-free nucleic acid molecules from the subject; and

(c) determining the progress of the condition based on the first state of the condition and the second state of the condition,

wherein each of the one or more cell-free nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence that are separated by at least one nucleotide.

500. The method of embodiment 499, wherein the progress of the condition is worsening of the condition.

501. The method of embodiment 499, wherein the progress of the condition is at least a partial remission of the condition.

502. The method of any one of embodiments 499-501, wherein a presence of the plurality

of phased variants is indicative of the first state or the second state of the condition of the subject.

503. The method of any one of embodiments 499-502, wherein the second plurality of nucleic acid molecules is obtained from the subject at least about 1 week, at least about 2 weeks, at least about 3 weeks, at least about 4 weeks, at least about 2 months, or at least about 3 months subsequent to obtaining the first plurality of nucleic acid molecules from the subject.

504. The method of any one of embodiments 499-503, wherein the subject is subjected to a treatment for the condition (i) prior to obtaining the second plurality of nucleic acid molecules from the subject and (ii) subsequent to obtaining the first plurality of nucleic acid molecules from the subject.

505. The method of any one of embodiments 499-504, wherein the progress of the condition is indicative of minimal residual disease of the condition of the subject.

506. The method of any one of embodiments 499-505, wherein the progress of the condition is indicative of tumor burden or cancer burden of the subject.

507. The method of any one of the preceding embodiments, wherein the one or more nucleic acid molecules are captured from among the plurality of cell-free nucleic acid molecules with a set of nucleic acid probes, wherein the set of nucleic acid probes is configured to hybridize to at least a portion of nucleic acid molecules comprising one or more genomic regions associated with the condition.

508. The method of any one of embodiments 499-507, wherein the subject has been determined to have the condition based at least in part on one or more insertions or deletions (indels) identified in the one or more nucleic acid molecules.

509. The method of any one of embodiments 499-508, wherein the subject has received an organ or tissue transplant, and wherein the condition comprises transplant rejection of the subject.

510. The method of embodiment 499-509, wherein the plurality of nucleic acid molecules are DNA molecules.

511. The method of embodiment 510, wherein the DNA molecules are cellular DNA molecules.

512. The method of embodiment 510, wherein the cellular DNA molecules are derived from hematological cancer cells or circulating tumor cells.

513. The method of embodiment 510, wherein the nucleic acid molecules are cell-free DNA molecules.

514. The method of embodiment 513, further comprising determining one or both of a start

position and a end position of the cfDNA molecules and, wherein identifying the subject for treatment for the condition is based at least in part on the one or both of the start position and end position of the cfDNA molecules.

515. The method of any one of embodiments 499-509, wherein the nucleic acid molecules are RNA molecules.

516. The method of embodiment 515, wherein the nucleic acid molecules are cell-free RNA molecules.

517. The method of any one of embodiments 499-516, wherein the subject had not been predetermined to have the condition.

518. The method of any one of embodiments 499-517, wherein subjecting the subject to the treatment comprising treating the subject for cancer, wherein the subject had not been previously diagnosed and/or suspected of having cancer.

519. The method of any one of embodiments 499-518, wherein the phased variants are within 180 bp, within 170 bp, within 160 bp, or within 150 bp of each other as determined by reference to the reference genomic sequence.

520. The method of any one of embodiments 499-519, wherein a first phased variant of the plurality of phased variants is a somatic single nucleotide variant (SNV).

521. The method of any one of embodiments 499-519, wherein a first phased variant of the plurality of phased variants is a somatic indel.

522. The method of any one of embodiments 499-519, wherein a first phased variant of the plurality of phased variants is a somatic translocation breakpoint.

523. The method of any one of embodiments 499-519, wherein a first phased variant of the plurality of phased variants is a somatic amplification or deletion breakpoint.

524. The method of any one of embodiments 499-519, wherein a first phased variant of the plurality of phased variants is a region of localized hypermutation.

525. The method of any one of embodiments 499-519, wherein a first phased variant of the plurality of phased variants is a methylation status change relative to a reference methylation status.

526. The method of any one of embodiments 499-519, wherein a first phased variant of the plurality of phased variants is a germline single nucleotide variant (SNV).

527. The method of any one of embodiments 499-519, wherein a first phased variant of the plurality of phased variants is a germline indel.

528. The method of any one of embodiments 499-519, wherein a first phased variant of the plurality of phased variants is a germline translocation breakpoint.

529. The method of any one of embodiments 499-519, wherein a first phased variant of the plurality of phased variants is a germline amplification or deletion breakpoint.

530. The method of any one of embodiments 520-529, wherein a second phased variant of the plurality of phased variants is a somatic single nucleotide variant (SNV).

531. The method of any one of embodiments 520-529, wherein a second phased variant of the plurality of phased variants is a somatic indel.

532. The method of any one of embodiments 520-529, wherein a second phased variant of the plurality of phased variants is a somatic translocation breakpoint.

533. The method of any one of embodiments 520-529, wherein a second phased variant of the plurality of phased variants is a somatic amplification or deletion breakpoint.

534. The method of any one of embodiments 520-529, wherein a second phased variant of the plurality of phased variants is a region of localized hypermutation.

535. The method of any one of embodiments 520-529, wherein a second phased variant of the plurality of phased variants is a methylation change relative to a reference methylation status.

536. The method of any one of embodiments 520-529, wherein a second phased variant of the plurality of phased variants is a germline single nucleotide variant (SNV).

537. The method of any one of embodiments 520-529, wherein a second phased variant of the plurality of phased variants is a germline indel.

538. The method of any one of embodiments 520-529, wherein a second phased variant of the plurality of phased variants is a germline translocation breakpoint.

539. The method of any one of embodiments 520-529, wherein a second phased variant of the plurality of phased variants is a germline amplification or deletion breakpoint.

540. The method of any one of the preceding embodiments, wherein analyzing the identified one or more nucleic acid molecules comprises analyzing (i) the identified one or more nucleic acid molecules and (ii) other nucleic acid molecules of the plurality of nucleic acid molecules that do not comprise the plurality of phased variants as different variables.

541. The method of any one of the preceding embodiments, wherein the analyzing of the identified one or more nucleic acid molecules is not based on other nucleic acid molecules of the plurality of nucleic acid molecules that do not comprise the plurality of phased variants.

542. The method of any one of the preceding embodiments, wherein a number of the plurality of phased variants from the identified one or more nucleic acid molecules is indicative of the condition of the subject.

543. The method of embodiment 542, wherein a ratio of (i) the number of the plurality of

phased variants from the one or more nucleic acid molecules and (ii) a number of single nucleotide variants (SNVs) from the one or more nucleic acid molecules is indicative of the condition of the subject.

544. The method of any one of the preceding embodiments, wherein a frequency of the plurality of phased variants in the identified one or more nucleic acid molecules is indicative of the condition of the subject.

545. The method of embodiment 544, wherein the frequency is indicative of a diseased cell associated with the condition.

546. The method of embodiment 545, wherein the condition is diffuse large B-cell lymphoma, and wherein the frequency is indicative of whether the one or more nucleic acid molecules are derived from germinal center B-cell (GCB) or activated B-cell (ABC).

547. The method of any one of the preceding embodiments, wherein genomic origin of the identified one or more nucleic acid molecules is indicative of the condition of the subject.

548. The method of any one of the preceding embodiments, wherein the first and second phased variants are separated by at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 nucleotides.

549. The method of any one of the preceding embodiments, wherein the first and second phased variants are separated by at most about 180, at most about 170, at most about 160, at most about 150, or at most about 140 nucleotides.

550. The method of any one of the preceding embodiments, wherein at least about 10%, at least about 20%, at least about 30%, at least about 40%, or at least about 50% of the one or more nucleic acid molecules comprising a plurality of phased variants comprises a single nucleotide variant (SNV) that is at least 2 nucleotides away from an adjacent SNV.

551. The method of any one of the preceding embodiments, wherein the plurality of phased variants comprises at least 3, at least 4, at least 5, at least 10, at least 15, at least 20, or at least 25 phased variants within the same nucleic acid molecule.

552. The method of any one of the preceding embodiments, wherein the one or more nucleic acid molecules identified comprises at least 2, at least 3, at least 4, at least 5, at least 10, at least 50, at least 100, at least 500, or at least 1,000 nucleic acid molecules.

553. The method of any one of the preceding embodiments, wherein the reference genomic sequence is derived from a reference cohort.

554. The method of embodiment 553, wherein the reference genomic sequence comprises a consensus sequence from the reference cohort.

555. The method of embodiment 553, wherein the reference genomic sequence comprises at

least a portion of hg19 human genome, hg18 genome, hg17 genome, hg16 genome, or hg38 genome.

556. The method of any one of the preceding embodiments, wherein the reference genomic sequence is derived from a sample of the subject.

557. The method of embodiment 556, wherein the sample is a healthy sample.

558. The method of embodiment 557, wherein the sample comprises a healthy cell.

559. The method of embodiment 558, wherein the healthy cell comprises a healthy leukocyte.

560. The method of embodiment 556, wherein the sample is a diseased sample.

561. The method of embodiment 560, wherein the diseased sample comprises a diseased cell.

562. The method of embodiment 561, wherein the diseased cell comprises a tumor cell.

563. The method of embodiment 560, wherein the diseased sample comprises a solid tumor.

564. The method of any one of the preceding embodiments, wherein the set of nucleic acid probes is designed based on the plurality of phased variants that are identified by comparing (i) sequencing data from a solid tumor, lymphoma, or blood tumor of the subject and (ii) sequencing data from a healthy cell of the subject or a healthy cohort.

565. The method of embodiment 564, wherein the healthy cell is from the subject.

566. The method of embodiment 564, wherein the healthy cell is from the healthy cohort.

567. The method of any one of the preceding embodiments, wherein the set of nucleic acid probes are designed to hybridize to at least a portion of sequences of genomic loci associated with the condition.

568. The method of embodiment 567, wherein the genomic loci associated with the condition are known to exhibit aberrant somatic hypermutation when the subject has the condition.

569. The method of any one of the preceding embodiments, wherein the set of nucleic acid probes are designed to hybridize to at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% of (i) the genomic regions identified in Table 1, (ii) the genomic regions identified in Table 3, or (iii) the genomic regions identified to have a plurality of phased variants in Table 3.

570. The method of any one of the preceding embodiments, wherein each nucleic acid probe of the set of nucleic acid probes has at least about 70%, at least about 80%, at least about 90% sequence identity, at least about 95% sequence identity, or about 100% sequence identity to a

probe sequence selected from Table 6.

571. The method of any one of the preceding embodiments, wherein the set of nucleic acid probes comprises at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90% of probe sequences in Table 6.

572. The method of any one of the preceding embodiments, further comprising determining that the subject has the condition or determining a degree or status of the condition of the subject, based on the identified one or more nucleic acid molecules comprising the plurality of phased variants.

573. The method of embodiment 572, further comprising determining that the one or more nucleic acid molecules are derived from a sample associated with the condition, based on performing a statistical model analysis of the identified one or more nucleic acid molecules.

574. The method of embodiment 573, wherein the statistical model analysis comprises a Monte Carlo statistical analysis.

575. The method of any one of the preceding embodiments, further comprising monitoring a progress of the condition of the subject based on the identified one or more nucleic acid molecules.

576. The method of any one of the preceding embodiments, further comprising performing a different procedure to confirm the condition of the subject.

577. The method of embodiment 576, wherein the different procedure comprises a blood test, genetic test, medical imaging, physical exam, or tissue biopsy.

578. The method of any one of the preceding embodiments, further comprising determining a treatment for the condition of the subject based on the identified one or more nucleic acid molecules.

579. The method of any one of the preceding embodiments, wherein the subject has been subjected to a treatment for the condition prior to (a).

580. The method of any one of the preceding embodiments, wherein the treatment comprises chemotherapy, radiotherapy, chemoradiotherapy, immunotherapy, adoptive cell therapy, hormone therapy, targeted drug therapy, surgery, transplant, transfusion, or medical surveillance.

581. The method of any one of the preceding embodiments, wherein the plurality of nucleic acid molecules comprise a plurality of cell-free deoxyribonucleic acid (DNA) molecules.

582. The method of any one of the preceding embodiments, wherein the condition comprises a disease.

583. The method of any one of the preceding embodiments, wherein the plurality of nucleic acid molecules are derived from a bodily sample of the subject.

584. The method of embodiment 583, wherein the bodily sample comprises plasma, serum, blood, cerebrospinal fluid, lymph fluid, saliva, urine, or stool.

585. The method of any one of the preceding embodiments, wherein the subject is a mammal.

586. The method of any one of the preceding embodiments, wherein the subject is a human.

587. The method of any one of the preceding embodiments, wherein the condition comprises neoplasm, cancer, or tumor.

588. The method of embodiment 587, wherein the condition comprises a solid tumor.

589. The method of embodiment 587, wherein the condition comprises a lymphoma.

590. The method of embodiment 589, wherein the condition comprises a B-cell lymphoma.

591. The method of embodiment 590, wherein the condition comprises a sub-type of B-cell lymphoma selected from the group consisting of diffuse large B-cell lymphoma, follicular lymphoma, Burkitt lymphoma, and B-cell chronic lymphocytic leukemia.

592. The method of any one of the preceding embodiments, wherein the plurality of phased variants have been previously identified as tumor-derived from sequencing a prior tumor sample or nucleic acid sample.

593. The method of any one of embodiments 499-592, wherein (b) further comprises identifying one or more insertions or deletions (indels) in the one or more nucleic acid molecules, and wherein (c) further comprises determining the condition of the subject based at least in part on the identified one or more indels.

594. The method of any one of embodiments 499-593, wherein the subject has received an organ or tissue transplant, and wherein the condition comprises transplant rejection of the subject.

595. A method for preferentially capturing nucleic acid molecules that comprise phased variants, the method comprising adding a set of nucleic acid probes to a sample comprising a plurality of nucleic acid molecules that have been obtained or derived from a subject, wherein each nucleic acid probe of the set of nucleic acid probes is configured to hybridize to a target nucleic acid molecule comprising a plurality of phased variants such that the nucleic acid probe is complementary to at least a region of the target nucleic acid molecule that extends from a first phased variant of the plurality of phased variants to a second phased variant of the plurality of phased variants.

596. The method of embodiment 595, wherein each nucleic acid probe of the set of nucleic

acid probes comprises a pull-down tag.

597. The method of embodiment 595 or 596, further comprising separation of target nucleic acid molecules that hybridize to the nucleic acid probes from nucleic acid molecules that do not hybridize to the nucleic acid probes to thereby capture target nucleic acid molecules.

598. The method of embodiment 595 or 597, wherein the pull-down tag comprises biotin.

599. The method of any one of embodiments 595-598, wherein the nucleic acid molecules are cell-free nucleic acid molecules (e.g., cell-free DNA molecules or cell-free RNA molecules).

600. The method of any one of embodiments 595-599, wherein the first phased variant is an SNV and the second phased variant is an SNV.

601. The method of any one of embodiments 595-600, wherein the first phased variant is selected from the group consisting of a somatic single nucleotide variant, a somatic indel, a somatic translocation breakpoint, a somatic amplification or deletion breakpoint, a germline SNV, a germline indel, a germline translocation breakpoint, a germline amplification or deletion breakpoint, and a region of localized hypermutation, and the second phased variant is selected from the group consisting of a somatic single nucleotide variant, a somatic indel, a somatic translocation breakpoint, a somatic amplification or deletion breakpoint, a germline SNV, a germline indel, a germline translocation breakpoint, a germline amplification or deletion breakpoint, and a region of localized hypermutation.

602. The method of any one of embodiments 595-601, wherein the first phased variant of the plurality of phased variants and the second phased variant of the plurality of phased variants are separated by at least 1, 2, 3, 4, 5, 10, or 20 nucleotides.

603. The method of any one of embodiments 595-602, wherein each nucleic acid probe of the set of nucleic acid probes is either (1) less than 40 nucleotides, less than 30 nucleotides, or less than 20 nucleotides in length or (2) no more than 5 nucleotides, nor more than 10 nucleotides, no more than 20 nucleotides, or no more than 30 nucleotides longer than the distance between the first phased variant of the plurality of phased variants and the second phased variant of the plurality of phased variants, wherein the first phased variant and the second phased variant are the most separated phased variants of the plurality of phased variants.

604. The method of any one of embodiments 595-603, wherein the target nucleic acid molecule is a molecule that is derived from a pre-identified portion of a genome of a cancer cell or a transplanted cell from the subject that differs in sequence from a reference genomic sequence, wherein the preidentified portion of the genome is less than 200, less than 180, or less than 150 nucleotides in length.

605. The method of any one of embodiments 595-604, wherein each nucleic acid probe of the plurality of nucleic acid probes has a lower ΔG of binding to the target nucleic acid molecule than to a corresponding molecule that is identical in length and sequence to the target nucleic acid molecule except that the corresponding molecule has a sequence that corresponds with a reference genomic sequence.

606. The method of embodiment 605, wherein the reference genomic sequence comprises a portion of either (1) a reference cohort, such as a portion of the hg19 human genome, hg18 genome, hg17 genome, hg16 genome, or hg38 genome or (2) a healthy sample from the subject.

607. The method of any one of embodiments 595-606, wherein the method involves the capture of the target nucleic acid derived from either the Watson strand or the Crick strand of a chromosome, but does not involve the capture of the corresponding complementary nucleic acid of the other strand.

608. The method of any one of embodiments 595-607, wherein the method comprises capture of at least 10, at least 100, at least 1000, or at least 10,000 target nucleic acid molecules.

609. The method of any one of embodiments 595-608, further comprising sequencing the captured target nucleic acids to obtain sequencing data derived from the plurality of nucleic acid molecules.

610. The method of embodiment 609, wherein the sequencing does not involve use of molecular barcodes.

611. The method of embodiment 609 or 610, wherein the sequencing does not comprise duplex sequencing.

612. A method for determining a condition of a subject, the method comprising:

obtaining, by a computer system, sequence information obtained by the method of embodiment any one of embodiments 609-611;

processing, by the computer system, the sequencing data to identify one or more nucleic acid molecules of the plurality of nucleic acid molecules, wherein each of the one or more nucleic acid molecules comprises a plurality of phased variants relative to a reference genomic sequence; and

analyzing, by the computer system, the identified one or more nucleic acid molecules to determine a condition of the subject.

613. The method of embodiment 612, wherein the method does not comprise duplex-mediated error suppression.

614. The method of embodiment 612 or 613, wherein the method does not comprise barcode-mediated error suppression.

615. A method for identifying sets of validated phased variants from a solid tumor sample of a subject, the method comprising:

(a) obtaining, by a computer system, sequencing data from a solid tumor sample of a subject;

(b) obtaining, by the computer system, sequencing data from a matched non-tumor sample of the subject;

(c) analyzing, using the computer system, the sequencing data from the solid tumor sample and the sequencing data from the matched non-tumor sample to identify a plurality of regions of a genome of the subject that include a first putative phased variant and a second putative phased variant, wherein each region is no more than 170 amino acids in length;

(d) after step (c), performing targeted sequencing on nucleic acids from the solid tumor sample of the subject that are from the plurality of regions identified in step (c) to a depth of at least 250×;

(e) identifying, using the computer system, sets of validated phased variants from the solid tumor sample of the subject based on sequencing data from the targeted sequencing of step (d).

616. The method of embodiment 615, wherein the first putative phased variant and the second putative phased variant are separated by at least one nucleotide.

617. The method of embodiment 615 or 616, wherein the first putative phased variant and the second putative phased variant are separated by at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 nucleotides.

618. The method of any one of embodiments 615-617, wherein step (c) comprises:

determining a plurality of single nucleotide variants in the genome of the subject that are present in the solid tumor sample relative to the matched non-tumor sample; and

from the identified single nucleotide variants, identifying the plurality regions of the genome that include the first phased variant and the second phased variant based on one or more of (1) a proximity (e.g., within 170 bp) of two or more of the identified the single nucleotide variants within a genome or (2) the presence of a plurality of the single nucleotide variants on a single read from the sequence data from the solid tumor sample of the subject.

619. The method of any one of embodiments 615-618, wherein the sequencing data from the solid tumor sample of the subject in step (a) comprises whole genome sequencing data.

620. The method of any one of embodiments 615-618, wherein the sequencing data of the solid tumor sample of the subject in step (a) comprises data for at least 50%, 75%, 80%, 90%, 95%, or 99% of the genome of the subject.

621. The method of any one of embodiments 615-618, wherein the sequencing data of the solid tumor sample of the subject in step (a) is whole exome data.

622. The method of any one of embodiments 615-621, wherein the sequencing data from the matched non-tumor sample of the subject in step (b) comprises whole genome sequencing data.

623. The method of any one of embodiments 615-621, wherein the sequencing data from the matched non-tumor sample of the subject in step (b) comprises data for at least 50%, 75%, 80%, 90%, 95%, or 99% of the genome of the subject.

624. The method of any one of embodiments 615-621, wherein the sequencing data from the matched non-tumor sample of the subject in step (b) comprises whole exome data.

625. The method of any one of embodiments 615-624, wherein the sequencing of step (a) is done at a depth of between 10× and 500×, between 10× and 250×, between 10× and 200×, between 10× and 100×, or between 10× and 50×.

626. The method of any one of embodiments 615-625, wherein the sequencing of step (b) is done at a depth of between 10× and 500×, between 10× and 250×, between 10× and 200×, between 10× and 100×, or between 10× and 50×.

627. The method of any one of embodiments 615-626, wherein the number of identified regions of the genome in step (c) comprises at least 400, at least 500, at least 700, at least 1000, at least 2000, at least 3000, at least 4000, or at least 5000 regions.

628. The method of any one of embodiments 615-627, wherein the number of identified regions of the genome in step (c) is no more than 15,000, 10,000, or 8,000 regions.

629. The method of any one of embodiments 615-618, wherein the identification of the plurality of regions of the genome in step (c) comprises determining one or more of (i) a presence in individual reads from the solid tumor sample of the subject of phased variants, (ii) the presence or absence of read support in the matched non-tumor sample, (iii) the presence of other non-reference bases on supporting reads, (iv) base quality, (v) mapping quality, and (vi) uniqueness of genomic positions.

630. The method of any one of embodiments 615-629, wherein the targeted sequencing of step (d) comprises (1) hybridization capture of nucleic acids from the tumor sample of the subject that correspond to the identified regions of the genome from step (c) and (2) sequencing of the captured nucleic acids from the tumor sample of the subject.

631. The method of any one of embodiments 615-630, wherein the number of sets of validated phased variants is less than 1000, less than 900, less than 800, or less than 700.

632. The method of any one of embodiments 615-631, wherein the number of sets of validated phased variants is greater than 10, greater than 20, greater than 50, or greater than 80.

633. The method of any one of embodiments 615-632, wherein the regions identified in step (c) are non-overlapping regions.

634. The method of any one of embodiments 615-633, wherein the nucleic acids of step (d) are DNA molecules.

635. The method of any one of embodiments 615-634, wherein the first phased variant and the second phased variant are each single nucleotide variants.

636. The method of any preceding embodiment, wherein the matched non-tumor sample is a healthy sample from the subject.

637. The method of any preceding embodiment, wherein the sets of validated phased variants are found in to have an allele fraction of greater than 5% and no read support in sequencing data from the matched non-tumor sample.

638. The method of any preceding embodiment, wherein the number of validated sets of phased variants identified in step (e) is at least 1.5-fold, 2-fold, 3-fold, 4-fold, or 5-fold lower than the number of putative sets of phased variants identified in step (c).

639. The method of any preceding embodiment, wherein step (d) further comprises performing targeted sequencing on nucleic acids from the matched non-tumor sample of the subject that are from the plurality of regions identified in step (c) to a depth of at least 500×;

640. A method comprising combining a set of nucleic acid probes with a plurality of cell-free nucleic acid molecules that are obtained or derived from a subject to form a mixture, wherein each nucleic acid probe of the set of nucleic acid probes is configured to hybridize to at least a portion of a cell-free nucleic acid molecule that comprises a set of phased variants identified by any preceding embodiment.

641. The method of embodiment 640, wherein each nucleic acid probe of the set of nucleic acid probes is configured to hybridize to a target nucleic acid molecule comprising a plurality of phased variants such that the nucleic acid probe is complementary to at least a region of the target nucleic acid molecule that extends from a first phased variant of the set of phased variants to a second phased variant of the set of phased variants.

642. The method of embodiment 640 or 641, wherein each nucleic acid probe of the set of nucleic acid probes comprises a pull-down tag.

643. The method of embodiment 642, wherein the pull-down tag comprises biotin.

644. The method of any one of embodiments 640-643, further comprising separating target nucleic acid molecules that hybridize to the nucleic acid probes from nucleic acid molecules that do not hybridize to the nucleic acid probes to thereby capture target nucleic acid molecules.

645. The method of any one of embodiments 640-644, further comprising sequencing the

cell-free nucleic acid molecules that hybridize to the nucleic acid probes.

646. The method of any one of embodiments 640-645, further comprising identifying one or more cell-free nucleic acid molecules as being a cancer-derived molecule with a limit of detection of less than about 1 out of 50,000 observations from sequencing data obtained from the sequencing of the cell-free nucleic acid molecules.

647. The method of embodiment 646, wherein the limit of detection of is less than about 1 out of 100,000, less than about 1 out of 500,000, less than about 1 out of 1,000,000, less than about 1 out of 1,500,000, or less than about 1 out of 2,000,000 observations from the sequencing data.

648. The method of any one of embodiments 645-647, wherein the sequencing does not involve use of molecular barcodes.

649. The method of any one of embodiments 645-648, wherein the sequencing does not comprise duplex sequencing.

650. The method of any one of embodiments 645-649, wherein the method does not comprise duplex-mediated error suppression.

651. The method of any one of embodiments 645-650, wherein the method does not comprise barcode-mediated error suppression.

652. The method of embodiment any one of embodiments 640-651, further comprising determining a condition of the subject.

653. The method of any one of embodiments 640-652, further comprising monitoring progress of a condition of the subject.

654. A computer program product comprising a non-transitory computer-readable medium having computer-executable code encoded therein, the computer-executable code adapted to be executed to implement a method according to any one of the preceding embodiments.

655. A system comprising one or more computer processors and computer memory coupled thereto, wherein the computer memory comprises machine executable code that, upon execution by the one or more computer processors, implements a method according to any one of the preceding embodiments.

[0745] While preferred embodiments of the present invention have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. It is not intended that the invention be limited by the specific examples provided within the specification. While the invention has been described with reference to the aforementioned specification, the descriptions and illustrations of the embodiments herein are not meant to be construed in a limiting sense. Numerous variations,

changes, and substitutions will now occur to those skilled in the art without departing from the invention. Furthermore, it shall be understood that all aspects of the invention are not limited to the specific depictions, configurations or relative proportions set forth herein which depend upon a variety of conditions and variables. It should be understood that various alternatives to the embodiments of the invention described herein may be employed in practicing the invention. It is therefore contemplated that the invention shall also cover any such alternatives, modifications, variations or equivalents. It is intended that the following claims define the scope of the invention and that methods and structures within the scope of these claims and their equivalents be covered thereby.

Table 1

#	Chromosome	Region Start	Region End	BL	CLL	DLBCL	FL	ClosestGene	Fisher_p_DLBCL_vs_FL	Fisher_p_DLBCL_vs_BL	Fisher_p_DLBCL_vs_CLL	Previously Identified	overSpecInAny Histology
1	chr1	756000	757000	0.028	0.000	0.015	0.000	AL669831.1	0.47887	1.00000	0.29694	0	0
2	chr1	1963000	1964000	0.028	0.000	0.015	0.000	GABRD	0.47887	1.00000	0.29694	0	0
3	chr1	2052000	2053000	0.028	0.000	0.000	0.014	PRKCZ	1.00000	0.34615	1.00000	0	0
4	chr1	3789000	3790000	0.000	0.000	0.029	0.000	DFFB	0.22755	0.54294	0.08726	0	0
5	chr1	6613000	6614000	0.000	0.000	0.044	0.014	NOL9	0.34948	0.54966	0.02537	1	0
6	chr1	6614000	6615000	0.000	0.000	0.088	0.027	NOL9	0.13270	0.09031	0.00058	1	1
7	chr1	6661000	6662000	0.000	0.000	0.029	0.014	KLHL21	0.60686	0.54294	0.08726	0	0
8	chr1	6662000	6663000	0.000	0.000	0.044	0.014	KLHL21	0.34948	0.54966	0.02537	0	0
9	chr1	9129000	9130000	0.000	0.000	0.044	0.000	SLC2A5	0.10727	0.54966	0.02537	0	0
10	chr1	10894000	10895000	0.028	0.000	0.000	0.014	C1orf127	1.00000	0.34615	1.00000	0	0
11	chr1	17019000	17020000	0.028	0.000	0.000	0.014	AL137798.1	1.00000	0.34615	1.00000	0	0
12	chr1	17231000	17232000	0.000	0.000	0.015	0.014	CROCC	1.00000	1.00000	0.29694	0	0
13	chr1	19935000	19936000	0.000	0.000	0.029	0.000	MINOS1-NBL1	0.22755	0.54294	0.08726	0	0
14	chr1	21091000	21092000	0.000	0.000	0.015	0.014	EPB41P3	1.00000	1.00000	0.29694	0	0
15	chr1	23885000	23886000	0.444	0.000	0.015	0.000	ID3	0.47887	0.00000	0.29694	1	1
16	chr1	28408000	28409000	0.000	0.000	0.029	0.000	EYA3	0.22755	0.54294	0.08726	0	0
17	chr1	32373000	32374000	0.000	0.000	0.029	0.000	PTPA2	0.22755	0.54294	0.08726	0	0
18	chr1	36722000	36723000	0.000	0.000	0.015	0.000	THRAP3	0.47887	1.00000	1.00000	0	0
19	chr1	46576000	46577000	0.000	0.000	0.015	0.014	PIK3R3	1.00000	1.00000	0.29694	0	0
20	chr1	51965000	51966000	0.000	0.006	0.015	0.000	EPS15	0.47887	1.00000	0.50663	0	0
21	chr1	51978000	51979000	0.000	0.000	0.029	0.000	EPS15	0.22755	0.54294	0.08726	0	0
22	chr1	51983000	51984000	0.000	0.006	0.029	0.000	EPS15	0.22755	0.54294	0.21104	0	0
23	chr1	72393000	72394000	0.000	0.000	0.015	0.014	NEGR1	1.00000	1.00000	0.29694	0	0
24	chr1	73719000	73720000	0.000	0.000	0.029	0.000	LRRIQ3	0.22755	0.54294	0.08726	0	0
25	chr1	77315000	77316000	0.028	0.006	0.000	0.000	ST6GALNAC5	1.00000	1.00000	1.00000	0	0
26	chr1	81306000	81307000	0.000	0.000	0.015	0.014	LPHN2	1.00000	1.00000	0.29694	0	0
27	chr1	81527000	81528000	0.000	0.000	0.029	0.000	LPHN2	0.22755	0.54294	0.08726	0	0
28	chr1	82009000	82010000	0.028	0.000	0.015	0.000	LPHN2	0.47887	1.00000	0.29694	0	0
29	chr1	84106000	84107000	0.000	0.006	0.015	0.000	TTLL7	0.47887	1.00000	0.50663	0	0
30	chr1	87524000	87525000	0.000	0.006	0.015	0.000	HS2ST1;HS2ST1LOC39524;	0.47887	1.00000	0.50663	0	0
31	chr1	94551000	94552000	0.000	0.000	0.029	0.000	ABCA4	0.22755	0.54294	0.08726	0	0
32	chr1	94552000	94553000	0.000	0.000	0.029	0.000	ABCA4	0.22755	0.54294	0.08726	0	0
33	chr1	103696000	103697000	0.000	0.000	0.000	0.027	COL11A1	0.49735	1.00000	1.00000	0	0
34	chr1	116979000	116980000	0.000	0.000	0.044	0.041	ATP1A1	1.00000	0.54966	0.02537	0	0
35	chr1	149784000	149785000	0.000	0.000	0.015	0.014	HIST2H3D	1.00000	1.00000	0.29694	1	0
36	chr1	149821000	149822000	0.000	0.000	0.044	0.000	HIST2H2AA4	0.10727	0.54966	0.02537	1	0
37	chr1	149857000	149858000	0.000	0.000	0.015	0.014	HIST2H2BE	1.00000	1.00000	0.29694	1	0
38	chr1	149858000	149859000	0.000	0.000	0.059	0.000	HIST2H2AC;HIST2H2BE;	0.05016	0.29551	0.00730	0	1
39	chr1	160616000	160617000	0.000	0.000	0.015	0.014	SLAMF1	1.00000	1.00000	0.29694	0	0
40	chr1	162711000	162712000	0.000	0.000	0.015	0.014	DDR2	1.00000	1.00000	0.29694	0	0
41	chr1	163684000	163685000	0.000	0.000	0.015	0.014	NUF2	1.00000	1.00000	0.29694	0	0
42	chr1	167598000	167599000	0.000	0.000	0.044	0.014	RCSD1	0.34948	0.54966	0.02537	0	0
43	chr1	167599000	167600000	0.000	0.000	0.029	0.014	RCSD1	0.60686	0.54294	0.08726	0	0
44	chr1	167600000	167601000	0.000	0.000	0.044	0.000	RCSD1	0.10727	0.54966	0.02537	0	0
45	chr1	174333000	174334000	0.000	0.000	0.015	0.014	RABGAP1L	1.00000	1.00000	0.29694	0	0
46	chr1	187263000	187264000	0.000	0.000	0.044	0.000	PLA2G4A	0.10727	0.54966	0.02537	0	0

47	chr1	187283000	187284000	0.000	0.000	0.029	0.000	PLA2G4A	0.22755	0.54294	0.08726	0	0	
48	chr1	187892000	187893000	0.028	0.000	0.015	0.000	PLA2G4A	0.47887	1.00000	0.29694	0	0	
49	chr1	195282000	195283000	0.000	0.000	0.015	0.014	KCNT2	1.00000	1.00000	0.29694	0	0	
50	chr1	198591000	198592000	0.000	0.000	0.029	0.000	PTPRC	0.22755	0.54294	0.08726	0	0	
51	chr1	198608000	198609000	0.000	0.000	0.029	0.000	PTPRC	0.22755	0.54294	0.08726	0	0	
52	chr1	198609000	198610000	0.000	0.000	0.029	0.000	PTPRC	0.22755	0.54294	0.08726	0	0	
53	chr1	202004000	202005000	0.028	0.000	0.029	0.000	ELF3	0.22755	1.00000	0.08726	0	0	
54	chr1	203273000	203274000	0.000	0.000	0.029	0.000	BTG2	0.22755	0.54294	0.08726	1	0	
55	chr1	203274000	203275000	0.000	0.000	0.176	0.014	BTG2	0.60078	0.60730	0.00000	1	1	
56	chr1	203275000	203276000	0.028	0.006	0.471	0.081	BTG2	0.00000	0.00000	0.00000	1	1	
57	chr1	203276000	203277000	0.028	0.000	0.059	0.000	BTG2	0.05016	0.58667	0.00730	1	1	
58	chr1	205780000	205781000	0.000	0.000	0.000	0.027	SLC41A1	0.49735	1.00000	1.00000	0	0	
59	chr1	205781000	205782000	0.000	0.000	0.000	0.027	SLC41A1	0.49735	1.00000	1.00000	0	0	
60	chr1	206283000	206284000	0.000	0.000	0.015	0.014	CTSE	1.00000	1.00000	0.29694	0	0	
61	chr1	206286000	206287000	0.000	0.000	0.029	0.014	CTSE	0.60686	0.54294	0.08726	0	0	
62	chr1	217044000	217045000	0.000	0.000	0.029	0.000	ESRRG	0.22755	0.54294	0.08726	0	0	
63	chr1	226924000	226925000	0.000	0.000	0.029	0.000	UPKB	0.22755	0.54294	0.08726	1	0	
64	chr1	226925000	226926000	0.000	0.000	0.044	0.000	UPKB	0.10727	0.54966	0.02537	1	0	
65	chr1	226926000	226927000	0.000	0.000	0.029	0.000	UPKB	0.22755	0.54294	0.08726	1	0	
66	chr1	229974000	229975000	0.028	0.000	0.015	0.027	URB2	1.00000	1.00000	0.29694	0	0	
67	chr1	235131000	235132000	0.000	0.000	0.000	0.027	TOMM20	0.49735	1.00000	1.00000	0	0	
68	chr1	235141000	235142000	0.000	0.000	0.015	0.014	TOMM20	1.00000	1.00000	0.29694	0	0	
69	chr1	238787000	238788000	0.000	0.000	0.029	0.000	MTRNR2L11	0.22755	0.54294	0.08726	0	0	
70	chr1	248088000	248089000	0.028	0.000	0.015	0.000	OR2T8	0.47887	1.00000	0.29694	0	0	
71	chr2	630000	631000	0.000	0.000	0.000	0.027	TMEM18	0.49735	1.00000	1.00000	0	0	
72	chr2	1484000	1485000	0.056	0.000	0.000	0.027	TPO	0.49735	1.00000	1.00000	0	0	
73	chr2	7991000	7992000	0.056	0.000	0.000	0.000	RNF144A	1.00000	0.11765	1.00000	0	1	
74	chr2	12173000	12174000	0.000	0.000	0.044	0.000	LPIN1	0.10727	0.54966	0.02537	0	0	
75	chr2	12175000	12176000	0.000	0.000	0.029	0.000	LPIN1	0.22755	0.54294	0.08726	0	0	
76	chr2	12249000	12250000	0.000	0.000	0.029	0.000	LPIN1	0.22755	0.54294	0.08726	0	0	
77	chr2	14113000	14114000	0.000	0.000	0.000	0.027	FAM84A	0.49735	1.00000	1.00000	0	0	
78	chr2	17577000	17578000	0.000	0.000	0.015	0.014	RAD51AP2	1.00000	1.00000	0.29694	0	0	
79	chr2	19253000	19254000	0.000	0.000	0.029	0.000	OSR1	0.22755	0.54294	0.08726	0	0	
80	chr2	24802000	24803000	0.056	0.000	0.029	0.000	NCOA1	0.22755	0.54294	0.08726	0	0	
81	chr2	31478000	31479000	0.000	0.000	0.015	0.014	EHD3	1.00000	1.00000	0.29694	0	0	
82	chr2	41728000	41729000	0.000	0.000	0.015	0.014	C2orf91	1.00000	1.00000	0.29694	0	0	
83	chr2	45404000	45405000	0.000	0.000	0.000	0.027	SIX2	0.49735	1.00000	1.00000	0	0	
84	chr2	47923000	47924000	0.000	0.000	0.015	0.014	MSH6	1.00000	1.00000	0.29694	0	0	
85	chr2	47944000	47945000	0.000	0.000	0.029	0.000	MSH6	0.22755	0.54294	0.08726	0	0	
86	chr2	51360000	51361000	0.000	0.000	0.015	0.014	NRXN1	1.00000	1.00000	0.29694	0	0	
87	chr2	51655000	51656000	0.000	0.000	0.000	0.027	NRXN1	0.49735	1.00000	1.00000	0	0	
88	chr2	56565000	56566000	0.000	0.000	0.029	0.000	CCDC85A	0.22755	0.54294	0.08726	0	0	
89	chr2	57860000	57861000	0.000	0.000	0.015	0.014	VRK2	1.00000	1.00000	0.29694	0	0	
90	chr2	60779000	60780000	0.000	0.000	0.029	0.027	BCL11A	1.00000	0.54294	0.08726	0	0	
91	chr2	60779000	60781000	0.000	0.000	0.029	0.000	BCL11A	0.22755	0.54294	0.08726	0	0	
92	chr2	63802000	63803000	0.000	0.000	0.000	0.027	WDPCP	0.49735	1.00000	1.00000	0	0	
93	chr2	63827000	63828000	0.000	0.000	0.015	0.014	MDH1	1.00000	1.00000	0.29694	0	0	
94	chr2	64319000	64320000	0.000	0.000	0.044	0.000	PELI1	0.10727	0.54966	0.02537	0	0	
95	chr2	65593000	65594000	0.000	0.000	0.044	0.054	SPRED2	1.00000	0.54966	0.02537	1	1	
96	chr2	67002000	67003000	0.028	0.000	0.029	0.000	MEIS1	0.22755	1.00000	0.08726	0	0	
97	chr2	70315000	70316000	0.083	0.000	0.000	0.000	PCBP1	1.00000	0.03921	1.00000	0	1	

98	chr2	79592000	79803000	0.028	0.000	0.015	0.000	REG3A	0.47887	1.00000	0.29694	0		0
99	chr2	79644000	79645000	0.000	0.000	0.000	0.027	CTNNA2	0.49735	1.00000	1.00000	0		0
100	chr2	81818000	81819000	0.000	0.000	0.000	0.027	CTNNA2	0.49735	1.00000	1.00000	0		0
101	chr2	82310000	82311000	0.028	0.000	0.015	0.000	CTNNA2	0.47887	1.00000	0.29694	0		0
102	chr2	82948000	82949000	0.000	0.000	0.029	0.000	SUCLG1	0.22755	0.54294	0.08726	0		0
103	chr2	85335000	85336000	0.000	0.000	0.000	0.027	TCF7L1	0.49735	1.00000	1.00000	0		0
104	chr2	88905000	88906000	0.000	0.000	0.059	0.000	EIF2AK3	0.05016	0.29551	0.00730	0		1
105	chr2	88906000	88907000	0.000	0.006	0.074	0.014	EIF2AK3	0.10420	0.16101	0.00953	0		1
106	chr2	88907000	88908000	0.000	0.000	0.059	0.000	EIF2AK3	0.05016	0.29551	0.00730	0		1
107	chr2	89052000	89053000	0.000	0.006	0.015	0.000	RPIA	0.47887	1.00000	0.50663	0		0
108	chr2	89065000	89066000	0.000	0.000	0.015	0.027	RPIA	1.00000	1.00000	0.29694	0		0
109	chr2	89066000	89067000	0.000	0.000	0.015	0.014	RPIA	1.00000	1.00000	0.29694	0		0
110	chr2	89095000	89096000	0.000	0.000	0.015	0.014	RPIA	1.00000	1.00000	0.29694	0		0
111	chr2	89127000	89128000	0.000	0.006	0.147	0.041	IGKC	0.03985	0.01464	0.00003	0		1
112	chr2	89128000	89129000	0.028	0.006	0.176	0.041	IGKC	0.01224	0.03142	0.00000	0		1
113	chr2	89129000	89130000	0.000	0.000	0.044	0.041	IGKC	1.00000	0.54966	0.02537	0		0
114	chr2	89130000	89131000	0.000	0.000	0.044	0.000	IGKC	0.10727	0.54966	0.02537	0		0
115	chr2	89131000	89132000	0.000	0.000	0.029	0.000	IGKC	0.22755	0.54294	0.08726	0		0
116	chr2	89132000	89133000	0.000	0.006	0.015	0.014	IGKC	1.00000	1.00000	0.50663	0		0
117	chr2	89133000	89134000	0.000	0.000	0.029	0.041	IGKC	1.00000	0.54294	0.08726	0		0
118	chr2	89137000	89138000	0.000	0.000	0.044	0.014	IGKC	0.34948	0.54966	0.02537	0		0
119	chr2	89138000	89139000	0.000	0.000	0.015	0.014	IGKC	1.00000	1.00000	0.29694	0		0
120	chr2	89139000	89140000	0.000	0.000	0.044	0.014	IGKC	0.34948	0.54966	0.02537	0		0
121	chr2	89140000	89141000	0.000	0.000	0.088	0.054	IGKC	0.52007	0.99031	0.00058	0		1
122	chr2	89141000	89142000	0.000	0.006	0.103	0.027	IGKC	0.08710	0.09269	0.00099	0		1
123	chr2	89142000	89143000	0.000	0.000	0.088	0.000	IGKC	0.01070	0.99031	0.00058	0		1
124	chr2	89143000	89144000	0.000	0.000	0.029	0.000	IGKC	0.22755	0.54294	0.08726	0		0
125	chr2	89144000	89145000	0.000	0.000	0.015	0.014	IGKC	1.00000	1.00000	0.29694	0		0
126	chr2	89145000	89146000	0.000	0.000	0.029	0.014	IGKC	0.60686	0.54294	0.08726	0		0
127	chr2	89146000	89147000	0.000	0.000	0.029	0.014	IGKC	0.60686	0.54294	0.08726	0		0
128	chr2	89153000	89154000	0.000	0.000	0.029	0.000	IGKC	0.22755	0.54294	0.08726	0		0
129	chr2	89155000	89156000	0.000	0.000	0.059	0.014	IGKC	0.19371	0.29551	0.00730	0		1
130	chr2	89156000	89157000	0.000	0.000	0.103	0.014	IGKC	0.02808	0.09269	0.00016	0		1
131	chr2	89157000	89158000	0.000	0.000	0.250	0.149	IGKC	0.14439	0.00048	0.00000	0		1
132	chr2	89158000	89159000	0.028	0.019	0.426	0.270	IGKC	0.05462	0.00061	0.00000	0		1
133	chr2	89159000	89160000	0.222	0.180	0.574	0.473	IGKJ5	0.24418	0.00083	0.00000	0		1
134	chr2	89160000	89161000	0.444	0.242	0.500	0.608	IGKJ3;IGKJ4;IGKJ5;	0.23729	0.68125	0.00019	0		1
135	chr2	89161000	89162000	0.222	0.081	0.265	0.405	IGKJ1;IGKJ2;	0.10957	0.81234	0.00049	0		1
136	chr2	89162000	89163000	0.056	0.012	0.221	0.108	IGKJ1	0.10913	0.04835	0.00000	0		1
137	chr2	89163000	89164000	0.000	0.068	0.235	0.176	IGKJ1	0.41068	0.00098	0.00117	0		1
138	chr2	89164000	89165000	0.028	0.137	0.294	0.216	IGKJ1	0.33637	0.00075	0.00821	0		1
139	chr2	89165000	89166000	0.083	0.143	0.279	0.216	IGKJ1	0.43812	0.02316	0.02379	0		1
140	chr2	89166000	89167000	0.028	0.012	0.044	0.027	IGKJ1	0.67043	1.00000	0.15671	0		0
141	chr2	89169000	89170000	0.000	0.000	0.015	0.014	IGKJ1	1.00000	1.00000	0.29694	0		0
142	chr2	89184000	89185000	0.000	0.006	0.015	0.054	IGKV4-1	0.36833	1.00000	0.50663	0		1
143	chr2	89185000	89186000	0.028	0.056	0.162	0.135	IGKV4-1	0.81354	0.05349	0.01836	0		1
144	chr2	89196000	89197000	0.000	0.000	0.059	0.014	IGKV5-2	0.19371	0.29551	0.00730	0		1
145	chr2	89197000	89198000	0.000	0.000	0.000	0.027	IGKV5-2	0.49735	1.00000	1.00000	0		0
146	chr2	89214000	89215000	0.000	0.012	0.000	0.000	IGKV5-2	1.00000	1.00000	1.00000	0		0
147	chr2	89246000	89247000	0.000	0.031	0.029	0.027	IGKV1-5	1.00000	0.34294	1.00000	0		0
148	chr2	89247000	89248000	0.028	0.019	0.118	0.054	IGKV1-5	0.25086	0.15803	0.00321	0		1

149	chr2	89248000	89249000	0.028	0.000	0.044	0.000	IGKV1-5	0.10727	1.00000	0.02537	0		0
150	chr2	89266000	89267000	0.000	0.000	0.015	0.014	IGKV1-6	1.00000	1.00000	0.29694	0		0
151	chr2	89291000	89292000	0.000	0.019	0.029	0.000	IGKV1-8	0.22755	0.54294	0.63492	0		0
152	chr2	89292000	89293000	0.000	0.025	0.044	0.000	IGKV1-8	0.10727	0.54966	0.42650	0		0
153	chr2	89326000	89327000	0.000	0.019	0.000	0.041	IGKV3-11	0.24663	1.00000	0.55662	0		0
154	chr2	89327000	89328000	0.000	0.012	0.015	0.027	IGKV3-11	1.00000	1.00000	1.00000	0		0
155	chr2	89442000	89443000	0.111	0.050	0.074	0.122	IGKV3-20	0.40586	0.71556	0.53493	0		1
156	chr2	89443000	89444000	0.000	0.000	0.015	0.041	IGKV3-20	0.62100	1.00000	0.29694	0		0
157	chr2	89476000	89477000	0.028	0.000	0.000	0.014	IGKV2-24	1.00000	0.34615	1.00000	0		0
158	chr2	89513000	89514000	0.000	0.000	0.029	0.000	IGKV1-27	0.22755	0.54294	0.08726	0		0
159	chr2	89521000	89522000	0.028	0.000	0.015	0.014	IGKV2-28	1.00000	1.00000	0.29694	0		0
160	chr2	89533000	89534000	0.028	0.000	0.044	0.014	IGKV2-30	0.34948	1.00000	0.02537	0		0
161	chr2	89534000	89535000	0.000	0.000	0.029	0.014	IGKV2-30	0.60686	0.54294	0.08726	0		0
162	chr2	89544000	89545000	0.028	0.012	0.059	0.014	IGKV2-30	0.19371	0.65667	0.06548	0		1
163	chr2	89545000	89546000	0.000	0.006	0.029	0.000	IGKV2-30	0.22755	0.54294	0.21104	0		0
164	chr2	90259000	90260000	0.000	0.000	0.015	0.014	IGKV1D-8	1.00000	1.00000	0.29694	0		0
165	chr2	90260000	90261000	0.000	0.000	0.059	0.014	IGKV1D-8	0.19371	0.29551	0.60730	0		1
166	chr2	96809000	96810000	0.000	0.000	0.044	0.000	DUSP2	0.10727	0.54966	0.02537	1		0
167	chr2	96810000	96811000	0.000	0.000	0.044	0.014	DUSP2	0.34948	0.54966	0.02537	1		0
168	chr2	96811000	96812000	0.000	0.000	0.029	0.000	DUSP2	0.22755	0.54294	0.08726	1		0
169	chr2	96811000	96812000	0.000	0.000	0.015	0.014	TMEM131	1.00000	1.00000	0.29694	0		0
170	chr2	100757000	100758000	0.000	0.000	0.029	0.027	AFF3	1.00000	0.54294	0.08726	0		0
171	chr2	100758000	100759000	0.000	0.000	0.044	0.014	AFF3	0.34948	0.54966	0.02537	0		0
172	chr2	106144000	106145000	0.000	0.000	0.029	0.000	FHL2	0.22755	0.54294	0.08726	0		0
173	chr2	111878000	111879000	0.000	0.000	0.029	0.014	BCL2L11	0.60686	0.54294	0.08726	0		0
174	chr2	111879000	111880000	0.000	0.000	0.044	0.014	BCL2L11	0.34948	0.54966	0.02537	0		0
175	chr2	112305000	112306000	0.000	0.000	0.015	0.014	ANAPC1	1.00000	1.00000	0.29694	0		0
176	chr2	116234000	116235000	0.000	0.000	0.015	0.014	DPP10	1.00000	1.00000	0.29694	0		0
177	chr2	116439000	116440000	0.028	0.000	0.000	0.014	DPP10	1.00000	0.34615	1.00000	0		0
178	chr2	124697000	124698000	0.028	0.000	0.015	0.000	CNTNAP5	0.47887	1.00000	0.29694	0		0
179	chr2	125235000	125236000	0.000	0.000	0.029	0.000	CNTNAP5	0.22755	0.54294	0.08726	0		0
180	chr2	127538000	127539000	0.028	0.000	0.015	0.000	GYPC	0.47887	1.00000	0.29694	0		0
181	chr2	136874000	136875000	0.000	0.000	0.191	0.014	CXCR4	0.00036	0.00372	0.00000	1		1
182	chr2	136875000	136876000	0.083	0.019	0.365	0.081	CXCR4	0.00626	0.03882	0.00000	1		1
183	chr2	136996000	136997000	0.000	0.000	0.029	0.000	CXCR4	0.22755	0.54294	0.08726	1		0
184	chr2	137082000	137083000	0.000	0.000	0.015	0.014	CXCR4	1.00000	1.00000	0.29694	1		0
185	chr2	140951000	140952000	0.000	0.000	0.029	0.000	LRP1B	0.22755	0.54294	0.08726	0		0
186	chr2	141335000	141336000	0.000	0.000	0.015	0.014	LRP1B	1.00000	1.00000	0.29694	0		0
187	chr2	141770000	141771000	0.000	0.000	0.029	0.000	LRP1B	0.22755	0.54294	0.08726	0		0
188	chr2	146445000	146446000	0.000	0.000	0.029	0.000	ZEB2	0.22755	0.54294	0.08726	0		0
189	chr2	146446000	146447000	0.000	0.000	0.029	0.014	ZEB2	0.60686	0.54294	0.08726	0		0
190	chr2	156443000	156444000	0.000	0.000	0.029	0.000	KCNJ3	0.22755	0.54294	0.08726	0		0
191	chr2	172590000	172591000	0.000	0.000	0.029	0.000	DYNC1I2	0.22755	0.54294	0.08726	0		0
192	chr2	176581000	176582000	0.028	0.000	0.000	0.014	KIAA1715	1.00000	0.34615	1.00000	0		0
193	chr2	179880000	179881000	0.000	0.000	0.015	0.014	CCDC141	1.00000	1.00000	0.29694	0		0
194	chr2	180358000	180359000	0.000	0.000	0.029	0.000	ZNF385B	0.22755	0.54294	0.08726	0		0
195	chr2	189285000	189286000	0.000	0.000	0.015	0.014	GULP1	1.00000	1.00000	0.29694	0		0
196	chr2	189432000	189433000	0.028	0.000	0.000	0.014	GULP1	1.00000	0.34615	1.00000	0		0
197	chr2	194115000	194116000	0.000	0.000	0.015	0.014	TMEFF2	1.00000	1.00000	0.29694	0		0
198	chr2	197035000	197036000	0.000	0.000	0.044	0.014	SIK1B	0.34948	0.54966	0.02537	0		0
199	chr2	197041000	197042000	0.000	0.000	0.029	0.000	SIK1B	0.22755	0.54294	0.08726	0		0

200	chr2	215999000	216000000	0.000	0.006	0.015	0.000	ABCA12	0.47887	1.00000	0.50663	0	0
201	chr2	216973000	216974000	0.028	0.000	0.000	0.014	XRCC5	1.00000	0.34615	1.00000	0	0
202	chr2	217247000	217248000	0.028	0.000	0.000	0.014	4-Mar-19	1.00000	0.34615	1.00000	0	0
203	chr2	225386000	225387000	0.000	0.000	0.029	0.000	CUL3	0.22755	0.54294	0.08726	0	0
204	chr2	225524000	225525000	0.000	0.000	0.029	0.000	CUL3	0.22755	0.54294	0.08726	0	0
205	chr2	233478000	233479000	0.028	0.000	0.015	0.000	EPHD1	0.47887	1.00000	0.29694	0	0
206	chr2	233980000	233981000	0.028	0.000	0.029	0.000	INPP5D	0.22755	1.00000	0.08726	0	0
207	chr2	240641000	240642000	0.028	0.000	0.000	0.027	AC093802.1	0.49735	0.34615	1.00000	0	0
208	chr2	241125000	241126000	0.000	0.000	0.000	0.027	OTOS	0.49735	1.00000	1.00000	0	0
209	chr3	8739000	8740000	0.000	0.000	0.000	0.027	CAV3	0.49735	1.00000	1.00000	0	0
210	chr3	16407000	16408000	0.000	0.000	0.000	0.027	RFTN1	0.49735	1.00000	1.00000	1	0
211	chr3	16409000	16410000	0.028	0.000	0.000	0.041	RFTN1	0.24603	0.34615	1.00000	1	0
212	chr3	16419000	16420000	0.000	0.006	0.044	0.000	RFTN1	0.10727	0.54966	0.07959	1	0
213	chr3	16472000	16473000	0.000	0.000	0.015	0.014	RFTN1	1.00000	1.00000	0.29694	1	0
214	chr3	16495000	16496000	0.000	0.000	0.029	0.000	RFTN1	0.22755	0.54294	0.08726	1	0
215	chr3	16552000	16553000	0.000	0.012	0.029	0.014	RFTN1	0.60686	0.54294	0.58408	1	0
216	chr3	16554000	16555000	0.000	0.000	0.103	0.027	RFTN1	0.08710	0.09569	0.00016	1	1
217	chr3	16555000	16556000	0.000	0.000	0.029	0.000	RFTN1	0.22755	0.54294	0.08726	1	0
218	chr3	21658000	21659000	0.000	0.000	0.029	0.000	ZNF385D	0.22755	0.54294	0.08726	0	0
219	chr3	25691000	25692000	0.000	0.000	0.029	0.000	TOP2B	0.22755	0.54294	0.08726	0	0
220	chr3	31969000	31970000	0.000	0.000	0.029	0.000	OSBPL10	0.22755	0.54294	0.08726	1	0
221	chr3	31993000	31994000	0.000	0.000	0.044	0.000	OSBPL10	0.10727	0.54966	0.02537	1	0
222	chr3	32001000	32002000	0.000	0.000	0.044	0.000	OSBPL10	0.10727	0.54966	0.02537	1	0
223	chr3	32022000	32023000	0.000	0.000	0.088	0.014	OSBPL10	0.05468	0.09031	0.00058	1	1
224	chr3	32023000	32024000	0.000	0.000	0.029	0.000	OSBPL10	0.22755	0.54294	0.08726	1	0
225	chr3	50128000	50129000	0.000	0.000	0.029	0.000	RBMS	0.22755	0.54294	0.08726	0	0
226	chr3	54913000	54914000	0.000	0.006	0.015	0.000	CACNA2D3	0.47887	1.00000	0.50663	0	0
227	chr3	56074000	56075000	0.028	0.000	0.000	0.014	ERC2	1.00000	0.34615	1.00000	0	0
228	chr3	59577000	59578000	0.000	0.000	0.029	0.000	FHIT	0.22755	0.54294	0.08726	0	0
229	chr3	60351000	60352000	0.000	0.000	0.044	0.000	FHIT	0.10727	0.54966	0.02537	0	0
230	chr3	60356000	60357000	0.028	0.000	0.000	0.014	FHIT	1.00000	0.34615	1.00000	0	0
231	chr3	60357000	60358000	0.000	0.000	0.015	0.014	FHIT	1.00000	1.00000	0.29694	0	0
232	chr3	60358000	60359000	0.000	0.000	0.015	0.014	FHIT	1.00000	1.00000	0.29694	0	0
233	chr3	60359000	60360000	0.000	0.000	0.029	0.000	FHIT	0.22755	0.54294	0.08726	0	0
234	chr3	60388000	60389000	0.000	0.000	0.015	0.027	FHIT	1.00000	1.00000	0.29694	0	0
235	chr3	60392000	60393000	0.000	0.000	0.029	0.000	FHIT	0.22755	0.54294	0.08726	0	0
236	chr3	60395000	60396000	0.000	0.000	0.000	0.027	FHIT	0.49735	1.00000	1.00000	0	0
237	chr3	60404000	60405000	0.000	0.000	0.029	0.000	FHIT	0.22755	0.54294	0.08726	0	0
238	chr3	60436000	60437000	0.000	0.000	0.000	0.027	FHIT	0.49735	1.00000	1.00000	0	0
239	chr3	60437000	60438000	0.000	0.000	0.029	0.000	FHIT	0.22755	0.54294	0.08726	0	0
240	chr3	60477000	60478000	0.000	0.000	0.029	0.000	FHIT	0.22755	0.54294	0.08726	0	0
241	chr3	60485000	60486000	0.000	0.000	0.015	0.014	FHIT	1.00000	1.00000	0.29694	0	0
242	chr3	60515000	60516000	0.000	0.000	0.015	0.014	FHIT	1.00000	1.00000	0.29694	0	0
243	chr3	60535000	60536000	0.000	0.006	0.015	0.000	FHIT	0.47887	1.00000	0.50663	0	0
244	chr3	60602000	60603000	0.000	0.000	0.029	0.014	FHIT	0.60686	0.54294	0.08726	0	0
245	chr3	60613000	60614000	0.000	0.000	0.029	0.014	FHIT	0.60686	0.54294	0.08726	0	0
246	chr3	60614000	60615000	0.000	0.000	0.029	0.000	FHIT	0.22755	0.54294	0.08726	0	0
247	chr3	60632000	60633000	0.000	0.000	0.000	0.027	FHIT	0.49735	1.00000	1.00000	0	0
248	chr3	60635000	60636000	0.000	0.000	0.029	0.000	FHIT	0.22755	0.54294	0.08726	0	0
249	chr3	60640000	60641000	0.000	0.000	0.000	0.027	FHIT	0.49735	1.00000	1.00000	0	0
250	chr3	60647000	60648000	0.000	0.000	0.015	0.014	FHIT	1.00000	1.00000	0.29694	0	0

251	chr3	66648000	66649000	0.000	0.000	0.015	0.014	FHIT	1.00000	1.00000	1.00000	0.29694	0	0
252	chr3	66652000	66653000	0.000	0.000	0.000	0.027	FHIT	0.49735	1.00000	1.00000	0	0	0
253	chr3	66660000	66661000	0.000	0.000	0.029	0.014	FHIT	0.60686	0.54294	1.00000	0.08726	0	0
254	chr3	66665000	66666000	0.000	0.000	0.015	0.027	FHIT	1.00000	1.00000	1.00000	0.29694	0	0
255	chr3	66666000	66667000	0.000	0.000	0.015	0.014	FHIT	1.00000	1.00000	1.00000	0.29694	0	0
256	chr3	66671000	66672000	0.000	0.000	0.000	0.041	FHIT	0.24603	1.00000	1.00000	0.02537	0	0
257	chr3	66673000	66674000	0.000	0.000	0.044	0.000	FHIT	0.10727	0.54966	1.00000	0.02537	0	0
258	chr3	66675000	66676000	0.000	0.000	0.015	0.014	FHIT	1.00000	1.00000	1.00000	0.29694	0	0
259	chr3	66678000	66679000	0.000	0.000	0.044	0.000	FHIT	0.10727	0.54966	0.02537	0	0	0
260	chr3	66683000	66684000	0.000	0.000	0.015	0.027	FHIT	1.00000	1.00000	1.00000	0.29694	0	0
261	chr3	66684000	66685000	0.000	0.000	0.015	0.041	FHIT	0.62100	1.00000	1.00000	0.29694	0	0
262	chr3	66688000	66689000	0.000	0.000	0.015	0.014	FHIT	1.00000	1.00000	1.00000	0.29694	0	0
263	chr3	66717000	66718000	0.000	0.000	0.000	0.027	FHIT	0.49735	1.00000	1.00000	0	0	0
264	chr3	66740000	66741000	0.000	0.000	0.029	0.000	FHIT	0.22755	0.54294	0.08726	0	0	0
265	chr3	66774000	66775000	0.000	0.000	0.029	0.000	FHIT	0.22755	0.54294	0.08726	0	0	0
266	chr3	66792000	66793000	0.000	0.000	0.000	0.027	FHIT	0.49735	1.00000	1.00000	0	0	0
267	chr3	66806000	66807000	0.028	0.000	0.000	0.014	FHIT	1.00000	0.34615	1.00000	0	0	0
268	chr3	66812000	66813000	0.000	0.000	0.000	0.027	FHIT	0.49735	1.00000	1.00000	0	0	0
269	chr3	66860000	66861000	0.000	0.000	0.000	0.027	FHIT	0.49735	1.00000	1.00000	0	0	0
270	chr3	71551000	71552000	0.000	0.000	0.000	0.027	EIF4E3	0.49735	1.00000	1.00000	0	0	0
271	chr3	78274000	78275000	0.000	0.000	0.015	0.014	ROBO1	1.00000	1.00000	0.29694	0	0	0
272	chr3	80273000	80274000	0.000	0.006	0.015	0.000	ROBO1	0.47887	1.00000	0.30663	0	0	0
273	chr3	83094000	83095000	0.028	0.000	0.015	0.000	GBE1	0.47887	1.00000	0.29694	0	0	0
274	chr3	83924000	83925000	0.028	0.000	0.000	0.014	CADM2	1.00000	0.34615	1.00000	0	0	0
275	chr3	84293000	84294000	0.000	0.000	0.015	0.014	CADM2	1.00000	1.00000	0.29694	0	0	0
276	chr3	85260000	85261000	0.000	0.000	0.044	0.000	CADM2	0.10727	0.54966	0.02537	0	0	0
277	chr3	85261000	85262000	0.000	0.000	0.029	0.000	CADM2	0.22755	0.54294	0.08726	0	0	0
278	chr3	85799000	85800000	0.000	0.000	0.029	0.000	CADM2	0.22755	0.54294	0.08726	0	0	0
279	chr3	86226000	86227000	0.000	0.000	0.029	0.000	CADM2	0.22755	0.54294	0.08726	0	0	0
280	chr3	88146000	88147000	0.000	0.000	0.029	0.000	CGGBP1	0.22755	0.54294	0.08726	0	0	0
281	chr3	94799000	94710000	0.000	0.000	0.029	0.000	NSUN3	0.22755	0.54294	0.08726	0	0	0
282	chr3	95460000	95461000	0.028	0.000	0.015	0.000	MTRNR2L12	0.47887	1.00000	0.29694	0	0	0
283	chr3	95724000	95725000	0.000	0.000	0.029	0.000	MTRNR2L12	0.22755	0.54294	0.08726	0	0	0
284	chr3	101569000	101570000	0.028	0.000	0.015	0.000	NFKBIZ	0.47887	1.00000	0.29694	0	0	0
285	chr3	111851000	111852000	0.000	0.000	0.044	0.000	GCSAM	0.10727	0.54966	0.02537	0	0	0
286	chr3	111852000	111853000	0.000	0.059	0.000	0.000	GCSAM	0.05016	0.29551	0.00730	0	1	1
287	chr3	122377000	122378000	0.028	0.000	0.044	0.000	PARP14	0.10727	1.00000	0.02537	0	0	0
288	chr3	150478000	150479000	0.000	0.000	0.029	0.000	SIAH2	0.22755	0.54294	0.08726	0	0	0
289	chr3	150479000	150480000	0.000	0.000	0.029	0.000	SIAH2	0.22755	0.54294	0.08726	0	0	0
290	chr3	150480000	150481000	0.000	0.000	0.015	0.014	SIAH2	1.00000	1.00000	0.29694	0	0	0
291	chr3	163237000	163238000	0.000	0.000	0.000	0.027	SI	0.49735	1.00000	1.00000	0	0	0
292	chr3	163238000	163239000	0.000	0.000	0.029	0.000	SI	0.22755	0.54294	0.08726	0	0	0
293	chr3	163615000	163616000	0.000	0.000	0.029	0.000	SI	0.22755	0.54294	0.08726	0	0	0
294	chr3	183270000	183271000	0.000	0.000	0.029	0.000	KLHL6	0.22755	0.54294	0.08726	0	0	0
295	chr3	183271000	183272000	0.000	0.000	0.029	0.014	KLHL6	0.60686	0.54294	0.08726	0	0	0
296	chr3	183272000	183273000	0.000	0.000	0.029	0.014	KLHL6	0.60686	0.54294	0.08726	0	0	0
297	chr3	183273000	183274000	0.000	0.019	0.044	0.027	KLHL6	0.67043	0.54966	0.36534	0	0	0
298	chr3	186648000	186649000	0.000	0.000	0.044	0.014	ADIPOQ	0.34948	0.54966	0.02537	0	0	0
299	chr3	186714000	186715000	0.000	0.006	0.132	0.027	ST6GAL1	0.02624	0.02564	0.00009	1	1	1
300	chr3	186713000	186716000	0.000	0.000	0.044	0.014	ST6GAL1	0.34948	0.54966	0.02537	1	0	0
301	chr3	186739000	186740000	0.000	0.006	0.074	0.014	ST6GAL1	0.10420	0.16101	0.00953	1	1	1

302	chr3	186744000	186741000	0.056	0.006	0.074	0.027	ST6GAL1	0.25970	1.00000	0.00953	1	1	
303	chr3	186742000	186743000	0.000	0.000	0.029	0.000	ST6GAL1	0.22755	0.54294	0.08726	1	0	
304	chr3	186783000	186784000	0.050	0.050	0.338	0.041	ST6GAL1	0.00001	0.00000	0.00000	1	1	
305	chr3	186784000	186785000	0.000	0.025	0.044	0.000	ST6GAL1	0.10727	0.54966	0.42650	1	0	
306	chr3	187458000	187459000	0.000	0.000	0.029	0.000	BCL6	0.22755	0.54294	0.08726	1	0	
307	chr3	187459000	187460000	0.000	0.000	0.029	0.000	BCL6	0.22755	0.54294	0.08726	1	0	
308	chr3	187460000	187461000	0.000	0.000	0.088	0.041	BCL6	0.31126	0.99031	0.00058	1	1	
309	chr3	187461000	187462000	0.000	0.006	0.353	0.122	BCL6	0.00137	0.00001	0.00000	1	1	
310	chr3	187462000	187463000	0.056	0.081	0.647	0.392	BCL6	0.00266	0.00000	0.00000	1	1	
311	chr3	187463000	187464000	0.000	0.037	0.485	0.239	BCL6	0.00164	0.00000	0.00000	1	1	
312	chr3	187464000	187465000	0.028	0.000	0.162	0.000	BCL6	0.00019	0.03349	0.00000	1	1	
313	chr3	187468000	187469000	0.000	0.000	0.044	0.000	BCL6	0.10727	0.54966	0.02537	1	0	
314	chr3	187635000	187636000	0.000	0.000	0.029	0.000	BCL6	0.22755	0.54294	0.08726	1	0	
315	chr3	187636000	187637000	0.000	0.000	0.000	0.027	BCL6	0.49735	1.00000	1.00000	1	0	
316	chr3	187653000	187654000	0.000	0.000	0.044	0.014	BCL6	0.34948	0.54966	0.02537	1	0	
317	chr3	187658000	187659000	0.000	0.000	0.029	0.000	BCL6	0.22755	0.54294	0.08726	1	0	
318	chr3	187660000	187661000	0.000	0.019	0.118	0.054	BCL6	0.25086	0.04825	0.00321	1	1	
319	chr3	187661000	187662000	0.000	0.012	0.191	0.081	BCL6	0.08249	0.00372	0.00000	1	1	
320	chr3	187664000	187665000	0.000	0.000	0.044	0.000	BCL6	0.10727	0.54966	0.02537	1	0	
321	chr3	187686000	187687000	0.028	0.000	0.029	0.014	ACO22498.1	0.00686	1.00000	0.08726	0	0	
322	chr3	187687000	187688000	0.000	0.006	0.000	0.014	ACO22498.1	1.00000	1.00000	1.00000	0	0	
323	chr3	187693000	187694000	0.000	0.000	0.015	0.014	ACO22498.1	1.00000	1.00000	0.29694	0	0	
324	chr3	187696000	187697000	0.000	0.006	0.059	0.000	ACO22498.1	0.05016	0.29551	0.02818	0	1	
325	chr3	187697000	187698000	0.000	0.000	0.044	0.000	ACO22498.1	0.10727	0.54966	0.02537	0	0	
326	chr3	187803000	187804000	0.000	0.000	0.029	0.000	ACO22498.1	0.22755	0.54294	0.08726	0	0	
327	chr3	187866000	187867000	0.000	0.000	0.059	0.014	ACO22498.1	0.19571	0.29551	0.00730	0	1	
328	chr3	187957000	187958000	0.000	0.006	0.132	0.014	ACO22498.1	0.00701	0.02564	0.00009	0	1	
329	chr3	187958000	187959000	0.028	0.025	0.221	0.095	ACO22498.1	0.06156	0.00936	0.00000	0	1	
330	chr3	187959000	187960000	0.000	0.012	0.118	0.000	ACO22498.1	0.00220	0.04825	0.00116	0	1	
331	chr3	187960000	187961000	0.000	0.000	0.029	0.000	ACO22498.1	0.22755	0.54294	0.08726	0	0	
332	chr3	188222000	188223000	0.000	0.000	0.029	0.000	LPP	0.22755	0.54294	0.08726	0	0	
333	chr3	188298000	188299000	0.000	0.000	0.000	0.014	LPP	1.00000	1.00000	0.29694	0	0	
334	chr3	188299000	188340000	0.000	0.006	0.088	0.027	LPP	0.15270	0.09031	0.00311	0	1	
335	chr3	188471000	188472000	0.000	0.006	0.191	0.068	LPP	0.04159	0.00372	0.00000	0	1	
336	chr3	188472000	188473000	0.000	0.000	0.044	0.027	LPP	0.67043	0.54966	0.02537	0	0	
337	chr4	50000	51000	0.000	0.000	0.029	0.000	ZNF595;ZNF718;	0.22755	0.54294	0.08726	0	0	
338	chr4	51000	52000	0.000	0.000	0.044	0.014	ZNF595;ZNF718;	0.34948	0.54966	0.02537	0	0	
339	chr4	54000	55000	0.000	0.000	0.029	0.000	ZNF595;ZNF718;	0.22755	0.54294	0.08726	0	0	
340	chr4	290000	291000	0.056	0.000	0.000	0.000	ZNF732	1.00000	0.11763	1.00000	0	1	
341	chr4	385000	386000	0.000	0.000	0.029	0.000	ZNF141	0.22755	0.54294	0.08726	0	0	
342	chr4	550000	551000	0.000	0.000	0.000	0.027	PIGG	0.49735	1.00000	1.00000	0	0	
343	chr4	2707000	2708000	0.028	0.000	0.015	0.000	FAM193A	0.47887	1.00000	0.29694	0	0	
344	chr4	5206000	5207000	0.000	0.000	0.029	0.000	STK32B	0.22755	0.54294	0.08726	0	0	
345	chr4	25863000	25864000	0.000	0.000	0.059	0.014	SELL3	0.19371	0.29551	0.00730	0	1	
346	chr4	25864000	25865000	0.000	0.006	0.044	0.027	SELL3	0.67043	0.54966	0.67959	0	0	
347	chr4	25865000	25866000	0.000	0.000	0.074	0.027	SELL3	0.25970	0.16161	0.60208	0	1	
348	chr4	29657000	29658000	0.000	0.000	0.015	0.014	PCDH7	1.00000	1.00000	0.29694	0	0	
349	chr4	30356000	30357000	0.000	0.006	0.015	0.000	PCDH7	0.47887	1.00000	0.50863	0	0	
350	chr4	33418000	33419000	0.000	0.000	0.029	0.000	PCDH7	0.22755	0.54294	0.08726	0	0	
351	chr4	33449000	33450000	0.028	0.000	0.015	0.000	PCDH7	0.47887	1.00000	0.29694	0	0	
352	chr4	39348000	39349000	0.000	0.000	0.015	0.014	REC1	1.00000	1.00000	0.29694	0	0	

353	chr4	39974000	39975000	0.000	0.000	0.000	0.027	PDSSA	0.49735	1.00000	1.00000	0	0	
354	chr4	40194000	40195000	0.000	0.000	0.044	0.027	N4BP2	0.67043	0.54966	0.02537	0	0	
355	chr4	40195000	40196000	0.000	0.000	0.015	0.027	N4BP2	1.00000	1.00000	0.29694	0	0	
356	chr4	40196000	40197000	0.000	0.000	0.074	0.014	N4BP2	0.10420	0.16101	0.00208	0	1	
357	chr4	40197000	40198000	0.000	0.000	0.015	0.027	N4BP2	1.00000	1.00000	0.29694	0	0	
358	chr4	40198000	40199000	0.000	0.000	0.088	0.041	N4BP2	0.31126	0.09031	0.00058	0	1	
359	chr4	40199000	40200000	0.056	0.000	0.279	0.162	N4BP2	0.10628	0.00895	0.00000	0	1	
360	chr4	40200000	40201000	0.000	0.006	0.118	0.041	RHOH	0.11795	0.04825	0.00030	1	1	
361	chr4	40201000	40202000	0.000	0.000	0.088	0.041	RHOH	0.31126	0.09031	0.00058	1	1	
362	chr4	40202000	40203000	0.000	0.000	0.029	0.014	RHOH	0.60686	0.54294	0.08726	1	0	
363	chr4	40204000	40205000	0.000	0.000	0.029	0.000	RHOH	0.22755	0.54294	0.08726	1	0	
364	chr4	45308000	45309000	0.000	0.000	0.029	0.000	GNPDA2	0.22755	0.54294	0.08726	0	0	
365	chr4	46360000	46361000	0.000	0.000	0.015	0.014	GABRA2	1.00000	1.00000	0.29694	0	0	
366	chr4	62375000	62376000	0.000	0.000	0.029	0.000	LPHN3	0.22755	0.54294	0.08726	0	0	
367	chr4	62530000	62531000	0.000	0.000	0.029	0.000	LPHN3	0.22755	0.54294	0.08726	0	0	
368	chr4	62911000	62912000	0.000	0.000	0.029	0.000	LPHN3	0.22755	0.54294	0.08726	0	0	
369	chr4	63120000	63121000	0.000	0.000	0.029	0.000	LPHN3	0.22755	0.54294	0.08726	0	0	
370	chr4	64015000	64016000	0.000	0.000	0.029	0.000	LPHN3	0.22755	0.54294	0.08726	0	0	
371	chr4	65038000	65039000	0.000	0.000	0.015	0.014	TECRL	1.00000	1.00000	0.29694	0	0	
372	chr4	65165000	65166000	0.000	0.000	0.015	0.014	TECRL	1.00000	1.00000	0.29694	0	0	
373	chr4	65966000	65967000	0.000	0.006	0.000	0.014	EPHA5	1.00000	1.00000	0.29694	0	0	
374	chr4	66827000	66828000	0.000	0.000	0.029	0.000	EPHA5	0.22755	0.54294	0.08726	0	0	
375	chr4	71531000	71532000	0.000	0.000	0.015	0.041	IGJ	0.62100	1.00000	0.29694	0	0	
376	chr4	71532000	71533000	0.000	0.000	0.000	0.027	IGJ	0.49735	1.00000	1.00000	0	0	
377	chr4	74456000	74457000	0.000	0.000	0.029	0.000	RASSF6	0.22755	0.54294	0.08726	0	0	
378	chr4	74483000	74484000	0.000	0.006	0.015	0.000	RASSF6	0.47887	1.00000	0.50663	0	0	
379	chr4	74484000	74485000	0.000	0.000	0.044	0.000	RASSF6	0.10727	0.54966	0.02537	0	0	
380	chr4	74485000	74486000	0.000	0.000	0.088	0.000	RASSF6	0.01070	0.09031	0.00058	0	1	
381	chr4	91886000	91887000	0.000	0.000	0.015	0.014	CCSER1	1.00000	1.00000	0.29694	0	0	
382	chr4	92787000	92788000	0.000	0.000	0.029	0.000	CCSER1	0.22755	0.54294	0.08726	0	0	
383	chr4	113206000	113207000	0.000	0.000	0.029	0.000	TIFA	0.22755	0.54294	0.08726	0	0	
384	chr4	114466000	114467000	0.000	0.000	0.029	0.000	CAMK2D	0.22755	0.54294	0.08726	0	0	
385	chr4	114681000	114682000	0.000	0.000	0.044	0.000	CAMK2D	0.10727	0.54966	0.02537	0	0	
386	chr4	117928000	117929000	0.000	0.000	0.029	0.000	TRAM1L1	0.22755	0.54294	0.08726	0	0	
387	chr4	123637000	123638000	0.000	0.000	0.000	0.027	BBS12	0.49735	1.00000	1.00000	0	0	
388	chr4	125227000	125228000	0.000	0.000	0.015	0.014	ANKRD50	1.00000	1.00000	0.29694	0	0	
389	chr4	127371000	127372000	0.000	0.000	0.029	0.000	FAT4	0.22755	0.54294	0.08726	0	0	
390	chr4	133455000	133456000	0.000	0.000	0.000	0.027	PCDH10	0.49735	1.00000	1.00000	0	0	
391	chr4	134538000	134539000	0.000	0.000	0.015	0.014	PCDH10	1.00000	1.00000	0.29694	0	0	
392	chr4	134743000	134744000	0.000	0.000	0.029	0.000	PABPC4L	0.22755	0.54294	0.08726	0	0	
393	chr4	134867000	134868000	0.000	0.000	0.029	0.000	PABPC4L	0.22755	0.54294	0.08726	0	0	
394	chr4	134949000	134950000	0.000	0.000	0.029	0.000	PABPC4L	0.22755	0.54294	0.08726	0	0	
395	chr4	135064000	135065000	0.000	0.000	0.015	0.014	PABPC4L	1.00000	1.00000	0.29694	0	0	
396	chr4	135077000	135078000	0.000	0.000	0.029	0.000	PABPC4L	0.22755	0.54294	0.08726	0	0	
397	chr4	136799000	136800000	0.028	0.006	0.000	0.000	PCDH18	1.00000	0.34615	1.00000	0	0	
398	chr4	136867000	136868000	0.000	0.000	0.015	0.014	PCDH18	1.00000	1.00000	0.29694	0	0	
399	chr4	140236000	140237000	0.000	0.000	0.015	0.014	NAA15	1.00000	1.00000	0.29694	0	0	
400	chr4	151723000	151724000	0.000	0.000	0.029	0.000	LRBA	0.22755	0.54294	0.08726	0	0	
401	chr4	151950000	151951000	0.000	0.000	0.000	0.027	LRBA	0.49735	1.00000	1.00000	0	0	
402	chr4	152125000	152126000	0.028	0.000	0.029	0.000	SH3D19	0.22755	1.00000	0.08726	0	0	
403	chr4	157246000	157247000	0.000	0.000	0.015	0.014	CTSO	1.00000	1.00000	0.29694	0	0	

404	chr4	164533000	164533000	0.000	0.000	0.000	0.027	1-Mar-19	0.49735	1.00000	1.00000	0	0	
405	chr4	178732000	178733000	0.028	0.000	0.000	0.014	AGA	1.00000	0.34615	1.00000	0	0	
406	chr4	178885000	178886000	0.000	0.000	0.029	0.000	AGA	0.22755	0.54294	0.08726	0	0	
407	chr4	179898000	179899000	0.000	0.000	0.029	0.000	AGA	0.22755	0.54294	0.08726	0	0	
408	chr4	180885000	180886000	0.000	0.006	0.029	0.000	TENM3	0.22755	0.54294	0.21104	0	0	
409	chr4	181554000	181555000	0.000	0.000	0.029	0.000	TENM3	0.22755	0.54294	0.08726	0	0	
410	chr4	182122000	182123000	0.000	0.000	0.015	0.014	TENM3	1.00000	1.00000	0.29694	0	0	
411	chr5	436000	437000	0.028	0.000	0.000	0.014	AHRR	1.00000	0.34615	1.00000	0	0	
412	chr5	3982000	3983000	0.000	0.000	0.029	0.000	IRX1	0.22755	0.54294	0.08726	0	0	
413	chr5	17218000	17219000	0.000	0.000	0.029	0.000	HASP1	0.22755	0.54294	0.08726	0	0	
414	chr5	17219000	17220000	0.000	0.000	0.029	0.000	HASP1	0.22755	0.54294	0.08726	0	0	
415	chr5	18514000	18515000	0.028	0.000	0.000	0.014	CDH18	1.00000	0.34615	1.00000	0	0	
416	chr5	22356000	22357000	0.000	0.000	0.029	0.000	CDH12	0.22755	0.54294	0.08726	0	0	
417	chr5	22517000	22518000	0.000	0.000	0.015	0.014	CDH12	1.00000	1.00000	0.29694	0	0	
418	chr5	24632000	24633000	0.000	0.000	0.029	0.000	CDH10	0.22755	0.54294	0.08726	0	0	
419	chr5	25275000	25276000	0.000	0.000	0.015	0.014	CDH10	1.00000	1.00000	0.29694	0	0	
420	chr5	25541000	25542000	0.000	0.000	0.029	0.000	CDH10	0.22755	0.54294	0.08726	0	0	
421	chr5	26119000	26120000	0.000	0.000	0.015	0.014	CDH9	1.00000	1.00000	0.29694	0	0	
422	chr5	26450000	26451000	0.000	0.000	0.029	0.000	CDH9	0.22755	0.54294	0.08726	0	0	
423	chr5	29224000	29225000	0.000	0.000	0.029	0.000	CDH6	0.22755	0.54294	0.08726	0	0	
424	chr5	29492000	29493000	0.000	0.000	0.029	0.000	CDH6	0.22755	0.54294	0.08726	0	0	
425	chr5	29648000	29649000	0.000	0.000	0.029	0.000	CDH6	0.22755	0.54294	0.08726	0	0	
426	chr5	51521000	51522000	0.000	0.000	0.044	0.014	CTD-2203A3.1	0.34948	0.54966	0.02537	0	0	
427	chr5	83841000	83842000	0.000	0.000	0.029	0.000	EDIL3	0.22755	0.54294	0.08726	0	0	
428	chr5	88177000	88178000	0.000	0.000	0.029	0.000	MEF2C	0.22755	0.54294	0.08726	0	0	
429	chr5	88178000	88179000	0.000	0.000	0.015	0.014	MEF2C	1.00000	1.00000	0.29694	0	0	
430	chr5	91417000	91418000	0.000	0.000	0.000	0.027	ARRDC3	0.49735	1.00000	1.00000	0	0	
431	chr5	103678000	103679000	0.000	0.000	0.015	0.014	NUDT12	1.00000	1.00000	0.29694	0	0	
432	chr5	123696000	123697000	0.000	0.000	0.000	0.027	ZNF608	0.49735	1.00000	1.00000	1	0	
433	chr5	124079000	124080000	0.000	0.000	0.029	0.014	ZNF608	0.60686	0.54294	0.08726	1	0	
434	chr5	124980000	124981000	0.000	0.000	0.029	0.014	ZNF608	0.60686	0.54294	0.08726	1	0	
435	chr5	127594000	127595000	0.000	0.000	0.015	0.014	FBN2	1.00000	1.00000	0.29694	0	0	
436	chr5	127875000	127876000	0.000	0.000	0.000	0.027	FBN2	0.49735	1.00000	1.00000	0	0	
437	chr5	131825000	131826000	0.000	0.000	0.074	0.000	IRF1	0.02326	0.16101	0.00208	0	1	
438	chr5	131826000	131827000	0.000	0.000	0.029	0.000	IRF1	0.22755	0.54294	0.08726	0	0	
439	chr5	149791000	149792000	0.000	0.000	0.132	0.014	CD74	0.00761	0.02564	0.00001	1	1	
440	chr5	149792000	149793000	0.000	0.000	0.015	0.014	CD74	1.00000	1.00000	0.29694	1	0	
441	chr5	158380000	158381000	0.028	0.000	0.015	0.000	EBF1	0.47887	1.00000	0.29694	0	0	
442	chr5	158479000	158480000	0.000	0.000	0.029	0.000	EBF1	0.22755	0.54294	0.08726	0	0	
443	chr5	158526000	158527000	0.028	0.000	0.044	0.000	EBF1	0.10727	1.00000	0.02537	0	0	
444	chr5	158527000	158528000	0.000	0.000	0.029	0.000	EBF1	0.22755	0.54294	0.08726	0	0	
445	chr5	158528000	158529000	0.000	0.000	0.059	0.000	EBF1	0.05016	0.29551	0.00739	0	1	
446	chr5	164247000	164248000	0.000	0.000	0.029	0.000	MAT2B	0.22755	0.54294	0.08726	0	0	
447	chr5	164441000	164442000	0.028	0.000	0.015	0.000	MAT2B	0.47887	1.00000	0.29694	0	0	
448	chr5	165932000	165933000	0.000	0.000	0.015	0.014	TENM2	1.00000	1.00000	0.29694	0	0	
449	chr5	173300000	173301000	0.000	0.000	0.000	0.027	CPEB4	0.49735	1.00000	1.00000	0	0	
450	chr5	179166000	179167000	0.000	0.000	0.015	0.027	MAML1	1.00000	1.00000	0.29694	0	0	
451	chr6	18010000	18010300	0.000	0.000	0.015	0.014	FLT4	1.00000	1.00000	0.29694	0	0	
452	chr6	392000	393000	0.000	0.000	0.074	0.000	IRF4	0.02326	0.16101	0.00208	1	1	
453	chr6	393000	394000	0.000	0.000	0.074	0.000	IRF4	0.02326	0.16101	0.00208	1	1	
454	chr6	14118000	14119000	0.000	0.000	0.279	0.041	CD83	0.00011	0.00013	0.00000	1	1	

455	chr6	14119000	14120000	0.000	0.000	0.044	0.027	CD83	0.67043	0.54966	0.02537	1		0
456	chr6	18111000	18112000	0.028	0.000	0.044	0.000	NFILRC1	0.10727	1.00000	0.02537	0		0
457	chr6	18387000	18388000	0.000	0.000	0.000	0.027	RNF144B	0.49735	1.00000	1.00000	1		0
458	chr6	18388000	18389000	0.000	0.000	0.000	0.027	RNF144B	0.49735	1.00000	1.00000	1		0
459	chr6	19573000	19574000	0.000	0.000	0.029	0.000	TD4	0.22755	0.54294	0.08726	0		0
460	chr6	22873000	22874000	0.000	0.000	0.015	0.014	EDGFL1	1.00000	1.00000	0.29694	0		0
461	chr6	26031000	26032000	0.000	0.000	0.000	0.027	HIST1H3B	0.49735	1.00000	1.00000	1		0
462	chr6	26032000	26033000	0.000	0.000	0.000	0.027	HIST1H3B	0.49735	1.00000	1.00000	1		0
463	chr6	26056000	26057000	0.000	0.000	0.059	0.027	HIST1H1C	0.42627	0.29551	0.60730	1		1
464	chr6	26123000	26124000	0.000	0.000	0.059	0.014	HIST1H2BC	0.19371	0.29551	0.60730	1		1
465	chr6	26124000	26125000	0.000	0.000	0.074	0.000	HIST1H2AC;HIST1H2BC;	0.02326	0.16101	0.60208	0		1
466	chr6	26125000	26126000	0.000	0.000	0.015	0.014	HIST1H2AC	1.00000	1.00000	0.29694	1		0
467	chr6	26156000	26157000	0.000	0.000	0.074	0.014	HIST1H1E	0.10420	0.16101	0.60208	1		1
468	chr6	26157000	26158000	0.000	0.000	0.029	0.014	HIST1H1E	0.60686	0.54294	0.08726	1		0
469	chr6	26216000	26217000	0.000	0.000	0.029	0.000	HIST1H2BG	0.22755	0.54294	0.08726	1		0
470	chr6	26233000	26234000	0.000	0.000	0.044	0.000	HIST1H1D	0.10727	0.54966	0.02537	0		0
471	chr6	27101000	27102000	0.000	0.000	0.029	0.000	HIST1H2AG	0.22755	0.54294	0.08726	1		0
472	chr6	27114000	27115000	0.000	0.000	0.059	0.014	HIST1H2AE;HIST1H2BK;	0.19371	0.29551	0.60730	0		1
473	chr6	27792000	27793000	0.000	0.000	0.044	0.014	HIST1H4J	0.34948	0.54966	0.02537	0		0
474	chr6	27833000	27834000	0.000	0.000	0.015	0.014	HIST1H2AL	1.00000	1.00000	0.29694	1		0
475	chr6	27860000	27861000	0.000	0.000	0.029	0.027	HIST1H2AM	1.00000	0.54294	0.08726	1		0
476	chr6	27861000	27862000	0.000	0.000	0.015	0.014	HIST1H2BO	1.00000	1.00000	0.29694	1		0
477	chr6	29778000	29779000	0.028	0.000	0.000	0.014	LOC554223	1.00000	0.34615	1.00000	0		0
478	chr6	29780000	29781000	0.000	0.000	0.015	0.014	HLA-G	1.00000	1.00000	0.29694	0		0
479	chr6	29911000	29912000	0.000	0.000	0.044	0.000	HLA-A	0.10727	0.54966	0.02537	0		0
480	chr6	29927000	29928000	0.000	0.000	0.015	0.014	HLA-A	1.00000	1.00000	0.29694	0		0
481	chr6	31324000	31325000	0.000	0.000	0.029	0.014	HLA-B	0.60686	0.54294	0.08726	1		0
482	chr6	31325000	31326000	0.028	0.000	0.000	0.014	HLA-B	1.00000	0.34615	1.00000	1		0
483	chr6	31543000	31544000	0.000	0.000	0.029	0.000	TNF	0.22755	0.54294	0.08726	1		0
484	chr6	31549000	31550000	0.000	0.026	0.191	0.068	LTB	0.04150	0.00372	0.00000	1		1
485	chr6	31550000	31551000	0.000	0.000	0.044	0.000	LTB	0.10727	0.54966	0.02537	1		0
486	chr6	32440000	32441000	0.000	0.000	0.044	0.027	HLA-DPA	0.67043	0.54966	0.02537	0		0
487	chr6	32451000	32452000	0.056	0.000	0.000	0.000	HLA-DRB5	1.00000	0.11763	1.00000	0		1
488	chr6	32452000	32453000	0.028	0.000	0.015	0.000	HLA-DRB5	0.47887	1.00000	0.29694	0		0
489	chr6	32455000	32456000	0.028	0.000	0.015	0.000	HLA-DRB5	0.47887	1.00000	0.29694	0		0
490	chr6	32457000	32458000	0.000	0.000	0.000	0.027	HLA-DRB5	0.49735	1.00000	1.00000	0		0
491	chr6	32498000	32499000	0.000	0.000	0.000	0.027	HLA-DRB5	0.49735	1.00000	1.00000	0		0
492	chr6	32505000	32506000	0.000	0.000	0.029	0.014	HLA-DRB5	0.60686	0.54294	0.08726	0		0
493	chr6	32511000	32512000	0.000	0.000	0.000	0.041	HLA-DRB5	0.24603	1.00000	1.00000	0		0
494	chr6	32522000	32523000	0.028	0.000	0.015	0.027	HLA-DRB1	1.00000	1.00000	0.29694	0		0
495	chr6	32525000	32526000	0.000	0.000	0.029	0.014	HLA-DRB1	0.60686	0.54294	0.08726	0		0
496	chr6	32526000	32527000	0.000	0.000	0.000	0.041	HLA-DRB1	0.24603	1.00000	1.00000	0		0
497	chr6	32527000	32528000	0.000	0.000	0.000	0.027	HLA-DRB1	0.49735	1.00000	1.00000	0		0
498	chr6	32548000	32549000	0.000	0.000	0.029	0.014	HLA-DRB1	0.60686	0.54294	0.08726	0		0
499	chr6	32552000	32553000	0.056	0.000	0.015	0.027	HLA-DRB1	1.00000	0.27446	0.29694	0		1
500	chr6	32557000	32558000	0.028	0.000	0.000	0.041	HLA-DRB1	0.24603	0.34615	1.00000	0		0
501	chr6	32609000	32610000	0.028	0.000	0.059	0.014	HLA-DQA1	0.19371	0.65667	0.60730	0		1
502	chr6	32630000	32631000	0.000	0.000	0.015	0.014	HLA-DQB1	1.00000	1.00000	0.29694	0		0
503	chr6	32632000	32633000	0.111	0.000	0.029	0.027	HLA-DQB1	1.00000	0.17874	0.08726	0		1

504	chr6	32727000	32728000	0.056	0.000	0.015	0.000	HLA-DQB2	0.47887	0.27446	0.29694	0	1
505	chr6	32729000	32730000	0.056	0.000	0.029	0.014	HLA-DQB2	0.60686	0.60763	0.08726	0	1
506	chr6	33045000	33049000	0.030	0.030	0.015	0.014	HLA-DPB1	1.00000	1.00000	0.29694	0	0
507	chr6	34179000	34180000	0.000	0.000	0.029	0.000	HMGA1	0.22755	0.54294	0.08726	0	0
508	chr6	37138000	37139000	0.000	0.000	0.191	0.081	PIM1	0.08249	0.00372	0.00000	1	1
509	chr6	37139000	37140000	0.000	0.000	0.088	0.041	PIM1	0.03031	0.00058	0.00058	1	1
510	chr6	37140000	37141000	0.000	0.000	0.029	0.014	PIM1	0.60686	0.54294	0.08726	1	0
511	chr6	58001000	58002000	0.000	0.000	0.015	0.014	PRIM2	1.00000	1.00000	0.29694	0	0
512	chr6	67923000	67924000	0.000	0.000	0.015	0.014	BAT3	1.00000	1.00000	0.29694	0	0
513	chr6	77257000	77258000	0.000	0.000	0.029	0.000	EMPG1	0.22755	0.54294	0.08726	0	0
514	chr6	81437000	81438000	0.000	0.000	0.015	0.014	BCKDHB	1.00000	1.00000	0.29694	0	0
515	chr6	88468000	88469000	0.000	0.000	0.015	0.014	AKIRIN2	1.00000	1.00000	0.29694	0	0
516	chr6	88630000	88631000	0.000	0.000	0.044	0.014	SPACA1	0.34948	0.54966	0.02537	0	0
517	chr6	88876000	88877000	0.028	0.000	0.015	0.000	CNR1	0.47887	1.00000	0.29694	0	0
518	chr6	89323000	89324000	0.000	0.000	0.029	0.014	RNGTT	0.60686	0.54294	0.08726	0	0
519	chr6	89338000	89339000	0.000	0.000	0.029	0.000	RNGTT	0.22755	0.54294	0.08726	0	0
520	chr6	89348000	89349000	0.000	0.000	0.044	0.000	RNGTT	0.10727	0.54966	0.02537	0	0
521	chr6	89470000	89471000	0.000	0.000	0.029	0.000	RNGTT	0.22755	0.54294	0.08726	0	0
522	chr6	89471000	89472000	0.000	0.000	0.029	0.000	RNGTT	0.22755	0.54294	0.08726	0	0
523	chr6	90061000	90062000	0.030	0.030	0.059	0.000	UBE2J1	0.05016	0.29551	0.00730	1	1
524	chr6	90062000	90063000	0.000	0.000	0.029	0.000	UBE2J1	0.22755	0.54294	0.08726	1	0
525	chr6	90994000	90995000	0.000	0.000	0.029	0.014	MAP3K7	0.60686	0.54294	0.08726	0	0
526	chr6	91004000	91005000	0.000	0.000	0.059	0.014	MAP3K7	0.19371	0.29551	0.00730	0	1
527	chr6	91005000	91006000	0.000	0.019	0.294	0.095	MAP3K7	0.00279	0.00011	0.00000	0	1
528	chr6	91006000	91007000	0.000	0.006	0.118	0.027	MAP3K7	0.04838	0.04825	0.00039	0	1
529	chr6	91007000	91008000	0.000	0.012	0.029	0.000	MAP3K7	0.22755	0.54294	0.58408	0	0
530	chr6	94822000	94823000	0.028	0.000	0.015	0.000	EPHA7	0.47887	1.00000	0.29694	0	0
531	chr6	107704000	107705000	0.028	0.000	0.000	0.014	PDSS2	1.00000	0.34615	1.00000	0	0
532	chr6	112885000	112886000	0.000	0.000	0.015	0.014	RFPL4B	1.00000	1.00000	0.29694	0	0
533	chr6	118244000	118245000	0.000	0.000	0.015	0.014	SLC35F1	1.00000	1.00000	0.29694	0	0
534	chr6	121288000	121289000	0.000	0.000	0.000	0.027	C6orf170	0.49735	1.00000	1.00000	0	0
535	chr6	121489000	121490000	0.000	0.000	0.029	0.000	C6orf170	0.22755	0.54294	0.08726	0	0
536	chr6	123504000	123505000	0.000	0.006	0.015	0.000	TRDN	0.47887	1.00000	0.50663	0	0
537	chr6	127313000	127314000	0.000	0.006	0.015	0.000	RSPO3	0.47887	1.00000	0.50663	0	0
538	chr6	133785000	133786000	0.000	0.000	0.029	0.000	EYA4	0.22755	0.54294	0.08726	0	0
539	chr6	134491000	134492000	0.000	0.000	0.029	0.000	SGK1	0.22755	0.54294	0.08726	1	0
540	chr6	134492000	134493000	0.000	0.000	0.044	0.014	SGK1	0.34948	0.54966	0.02537	1	0
541	chr6	134493000	134494000	0.000	0.000	0.029	0.000	SGK1	0.22755	0.54294	0.08726	1	0
542	chr6	134494000	134495000	0.000	0.000	0.029	0.000	SGK1	0.22755	0.54294	0.08726	1	0
543	chr6	134495000	134496000	0.000	0.000	0.162	0.041	SGK1	0.02233	0.01471	0.00000	1	1
544	chr6	134496000	134497000	0.000	0.000	0.029	0.000	SGK1	0.22755	0.54294	0.08726	1	0
545	chr6	142046000	142047000	0.000	0.000	0.059	0.000	NMBR	0.05016	0.29551	0.00730	0	1
546	chr6	147860000	147861000	0.028	0.000	0.015	0.000	SAMD5	0.47887	1.00000	0.29694	0	0
547	chr6	150954000	150955000	0.000	0.000	0.044	0.014	PLEKHG1	0.34948	0.54966	0.02537	0	0
548	chr6	159238000	159239000	0.000	0.012	0.044	0.014	EZR	0.34948	0.54966	0.15671	0	0
549	chr6	159239000	159240000	0.000	0.000	0.029	0.014	EZR	0.60686	0.54294	0.08726	0	0
550	chr6	159240000	159241000	0.000	0.000	0.029	0.014	EZR	0.60686	0.54294	0.08726	0	0
551	chr6	159464000	159465000	0.000	0.000	0.015	0.014	TAGAP	1.00000	1.00000	0.29694	0	0
552	chr6	159465000	159466000	0.000	0.000	0.029	0.000	TAGAP	0.22755	0.54294	0.08726	0	0
553	chr6	161263000	161266000	0.028	0.000	0.000	0.027	PLG	0.49735	0.34615	1.00000	0	0
554	chr6	161833000	161834000	0.028	0.000	0.000	0.027	PARK2	0.49735	0.34615	1.00000	0	0

555	chr6	162713000	162713000	0.000	0.000	0.029	0.000	PARK2	0.22755	0.54294	0.08726	0	0
556	chr6	164941000	164942000	0.000	0.000	0.029	0.000	C6orf118	0.22755	0.54294	0.08726	0	0
557	chr6	168813000	168814000	0.028	0.000	0.015	0.000	SMOC2	0.47887	1.00000	0.29694	0	0
558	chr7	1898000	1899000	0.000	0.000	0.029	0.000	AC110781.3	0.22755	0.54294	0.08726	0	0
559	chr7	1961000	1964000	0.028	0.000	0.015	0.000	MAD1L1	0.47887	1.00000	0.29694	0	0
560	chr7	2080000	2081000	0.000	0.000	0.015	0.014	MAD1L1	1.00000	1.00000	0.29694	0	0
561	chr7	5568000	5569000	0.000	0.000	0.059	0.014	ACTB	0.19371	0.29551	0.00730	1	1
562	chr7	5569000	5570000	0.000	0.000	0.059	0.014	ACTB	0.19371	0.29551	0.00730	1	1
563	chr7	5570000	5571000	0.000	0.000	0.015	0.027	ACTB	1.00000	1.00000	0.29694	1	0
564	chr7	9933000	9934000	0.000	0.000	0.029	0.014	NDUFA4	0.60686	0.54294	0.08726	0	0
565	chr7	13017000	13018000	0.028	0.000	0.015	0.000	ARL4A	0.47887	1.00000	0.29694	0	0
566	chr7	13346000	13347000	0.000	0.000	0.000	0.027	ETV1	0.49735	1.00000	0.00000	0	0
567	chr7	15459000	15460000	0.000	0.000	0.000	0.027	AGMO	0.49735	1.00000	0.00000	0	0
568	chr7	16382000	16383000	0.000	0.000	0.015	0.014	ISPD	1.00000	1.00000	0.29694	0	0
569	chr7	28600000	28601000	0.028	0.000	0.015	0.000	CREB5	0.47887	1.00000	0.29694	0	0
570	chr7	40846000	40847000	0.000	0.000	0.015	0.041	C7orf10	0.62100	1.00000	0.29694	0	0
571	chr7	50349000	50350000	0.000	0.000	0.059	0.014	IKZF1	0.19371	0.29551	0.00730	0	1
572	chr7	50350000	50351000	0.000	0.000	0.044	0.000	IKZF1	0.10727	0.54966	0.02537	0	0
573	chr7	53335000	53336000	0.000	0.000	0.000	0.027	POM121L12	0.49735	1.00000	0.00000	0	0
574	chr7	57713000	57714000	0.000	0.000	0.029	0.000	ZNF716	0.22755	0.54294	0.08726	0	0
575	chr7	62475000	62476000	0.000	0.000	0.015	0.027	AC006455.1	1.00000	1.00000	0.29694	0	0
576	chr7	70669000	70670000	0.000	0.000	0.029	0.000	WBSCR17	0.22755	0.54294	0.08726	0	0
577	chr7	71553000	71554000	0.000	0.000	0.015	0.014	CALN1	1.00000	1.00000	0.29694	0	0
578	chr7	79847000	79848000	0.000	0.000	0.015	0.014	GNAI1	1.00000	1.00000	0.29694	0	0
579	chr7	80694000	80695000	0.000	0.000	0.029	0.000	AC005008.2	0.22755	0.54294	0.08726	0	0
580	chr7	81556000	81557000	0.000	0.000	0.000	0.027	CACNA2D1	0.49735	1.00000	0.00000	0	0
581	chr7	84127000	84128000	0.028	0.000	0.015	0.000	SEMA3A	0.47887	1.00000	0.29694	0	0
582	chr7	84247000	84248000	0.000	0.000	0.029	0.000	SEMA3D	0.22755	0.54294	0.08726	0	0
583	chr7	84257000	84258000	0.028	0.000	0.015	0.000	SEMA3D	0.47887	1.00000	0.29694	0	0
584	chr7	86914000	86915000	0.000	0.000	0.015	0.014	CROT	1.00000	1.00000	0.29694	0	0
585	chr7	90356000	90357000	0.000	0.000	0.029	0.000	CDK14	0.22755	0.54294	0.08726	0	0
586	chr7	93304000	93305000	0.000	0.000	0.029	0.000	CALCR	0.22755	0.54294	0.08726	0	0
587	chr7	93682000	93683000	0.000	0.000	0.015	0.014	BET1	1.00000	1.00000	0.29694	0	0
588	chr7	102644000	102645000	0.028	0.000	0.000	0.014	FBXL13	1.00000	0.34615	1.00000	0	0
589	chr7	105699000	105700000	0.000	0.000	0.015	0.027	CHRM3	1.00000	1.00000	0.29694	0	0
590	chr7	110521000	110522000	0.000	0.000	0.029	0.000	EMMPRL	0.22755	0.54294	0.08726	0	0
591	chr7	110543000	110544000	0.000	0.000	0.029	0.000	EMMPRL	0.22755	0.54294	0.08726	0	0
592	chr7	110545000	110546000	0.000	0.000	0.015	0.014	EMMPRL	1.00000	1.00000	0.29694	0	0
593	chr7	110597000	110598000	0.000	0.000	0.015	0.014	EMMPRL	1.00000	1.00000	0.29694	0	0
594	chr7	110601000	110602000	0.000	0.000	0.029	0.000	EMMPRL	0.22755	0.54294	0.08726	0	0
595	chr7	110602000	110603000	0.000	0.000	0.029	0.000	EMMPRL	0.22755	0.54294	0.08726	0	0
596	chr7	110609000	110610000	0.000	0.000	0.029	0.000	EMMPRL	0.22755	0.54294	0.08726	0	0
597	chr7	110610000	110611000	0.000	0.000	0.044	0.000	EMMPRL	0.10727	0.54966	0.02537	0	0
598	chr7	110617000	110618000	0.000	0.000	0.029	0.000	EMMPRL	0.22755	0.54294	0.08726	0	0
599	chr7	110618000	110619000	0.000	0.000	0.044	0.000	EMMPRL	0.10727	0.54966	0.02537	0	0
600	chr7	110619000	110620000	0.000	0.000	0.029	0.000	EMMPRL	0.22755	0.54294	0.08726	0	0
601	chr7	110621000	110622000	0.000	0.000	0.029	0.000	EMMPRL	0.22755	0.54294	0.08726	0	0
602	chr7	110628000	110629000	0.000	0.000	0.029	0.000	EMMPRL	0.22755	0.54294	0.08726	0	0
603	chr7	110629000	110630000	0.000	0.000	0.015	0.027	EMMPRL	1.00000	1.00000	0.29694	0	0
604	chr7	110631000	110632000	0.000	0.000	0.044	0.000	EMMPRL	0.10727	0.54966	0.02537	0	0
605	chr7	110632000	110633000	0.000	0.000	0.029	0.014	EMMPRL	0.60686	0.54294	0.08726	0	0

606	chr7	106636000	106637000	0.000	0.000	0.029	0.014	EMMP2L	0.60686	0.54294	0.08726	0	0	
607	chr7	106637000	106638000	0.000	0.000	0.029	0.014	EMMP2L	0.60686	0.54294	0.08726	0	0	
608	chr7	106638000	106639000	0.000	0.000	0.029	0.027	EMMP2L	1.00000	0.54294	0.08726	0	0	
609	chr7	106639000	106640000	0.000	0.000	0.044	0.000	EMMP2L	0.10727	0.54966	0.02537	0	0	
610	chr7	106641000	106642000	0.000	0.000	0.029	0.000	EMMP2L	0.22755	0.54294	0.08726	0	0	
611	chr7	106650000	106651000	0.000	0.000	0.029	0.000	EMMP2L	0.22755	0.54294	0.08726	0	0	
612	chr7	106651000	106652000	0.000	0.000	0.029	0.014	EMMP2L	0.60686	0.54294	0.08726	0	0	
613	chr7	106666000	106667000	0.000	0.000	0.000	0.027	EMMP2L	0.49735	1.00000	1.00000	0	0	
614	chr7	106671000	106672000	0.000	0.000	0.029	0.000	EMMP2L	0.22755	0.54294	0.08726	0	0	
615	chr7	106677000	106678000	0.000	0.000	0.029	0.014	EMMP2L	0.60686	0.54294	0.08726	0	0	
616	chr7	106679000	106680000	0.000	0.000	0.029	0.000	EMMP2L	0.22755	0.54294	0.08726	0	0	
617	chr7	106680000	106681000	0.000	0.000	0.074	0.000	EMMP2L	0.62326	0.16101	0.00208	0	1	
618	chr7	106685000	106686000	0.000	0.000	0.029	0.000	LRRN3	0.22755	0.54294	0.08726	0	0	
619	chr7	106686000	106687000	0.028	0.000	0.044	0.027	LRRN3	0.67043	1.00000	0.02537	0	0	
620	chr7	106688000	106689000	0.000	0.000	0.029	0.000	LRRN3	0.22755	0.54294	0.08726	0	0	
621	chr7	106699000	106700000	0.000	0.000	0.059	0.000	LRRN3	0.05016	0.29551	0.00730	0	1	
622	chr7	106700000	106701000	0.000	0.000	0.029	0.000	LRRN3	0.22755	0.54294	0.08726	0	0	
623	chr7	106709000	106710000	0.000	0.000	0.029	0.000	LRRN3	0.22755	0.54294	0.08726	0	0	
624	chr7	106711000	106712000	0.000	0.000	0.044	0.000	LRRN3	0.10727	0.54966	0.02537	0	0	
625	chr7	106714000	106715000	0.000	0.000	0.015	0.014	LRRN3	1.00000	1.00000	0.29694	0	0	
626	chr7	106727000	106728000	0.000	0.000	0.029	0.000	LRRN3	0.22755	0.54294	0.08726	0	0	
627	chr7	106728000	106729000	0.000	0.000	0.015	0.014	LRRN3	1.00000	1.00000	0.29694	0	0	
628	chr7	106729000	106730000	0.000	0.000	0.029	0.014	LRRN3	0.60686	0.54294	0.08726	0	0	
629	chr7	106734000	106735000	0.000	0.000	0.015	0.014	LRRN3	1.00000	1.00000	0.29694	0	0	
630	chr7	106737000	106738000	0.000	0.000	0.015	0.027	LRRN3	1.00000	1.00000	0.29694	0	0	
631	chr7	106740000	106741000	0.000	0.000	0.029	0.027	LRRN3	1.00000	0.54294	0.08726	0	0	
632	chr7	106744000	106745000	0.000	0.000	0.029	0.000	LRRN3	0.22755	0.54294	0.08726	0	0	
633	chr7	106746000	106747000	0.000	0.000	0.029	0.014	LRRN3	0.60686	0.54294	0.08726	0	0	
634	chr7	106747000	106748000	0.000	0.000	0.029	0.000	LRRN3	0.22755	0.54294	0.08726	0	0	
635	chr7	106748000	106749000	0.000	0.000	0.029	0.000	LRRN3	0.22755	0.54294	0.08726	0	0	
636	chr7	106755000	106756000	0.000	0.000	0.044	0.000	LRRN3	0.10727	0.54966	0.02537	0	0	
637	chr7	106764000	106765000	0.000	0.000	0.029	0.000	LRRN3	0.22755	0.54294	0.08726	0	0	
638	chr7	106767000	106768000	0.000	0.000	0.029	0.014	LRRN3	0.60686	0.54294	0.08726	0	0	
639	chr7	106769000	106770000	0.000	0.000	0.044	0.000	LRRN3	0.10727	0.54966	0.02537	0	0	
640	chr7	106771000	106772000	0.000	0.000	0.029	0.014	LRRN3	0.60686	0.54294	0.08726	0	0	
641	chr7	106779000	106780000	0.000	0.000	0.015	0.027	LRRN3	1.00000	1.00000	0.29694	0	0	
642	chr7	106780000	106781000	0.000	0.000	0.029	0.000	LRRN3	0.22755	0.54294	0.08726	0	0	
643	chr7	106783000	106784000	0.000	0.000	0.044	0.000	LRRN3	0.10727	0.54966	0.02537	0	0	
644	chr7	106785000	106786000	0.000	0.000	0.029	0.000	LRRN3	0.22755	0.54294	0.08726	0	0	
645	chr7	106801000	106802000	0.000	0.000	0.015	0.027	LRRN3	1.00000	1.00000	0.29694	0	0	
646	chr7	106802000	106803000	0.000	0.000	0.029	0.000	LRRN3	0.22755	0.54294	0.08726	0	0	
647	chr7	106810000	106811000	0.000	0.000	0.029	0.000	LRRN3	0.22755	0.54294	0.08726	0	0	
648	chr7	106816000	106817000	0.000	0.000	0.044	0.000	LRRN3	0.10727	0.54966	0.02537	0	0	
649	chr7	106821000	106822000	0.000	0.000	0.029	0.000	LRRN3	0.22755	0.54294	0.08726	0	0	
650	chr7	106824000	106825000	0.000	0.000	0.029	0.000	LRRN3	0.22755	0.54294	0.08726	0	0	
651	chr7	106827000	106828000	0.000	0.000	0.015	0.014	LRRN3	1.00000	1.00000	0.29694	0	0	
652	chr7	106836000	106837000	0.000	0.000	0.044	0.000	LRRN3	0.10727	0.54966	0.02537	0	0	
653	chr7	106847000	106848000	0.000	0.000	0.029	0.000	LRRN3	0.22755	0.54294	0.08726	0	0	
654	chr7	111567000	111568000	0.028	0.000	0.000	0.014	DOCK4	1.00000	0.34615	1.00000	0	0	
655	chr7	119056000	119057000	0.000	0.000	0.015	0.014	KCND2	1.00000	1.00000	0.29694	0	0	
656	chr7	121380000	121381000	0.000	0.036	0.015	0.014	PTPRZ1	1.00000	1.00000	0.50663	0	0	

657	chr7	123887000	123886000	0.000	0.000	0.029	0.000	TMEM229A	0.22755	0.54294	0.08726	0	0	
658	chr7	125263000	125263000	0.000	0.000	0.015	0.014	POT1	1.00000	1.00000	0.29694	0	0	
659	chr7	145723000	145724000	0.000	0.000	0.029	0.000	CNTNAP2	0.22755	0.54294	0.08726	0	0	
660	chr7	148508000	148509000	0.000	0.000	0.000	0.041	EZH2	0.24603	1.00000	1.00000	0	0	
661	chr7	155127000	155128000	0.000	0.000	0.000	0.027	BLACE	0.49735	1.00000	1.00000	0	0	
662	chr7	157162000	157163000	0.056	0.000	0.000	0.000	DNAJB6	1.00000	0.11763	1.00000	0	1	
663	chr8	1586844000	1586845000	0.000	0.000	0.015	0.014	WDR60	1.00000	1.00000	0.29694	0	0	
664	chr8	1646000	1647000	0.000	0.000	0.015	0.027	DLGAP2	1.00000	1.00000	0.29694	0	0	
665	chr8	5558000	5559000	0.000	0.000	0.029	0.000	MCPH1	0.22755	0.54294	0.08726	0	0	
666	chr8	5612000	5613000	0.000	0.000	0.000	0.027	MCPH1	0.49735	1.00000	1.00000	0	0	
667	chr8	8602000	8603000	0.000	0.000	0.029	0.014	MIR4S1	0.60686	0.54294	0.08726	0	0	
668	chr8	8706000	8707000	0.000	0.000	0.029	0.000	MIR4S1	0.22755	0.54294	0.08726	0	0	
669	chr8	8717000	8718000	0.000	0.000	0.029	0.000	MIR4S1	0.22755	0.54294	0.08726	0	0	
670	chr8	11352000	11353000	0.000	0.000	0.029	0.014	BLK	0.60686	0.54294	0.08726	0	0	
671	chr8	14080000	14081000	0.000	0.000	0.015	0.014	SGCZ	1.00000	1.00000	0.29694	0	0	
672	chr8	14796000	14797000	0.000	0.006	0.015	0.000	SGCZ	0.47887	1.00000	0.50663	0	0	
673	chr8	16090000	16091000	0.000	0.000	0.015	0.014	MSR1	1.00000	1.00000	0.29694	0	0	
674	chr8	16187000	16188000	0.028	0.000	0.015	0.000	MSR1	0.47887	1.00000	0.29694	0	0	
675	chr8	23101000	23102000	0.000	0.000	0.015	0.014	CHMP7	1.00000	1.00000	0.29694	0	0	
676	chr8	24207000	24208000	0.000	0.000	0.029	0.000	ADAM28	0.22755	0.54294	0.08726	0	0	
677	chr8	29155000	29156000	0.028	0.000	0.000	0.014	KIF13B	1.00000	0.34615	1.00000	0	0	
678	chr8	35657000	35658000	0.000	0.000	0.029	0.000	ADO22L1	0.22755	0.54294	0.08726	0	0	
679	chr8	38759000	38760000	0.000	0.000	0.029	0.000	PLEKHA2	0.22755	0.54294	0.08726	0	0	
680	chr8	54986000	54987000	0.000	0.000	0.029	0.000	LYPLA1	0.22755	0.54294	0.08726	0	0	
681	chr8	60031000	60032000	0.000	0.000	0.015	0.014	TOX	1.00000	1.00000	0.29694	0	0	
682	chr8	67525000	67526000	0.000	0.000	0.015	0.014	MYBL1	1.00000	1.00000	0.29694	0	0	
683	chr8	77105000	77106000	0.000	0.000	0.029	0.000	ZFHX4	0.22755	0.54294	0.08726	0	0	
684	chr8	78400000	78401000	0.000	0.000	0.029	0.000	PEX2	0.22755	0.54294	0.08726	0	0	
685	chr8	90322000	90323000	0.000	0.000	0.029	0.000	RIPK2	0.22755	0.54294	0.08726	0	0	
686	chr8	93199000	93200000	0.000	0.000	0.029	0.000	RUNX1T1	0.22755	0.54294	0.08726	0	0	
687	chr8	94618000	94619000	0.028	0.000	0.015	0.000	FAM92A1	0.47887	1.00000	0.29694	0	0	
688	chr8	110586000	110587000	0.000	0.000	0.015	0.014	SYBU	1.00000	1.00000	0.29694	0	0	
689	chr8	126687000	126688000	0.028	0.000	0.015	0.014	TRIB1	1.00000	1.00000	0.29694	0	0	
690	chr8	128748000	128749000	0.500	0.000	0.132	0.000	MYC	0.00699	0.00010	0.00001	1	1	
691	chr8	128749000	128750000	0.583	0.000	0.103	0.014	MYC	0.02808	0.00000	0.00016	1	1	
692	chr8	128750000	128751000	0.444	0.000	0.088	0.014	MYC	0.05468	0.00007	0.00058	1	1	
693	chr8	128751000	128752000	0.111	0.000	0.044	0.000	MYC	0.10727	0.23165	0.02537	1	1	
694	chr8	128752000	128753000	0.056	0.000	0.015	0.000	MYC	0.47887	0.27446	0.29694	1	1	
695	chr8	137918000	137919000	0.028	0.000	0.015	0.000	FAM135B	0.47887	1.00000	0.29694	0	0	
696	chr8	138274000	138275000	0.000	0.000	0.000	0.027	FAM135B	0.49735	1.00000	1.00000	0	0	
697	chr8	143183000	143184000	0.028	0.000	0.015	0.000	TSNARE1	0.47887	1.00000	0.29694	0	0	
698	chr8	144123000	144124000	0.000	0.000	0.029	0.000	C8orf31	0.22755	0.54294	0.08726	0	0	
699	chr9	6411000	6412000	0.000	0.000	0.029	0.000	UHRF2	0.22755	0.54294	0.08726	0	0	
700	chr9	6413000	6414000	0.000	0.000	0.015	0.014	UHRF2	1.00000	1.00000	0.29694	0	0	
701	chr9	6414000	6415000	0.000	0.000	0.029	0.014	UHRF2	0.60686	0.54294	0.08726	0	0	
702	chr9	9928000	9929000	0.000	0.000	0.000	0.027	PTPRD	0.49735	1.00000	1.00000	0	0	
703	chr9	13965000	13966000	0.000	0.000	0.029	0.000	NFIB	0.22755	0.54294	0.08726	0	0	
704	chr9	22824000	22825000	0.000	0.000	0.029	0.000	DMRTA1	0.22755	0.54294	0.08726	0	0	
705	chr9	25260000	25261000	0.000	0.000	0.029	0.000	TUSC1	0.22755	0.54294	0.08726	0	0	
706	chr9	29890000	29891000	0.000	0.000	0.015	0.014	LINGO2	1.00000	1.00000	0.29694	0	0	
707	chr9	30656000	30657000	0.000	0.000	0.015	0.014	ACO1	1.00000	1.00000	0.29694	0	0	

708	chr9	37003000	37004000	0.000	0.006	0.015	0.000	PAX5	0.47887	1.00000	0.50663	1		0
709	chr9	37003000	37006000	0.000	0.000	0.015	0.014	PAX5	1.00000	1.00000	0.29694	1		0
710	chr9	37024000	37025000	0.000	0.000	0.044	0.027	PAX5	0.67043	0.54966	0.02537	1		0
711	chr9	37025000	37026000	0.000	0.000	0.132	0.054	PAX5	0.14640	0.02564	0.00001	1		1
712	chr9	37026000	37027000	0.000	0.006	0.221	0.108	PAX5	0.10913	0.00167	0.00000	1		1
713	chr9	37027000	37028000	0.000	0.000	0.029	0.014	PAX5	0.60686	0.54294	0.08726	1		0
714	chr9	37033000	37034000	0.000	0.000	0.044	0.014	PAX5	0.34948	0.54966	0.02537	1		0
715	chr9	37034000	37035000	0.000	0.000	0.074	0.041	PAX5	0.47996	0.16101	0.00208	1		1
716	chr9	37035000	37036000	0.000	0.000	0.015	0.014	PAX5	1.00000	1.00000	0.29694	1		0
717	chr9	37196000	37197000	0.000	0.000	0.029	0.014	ZCCHC7	0.60686	0.54294	0.08726	0		0
718	chr9	37197000	37198000	0.000	0.000	0.029	0.000	ZCCHC7	0.22755	0.54294	0.08726	0		0
719	chr9	37293000	37294000	0.000	0.000	0.029	0.027	ZCCHC7	1.00000	0.54294	0.08726	0		0
720	chr9	37294000	37295000	0.000	0.000	0.044	0.027	ZCCHC7	0.67043	0.54966	0.02537	0		0
721	chr9	37327000	37328000	0.000	0.000	0.015	0.014	ZCCHC7	1.00000	1.00000	0.29694	0		0
722	chr9	37336000	37337000	0.000	0.000	0.044	0.014	ZCCHC7	0.34948	0.54966	0.02537	0		0
723	chr9	37337000	37338000	0.000	0.012	0.015	0.041	ZCCHC7	0.62100	1.00000	1.00000	0		0
724	chr9	37338000	37339000	0.000	0.000	0.029	0.014	ZCCHC7	0.60686	0.54294	0.08726	0		0
725	chr9	37369000	37370000	0.000	0.000	0.029	0.000	ZCCHC7	0.22755	0.54294	0.08726	0		0
726	chr9	37371000	37372000	0.028	0.025	0.118	0.068	ZCCHC7	0.38669	0.15803	0.00732	0		1
727	chr9	37372000	37373000	0.000	0.000	0.015	0.014	ZCCHC7	1.00000	1.00000	0.29694	0		0
728	chr9	37383000	37384000	0.000	0.000	0.059	0.027	ZCCHC7	0.42627	0.29551	0.00730	0		1
729	chr9	37384000	37385000	0.000	0.000	0.059	0.054	ZCCHC7	1.00000	0.29551	0.00730	0		1
730	chr9	37385000	37386000	0.000	0.000	0.029	0.014	ZCCHC7	0.60686	0.54294	0.08726	0		0
731	chr9	37387000	37388000	0.000	0.000	0.059	0.014	ZCCHC7	0.19371	0.29551	0.00730	0		1
732	chr9	37397000	37398000	0.000	0.000	0.044	0.000	GRHPR	0.10727	0.54966	0.02537	0		0
733	chr9	37398000	37399000	0.000	0.000	0.029	0.000	GRHPR	0.22755	0.54294	0.08726	0		0
734	chr9	37399000	37400000	0.000	0.000	0.029	0.000	GRHPR	0.22755	0.54294	0.08726	0		0
735	chr9	37402000	37403000	0.000	0.006	0.029	0.000	GRHPR	0.22755	0.54294	0.21104	0		0
736	chr9	37406000	37407000	0.000	0.000	0.015	0.014	GRHPR	1.00000	1.00000	0.29694	0		0
737	chr9	37407000	37408000	0.000	0.000	0.132	0.149	GRHPR	0.81382	0.02564	0.00001	0		1
738	chr9	37408000	37409000	0.000	0.006	0.029	0.027	GRHPR	1.00000	0.54294	0.21104	0		0
739	chr9	37410000	37411000	0.000	0.000	0.029	0.000	GRHPR	0.22755	0.54294	0.08726	0		0
740	chr9	37424000	37425000	0.000	0.000	0.044	0.000	GRHPR	0.10727	0.54966	0.02537	0		0
741	chr9	37425000	37426000	0.000	0.000	0.029	0.000	GRHPR	0.22755	0.54294	0.08726	0		0
742	chr9	112811000	112812000	0.000	0.000	0.059	0.014	AKAP2	0.19371	0.29551	0.00730	0		1
743	chr9	117037000	117038000	0.056	0.000	0.000	0.014	COL27A1	1.00000	0.11763	1.00000	0		1
744	chr9	119779000	119780000	0.000	0.000	0.044	0.000	ASTN2	0.10727	0.54966	0.02537	0		0
745	chr9	126232000	126233000	0.056	0.000	0.000	0.000	DENND1A	1.00000	0.11763	1.00000	0		1
746	chr9	130741000	130742000	0.000	0.000	0.059	0.000	FAM102A	0.05916	0.29551	0.00730	1		1
747	chr9	130742000	130743000	0.000	0.000	0.059	0.027	FAM102A	0.42627	0.29551	0.00730	1		1
748	chr9	132767000	132768000	0.000	0.000	0.015	0.014	FNBP1	1.00000	1.00000	0.29694	0		0
749	chr9	132785000	132786000	0.000	0.000	0.029	0.000	FNBP1	0.22755	0.54294	0.08726	0		0
750	chr9	132803000	132804000	0.000	0.000	0.015	0.014	FNBP1	1.00000	1.00000	0.29694	0		0
751	chr9	132804000	132805000	0.000	0.000	0.029	0.027	FNBP1	1.00000	0.54294	0.08726	0		0
752	chr9	134551000	134552000	0.000	0.000	0.029	0.000	RAPGEF1	0.22755	0.54294	0.08726	0		0
753	chr9	138874000	138875000	0.056	0.000	0.029	0.014	UBAC1	0.60686	0.60763	0.08726	0		1
754	chr10	3333000	3334000	0.000	0.000	0.000	0.027	PITRM1	0.49735	1.00000	1.00000	0		0
755	chr10	5707000	5708000	0.000	0.000	0.029	0.014	ASB13	0.60686	0.54294	0.08726	0		0
756	chr10	5728000	5729000	0.000	0.006	0.015	0.000	ASB13	0.47887	1.00000	0.50663	0		0
757	chr10	15393000	15394000	0.028	0.000	0.015	0.000	FAM171A1	0.47887	1.00000	0.29694	0		0
758	chr10	20796000	20797000	0.000	0.006	0.015	0.000	PLXDC2	0.47887	1.00000	0.50663	0		0

759	chr10	35424000	35425000	0.000	0.000	0.029	0.000	CREM	0.22755	0.54294	0.08726	0	0	0
760	chr10	36678000	36679000	0.000	0.000	0.000	0.027	PCDH15	0.49735	1.00000	1.00000	0	0	0
761	chr10	63440000	63441000	0.000	0.015	0.000	0.000	C10orf107	0.47887	1.00000	0.29694	0	0	0
762	chr10	63659000	63660000	0.000	0.000	0.044	0.014	ARID5B	0.34948	0.54966	0.02537	1	0	0
763	chr10	63660000	63661000	0.000	0.000	0.059	0.014	ARID5B	0.19371	0.29551	0.00730	1	1	1
764	chr10	63662000	63663000	0.000	0.000	0.029	0.014	ARID5B	0.60686	0.54294	0.08726	1	0	0
765	chr10	63720000	63721000	0.000	0.000	0.029	0.000	ARID5B	0.22755	0.54294	0.08726	1	0	0
766	chr10	63803000	63804000	0.000	0.000	0.000	0.027	ARID5B	0.49735	1.00000	1.00000	1	0	0
767	chr10	63809000	63810000	0.000	0.000	0.015	0.014	ARID5B	1.00000	1.00000	0.29694	1	0	0
768	chr10	63810000	63811000	0.000	0.000	0.000	0.027	ARID5B	0.49735	1.00000	1.00000	1	0	0
769	chr10	67907000	67908000	0.000	0.006	0.015	0.000	CTNNA3	0.47887	1.00000	0.50663	0	0	0
770	chr10	68474000	68475000	0.000	0.000	0.000	0.027	CTNNA3	0.49735	1.00000	1.00000	0	0	0
771	chr10	98510000	98511000	0.000	0.000	0.029	0.000	PIK3AP1	0.22755	0.54294	0.08726	0	0	0
772	chr10	101384000	101385000	0.028	0.000	0.015	0.014	SLC25A28	1.00000	1.00000	0.29694	0	0	0
773	chr10	108276000	108277000	0.000	0.000	0.029	0.000	SORCS1	0.22755	0.54294	0.08726	0	0	0
774	chr10	113473000	113474000	0.028	0.000	0.015	0.000	GPAM	0.47887	1.00000	0.29694	0	0	0
775	chr10	113636000	113637000	0.000	0.000	0.029	0.000	GPAM	0.22755	0.54294	0.08726	0	0	0
776	chr10	116458000	116459000	0.000	0.000	0.044	0.000	ABLIM1	0.10727	0.54966	0.02537	0	0	0
777	chr10	121623000	121624000	0.000	0.000	0.029	0.000	MCMBP	0.22755	0.54294	0.08726	0	0	0
778	chr10	132973000	132974000	0.000	0.000	0.015	0.027	TCERG1L	1.00000	1.00000	0.29694	0	0	0
779	chr10	134326000	134327000	0.028	0.000	0.015	0.000	INPP5A	0.47887	1.00000	0.29694	0	0	0
780	chr11	871000	872000	0.028	0.000	0.029	0.000	CHID1	0.22755	1.00000	0.08726	0	0	0
781	chr11	1149000	1150000	0.028	0.000	0.015	0.000	MUC5AC	0.47887	1.00000	0.29694	0	0	0
782	chr11	25065000	25066000	0.000	0.000	0.029	0.000	LUZP2	0.22755	0.54294	0.08726	0	0	0
783	chr11	25289000	25290000	0.000	0.000	0.029	0.000	LUZP2	0.22755	0.54294	0.08726	0	0	0
784	chr11	27216000	27217000	0.028	0.000	0.029	0.014	BBOX1	0.60686	1.00000	0.08726	0	0	0
785	chr11	28849000	28850000	0.000	0.000	0.000	0.027	METTL15	0.49735	1.00000	1.00000	0	0	0
786	chr11	29253000	29254000	0.000	0.000	0.029	0.000	KCNA4	0.22755	0.54294	0.08726	0	0	0
787	chr11	29900000	29901000	0.000	0.000	0.029	0.000	KCNA4	0.22755	0.54294	0.08726	0	0	0
788	chr11	40626000	40627000	0.000	0.000	0.029	0.000	LRRC4C	0.22755	0.54294	0.08726	0	0	0
789	chr11	40845000	40846000	0.000	0.000	0.029	0.000	LRRC4C	0.22755	0.54294	0.08726	0	0	0
790	chr11	40868000	40869000	0.000	0.000	0.029	0.000	LRRC4C	0.22755	0.54294	0.08726	0	0	0
791	chr11	41066000	41067000	0.000	0.000	0.029	0.000	LRRC4C	0.22755	0.54294	0.08726	0	0	0
792	chr11	41844000	41845000	0.028	0.000	0.015	0.000	AP5	0.47887	1.00000	0.29694	0	0	0
793	chr11	57171000	57172000	0.000	0.000	0.029	0.014	SLC43A3	0.60686	0.54294	0.08726	0	0	0
794	chr11	60224000	60225000	0.000	0.000	0.074	0.014	MS4A1	0.10420	0.16101	0.00208	1	1	1
795	chr11	65190000	65191000	0.000	0.000	0.074	0.027	FRMD8	0.25970	0.16101	0.00208	0	1	1
796	chr11	65191000	65192000	0.000	0.000	0.103	0.014	FRMD8	0.02808	0.09269	0.00016	0	1	1
797	chr11	65266000	65267000	0.000	0.000	0.029	0.014	SCYL1	0.60686	0.54294	0.08726	0	0	0
798	chr11	65267000	65268000	0.000	0.000	0.103	0.000	SCYL1	0.60488	0.09269	0.00016	0	1	1
799	chr11	85963000	85964000	0.000	0.000	0.029	0.000	EED	0.22755	0.54294	0.08726	0	0	0
800	chr11	92261000	92263000	0.000	0.000	0.029	0.000	FAT3	0.22755	0.54294	0.08726	0	0	0
801	chr11	102117000	102118000	0.000	0.000	0.000	0.027	YAP1	0.49735	1.00000	1.00000	0	0	0
802	chr11	102188000	102189000	0.000	0.012	0.206	0.108	BIRC3	0.16270	0.00197	0.00000	1	1	1
803	chr11	102189000	102190000	0.000	0.000	0.059	0.000	BIRC3	0.03916	0.29551	0.00730	1	1	1
804	chr11	107497000	107498000	0.028	0.000	0.015	0.000	ELMOD1	0.47887	1.00000	0.29694	0	0	0
805	chr11	108781000	108782000	0.000	0.000	0.015	0.014	DDX10	1.00000	1.00000	0.29694	0	0	0
806	chr11	108975000	108976000	0.000	0.000	0.015	0.014	DDX10	1.00000	1.00000	0.29694	0	0	0
807	chr11	109066000	109067000	0.028	0.000	0.015	0.000	C11orf87	0.47887	1.00000	0.29694	0	0	0
808	chr11	111248000	111249000	0.000	0.000	0.029	0.014	POU2AF1	0.60686	0.54294	0.08726	1	0	0
809	chr11	111249000	111250000	0.000	0.012	0.103	0.081	POU2AF1	0.77363	0.09269	0.00337	1	1	1

810	chr11	115761000	115762000	0.028	0.000	0.015	0.041	CADM1	0.62100	1.00000	0.29694	0	0
811	chr11	118723000	118724000	0.000	0.029	0.000	CXCR5	0.22755	1.00000	0.54294	0.08726	0	0
812	chr11	126496000	126497000	0.028	0.000	0.015	0.014	KIRREL3	1.00000	1.00000	0.29694	0	0
813	chr11	128390000	128391000	0.000	0.000	0.044	0.014	ETS1	0.34948	0.54966	0.02537	1	0
814	chr11	128391000	128392000	0.000	0.000	0.118	0.014	ETS1	0.01415	0.04825	0.00004	1	1
815	chr12	6554000	6555000	0.000	0.000	0.029	0.000	CD27	0.22755	0.54294	0.08726	0	0
816	chr12	8762000	8763000	0.000	0.000	0.015	0.014	AICDA	1.00000	1.00000	0.29694	0	0
817	chr12	8763000	8764000	0.000	0.000	0.044	0.041	AICDA	1.00000	0.54966	0.02537	0	0
818	chr12	8764000	8765000	0.000	0.000	0.029	0.068	AICDA	0.44431	0.54294	0.08726	0	1
819	chr12	8765000	8766000	0.000	0.000	0.015	0.027	AICDA	1.00000	1.00000	0.29694	0	0
820	chr12	9823000	9824000	0.000	0.000	0.015	0.014	CLEC2D	1.00000	1.00000	0.29694	0	0
821	chr12	11716000	11717000	0.000	0.000	0.029	0.000	ETV6	0.22755	0.54294	0.08726	1	0
822	chr12	11803000	11804000	0.000	0.000	0.015	0.014	ETV6	1.00000	1.00000	0.29694	1	0
823	chr12	14923000	14924000	0.000	0.000	0.015	0.014	HIST1H4	1.00000	1.00000	0.29694	1	0
824	chr12	16717000	16718000	0.000	0.000	0.000	0.027	LMO3	0.49735	1.00000	1.00000	0	0
825	chr12	23805000	23806000	0.000	0.000	0.029	0.000	SOX5	0.22755	0.54294	0.08726	0	0
826	chr12	25149000	25150000	0.000	0.000	0.029	0.000	C12orf77	0.22755	0.54294	0.08726	0	0
827	chr12	25151000	25152000	0.000	0.000	0.015	0.014	C12orf77	1.00000	1.00000	0.29694	0	0
828	chr12	25174000	25175000	0.000	0.000	0.044	0.000	C12orf77	0.10727	0.54966	0.02537	0	0
829	chr12	25205000	25206000	0.000	0.000	0.015	0.000	LRMP	0.47887	1.00000	0.50663	1	0
830	chr12	25296000	25297000	0.000	0.006	0.103	0.014	LRMP	0.02808	0.09269	0.00099	1	1
831	chr12	25297000	25298000	0.000	0.006	0.118	0.014	LRMP	0.01415	0.04825	0.00030	1	1
832	chr12	25298000	25299000	0.000	0.000	0.029	0.014	LRMP	0.60686	0.54294	0.08726	1	0
833	chr12	25665000	25666000	0.028	0.000	0.015	0.000	ELT3D1	0.47887	1.00000	0.29694	0	0
834	chr12	38920000	38921000	0.000	0.000	0.029	0.000	CPNE8	0.22755	0.54294	0.08726	0	0
835	chr12	48027000	48028000	0.028	0.000	0.059	0.027	RPAP3	0.42627	0.65667	0.00730	0	1
836	chr12	57496000	57497000	0.000	0.000	0.015	0.014	STAT6	1.00000	1.00000	0.29694	0	0
837	chr12	69203000	69204000	0.000	0.006	0.015	0.000	MDM2	0.47887	1.00000	0.50663	0	0
838	chr12	76202000	76203000	0.000	0.000	0.000	0.027	PHLDA1	0.49735	1.00000	1.00000	0	0
839	chr12	79270000	79271000	0.000	0.000	0.029	0.027	SYT1	1.00000	0.54294	0.08726	0	0
840	chr12	82572000	82573000	0.000	0.000	0.015	0.014	CCDC59	1.00000	1.00000	0.29694	0	0
841	chr12	84837000	84838000	0.000	0.000	0.000	0.027	SLC6A15	0.49735	1.00000	1.00000	0	0
842	chr12	86114000	86115000	0.000	0.000	0.029	0.000	RASSF9	0.22755	0.54294	0.08726	0	0
843	chr12	86115000	86116000	0.000	0.000	0.029	0.000	RASSF9	0.22755	0.54294	0.08726	0	0
844	chr12	92538000	92539000	0.000	0.000	0.088	0.027	BTG1	0.15270	0.09631	0.00058	1	1
845	chr12	92539000	92540000	0.000	0.000	0.074	0.014	BTG1	0.10420	0.16101	0.00208	1	1
846	chr12	96036000	96037000	0.028	0.000	0.015	0.000	NTN4	0.47887	1.00000	0.29694	0	0
847	chr12	110171000	110172000	0.000	0.006	0.015	0.000	FAM222A	0.47887	1.00000	0.50663	0	0
848	chr12	110980000	110981000	0.000	0.000	0.015	0.014	PPTC7	1.00000	1.00000	0.29694	0	0
849	chr12	113493000	113494000	0.000	0.000	0.059	0.000	DTX1	0.05016	0.29551	0.00730	1	1
850	chr12	113494000	113495000	0.000	0.000	0.176	0.041	DTX1	0.01224	0.09730	0.00000	1	1
851	chr12	113495000	113496000	0.000	0.000	0.162	0.068	DTX1	0.11064	0.01471	0.00000	1	1
852	chr12	113496000	113497000	0.000	0.000	0.132	0.054	DTX1	0.14640	0.02564	0.00001	1	1
853	chr12	113497000	113498000	0.000	0.000	0.074	0.000	DTX1	0.02326	0.16101	0.00208	1	1
854	chr12	113499000	113500000	0.000	0.000	0.029	0.000	DTX1	0.22755	0.54294	0.08726	1	0
855	chr12	113512000	113513000	0.000	0.000	0.029	0.000	DTX1	0.22755	0.54294	0.08726	1	0
856	chr12	115966000	115967000	0.000	0.000	0.000	0.027	MED13L	0.49735	1.00000	1.00000	0	0
857	chr12	122432000	122433000	0.000	0.000	0.029	0.000	WDR66	0.22755	0.54294	0.08726	0	0
858	chr12	122433000	122434000	0.000	0.000	0.059	0.014	WDR66	0.19371	0.29551	0.00730	0	1
859	chr12	122447000	122448000	0.000	0.000	0.000	0.027	WDR66	0.49735	1.00000	1.00000	0	0
860	chr12	122458000	122459000	0.000	0.006	0.118	0.068	BCL7A	0.38669	0.04825	0.00030	1	1

861	chr12	122459000	122460000	0.000	0.006	0.324	0.108	BCL7A	0.00197	0.00003	0.00000	1	1	
862	chr12	122460000	122461000	0.000	0.000	0.176	0.081	BCL7A	0.12879	0.00730	0.00000	1	1	
863	chr12	122461000	122462000	0.000	0.006	0.279	0.162	BCL7A	0.10628	0.00013	0.00000	1	1	
864	chr12	122462000	122463000	0.000	0.012	0.191	0.027	BCL7A	0.00186	0.00372	0.00000	1	1	
865	chr12	122463000	122464000	0.000	0.012	0.132	0.054	BCL7A	0.14640	0.02564	0.00038	1	1	
866	chr12	124054000	124055000	0.028	0.000	0.015	0.014	TMED2	1.00000	1.00000	0.29694	0	0	
867	chr12	127965000	127966000	0.000	0.000	0.000	0.027	TMEM132C	0.49735	1.00000	1.00000	0	0	
868	chr12	131303000	131304000	0.056	0.000	0.015	0.014	STX2	1.00000	0.27446	0.29694	0	1	
869	chr12	131649000	131650000	0.000	0.000	0.000	0.027	GPR133	0.49735	1.00000	1.00000	0	0	
870	chr12	133306000	133307000	0.028	0.000	0.015	0.027	ANKLE2	1.00000	1.00000	0.29694	0	0	
871	chr13	21913000	21914000	0.000	0.000	0.029	0.000	ZDHHC20	0.22755	0.54294	0.08726	0	0	
872	chr13	32116000	32117000	0.028	0.000	0.015	0.000	RXFP2	0.47887	1.00000	0.29694	0	0	
873	chr13	35498000	35499000	0.000	0.000	0.015	0.027	KBTBD4	1.00000	1.00000	0.29694	0	0	
874	chr13	38371000	38372000	0.028	0.000	0.015	0.000	TPPC4	0.47887	1.00000	0.29694	0	0	
875	chr13	38630000	38631000	0.000	0.000	0.029	0.000	TPPC4	0.22755	0.54294	0.08726	0	0	
876	chr13	41156000	41157000	0.000	0.000	0.029	0.000	FOXO1	0.22755	0.54294	0.08726	1	0	
877	chr13	41240000	41241000	0.028	0.000	0.029	0.000	FOXO1	0.22755	1.00000	0.08726	1	0	
878	chr13	46958000	46959000	0.000	0.000	0.029	0.000	KIAA0226L	0.22755	0.54294	0.08726	0	0	
879	chr13	46959000	46960000	0.000	0.000	0.029	0.000	KIAA0226L	0.22755	0.54294	0.08726	0	0	
880	chr13	46960000	46961000	0.000	0.000	0.088	0.027	KIAA0226L	0.15270	0.09031	0.00058	0	1	
881	chr13	46961000	46962000	0.000	0.000	0.015	0.014	KIAA0226L	1.00000	1.00000	0.29694	0	0	
882	chr13	46962000	46963000	0.000	0.000	0.015	0.014	KIAA0226L	1.00000	1.00000	0.29694	0	0	
883	chr13	55239000	55240000	0.000	0.000	0.029	0.000	OLFM4	0.22755	0.54294	0.08726	0	0	
884	chr13	55386000	55387000	0.000	0.000	0.029	0.000	OLFM4	0.22755	0.54294	0.08726	0	0	
885	chr13	55598000	55599000	0.000	0.000	0.029	0.000	OLFM4	0.22755	0.54294	0.08726	0	0	
886	chr13	57222000	57223000	0.000	0.000	0.029	0.000	FRP20A;FRP20D;FRP20E;20BPRR20E;	0.22755	0.54294	0.08726	0	0	
887	chr13	61343000	61344000	0.028	0.000	0.015	0.000	TDRD3	0.47887	1.00000	0.29694	0	0	
888	chr13	62830000	62831000	0.000	0.000	0.000	0.027	PCDH20	0.49735	1.00000	1.00000	0	0	
889	chr13	63049000	63050000	0.000	0.000	0.029	0.000	PCDH20	0.22755	0.54294	0.08726	0	0	
890	chr13	63157000	63158000	0.028	0.000	0.015	0.000	AL445989.1	0.47887	1.00000	0.29694	0	0	
891	chr13	63214000	63215000	0.028	0.000	0.015	0.000	AL445989.1	0.47887	1.00000	0.29694	0	0	
892	chr13	64802000	64803000	0.000	0.000	0.015	0.014	AL445989.1	1.00000	1.00000	0.29694	0	0	
893	chr13	65637000	65638000	0.000	0.000	0.029	0.000	PCDH9	0.22755	0.54294	0.08726	0	0	
894	chr13	68656000	68657000	0.000	0.000	0.000	0.027	PCDH9	0.49735	1.00000	1.00000	0	0	
895	chr13	69418000	69419000	0.000	0.000	0.029	0.014	KLHL1	0.60686	0.54294	0.08726	0	0	
896	chr13	70956000	70957000	0.000	0.012	0.015	0.000	KLHL1	0.47887	1.00000	1.00000	0	0	
897	chr13	74542000	74543000	0.000	0.000	0.029	0.000	KLF12	0.22755	0.54294	0.08726	0	0	
898	chr13	75983000	75984000	0.000	0.000	0.074	0.014	TBC1D4	0.10420	0.16101	0.00208	0	1	
899	chr13	75984000	75985000	0.000	0.000	0.118	0.027	TBC1D4	0.04838	0.04825	0.00004	0	1	
900	chr13	83450000	83451000	0.000	0.000	0.029	0.000	SLITRK1	0.22755	0.54294	0.08726	0	0	
901	chr13	84641000	84642000	0.000	0.000	0.015	0.014	SLITRK1	1.00000	1.00000	0.29694	0	0	
902	chr13	87793000	87794000	0.000	0.000	0.015	0.014	SLITRK5	1.00000	1.00000	0.29694	0	0	
903	chr13	91480000	91481000	0.000	0.000	0.000	0.027	GPC5	0.49735	1.00000	1.00000	0	0	
904	chr13	106081000	106082000	0.000	0.000	0.015	0.014	DAOA	1.00000	1.00000	0.29694	0	0	
905	chr13	114786000	114787000	0.000	0.000	0.015	0.027	RASA3	1.00000	1.00000	0.29694	0	0	
906	chr13	114916000	114917000	0.028	0.000	0.000	0.014	RASA3	1.00000	0.34613	1.00000	0	0	
907	chr14	22948000	22949000	0.000	0.000	0.029	0.000	TRAJ56	0.22755	0.54294	0.08726	0	0	
908	chr14	22949000	22950000	0.000	0.000	0.044	0.000	TRAJ56	0.10727	0.54966	0.07537	0	0	
909	chr14	22950000	22951000	0.000	0.000	0.029	0.000	TRAJ54	0.22755	0.54294	0.08726	0	0	
910	chr14	22970000	22978000	0.000	0.000	0.015	0.014	TRAJ33	1.00000	1.00000	0.29694	0	0	

911	chr14	27286000	27287000	0.000	0.000	0.029	0.000	NOVA1	0.22755	0.54294	0.08726	0	0	
912	chr14	28646000	28646000	0.000	0.000	0.000	0.027	FOXG1	0.49735	1.00000	1.00000	0	0	
913	chr14	49407000	49408000	0.000	0.000	0.000	0.041	RPS29	0.24603	1.00000	1.00000	0	0	
914	chr14	50864000	50865000	0.000	0.000	0.029	0.000	CDKL1	0.22755	0.54294	0.08726	0	0	
915	chr14	54812000	54813000	0.000	0.000	0.000	0.027	CDKN3	0.49735	1.00000	1.00000	0	0	
916	chr14	55348000	55349000	0.000	0.000	0.029	0.000	GCH1	0.22755	0.54294	0.08726	0	0	
917	chr14	59827000	59828000	0.000	0.000	0.029	0.000	DAAM1	0.22755	0.54294	0.08726	0	0	
918	chr14	63143000	63144000	0.000	0.000	0.015	0.014	KCNH5	1.00000	1.00000	0.29694	0	0	
919	chr14	64194000	64195000	0.000	0.000	0.015	0.014	SGPP1	1.00000	1.00000	0.29694	0	0	
920	chr14	69258000	69259000	0.000	0.000	0.191	0.027	ZFP36L1	0.00186	0.00372	0.00000	1	1	
921	chr14	69259000	69260000	0.000	0.012	0.265	0.068	ZFP36L1	0.00024	0.00024	0.00000	1	1	
922	chr14	78418000	78419000	0.000	0.000	0.029	0.000	ADCK1	0.22755	0.54294	0.08726	0	0	
923	chr14	81685000	81686000	0.028	0.000	0.015	0.000	GTF2A1	0.47887	1.00000	0.29694	0	0	
924	chr14	84420000	84421000	0.000	0.006	0.015	0.000	FLRT2	0.47887	1.00000	0.50663	0	0	
925	chr14	91883000	91884000	0.000	0.000	0.015	0.014	CCDC88C	1.00000	1.00000	0.29694	0	0	
926	chr14	94941000	94942000	0.000	0.006	0.029	0.014	SERPINA9	0.60686	0.54294	0.21104	1	0	
927	chr14	94942000	94943000	0.000	0.000	0.118	0.014	SERPINA9	0.01415	0.04825	0.00004	1	1	
928	chr14	96179000	96180000	0.028	0.037	0.132	0.108	TCL1A	0.79702	0.15881	0.01586	1	1	
929	chr14	96180000	96181000	0.028	0.025	0.088	0.054	TCL1A	0.52067	0.41714	0.06858	1	1	
930	chr14	101597000	101598000	0.000	0.000	0.000	0.027	AL117190.3	0.49735	1.00000	1.00000	0	0	
931	chr14	102285000	102286000	0.000	0.000	0.015	0.014	PPP2R5C	1.00000	1.00000	0.29694	0	0	
932	chr14	105954000	105955000	0.000	0.000	0.044	0.014	CRIP1	0.34948	0.54966	0.02537	0	0	
933	chr14	106031000	106032000	0.000	0.000	0.015	0.014	IGHA2	1.00000	1.00000	0.29694	0	0	
934	chr14	106042000	106043000	0.000	0.019	0.103	0.041	IGHA2	0.19468	0.09269	0.00855	0	1	
935	chr14	106048000	106049000	0.000	0.006	0.015	0.000	IGHA2	0.47887	1.00000	0.50663	0	0	
936	chr14	106054000	106055000	0.000	0.000	0.029	0.014	IGHA2	0.60686	0.54294	0.08726	0	0	
937	chr14	106055000	106056000	0.056	0.000	0.103	0.027	IGHA2	0.08710	0.49267	0.00016	0	1	
938	chr14	106056000	106057000	0.056	0.006	0.074	0.027	IGHA2	0.25970	1.00000	0.00953	0	1	
939	chr14	106057000	106058000	0.000	0.000	0.059	0.000	IGHA2	0.05016	0.29551	0.00730	0	1	
940	chr14	106058000	106059000	0.000	0.000	0.029	0.000	IGHA2	0.22755	0.54294	0.08726	0	0	
941	chr14	106066000	106067000	0.000	0.000	0.059	0.000	IGHE	0.05016	0.29551	0.00730	0	1	
942	chr14	106067000	106068000	0.000	0.000	0.044	0.014	IGHE	0.34948	0.54966	0.02537	0	0	
943	chr14	106068000	106069000	0.000	0.000	0.103	0.027	IGHE	0.08710	0.09269	0.00016	0	1	
944	chr14	106069000	106070000	0.000	0.006	0.206	0.216	IGHE	1.00000	0.00197	0.00000	0	1	
945	chr14	106070000	106071000	0.000	0.000	0.088	0.068	IGHE	0.75773	0.09031	0.00058	0	1	
946	chr14	106071000	106072000	0.000	0.000	0.074	0.068	IGHE	1.00000	0.16101	0.00208	0	1	
947	chr14	106072000	106073000	0.000	0.000	0.029	0.014	IGHE	0.60686	0.54294	0.08726	0	0	
948	chr14	106082000	106083000	0.000	0.000	0.015	0.027	IGHG4	1.00000	1.00000	0.29694	0	0	
949	chr14	106092000	106093000	0.000	0.000	0.029	0.000	IGHG4	0.22755	0.54294	0.08726	0	0	
950	chr14	106094000	106095000	0.000	0.006	0.147	0.027	IGHG4	0.01393	0.01464	0.00003	0	1	
951	chr14	106095000	106096000	0.000	0.000	0.103	0.081	IGHG4	0.77363	0.09269	0.00016	0	1	
952	chr14	106110000	106111000	0.000	0.000	0.074	0.014	IGHG2	0.10420	0.16101	0.00208	0	1	
953	chr14	106111000	106112000	0.000	0.000	0.015	0.014	IGHG2	1.00000	1.00000	0.29694	0	0	
954	chr14	106112000	106113000	0.000	0.056	0.294	0.257	IGHG2	0.76749	0.00311	0.00000	0	1	
955	chr14	106113000	106114000	0.028	0.068	0.397	0.284	IGHG2	0.16121	0.00062	0.00000	0	1	
956	chr14	106114000	106115000	0.000	0.000	0.279	0.122	IGHG2	0.02111	0.00013	0.00000	0	1	
957	chr14	106146000	106147000	0.000	0.000	0.029	0.000	IGHA1	0.22755	0.54294	0.08726	0	0	
958	chr14	106151000	106152000	0.000	0.006	0.015	0.014	IGHA1	1.00000	1.00000	0.50663	0	0	
959	chr14	106152000	106153000	0.000	0.006	0.015	0.027	IGHA1	1.00000	1.00000	0.50663	0	0	
960	chr14	106161000	106162000	0.000	0.000	0.015	0.014	IGHA1	1.00000	1.00000	0.29694	0	0	
961	chr14	106173000	106174000	0.028	0.006	0.029	0.027	IGHA1	1.00000	1.00000	0.21104	0	0	

962	chr14	106174000	106175000	0.000	0.006	0.029	0.000	IGHA1	0.22755	0.54294	0.21104	0	0	
963	chr14	106175000	106176000	0.028	0.006	0.059	0.014	IGHA1	0.19371	0.65667	0.02818	0	1	
964	chr14	106176000	106177000	0.139	0.031	0.103	0.068	IGHA1	0.55139	0.74810	0.04551	0	1	
965	chr14	106177000	106178000	0.000	0.019	0.059	0.027	IGHA1	0.42627	0.29551	0.20627	0	1	
966	chr14	106178000	106179000	0.000	0.006	0.059	0.014	IGHA1	0.19371	0.29551	0.02818	0	1	
967	chr14	106208000	106209000	0.000	0.000	0.103	0.027	IGHG1	0.08710	0.09269	0.00016	0	1	
968	chr14	106209000	106210000	0.000	0.006	0.118	0.054	IGHG1	0.23986	0.04825	0.00030	0	1	
969	chr14	106210000	106211000	0.000	0.000	0.118	0.068	IGHG1	0.38669	0.04825	0.00004	0	1	
970	chr14	106211000	106212000	0.000	0.056	0.235	0.149	IGHG1	0.20587	0.00098	0.00025	0	1	
971	chr14	106212000	106213000	0.028	0.106	0.309	0.270	IGHG1	0.71144	0.00070	0.00035	0	1	
972	chr14	106213000	106214000	0.056	0.068	0.382	0.216	IGHG1	0.04243	0.00034	0.00000	0	1	
973	chr14	106214000	106215000	0.000	0.000	0.147	0.000	IGHG1	0.00044	0.01464	0.00000	0	1	
974	chr14	106237000	106238000	0.000	0.000	0.088	0.000	IGHG3	0.01070	0.09031	0.00058	0	1	
975	chr14	106238000	106239000	0.000	0.000	0.176	0.027	IGHG3	0.00370	0.00730	0.00000	0	1	
976	chr14	106239000	106240000	0.056	0.062	0.206	0.135	IGHG3	0.27339	0.04910	0.00349	0	1	
977	chr14	106240000	106241000	0.028	0.130	0.324	0.230	IGHG3	0.25971	0.00034	0.00136	0	1	
978	chr14	106241000	106242000	0.000	0.025	0.221	0.081	IGHG3	0.03144	0.00107	0.00000	0	1	
979	chr14	106242000	106243000	0.000	0.000	0.044	0.014	IGHG3	0.34948	0.54966	0.02537	0	0	
980	chr14	106321000	106322000	0.000	0.000	0.059	0.000	IGHM	0.05016	0.29551	0.00730	0	1	
981	chr14	106322000	106323000	0.000	0.006	0.221	0.054	IGHM	0.00556	0.00107	0.00000	0	1	
982	chr14	106323000	106324000	0.056	0.062	0.235	0.162	IGHM	0.29797	0.02782	0.00040	0	1	
983	chr14	106324000	106325000	0.250	0.193	0.221	0.284	IGHM	0.44266	0.80827	0.71834	0	1	
984	chr14	106325000	106326000	0.694	0.335	0.279	0.365	IGHM	0.28848	0.00006	0.44111	0	1	
985	chr14	106326000	106327000	0.833	0.540	0.838	0.838	IGHJ6	1.00000	1.00000	0.00001	0	1	
986	chr14	106327000	106328000	0.333	0.335	0.926	0.905	IGHJ6	0.76658	0.00000	0.00000	0	1	
987	chr14	106328000	106329000	0.250	0.248	0.809	0.730	IGHJ6	0.32171	0.00000	0.00000	0	1	
988	chr14	106329000	106330000	0.694	0.441	0.882	0.932	IGHJ6	0.38669	0.03986	0.00000	0	1	
989	chr14	106330000	106331000	0.694	0.298	0.574	0.649	IGHJ3;IGHJ4;IGHJ5;IGHJ6	0.39187	0.29080	0.00017	0	1	
990	chr14	106331000	106332000	0.028	0.012	0.044	0.027	IGHD7-27;IGHJ1;IGHJ2;IGHJ3	0.67043	1.00000	0.15671	0	0	
991	chr14	106338000	106339000	0.028	0.006	0.000	0.000	IGHD7-27	1.00000	0.34615	1.00000	0	0	
992	chr14	106350000	106351000	0.000	0.006	0.029	0.000	IGHD4-23	0.22755	0.54294	0.21104	0	0	
993	chr14	106352000	106353000	0.000	0.000	0.029	0.000	IGHD3-22	0.22755	0.54294	0.08726	0	0	
994	chr14	106353000	106354000	0.000	0.006	0.029	0.000	IGHD2-21	0.22755	0.54294	0.21104	0	0	
995	chr14	106354000	106355000	0.000	0.006	0.015	0.000	IGHD2-21	0.47887	1.00000	0.50663	0	0	
996	chr14	106355000	106356000	0.000	0.000	0.044	0.000	IGHD2-21	0.10727	0.54966	0.02537	0	0	
997	chr14	106357000	106358000	0.028	0.000	0.059	0.000	IGHD1-20;IGHD6-19;	0.05016	0.65667	0.00730	0	1	
998	chr14	106358000	106359000	0.000	0.006	0.029	0.000	IGHD5-18	0.22755	0.54294	0.21104	0	0	
999	chr14	106362000	106363000	0.028	0.006	0.000	0.000	IGHD3-16	1.00000	0.34615	1.00000	0	0	
1000	chr14	106364000	106365000	0.000	0.000	0.029	0.000	IGHD2-15	0.22755	0.54294	0.08726	0	0	
1001	chr14	106367000	106368000	0.000	0.000	0.029	0.000	IGHD6-13	0.22755	0.54294	0.08726	0	0	
1002	chr14	106370000	106371000	0.000	0.012	0.044	0.014	IGHD3-10;IGHD3-9;	0.34948	0.54966	0.13671	0	0	
1003	chr14	106371000	106372000	0.000	0.012	0.029	0.014	IGHD3-9	0.60686	0.54294	0.58498	0	0	
1004	chr14	106372000	106373000	0.000	0.006	0.015	0.000	IGHD2-8	0.47887	1.00000	0.50663	0	0	
1005	chr14	106375000	106376000	0.000	0.019	0.015	0.000	IGHD1-7	0.47887	1.00000	1.00000	0	0	
1006	chr14	106376000	106377000	0.000	0.012	0.015	0.000	IGHD6-6	0.47887	1.00000	1.00000	0	0	
1007	chr14	106380000	106381000	0.000	0.031	0.000	0.000	IGHD3-3	1.00000	1.00000	0.32529	0	0	
1008	chr14	106381000	106382000	0.000	0.031	0.000	0.000	IGHD2-2	1.00000	1.00000	0.32529	0	0	
1009	chr14	106382000	106383000	0.000	0.037	0.044	0.014	IGHD2-2	0.34948	0.54966	0.72719	0	0	
1010	chr14	106383000	106384000	0.000	0.000	0.044	0.014	IGHD2-2	0.34948	0.54966	0.02537	0	0	
1011	chr14	106384000	106385000	0.000	0.012	0.044	0.014	IGHD1-1	0.34948	0.54966	0.15671	0	0	

1012	chr14	106385000	106386000	0.000	0.000	0.029	0.014	IGHD1-1	0.60686	0.54294	0.08726	0	0	
1013	chr14	106387000	106388000	0.000	0.000	0.029	0.014	KIAA0125	0.60686	0.54294	0.08726	0	0	
1014	chr14	106403000	106406000	0.030	0.036	0.015	0.014	IGHV6-1	1.00000	1.00000	0.50663	0	0	
1015	chr14	106406000	106407000	0.000	0.006	0.015	0.014	IGHV6-1	1.00000	1.00000	0.50663	0	0	
1016	chr14	106419000	106420000	0.000	0.006	0.015	0.000	IGHV6-1	0.47887	1.00000	0.50663	0	0	
1017	chr14	106452000	106453000	0.000	0.006	0.029	0.000	IGHV1-2	0.22755	0.54294	0.21104	0	0	
1018	chr14	106453000	106454000	0.000	0.006	0.044	0.000	IGHV1-2	0.10727	0.54966	0.07959	0	0	
1019	chr14	106454000	106455000	0.000	0.000	0.029	0.000	IGHV1-2	0.22755	0.54294	0.08726	0	0	
1020	chr14	106494000	106495000	0.000	0.019	0.000	0.014	IGHV2-5	1.00000	1.00000	0.55662	0	0	
1021	chr14	106518000	106519000	0.028	0.037	0.000	0.054	IGHV3-7	0.12104	0.34615	0.18288	0	1	
1022	chr14	106519000	106520000	0.000	0.012	0.000	0.027	IGHV3-7	0.49735	1.00000	1.00000	0	0	
1023	chr14	106539000	106540000	0.000	0.031	0.015	0.000	IGHV1-8	0.47887	1.00000	0.67240	0	0	
1024	chr14	106552000	106553000	0.000	0.006	0.029	0.014	IGHV3-9	0.60686	0.54294	0.21104	0	0	
1025	chr14	106573000	106574000	0.000	0.019	0.029	0.068	IGHV3-11	0.44431	0.54294	0.63492	0	1	
1026	chr14	106574000	106575000	0.000	0.006	0.029	0.041	IGHV3-11	1.00000	0.54294	0.21104	0	0	
1027	chr14	106578000	106579000	0.000	0.000	0.015	0.027	IGHV3-11	1.00000	1.00000	0.29694	0	0	
1028	chr14	106579000	106580000	0.000	0.000	0.015	0.027	IGHV3-11	1.00000	1.00000	0.29694	0	0	
1029	chr14	106610000	106611000	0.056	0.012	0.029	0.000	IGHV3-15	0.22755	0.60763	0.58408	0	1	
1030	chr14	106641000	106642000	0.000	0.019	0.015	0.000	IGHV1-18	0.47887	1.00000	1.00000	0	0	
1031	chr14	106642000	106643000	0.000	0.012	0.015	0.000	IGHV1-18	0.47887	1.00000	1.00000	0	0	
1032	chr14	106691000	106692000	0.000	0.012	0.029	0.027	IGHV3-21	1.00000	0.54294	0.58408	0	0	
1033	chr14	106692000	106693000	0.000	0.006	0.015	0.041	IGHV3-21	0.62100	1.00000	1.00000	0	0	
1034	chr14	106725000	106726000	0.083	0.068	0.103	0.135	IGHV3-23	0.61250	1.00000	0.42238	0	1	
1035	chr14	106726000	106727000	0.028	0.019	0.088	0.095	IGHV3-23	1.00000	0.41714	0.02173	0	1	
1036	chr14	106733000	106734000	0.028	0.006	0.015	0.027	IGHV1-24	1.00000	1.00000	0.50663	0	0	
1037	chr14	106757000	106758000	0.056	0.000	0.015	0.000	IGHV2-26	0.47887	0.27446	0.29694	0	1	
1038	chr14	106758000	106759000	0.056	0.000	0.000	0.000	IGHV2-26	1.00000	0.11763	1.00000	0	1	
1039	chr14	106791000	106792000	0.056	0.006	0.015	0.000	IGHV3-30	0.47887	0.27446	0.50663	0	1	
1040	chr14	106804000	106805000	0.000	0.006	0.029	0.000	IGHV4-31	0.22755	0.54294	0.21104	0	0	
1041	chr14	106805000	106806000	0.000	0.006	0.044	0.014	IGHV4-31	0.34948	0.54966	0.07959	0	0	
1042	chr14	106806000	106807000	0.000	0.006	0.015	0.000	IGHV4-31	0.47887	1.00000	0.50663	0	0	
1043	chr14	106815000	106816000	0.000	0.012	0.044	0.027	IGHV3-33	0.67043	0.54966	0.15671	0	0	
1044	chr14	106816000	106817000	0.000	0.006	0.074	0.014	IGHV3-33	0.10420	0.16101	0.00953	0	1	
1045	chr14	106817000	106818000	0.000	0.000	0.029	0.000	IGHV3-33	0.22755	0.54294	0.08726	0	0	
1046	chr14	106829000	106830000	0.167	0.050	0.162	0.135	IGHV4-34	0.81354	1.00000	0.00804	0	1	
1047	chr14	106830000	106831000	0.028	0.043	0.118	0.135	IGHV4-34	0.80514	0.15803	0.07447	0	1	
1048	chr14	106877000	106878000	0.056	0.006	0.015	0.041	IGHV4-39	0.62160	0.27446	0.50663	0	1	
1049	chr14	106878000	106879000	0.028	0.012	0.044	0.041	IGHV4-39	1.00000	1.00000	0.15671	0	0	
1050	chr14	106967000	106968000	0.056	0.000	0.015	0.000	IGHV1-46	0.47887	0.27446	0.29694	0	1	
1051	chr14	106994000	106995000	0.028	0.012	0.088	0.122	IGHV3-48	0.59201	0.41714	0.00949	0	1	
1052	chr14	106995000	106996000	0.000	0.000	0.000	0.027	IGHV3-48	0.49735	1.00000	1.00000	0	0	
1053	chr14	107034000	107035000	0.028	0.000	0.000	0.014	IGHV3-51	1.00000	0.34615	1.00000	0	0	
1054	chr14	107035000	107036000	0.000	0.006	0.029	0.014	IGHV3-51	0.60686	0.54294	0.21104	0	0	
1055	chr14	107048000	107049000	0.028	0.006	0.000	0.000	IGHV3-53	1.00000	0.34615	1.00000	0	0	
1056	chr14	107049000	107050000	0.000	0.012	0.044	0.027	IGHV3-53	0.67043	0.54966	0.15671	0	0	
1057	chr14	107083000	107084000	0.000	0.006	0.044	0.054	IGHV4-59	1.00000	0.54966	0.07959	0	1	
1058	chr14	107084000	107085000	0.000	0.006	0.029	0.027	IGHV4-59	1.00000	0.54294	0.21104	0	0	
1059	chr14	107095000	107096000	0.000	0.006	0.015	0.000	IGHV4-61	0.47887	1.00000	0.50663	0	0	
1060	chr14	107113000	107114000	0.000	0.000	0.029	0.000	IGHV3-64	0.22755	0.54294	0.08726	0	0	
1061	chr14	107114000	107115000	0.000	0.000	0.029	0.000	IGHV3-64	0.22755	0.54294	0.08726	0	0	
1062	chr14	107169000	107170000	0.056	0.068	0.206	0.041	IGHV1-69	0.00346	0.03910	0.00442	0	1	

1063	chr14	107170000	107171000	0.028	0.075	0.294	0.095	IGHV1-69	0.60279	0.60675	0.60604	0	1
1064	chr14	107176000	107177000	0.028	0.006	0.118	0.027	IGHV2-70	0.04838	0.15863	0.60730	0	1
1065	chr14	107177000	107178000	0.030	0.030	0.044	0.027	IGHV2-70	0.67043	0.54966	0.02537	0	0
1066	chr14	107178000	107179000	0.056	0.161	0.456	0.284	IGHV2-70	0.03781	0.60602	0.60601	0	1
1067	chr14	107179000	107180000	0.056	0.180	0.382	0.338	IGHV2-70	0.60350	0.60034	0.60206	0	1
1068	chr14	107183000	107184000	0.000	0.006	0.029	0.000	IGHV2-70	0.22755	0.54294	0.21104	0	0
1069	chr14	107199000	107200000	0.000	0.012	0.015	0.000	IGHV3-72	0.47887	1.00000	1.00000	0	0
1070	chr14	107218000	107219000	0.028	0.012	0.015	0.000	IGHV3-74	0.47887	1.00000	1.00000	0	0
1071	chr14	107219000	107220000	0.000	0.012	0.074	0.027	IGHV3-74	0.25970	0.16101	0.02559	0	1
1072	chr14	107221000	107222000	0.000	0.000	0.059	0.000	IGHV3-74	0.05016	0.29551	0.60730	0	1
1073	chr14	107223000	107233000	0.000	0.000	0.029	0.000	IGHV3-74	0.22755	0.54294	0.08726	0	0
1074	chr14	107253000	107254000	0.000	0.000	0.044	0.014	IGHV7-81	0.34948	0.54966	0.02537	0	0
1075	chr14	107258000	107259000	0.000	0.000	0.015	0.014	IGHV7-81	1.00000	1.00000	0.29694	0	0
1076	chr14	107259000	107260000	0.000	0.025	0.235	0.027	IGHV7-81	0.60021	0.60098	0.60000	0	1
1077	chr15	45003000	45004000	0.000	0.000	0.044	0.000	B2M	0.10727	0.54966	0.02537	0	0
1078	chr15	45007000	45008000	0.000	0.000	0.044	0.000	B2M	0.10727	0.54966	0.02537	0	0
1079	chr15	45814000	45815000	0.000	0.000	0.015	0.014	SLC30A4	1.00000	1.00000	0.29694	0	0
1080	chr15	59664000	59665000	0.000	0.000	0.044	0.041	MYO1E	1.00000	0.54966	0.02537	0	0
1081	chr15	65588000	65589000	0.028	0.000	0.000	0.014	PARP16	1.00000	0.34615	1.00000	0	0
1082	chr15	78332000	78333000	0.028	0.000	0.000	0.014	TBC1D2B	1.00000	0.34615	1.00000	0	0
1083	chr15	83227000	83228000	0.000	0.000	0.029	0.000	CPEB1	0.22755	0.54294	0.08726	0	0
1084	chr15	86226000	86227000	0.000	0.000	0.044	0.000	AKAP13	0.10727	0.54966	0.02537	0	0
1085	chr15	86233000	86234000	0.000	0.000	0.029	0.014	AKAP13	0.60686	0.54294	0.08726	0	0
1086	chr15	86245000	86246000	0.000	0.000	0.059	0.000	AKAP13	0.05016	0.29551	0.60730	0	1
1087	chr16	368000	369000	0.000	0.000	0.015	0.014	AXIN1	1.00000	1.00000	0.29694	0	0
1088	chr16	3788000	3789000	0.000	0.000	0.015	0.014	CREBBP	1.00000	1.00000	0.29694	0	0
1089	chr16	10971000	10972000	0.000	0.000	0.162	0.041	CIITA	0.02223	0.01471	0.00000	1	1
1090	chr16	10972000	10973000	0.000	0.000	0.191	0.081	CIITA	0.08249	0.00372	0.00000	1	1
1091	chr16	10973000	10974000	0.000	0.000	0.162	0.095	CIITA	0.31342	0.01471	0.60660	1	1
1092	chr16	10974000	10975000	0.000	0.000	0.059	0.000	CIITA	0.05016	0.29551	0.60730	1	1
1093	chr16	11348000	11349000	0.000	0.000	0.191	0.027	SOCS1	0.60186	0.00372	0.00000	1	1
1094	chr16	11349000	11350000	0.000	0.000	0.221	0.041	SOCS1	0.60179	0.00107	0.60660	1	1
1095	chr16	21167000	21168000	0.000	0.000	0.015	0.014	DNAH3	1.00000	1.00000	0.29694	0	0
1096	chr16	27325000	27326000	0.000	0.000	0.029	0.041	CTD-3203P2.2	1.00000	0.54294	0.08726	0	0
1097	chr16	27326000	27327000	0.000	0.000	0.088	0.041	CTD-3203P2.2	0.31126	0.60631	0.60058	0	1
1098	chr16	27327000	27328000	0.000	0.000	0.029	0.000	IL4R	0.22755	0.54294	0.08726	0	0
1099	chr16	27414000	27415000	0.000	0.000	0.029	0.000	IL21R	0.22755	0.54294	0.08726	0	0
1100	chr16	29248000	29249000	0.000	0.000	0.029	0.000	61E3.4	0.22755	0.54294	0.08726	0	0
1101	chr16	31910000	31911000	0.000	0.000	0.015	0.014	ZNF267	1.00000	1.00000	0.29694	0	0
1102	chr16	46821000	46822000	0.000	0.000	0.015	0.014	C16orf87	1.00000	1.00000	0.29694	0	0
1103	chr16	50985000	50986000	0.000	0.000	0.015	0.014	CYLD	1.00000	1.00000	0.29694	0	0
1104	chr16	64351000	64352000	0.000	0.000	0.029	0.014	CDH11	0.60686	0.54294	0.08726	0	0
1105	chr16	78398000	78399000	0.000	0.000	0.000	0.027	WWOX	0.49735	1.00000	1.00000	0	0
1106	chr16	78615000	78616000	0.000	0.000	0.015	0.014	WWOX	1.00000	1.00000	0.29694	0	0
1107	chr16	78753000	78754000	0.000	0.000	0.015	0.014	WWOX	1.00000	1.00000	0.29694	0	0
1108	chr16	78811000	78812000	0.000	0.000	0.000	0.027	WWOX	0.49735	1.00000	1.00000	0	0
1109	chr16	79988000	79989000	0.000	0.000	0.015	0.014	MAF	1.00000	1.00000	0.29694	0	0
1110	chr16	81836000	81837000	0.000	0.000	0.029	0.000	PLCG2	0.22755	0.54294	0.08726	0	0
1111	chr16	85932000	85933000	0.000	0.000	0.059	0.027	IRF8	0.42627	0.29551	0.60730	1	1
1112	chr16	85933000	85934000	0.000	0.012	0.221	0.081	IRF8	0.03144	0.00107	0.00000	1	1
1113	chr16	85934000	85935000	0.000	0.006	0.015	0.027	IRF8	1.00000	1.00000	0.50663	1	0

1114	chr16	85936000	85937000	0.000	0.000	0.029	0.000	IRF8	0.22755	0.54294	0.08726	1		0	
1115	chr16	88441000	88442000	0.000	0.000	0.015	0.014	ZNF469	1.00000	1.00000	0.29694	0		0	
1116	chr17	3598000	3599000	0.000	0.000	0.029	0.014	P2RX5-P2RX5-TAX1BP3-P2RX5;	0.60686	0.54294	0.08726	0		0	
1117	chr17	17286000	17287000	0.000	0.000	0.029	0.000	SMCR9	0.22755	0.54294	0.08726	0		0	
1118	chr17	21194000	21195000	0.000	0.000	0.015	0.041	MAP3K3	0.62100	1.00000	0.29694	0		0	
1119	chr17	29646000	29647000	0.000	0.000	0.029	0.014	EVI2A	0.60686	0.54294	0.08726	0		0	
1120	chr17	38025000	38026000	0.000	0.000	0.029	0.014	IKZF3	0.60686	0.54294	0.08726	0		0	
1121	chr17	43662000	43663000	0.000	0.000	0.029	0.000	PLEKHM1	0.22755	0.54294	0.08726	0		0	
1122	chr17	56408000	56409000	0.000	0.006	0.059	0.027	BZRAP1	0.42627	0.29551	0.02818	0		1	
1123	chr17	56409000	56410000	0.000	0.000	0.265	0.027	BZRAP1	0.60695	0.00023	0.00000	0		1	
1124	chr17	57916000	57917000	0.000	0.000	0.029	0.014	VMP1	0.60686	0.54294	0.08726	1		0	
1125	chr17	57917000	57918000	0.000	0.000	0.029	0.000	VMP1	0.22755	0.54294	0.08726	1		0	
1126	chr17	62007000	62008000	0.000	0.000	0.029	0.000	CD79B	0.22755	0.54294	0.08726	0		0	
1127	chr17	62008000	62009000	0.000	0.000	0.044	0.014	CD79B	0.34948	0.54966	0.02537	0		0	
1128	chr17	63067000	63068000	0.000	0.000	0.015	0.014	GNA13	1.00000	1.00000	0.29694	0		0	
1129	chr17	65676000	65677000	0.000	0.000	0.029	0.000	PITPNC1	0.22755	0.54294	0.08726	0		0	
1130	chr17	69365000	69366000	0.000	0.000	0.015	0.014	AC007361.1	1.00000	1.00000	0.29694	0		0	
1131	chr17	70083000	70084000	0.028	0.000	0.000	0.014	SOX9	1.00000	0.34615	1.00000	0		0	
1132	chr17	74733000	74734000	0.000	0.000	0.000	0.027	SRSF2	0.49735	1.00000	1.00000	0		0	
1133	chr17	75447000	75448000	0.000	0.000	0.044	0.000	9-Sep-19	0.10727	0.54966	0.02537	0		0	
1134	chr17	75448000	75449000	0.000	0.000	0.044	0.000	9-Sep-19	0.10727	0.54966	0.02537	0		0	
1135	chr17	76775000	76776000	0.000	0.000	0.000	0.027	CYTH1	0.49735	1.00000	1.00000	0		0	
1136	chr17	80928000	80929000	0.000	0.000	0.029	0.000	B3GNTL1	0.22755	0.54294	0.08726	0		0	
1137	chr17	80976000	80977000	0.000	0.000	0.015	0.014	B3GNTL1	1.00000	1.00000	0.29694	0		0	
1138	chr18	2709000	2710000	0.000	0.000	0.029	0.000	SMCHD1	0.22755	0.54294	0.08726	0		0	
1139	chr18	3600000	3601000	0.000	0.000	0.015	0.014	DLGAP1	1.00000	1.00000	0.29694	0		0	
1140	chr18	12062000	12063000	0.000	0.000	0.000	0.041	ANKRD62	0.24603	1.00000	1.00000	0		0	
1141	chr18	27771000	27772000	0.000	0.000	0.029	0.000	DSC3	0.22755	0.54294	0.08726	0		0	
1142	chr18	28066000	28067000	0.000	0.000	0.029	0.000	DSC3	0.22755	0.54294	0.08726	0		0	
1143	chr18	30349000	30350000	0.030	0.000	0.000	0.027	AC012121.1;KLHL14;	0.49735	1.00000	1.00000	0		0	
1144	chr18	36806000	36807000	0.000	0.000	0.029	0.000	CELF4	0.22755	0.54294	0.08726	0		0	
1145	chr18	37751000	37752000	0.000	0.000	0.015	0.014	PIK3C3	1.00000	1.00000	0.29694	0		0	
1146	chr18	38672000	38673000	0.028	0.000	0.000	0.014	PIK3C3	1.00000	0.34615	1.00000	0		0	
1147	chr18	42168000	42169000	0.028	0.000	0.000	0.014	SETBP1	1.00000	0.34615	1.00000	0		0	
1148	chr18	51952000	51953000	0.000	0.000	0.029	0.000	C18orf54	0.22755	0.54294	0.08726	0		0	
1149	chr18	52447000	52448000	0.000	0.000	0.015	0.014	RAB27B	1.00000	1.00000	0.29694	0		0	
1150	chr18	52988000	52989000	0.000	0.000	0.029	0.000	TCF4	0.22755	0.54294	0.08726	0		0	
1151	chr18	54653000	54654000	0.000	0.000	0.000	0.027	WDR7	0.49735	1.00000	1.00000	0		0	
1152	chr18	60794000	60795000	0.000	0.000	0.029	0.000	BCL2	0.22755	0.54294	0.08726	1		0	
1153	chr18	60805000	60806000	0.000	0.000	0.074	0.081	BCL2	1.00000	0.16101	0.00268	1		1	
1154	chr18	60806000	60807000	0.000	0.006	0.132	0.122	BCL2	1.00000	0.02564	0.00009	1		1	
1155	chr18	60809000	60810000	0.000	0.000	0.059	0.027	BCL2	0.42627	0.29551	0.00730	1		1	
1156	chr18	60821000	60822000	0.000	0.000	0.029	0.000	BCL2	0.22755	0.54294	0.08726	1		0	
1157	chr18	60825000	60826000	0.000	0.000	0.044	0.027	BCL2	0.67043	0.54966	0.02537	1		0	
1158	chr18	60826000	60827000	0.000	0.000	0.029	0.000	BCL2	0.22755	0.54294	0.08726	1		0	
1159	chr18	60828000	60829000	0.000	0.000	0.015	0.027	BCL2	1.00000	1.00000	0.29694	1		0	
1160	chr18	60873000	60874000	0.030	0.000	0.044	0.027	BCL2	0.67043	0.54966	0.02537	1		0	
1161	chr18	60875000	60876000	0.000	0.000	0.044	0.027	BCL2	0.67043	0.54966	0.02537	1		0	
1162	chr18	60876000	60877000	0.000	0.000	0.015	0.054	BCL2	0.36833	1.00000	0.29694	1		1	
1163	chr18	60983000	60984000	0.000	0.006	0.059	0.068	BCL2	1.00000	0.29551	0.02818	1		1	

1164	chr18	60984000	60985000	0.000	0.012	0.176	0.459	BCL2	0.00034	0.00730	0.00001	1	1		
1165	chr18	60985000	60986000	0.000	0.000	0.221	0.635	BCL2	0.00000	0.00167	0.00000	1	1		
1166	chr18	60986000	60987000	0.000	0.019	0.235	0.730	BCL2	0.00000	0.00098	0.00000	1	1		
1167	chr18	60987000	60988000	0.000	0.019	0.191	0.500	BCL2	0.00019	0.00372	0.00001	1	1		
1168	chr18	60988000	60989000	0.000	0.012	0.221	0.595	BCL2	0.00001	0.00167	0.00000	1	1		
1169	chr18	61810000	61811000	0.000	0.000	0.015	0.014	SERPINB8	1.00000	1.00000	0.29694	0	0		
1170	chr18	63080000	63081000	0.000	0.000	0.029	0.000	CDH7	0.22755	0.54294	0.08726	0	0		
1171	chr18	63791000	63792000	0.028	0.000	0.015	0.000	CDH7	0.47887	1.00000	0.29694	0	0		
1172	chr18	63876000	63877000	0.000	0.000	0.029	0.000	CDH19	0.22755	0.54294	0.08726	0	0		
1173	chr18	64643000	64644000	0.000	0.000	0.029	0.000	CDH19	0.22755	0.54294	0.08726	0	0		
1174	chr18	65863000	65864000	0.000	0.000	0.000	0.027	TMX3	0.49735	1.00000	1.00000	0	0		
1175	chr18	66328000	66329000	0.000	0.000	0.015	0.014	TMX3	1.00000	1.00000	0.29694	0	0		
1176	chr18	70462000	70463000	0.000	0.000	0.015	0.014	NETO1	1.00000	1.00000	0.29694	0	0		
1177	chr18	73767000	73768000	0.000	0.000	0.015	0.014	ZNF516	1.00000	1.00000	0.29694	0	0		
1178	chr18	76515000	76516000	0.000	0.000	0.029	0.014	SALL3	0.60686	0.54294	0.08726	0	0		
1179	chr18	76724000	76725000	0.000	0.000	0.015	0.014	SALL3	1.00000	1.00000	0.29694	0	0		
1180	chr18	76725000	76726000	0.000	0.000	0.015	0.014	SALL3	1.00000	1.00000	0.29694	0	0		
1181	chr19	1612000	1613000	0.056	0.000	0.000	0.000	TCF3	1.00000	0.11763	1.00000	0	1		
1182	chr19	2476000	2477000	0.000	0.000	0.029	0.000	GADD45B	0.22755	0.54294	0.08726	1	0		
1183	chr19	10304000	10305000	0.000	0.000	0.059	0.000	DNMT1	0.05016	0.29551	0.00730	0	1		
1184	chr19	10305000	10306000	0.000	0.000	0.044	0.000	DNMT1	0.10727	0.54966	0.02537	0	0		
1185	chr19	10335000	10336000	0.000	0.000	0.015	0.014	SIPR2	1.00000	1.00000	0.29694	1	0		
1186	chr19	10340000	10341000	0.000	0.000	0.118	0.041	SIPR2	0.11795	0.03825	0.00004	1	1		
1187	chr19	10341000	10342000	0.000	0.012	0.206	0.054	SIPR2	0.01013	0.00197	0.00000	1	1		
1188	chr19	16030000	16031000	0.028	0.000	0.015	0.000	CYP4F11	0.47887	1.00000	0.29694	0	0		
1189	chr19	16436000	16437000	0.000	0.000	0.029	0.014	KLF2	0.60686	0.54294	0.08726	1	0		
1190	chr19	20889000	20890000	0.000	0.006	0.015	0.000	ZNF626	0.47887	1.00000	0.50663	0	0		
1191	chr19	21073000	21074000	0.000	0.000	0.015	0.027	ZNF85	1.00000	1.00000	0.29694	0	0		
1192	chr19	21092000	21093000	0.000	0.000	0.029	0.000	ZNF85	0.22755	0.54294	0.08726	0	0		
1193	chr19	23841000	23842000	0.000	0.000	0.015	0.027	ZNF675	1.00000	1.00000	0.29694	0	0		
1194	chr19	29256000	29257000	0.000	0.000	0.029	0.000	UQCRFS1	0.22755	0.54294	0.08726	0	0		
1195	chr19	44183000	44184000	0.000	0.000	0.029	0.000	PLAUR	0.22755	0.54294	0.08726	0	0		
1196	chr19	50399000	50400000	0.000	0.000	0.029	0.000	IL4I1	0.22755	0.54294	0.08726	0	0		
1197	chr19	53419000	53420000	0.028	0.000	0.015	0.014	ZNF321P,ZNF816,ZNF816-ZNF321PZNF321P,ZNF816-ZNF321P,	1.00000	1.00000	0.29694	0	0		
1198	chr20	1547000	1547100	0.028	0.006	0.000	0.000	MACROD2	1.00000	0.34615	1.00000	0	0		
1199	chr20	23359000	23360000	0.056	0.000	0.000	0.000	NAPB	1.00000	0.11763	1.00000	0	1		
1200	chr20	23912000	23913000	0.000	0.000	0.000	0.027	CST5	0.49735	1.00000	1.00000	0	0		
1201	chr20	46133000	46134000	0.000	0.000	0.059	0.014	NCOA3	0.19371	0.29551	0.00730	1	1		
1202	chr20	49127000	49128000	0.000	0.000	0.029	0.014	PTPN1	0.60686	0.54294	0.08726	0	0		
1203	chr20	49648000	49649000	0.000	0.000	0.029	0.000	KCNG1	0.22755	0.54294	0.08726	0	0		
1204	chr20	61607000	61608000	0.000	0.000	0.000	0.027	SLC17A9	0.49735	1.00000	1.00000	0	0		
1205	chr21	21597000	21598000	0.000	0.000	0.029	0.000	NCAM2	0.22755	0.54294	0.08726	0	0		
1206	chr21	23458000	23459000	0.000	0.000	0.029	0.000	NCAM2	0.22755	0.54294	0.08726	0	0		
1207	chr21	24998000	24999000	0.000	0.000	0.029	0.000	MRPL39	0.22755	0.54294	0.08726	0	0		
1208	chr21	26935000	26936000	0.000	0.000	0.015	0.014	MRPL39	1.00000	1.00000	0.29694	0	0		
1209	chr21	35779000	35780000	0.000	0.000	0.000	0.027	SMEM1	0.49735	1.00000	1.00000	0	0		
1210	chr21	38779000	38780000	0.000	0.000	0.000	0.027	DYRK1A	0.49735	1.00000	1.00000	0	0		
1211	chr21	43254000	43255000	0.000	0.000	0.029	0.000	PRDM15	0.22755	0.54294	0.08726	0	0		

1212	chr21	44612060	44613000	0.000	0.000	0.000	0.027	CRYAA	0.49735	1.00000	1.00000	0	0	0
1213	chr21	45381000	45382000	0.000	0.000	0.029	0.000	AGPAT3	0.22755	0.54294	0.08726	0		0
1214	chr21	46058000	46059000	0.030	0.030	0.015	0.027	KRTAP10-10	1.00000	1.00000	0.29694	0	0	0
1215	chr22	19050000	19051000	0.000	0.006	0.000	0.027	DGCR2	0.49735	1.00000	1.00000	0	0	0
1216	chr22	20212000	20213000	0.000	0.000	0.029	0.014	RTN4R	0.60686	0.54294	0.08726	0		0
1217	chr22	20708000	20709000	0.000	0.000	0.029	0.000	FAM230A	0.22755	0.54294	0.08726	0	0	0
1218	chr22	21994000	21995000	0.028	0.000	0.015	0.000	SDF2L1	0.47887	1.00000	0.29694	0	0	0
1219	chr22	22379000	22380000	0.000	0.000	0.029	0.027	IGLV4-69	1.00000	1.00000	0.08726	0		0
1220	chr22	22380000	22381000	0.000	0.012	0.044	0.068	IGLV4-69	0.72064	0.54966	0.15671	0	0	1
1221	chr22	22381000	22382000	0.000	0.012	0.015	0.027	IGLV4-69	1.00000	1.00000	1.00000	0		0
1222	chr22	22385000	22386000	0.028	0.031	0.029	0.068	IGLV4-69	0.44431	1.00000	1.00000	0		1
1223	chr22	22452000	22453000	0.000	0.012	0.015	0.014	IGLV8-61	1.00000	1.00000	1.00000	0	0	0
1224	chr22	22453000	22454000	0.000	0.012	0.015	0.014	IGLV8-61	1.00000	1.00000	1.00000	0		0
1225	chr22	22516000	22517000	0.000	0.025	0.015	0.054	IGLV4-60	0.36833	1.00000	1.00000	0		1
1226	chr22	22517000	22518000	0.000	0.019	0.000	0.014	IGLV4-60	1.00000	1.00000	0.55662	0	0	0
1227	chr22	22550000	22551000	0.056	0.006	0.044	0.054	IGLV6-57	1.00000	1.00000	0.07959	0		1
1228	chr22	22569000	22570000	0.000	0.006	0.015	0.014	IGLV10-54	1.00000	1.00000	0.50663	0	0	0
1229	chr22	22676000	22677000	0.028	0.000	0.015	0.000	IGLV1-51	0.47887	1.00000	0.29694	0		0
1230	chr22	22677000	22678000	0.083	0.012	0.015	0.014	IGLV1-51	1.00000	0.11840	1.00000	0		1
1231	chr22	22707000	22708000	0.028	0.006	0.044	0.014	IGLV5-48	0.34948	1.00000	0.07959	0		0
1232	chr22	22712000	22713000	0.083	0.012	0.088	0.041	IGLV1-47	0.31126	1.00000	0.60949	0		1
1233	chr22	22723000	22724000	0.000	0.006	0.015	0.027	IGLV7-46	1.00000	1.00000	0.50663	0		0
1234	chr22	22724000	22725000	0.028	0.012	0.088	0.041	IGLV7-46	0.31126	0.41714	0.60949	0		1
1235	chr22	22730000	22731000	0.000	0.006	0.059	0.054	IGLV5-45	1.00000	0.29551	0.02818	0		1
1236	chr22	22731000	22732000	0.000	0.006	0.029	0.000	IGLV8-45	0.22755	0.54294	0.21104	0		0
1237	chr22	22735000	22736000	0.028	0.037	0.059	0.068	IGLV1-44	1.00000	0.65667	0.48849	0		1
1238	chr22	22749000	22750000	0.000	0.006	0.059	0.027	IGLV7-43	0.42627	0.29551	0.02818	0		1
1239	chr22	22758000	22759000	0.028	0.006	0.029	0.014	IGLV1-40	0.60686	1.00000	0.21104	0		0
1240	chr22	22759000	22760000	0.056	0.006	0.044	0.027	IGLV1-40	0.67043	1.00000	0.07959	0		1
1241	chr22	22764000	22765000	0.111	0.006	0.044	0.068	IGLV1-40	0.72064	0.23165	0.07959	0		1
1242	chr22	23028000	23029000	0.000	0.006	0.015	0.000	IGLV3-25	0.47887	1.00000	0.50663	0		0
1243	chr22	23029000	23030000	0.028	0.062	0.132	0.108	IGLV3-25	0.79702	0.15881	0.11274	0		1
1244	chr22	23035000	23036000	0.000	0.000	0.015	0.014	IGLV2-23	1.00000	1.00000	0.29694	0		0
1245	chr22	23039000	23040000	0.000	0.000	0.000	0.027	IGLV2-23	0.49735	1.00000	1.00000	0		0
1246	chr22	23040000	23041000	0.000	0.043	0.103	0.054	IGLV2-23	0.35266	0.69269	0.12716	0		1
1247	chr22	23041000	23042000	0.000	0.006	0.044	0.000	IGLV2-23	0.10727	0.54966	0.07959	0		0
1248	chr22	23055000	23056000	0.028	0.056	0.059	0.014	IGLV3-21	0.19371	0.65667	1.00000	0		1
1249	chr22	23063000	23064000	0.000	0.000	0.074	0.041	IGLV3-19	0.47996	0.16101	0.60208	0		1
1250	chr22	23090000	23091000	0.000	0.000	0.059	0.041	IGLV3-16	0.70990	0.29551	0.60730	0		1
1251	chr22	23100000	23101000	0.000	0.019	0.044	0.054	IGLV2-14	1.00000	0.54966	0.36534	0		1
1252	chr22	23101000	23102000	0.028	0.031	0.074	0.081	IGLV2-14	1.00000	0.66188	0.16714	0		1
1253	chr22	23114000	23115000	0.000	0.000	0.015	0.027	IGLV3-12	1.00000	1.00000	0.29694	0		0
1254	chr22	23134000	23135000	0.000	0.000	0.029	0.014	IGLV2-11	0.60686	0.54294	0.08726	0		0
1255	chr22	23154000	23155000	0.000	0.019	0.074	0.027	IGLV3-10	0.25970	0.16101	0.05242	0		1
1256	chr22	23161000	23162000	0.000	0.006	0.000	0.014	IGLV3-9	1.00000	1.00000	1.00000	0		0
1257	chr22	23162000	23163000	0.000	0.012	0.000	0.014	IGLV3-9	1.00000	1.00000	1.00000	0		0
1258	chr22	23165000	23166000	0.000	0.012	0.000	0.041	IGLV2-8	0.24603	1.00000	1.00000	0		0
1259	chr22	23192000	23193000	0.000	0.006	0.088	0.041	IGLV4-3	0.31126	0.69031	0.60311	0		1
1260	chr22	23197000	23198000	0.000	0.006	0.015	0.000	IGLV4-3	0.47887	1.00000	0.50663	0		0
1261	chr22	23198000	23199000	0.000	0.025	0.147	0.068	IGLV4-3	0.17231	0.01404	0.00108	0		1
1262	chr22	23199000	23200000	0.000	0.031	0.221	0.068	IGLV4-3	0.01424	0.00107	0.00002	0		1

1263	chr22	23203000	23204000	0.000	0.000	0.029	0.000	IGLV4-3	0.22755	0.54294	0.08726	0	0	
1264	chr22	23204000	23205000	0.056	0.000	0.059	0.041	IGLV4-3	0.70990	1.00000	0.60730	0	1	
1265	chr22	23205000	23206000	0.000	0.000	0.015	0.027	IGLV4-3	1.00000	1.00000	0.29694	0	0	
1266	chr22	23206000	23208000	0.000	0.000	0.029	0.000	IGLV4-3	0.22755	0.54294	0.08726	0	0	
1267	chr22	23208000	23210000	0.000	0.000	0.029	0.000	IGLV4-3	0.22755	0.54294	0.08726	0	0	
1268	chr22	23213000	23214000	0.000	0.000	0.088	0.027	IGLV4-3	0.13270	0.09931	0.00058	0	1	
1269	chr22	23214000	23215000	0.000	0.000	0.074	0.027	IGLV4-3	0.25970	0.16101	0.00208	0	1	
1270	chr22	23219000	23220000	0.000	0.000	0.044	0.000	IGLV3-1	0.10727	0.54966	0.02537	0	0	
1271	chr22	23220000	23221000	0.000	0.000	0.059	0.000	IGLV3-1	0.05016	0.29551	0.00730	0	1	
1272	chr22	23222000	23223000	0.000	0.006	0.147	0.014	IGLV3-1	0.00342	0.01404	0.00003	0	1	
1273	chr22	23223000	23224000	0.083	0.149	0.544	0.432	IGLV3-1	0.23940	0.00000	0.00000	0	1	
1274	chr22	23224000	23225000	0.000	0.000	0.118	0.027	IGLV3-1	0.04838	0.04825	0.00664	0	1	
1275	chr22	23226000	23227000	0.000	0.000	0.029	0.000	IGLV3-1	0.22755	0.54294	0.08726	0	0	
1276	chr22	23227000	23228000	0.028	0.056	0.412	0.257	IGLL5	0.67371	0.00001	0.00000	0	1	
1277	chr22	23228000	23229000	0.028	0.019	0.309	0.095	IGLL5	0.00152	0.00070	0.00000	0	1	
1278	chr22	23229000	23230000	0.000	0.000	0.118	0.041	IGLL5	0.11795	0.04825	0.00004	0	1	
1279	chr22	23230000	23231000	0.222	0.161	0.647	0.514	IGLL5	0.12719	0.00007	0.00000	0	1	
1280	chr22	23231000	23232000	0.250	0.155	0.647	0.514	IGLL5	0.12719	0.00017	0.00000	0	1	
1281	chr22	23232000	23233000	0.000	0.012	0.426	0.162	IGLL5	0.00075	0.00000	0.00000	0	1	
1282	chr22	23233000	23234000	0.000	0.006	0.162	0.054	IGLJ1	0.05410	0.01471	0.00001	0	1	
1283	chr22	23234000	23235000	0.056	0.000	0.147	0.041	IGLJ1	0.03985	0.20979	0.00000	0	1	
1284	chr22	23235000	23236000	0.056	0.031	0.176	0.068	IGLJ1;IGLL5;	0.06843	0.13046	0.00035	0	1	
1285	chr22	23236000	23237000	0.111	0.043	0.250	0.095	IGLJ1;IGLL5;	0.02356	0.12484	0.00001	0	1	
1286	chr22	23237000	23238000	0.083	0.006	0.103	0.054	IGLC1;IGLL5;	0.35266	1.00000	0.00099	0	1	
1287	chr22	23241000	23242000	0.028	0.012	0.074	0.000	IGLJ2	0.02326	0.66188	0.02559	0	1	
1288	chr22	23242000	23243000	0.028	0.050	0.147	0.108	IGLC2	0.61516	0.09212	0.02792	0	1	
1289	chr22	23243000	23244000	0.000	0.000	0.029	0.000	IGLC2	0.22755	0.54294	0.08726	0	0	
1290	chr22	23244000	23245000	0.000	0.012	0.015	0.014	IGLC2	1.00000	1.00000	1.00000	0	0	
1291	chr22	23247000	23248000	0.111	0.099	0.088	0.122	IGLJ3	0.59261	0.73481	1.00000	0	1	
1292	chr22	23248000	23249000	0.000	0.012	0.015	0.027	IGLC3	1.00000	1.00000	1.00000	0	0	
1293	chr22	23249000	23250000	0.000	0.006	0.029	0.027	IGLC3	1.00000	0.54294	0.21104	0	0	
1294	chr22	23260000	23261000	0.000	0.025	0.015	0.000	IGLJ6	0.47887	1.00000	1.00000	0	0	
1295	chr22	23261000	23262000	0.000	0.012	0.015	0.014	IGLJ6	1.00000	1.00000	1.00000	0	0	
1296	chr22	23263000	23264000	0.000	0.006	0.044	0.014	IGLJ7	0.34948	0.54966	0.07959	0	0	
1297	chr22	23264000	23265000	0.000	0.006	0.044	0.027	IGLC7	0.67043	0.54966	0.07959	0	0	
1298	chr22	23273000	23274000	0.000	0.000	0.044	0.000	IGLC7	0.10727	0.54966	0.02537	0	0	
1299	chr22	23277000	23278000	0.000	0.000	0.029	0.014	IGLC7	0.60686	0.54294	0.08726	0	0	
1300	chr22	23278000	23279000	0.000	0.006	0.059	0.014	IGLC7	0.19371	0.29551	0.02818	0	1	
1301	chr22	23281000	23282000	0.000	0.000	0.029	0.014	IGLC7	0.60686	0.54294	0.08726	0	0	
1302	chr22	23282000	23283000	0.000	0.006	0.147	0.027	IGLC7	0.01393	0.01404	0.00003	0	1	
1303	chr22	23284000	23285000	0.000	0.000	0.029	0.000	IGLC7	0.22755	0.54294	0.08726	0	0	
1304	chr22	23523000	23524000	0.000	0.000	0.015	0.041	BCR	0.62100	1.00000	0.29694	0	0	
1305	chr22	23524000	23525000	0.000	0.000	0.029	0.014	BCR	0.60686	0.54294	0.08726	0	0	
1306	chr22	27236000	27237000	0.028	0.000	0.029	0.000	CRYBA4	0.22755	1.00000	0.08726	0	0	
1307	chr22	29195000	29196000	0.000	0.000	0.088	0.000	XBP1	0.01070	0.09931	0.00058	0	1	
1308	chr22	29196000	29197000	0.000	0.000	0.059	0.041	XBP1	0.70990	0.29551	0.00730	0	1	
1309	chr22	31826000	31827000	0.000	0.000	0.029	0.000	DRG1	0.22755	0.54294	0.08726	0	0	
1310	chr22	32982000	32983000	0.028	0.000	0.015	0.000	SYN3	0.47887	1.00000	0.29694	0	0	
1311	chr22	39852000	39853000	0.000	0.000	0.029	0.000	TAB1	0.22755	0.54294	0.08726	0	0	
1312	chr22	39854000	39855000	0.000	0.000	0.029	0.000	TAB1	0.22755	0.54294	0.08726	0	0	
1313	chr22	43360000	43361000	0.000	0.000	0.029	0.000	PACSIN2	0.22755	0.54294	0.08726	0	0	

1314	chr22	47186000	47187000	0.000	0.000	0.029	0.000	TBC1D22A	0.22755	0.54294	0.08726	0	0	
1315	chr22	47738000	47739000	0.000	0.000	0.000	0.027	LL22NC03-75H12.2	0.49735	1.00000	1.00000	0	0	
1316	chr22	50336000	50337000	0.028	0.000	0.015	0.000	CRELD2	0.47887	1.00000	0.29694	0	0	
1317	chrX	228000	229000	0.000	0.000	0.000	0.027	GTPBP6	0.49735	1.00000	1.00000	0	0	
1318	chrX	1514000	1515000	0.000	0.000	0.015	0.014	SLC25A6	1.00000	1.00000	0.29694	0	0	
1319	chrX	1611000	1612000	0.000	0.000	0.029	0.000	P2RY8	0.22755	0.54294	0.08726	1	0	
1320	chrX	12993000	12994000	0.000	0.000	0.235	0.041	TMSB4X	0.00091	0.00098	0.00000	1	1	
1321	chrX	12994000	12995000	0.000	0.000	0.221	0.027	TMSB4X	0.00045	0.00167	0.00000	1	1	
1322	chrX	13419000	13420000	0.028	0.000	0.029	0.027	ATYN3L	1.00000	1.00000	0.08726	0	0	
1323	chrX	27031000	27032000	0.000	0.000	0.059	0.000	DCAF8L2	0.05016	0.29551	0.00730	0	1	
1324	chrX	32315000	32316000	0.000	0.000	0.000	0.027	DMD	0.49735	1.00000	1.00000	1	0	
1325	chrX	32317000	32318000	0.028	0.000	0.000	0.014	DMD	1.00000	0.34615	1.00000	1	0	
1326	chrX	33144000	33145000	0.000	0.000	0.029	0.014	DMD	0.60686	0.54294	0.08726	1	0	
1327	chrX	33145000	33146000	0.000	0.000	0.044	0.027	DMD	0.67043	0.54966	0.02537	1	0	
1328	chrX	33146000	33147000	0.000	0.000	0.162	0.068	DMD	0.11004	0.01471	0.00000	1	1	
1329	chrX	41366000	41367000	0.000	0.000	0.015	0.027	CASK	1.00000	1.00000	0.29694	0	0	
1330	chrX	42802000	42803000	0.000	0.000	0.074	0.027	MAOA	0.25970	0.16161	0.00208	0	1	
1331	chrX	48775000	48776000	0.000	0.000	0.044	0.014	PIM2	0.34948	0.54966	0.02537	1	0	
1332	chrX	48776000	48777000	0.000	0.000	0.029	0.014	PIM2	0.60686	0.54294	0.08726	1	0	
1333	chrX	64071000	64072000	0.000	0.000	0.059	0.014	ZC4H2	0.19371	0.29551	0.00730	0	1	
1334	chrX	67036000	67037000	0.028	0.000	0.015	0.000	AR	0.47887	1.00000	0.29694	0	0	
1335	chrX	80258000	80259000	0.000	0.000	0.000	0.027	HMGN5	0.49735	1.00000	1.00000	0	0	
1336	chrX	81172000	81173000	0.000	0.000	0.015	0.027	SH3BGRL	1.00000	1.00000	0.29694	0	0	
1337	chrX	87742000	87743000	0.000	0.000	0.029	0.000	CPXCR1	0.22755	0.54294	0.08726	0	0	
1338	chrX	87831000	87832000	0.000	0.000	0.000	0.027	CPXCR1	0.49735	1.00000	1.00000	0	0	
1339	chrX	88263000	88264000	0.000	0.000	0.000	0.027	CPXCR1	0.49735	1.00000	1.00000	0	0	
1340	chrX	88458000	88459000	0.000	0.000	0.029	0.000	CPXCR1	0.22755	0.54294	0.08726	0	0	
1341	chrX	92647000	92648000	0.000	0.000	0.000	0.027	NAP1L3	0.49735	1.00000	1.00000	0	0	
1342	chrX	93378000	93380000	0.000	0.000	0.015	0.014	FAM133A	1.00000	1.00000	0.29694	0	0	
1343	chrX	94078000	94080000	0.000	0.000	0.015	0.014	FAM133A	1.00000	1.00000	0.29694	0	0	
1344	chrX	104006000	104007000	0.000	0.000	0.015	0.014	IL1RAPL2	1.00000	1.00000	0.29694	0	0	
1345	chrX	104269000	104270000	0.000	0.000	0.015	0.014	IL1RAPL2	1.00000	1.00000	0.29694	0	0	
1346	chrX	106132000	106133000	0.000	0.000	0.000	0.027	RIPPLY1	0.49735	1.00000	1.00000	0	0	
1347	chrX	113095000	113096000	0.056	0.000	0.015	0.000	HTR2C	0.47887	1.00000	0.50663	0	0	
1348	chrX	115676000	115677000	0.000	0.000	0.015	0.014	CXorf61	1.00000	1.00000	0.29694	0	0	
1349	chrX	124996000	124997000	0.000	0.000	0.029	0.000	DCAF12L2	0.22755	0.54294	0.08726	0	0	
1350	chrX	125708000	125709000	0.000	0.000	0.029	0.000	DCAF12L1	0.22755	0.54294	0.08726	0	0	
1351	chrX	128565000	128566000	0.000	0.000	0.015	0.014	SMARCA1	1.00000	1.00000	0.29694	0	0	
1352	chrX	129643000	129644000	0.000	0.000	0.015	0.027	RBMX2	1.00000	1.00000	0.29694	0	0	
1353	chrX	134903000	134904000	0.000	0.000	0.029	0.014	CT45A3;CT45A4;	0.60686	0.54294	0.08726	0	0	
1354	chrX	140846000	140847000	0.000	0.000	0.029	0.000	SPANXD;SPANXE;	0.22755	0.54294	0.08726	0	0	
1355	chrX	143750000	143751000	0.000	0.000	0.000	0.027	SPANXN1	0.49735	1.00000	1.00000	0	0	
1356	chrX	145016000	145017000	0.028	0.000	0.000	0.027	TMEM257	0.49735	0.34615	1.00000	0	0	

Table 2

#	Chromosome	Region Start	Region End	ABC-subtype	GCB-subtype	ClosestGene	p_ABC_vs_GCB	PreviouslyIdentified
1	chr1	756000	757000	0.040	0.000	AL669831.1	1.00000	0
2	chr1	1963000	1964000	0.000	0.000	GABRD	1.00000	0
3	chr1	2052000	2053000	0.000	0.040	PRKCZ	1.00000	0
4	chr1	3789000	3790000	0.000	0.000	DFFB	1.00000	0
5	chr1	6613000	6614000	0.000	0.000	NOL9	1.00000	1
6	chr1	6614000	6615000	0.120	0.040	NOL9	0.60921	1
7	chr1	6661000	6662000	0.000	0.000	KLHL21	1.00000	0
8	chr1	6662000	6663000	0.120	0.000	KLHL21	0.23469	0
9	chr1	9129000	9130000	0.000	0.080	SLC2A5	0.48980	0
10	chr1	10894000	10895000	0.040	0.000	C1orf127	1.00000	0
11	chr1	17019000	17020000	0.000	0.000	AL137798.1	1.00000	0
12	chr1	17231000	17232000	0.040	0.000	CROCC	1.00000	0
13	chr1	19935000	19936000	0.080	0.000	MINOS1-NBL1	0.48980	0
14	chr1	21091000	21092000	0.040	0.000	HP1BP3	1.00000	0
15	chr1	23885000	23886000	0.080	0.040	ID3	1.00000	1
16	chr1	28408000	28409000	0.000	0.040	EYA3	1.00000	0
17	chr1	32373000	32374000	0.000	0.040	PTP4A2	1.00000	0
18	chr1	36722000	36723000	0.040	0.000	THRAP3	1.00000	0
19	chr1	46576000	46577000	0.040	0.000	PIK3R3	1.00000	0
20	chr1	51965000	51966000	0.000	0.040	EPS15	1.00000	0
21	chr1	51978000	51979000	0.040	0.080	EPS15	1.00000	0
22	chr1	51983000	51984000	0.040	0.000	EPS15	1.00000	0
23	chr1	72393000	72394000	0.040	0.000	NEGR1	1.00000	0
24	chr1	73719000	73720000	0.040	0.040	LRRIQ3	1.00000	0
25	chr1	77315000	77316000	0.000	0.040	ST6GALNAC5	1.00000	0
26	chr1	81306000	81307000	0.040	0.000	LPHN2	1.00000	0
27	chr1	81527000	81528000	0.000	0.000	LPHN2	1.00000	0
28	chr1	82009000	82010000	0.000	0.000	LPHN2	1.00000	0
29	chr1	84106000	84107000	0.040	0.000	TTLL7	1.00000	0
30	chr1	87524000	87525000	0.000	0.040	HS2ST1;HS2ST1LOC339524;	1.00000	0
31	chr1	94551000	94552000	0.000	0.040	ABCA4	1.00000	0
32	chr1	94552000	94553000	0.000	0.040	ABCA4	1.00000	0
33	chr1	103696000	103697000	0.000	0.000	COL11A1	1.00000	0

34	chr1	116979000	116980000	0.000	0.040	ATP1A1	1.00000	0
35	chr1	149784000	149785000	0.040	0.040	HIST2H3D	1.00000	1
36	chr1	149821000	149822000	0.040	0.000	HIST2H2AA4	1.00000	1
37	chr1	149857000	149858000	0.000	0.040	HIST2H2BE	1.00000	1
38	chr1	149858000	149859000	0.080	0.040	HIST2H2AC;HIST2H2BE;	1.00000	0
39	chr1	160616000	160617000	0.040	0.040	SLAMF1	1.00000	0
40	chr1	162711000	162712000	0.040	0.000	DDR2	1.00000	0
41	chr1	163684000	163685000	0.040	0.000	NUF2	1.00000	0
42	chr1	167598000	167599000	0.080	0.000	RCSD1	0.48980	0
43	chr1	167599000	167600000	0.040	0.000	RCSD1	1.00000	0
44	chr1	167600000	167601000	0.040	0.040	RCSD1	1.00000	0
45	chr1	174333000	174334000	0.040	0.000	RABGAP1L	1.00000	0
46	chr1	187263000	187264000	0.000	0.000	PLA2G4A	1.00000	0
47	chr1	187283000	187284000	0.040	0.000	PLA2G4A	1.00000	0
48	chr1	187892000	187893000	0.040	0.000	PLA2G4A	1.00000	0
49	chr1	195282000	195283000	0.000	0.040	KCNT2	1.00000	0
50	chr1	198591000	198592000	0.000	0.040	PTPRC	1.00000	0
51	chr1	198608000	198609000	0.040	0.000	PTPRC	1.00000	0
52	chr1	198609000	198610000	0.080	0.000	PTPRC	0.48980	0
53	chr1	202004000	202005000	0.040	0.040	ELF3	1.00000	0
54	chr1	203273000	203274000	0.040	0.000	BTG2	1.00000	1
55	chr1	203274000	203275000	0.160	0.160	BTG2	1.00000	1
56	chr1	203275000	203276000	0.400	0.280	BTG2	0.55122	1
57	chr1	203276000	203277000	0.080	0.040	BTG2	1.00000	1
58	chr1	205780000	205781000	0.000	0.000	SLC41A1	1.00000	0
59	chr1	205781000	205782000	0.000	0.000	SLC41A1	1.00000	0
60	chr1	206283000	206284000	0.000	0.040	CTSE	1.00000	0
61	chr1	206286000	206287000	0.040	0.000	CTSE	1.00000	0
62	chr1	217044000	217045000	0.040	0.000	ESRRG	1.00000	0
63	chr1	226924000	226925000	0.080	0.120	ITPKB	1.00000	1
64	chr1	226925000	226926000	0.120	0.000	ITPKB	0.23469	1
65	chr1	226926000	226927000	0.120	0.000	ITPKB	0.23469	1
66	chr1	229974000	229975000	0.040	0.040	URB2	1.00000	0
67	chr1	235131000	235132000	0.000	0.000	TOMM20	1.00000	0
68	chr1	235141000	235142000	0.040	0.000	TOMM20	1.00000	0

69	chr1	238787000	238788000	0.040	0.000	MTRNR2L11	1.00000	0
70	chr1	248088000	248089000	0.040	0.000	OR2T8	1.00000	0
71	chr2	630000	631000	0.000	0.000	TMEM18	1.00000	0
72	chr2	1484000	1485000	0.000	0.000	TPO	1.00000	0
73	chr2	7991000	7992000	0.000	0.040	RNF144A	1.00000	0
74	chr2	12173000	12174000	0.000	0.040	LPIN1	1.00000	0
75	chr2	12175000	12176000	0.000	0.000	LPIN1	1.00000	0
76	chr2	12249000	12250000	0.000	0.040	LPIN1	1.00000	0
77	chr2	14113000	14114000	0.000	0.000	FAM84A	1.00000	0
78	chr2	17577000	17578000	0.000	0.040	RAD51AP2	1.00000	0
79	chr2	19253000	19254000	0.000	0.000	OSR1	1.00000	0
80	chr2	24802000	24803000	0.040	0.000	NCOA1	1.00000	0
81	chr2	31478000	31479000	0.040	0.000	EHD3	1.00000	0
82	chr2	41728000	41729000	0.040	0.000	C2orf91	1.00000	0
83	chr2	45404000	45405000	0.000	0.000	SIX2	1.00000	0
84	chr2	47923000	47924000	0.000	0.040	MSH6	1.00000	0
85	chr2	47944000	47945000	0.000	0.000	MSH6	1.00000	0
86	chr2	51360000	51361000	0.040	0.000	NRXN1	1.00000	0
87	chr2	51655000	51656000	0.000	0.000	NRXN1	1.00000	0
88	chr2	56565000	56566000	0.040	0.000	CCDC85A	1.00000	0
89	chr2	57800000	57801000	0.040	0.000	VRK2	1.00000	0
90	chr2	60779000	60780000	0.000	0.040	BCL11A	1.00000	0
91	chr2	60780000	60781000	0.080	0.000	BCL11A	0.48980	0
92	chr2	63802000	63803000	0.000	0.000	WDPCP	1.00000	0
93	chr2	63827000	63828000	0.000	0.040	MDH1	1.00000	0
94	chr2	64319000	64320000	0.000	0.040	PELI1	1.00000	0
95	chr2	65593000	65594000	0.000	0.040	SPRED2	1.00000	1
96	chr2	67002000	67003000	0.040	0.040	MEIS1	1.00000	0
97	chr2	70315000	70316000	0.040	0.000	PCBP1	1.00000	0
98	chr2	79502000	79503000	0.000	0.000	REG3A	1.00000	0
99	chr2	79644000	79645000	0.000	0.000	CTNNA2	1.00000	0
100	chr2	81818000	81819000	0.000	0.000	CTNNA2	1.00000	0
101	chr2	82310000	82311000	0.000	0.000	CTNNA2	1.00000	0
102	chr2	82948000	82949000	0.000	0.040	SUCLG1	1.00000	0
103	chr2	85335000	85336000	0.000	0.000	TCF7L1	1.00000	0
104	chr2	88905000	88906000	0.080	0.000	EIF2AK3	0.48980	0

105	chr2	88906000	88907000	0.160	0.040	EIF2AK3	0.34868	0	
106	chr2	88907000	88908000	0.040	0.040	EIF2AK3	1.00000	0	
107	chr2	89052000	89053000	0.000	0.080	RPIA	0.48980	0	
108	chr2	89065000	89066000	0.000	0.000	RPIA	1.00000	0	
109	chr2	89066000	89067000	0.040	0.000	RPIA	1.00000	0	
110	chr2	89095000	89096000	0.000	0.040	RPIA	1.00000	0	
111	chr2	89127000	89128000	0.120	0.080	IGKC	1.00000	0	
112	chr2	89128000	89129000	0.160	0.160	IGKC	1.00000	0	
113	chr2	89129000	89130000	0.120	0.000	IGKC	0.23469	0	
114	chr2	89130000	89131000	0.080	0.000	IGKC	0.48980	0	
115	chr2	89131000	89132000	0.040	0.040	IGKC	1.00000	0	
116	chr2	89132000	89133000	0.040	0.000	IGKC	1.00000	0	
117	chr2	89133000	89134000	0.000	0.040	IGKC	1.00000	0	
118	chr2	89137000	89138000	0.000	0.040	IGKC	1.00000	0	
119	chr2	89138000	89139000	0.040	0.000	IGKC	1.00000	0	
120	chr2	89139000	89140000	0.000	0.040	IGKC	1.00000	0	
121	chr2	89140000	89141000	0.040	0.120	IGKC	0.60921	0	
122	chr2	89141000	89142000	0.080	0.120	IGKC	1.00000	0	
123	chr2	89142000	89143000	0.040	0.200	IGKC	0.18946	0	
124	chr2	89143000	89144000	0.000	0.080	IGKC	0.48980	0	
125	chr2	89144000	89145000	0.040	0.040	IGKC	1.00000	0	
126	chr2	89145000	89146000	0.040	0.000	IGKC	1.00000	0	
127	chr2	89146000	89147000	0.000	0.000	IGKC	1.00000	0	
128	chr2	89153000	89154000	0.000	0.000	IGKC	1.00000	0	
129	chr2	89155000	89156000	0.080	0.080	IGKC	1.00000	0	
130	chr2	89156000	89157000	0.120	0.000	IGKC	0.23469	0	
131	chr2	89157000	89158000	0.240	0.160	IGKC	0.72520	0	
132	chr2	89158000	89159000	0.240	0.280	IGKC	1.00000	0	
133	chr2	89159000	89160000	0.360	0.640	IGKJ5	0.08874	0	
134	chr2	89160000	89161000	0.320	0.680	IGKJ3;IGKJ4;IGKJ5;	0.02271	0	
135	chr2	89161000	89162000	0.240	0.320	IGKJ1;IGKJ2;	0.75361	0	
136	chr2	89162000	89163000	0.200	0.200	IGKJ1	1.00000	0	
137	chr2	89163000	89164000	0.120	0.240	IGKJ1	0.46349	0	
138	chr2	89164000	89165000	0.160	0.280	IGKJ1	0.49620	0	
139	chr2	89165000	89166000	0.160	0.360	IGKJ1	0.19633	0	

140	chr2	89166000	89167000	0.000	0.040	IGKJ1	1.00000	0
141	chr2	89169000	89170000	0.000	0.040	IGKJ1	1.00000	0
142	chr2	89184000	89185000	0.000	0.000	IGKV4-1	1.00000	0
143	chr2	89185000	89186000	0.120	0.320	IGKV4-1	0.17062	0
144	chr2	89196000	89197000	0.000	0.160	IGKV5-2	0.10986	0
145	chr2	89197000	89198000	0.000	0.040	IGKV5-2	1.00000	0
146	chr2	89214000	89215000	0.000	0.040	IGKV5-2	1.00000	0
147	chr2	89246000	89247000	0.040	0.000	IGKV1-5	1.00000	0
148	chr2	89247000	89248000	0.160	0.000	IGKV1-5	0.10986	0
149	chr2	89248000	89249000	0.040	0.000	IGKV1-5	1.00000	0
150	chr2	89266000	89267000	0.000	0.040	IGKV1-6	1.00000	0
151	chr2	89291000	89292000	0.040	0.040	IGKV1-8	1.00000	0
152	chr2	89292000	89293000	0.000	0.040	IGKV1-8	1.00000	0
153	chr2	89326000	89327000	0.040	0.000	IGKV3-11	1.00000	0
154	chr2	89327000	89328000	0.040	0.000	IGKV3-11	1.00000	0
155	chr2	89442000	89443000	0.040	0.160	IGKV3-20	0.34868	0
156	chr2	89443000	89444000	0.000	0.000	IGKV3-20	1.00000	0
157	chr2	89476000	89477000	0.000	0.000	IGKV2-24	1.00000	0
158	chr2	89513000	89514000	0.040	0.000	IGKV1-27	1.00000	0
159	chr2	89521000	89522000	0.040	0.040	IGKV2-28	1.00000	0
160	chr2	89533000	89534000	0.040	0.000	IGKV2-30	1.00000	0
161	chr2	89534000	89535000	0.080	0.000	IGKV2-30	0.48980	0
162	chr2	89544000	89545000	0.000	0.080	IGKV2-30	0.48980	0
163	chr2	89545000	89546000	0.040	0.000	IGKV2-30	1.00000	0
164	chr2	90259000	90260000	0.040	0.000	IGKV1D-8	1.00000	0
165	chr2	90260000	90261000	0.120	0.000	IGKV1D-8	0.23469	0
166	chr2	96809000	96810000	0.040	0.080	DUSP2	1.00000	1
167	chr2	96810000	96811000	0.080	0.120	DUSP2	1.00000	1
168	chr2	96811000	96812000	0.000	0.080	DUSP2	0.48980	1
169	chr2	98611000	98612000	0.000	0.040	TMEM131	1.00000	0
170	chr2	100757000	100758000	0.080	0.000	AFF3	0.48980	0
171	chr2	100758000	100759000	0.120	0.000	AFF3	0.23469	0
172	chr2	106144000	106145000	0.000	0.080	FHL2	0.48980	0
173	chr2	111878000	111879000	0.000	0.120	BCL2L11	0.23469	0
174	chr2	111879000	111880000	0.040	0.120	BCL2L11	0.60921	0
175	chr2	112305000	112306000	0.000	0.040	ANAPC1	1.00000	0

176	chr2	116234000	116235000	0.040	0.000	DPP10	1.00000	0
177	chr2	116439000	116440000	0.040	0.000	DPP10	1.00000	0
178	chr2	124697000	124698000	0.000	0.040	CNTNAP5	1.00000	0
179	chr2	125235000	125236000	0.000	0.000	CNTNAP5	1.00000	0
180	chr2	127538000	127539000	0.000	0.000	GYPC	1.00000	0
181	chr2	136874000	136875000	0.200	0.120	CXCR4	0.70194	1
182	chr2	136875000	136876000	0.240	0.240	CXCR4	1.00000	1
183	chr2	136996000	136997000	0.000	0.040	CXCR4	1.00000	1
184	chr2	137082000	137083000	0.040	0.000	CXCR4	1.00000	1
185	chr2	140951000	140952000	0.040	0.000	LRP1B	1.00000	0
186	chr2	141335000	141336000	0.040	0.000	LRP1B	1.00000	0
187	chr2	141770000	141771000	0.000	0.000	LRP1B	1.00000	0
188	chr2	146445000	146446000	0.000	0.000	ZEB2	1.00000	0
189	chr2	146446000	146447000	0.000	0.080	ZEB2	0.48980	0
190	chr2	156443000	156444000	0.000	0.000	KCNJ3	1.00000	0
191	chr2	172590000	172591000	0.040	0.000	DYNC1I2	1.00000	0
192	chr2	176581000	176582000	0.000	0.000	KIAA1715	1.00000	0
193	chr2	179880000	179881000	0.000	0.040	CCDC141	1.00000	0
194	chr2	180358000	180359000	0.040	0.000	ZNF385B	1.00000	0
195	chr2	189285000	189286000	0.040	0.000	GULP1	1.00000	0
196	chr2	189432000	189433000	0.000	0.040	GULP1	1.00000	0
197	chr2	194115000	194116000	0.040	0.000	TMEFF2	1.00000	0
198	chr2	197035000	197036000	0.040	0.080	STK17B	1.00000	0
199	chr2	197041000	197042000	0.080	0.000	STK17B	0.48980	0
200	chr2	215999000	216000000	0.040	0.000	ABCA12	1.00000	0
201	chr2	216973000	216974000	0.000	0.000	XRCC5	1.00000	0
202	chr2	217247000	217248000	0.000	0.000	4-Mar-19	1.00000	0
203	chr2	225386000	225387000	0.040	0.000	CUL3	1.00000	0
204	chr2	225524000	225525000	0.000	0.040	CUL3	1.00000	0
205	chr2	233478000	233479000	0.040	0.000	EFHD1	1.00000	0
206	chr2	233980000	233981000	0.000	0.080	INPP5D	0.48980	0
207	chr2	240641000	240642000	0.000	0.000	AC093802.1	1.00000	0
208	chr2	241125000	241126000	0.000	0.000	OTOS	1.00000	0
209	chr3	8739000	8740000	0.000	0.000	CAV3	1.00000	0
210	chr3	16407000	16408000	0.000	0.000	RFTN1	1.00000	1
211	chr3	16409000	16410000	0.000	0.000	RFTN1	1.00000	1

212	chr3	164190000	164200000	0.040	0.080	RFTN1	1.00000	1
213	chr3	164720000	164730000	0.040	0.000	RFTN1	1.00000	1
214	chr3	164950000	164960000	0.000	0.080	RFTN1	0.48980	1
215	chr3	165520000	165530000	0.000	0.080	RFTN1	0.48980	1
216	chr3	165540000	165550000	0.120	0.120	RFTN1	1.00000	1
217	chr3	165550000	165560000	0.000	0.040	RFTN1	1.00000	1
218	chr3	216580000	216590000	0.040	0.000	ZNF385D	1.00000	0
219	chr3	256910000	256920000	0.040	0.040	TOP2B	1.00000	0
220	chr3	319690000	319700000	0.000	0.040	OSBPL10	1.00000	1
221	chr3	319930000	319940000	0.040	0.000	OSBPL10	1.00000	1
222	chr3	320010000	320020000	0.080	0.040	OSBPL10	1.00000	1
223	chr3	320220000	320230000	0.120	0.080	OSBPL10	1.00000	1
224	chr3	320230000	320240000	0.080	0.000	OSBPL10	0.48980	1
225	chr3	501280000	501290000	0.000	0.040	RBM5	1.00000	0
226	chr3	549130000	549140000	0.040	0.000	CACNA2D3	1.00000	0
227	chr3	560740000	560750000	0.040	0.040	ERC2	1.00000	0
228	chr3	595770000	595780000	0.000	0.000	FHIT	1.00000	0
229	chr3	603510000	603520000	0.000	0.040	FHIT	1.00000	0
230	chr3	603560000	603570000	0.000	0.000	FHIT	1.00000	0
231	chr3	603570000	603580000	0.040	0.000	FHIT	1.00000	0
232	chr3	603580000	603590000	0.040	0.000	FHIT	1.00000	0
233	chr3	603590000	603600000	0.000	0.000	FHIT	1.00000	0
234	chr3	603890000	603900000	0.000	0.040	FHIT	1.00000	0
235	chr3	603920000	603930000	0.040	0.000	FHIT	1.00000	0
236	chr3	603950000	603960000	0.000	0.000	FHIT	1.00000	0
237	chr3	604040000	604050000	0.040	0.000	FHIT	1.00000	0
238	chr3	604360000	604370000	0.000	0.000	FHIT	1.00000	0
239	chr3	604370000	604380000	0.000	0.040	FHIT	1.00000	0
240	chr3	604770000	604780000	0.040	0.040	FHIT	1.00000	0
241	chr3	604850000	604860000	0.040	0.000	FHIT	1.00000	0
242	chr3	605150000	605160000	0.000	0.040	FHIT	1.00000	0
243	chr3	605350000	605360000	0.040	0.000	FHIT	1.00000	0
244	chr3	606020000	606030000	0.000	0.000	FHIT	1.00000	0
245	chr3	606130000	606140000	0.000	0.040	FHIT	1.00000	0
246	chr3	606140000	606150000	0.000	0.040	FHIT	1.00000	0
247	chr3	606320000	606330000	0.000	0.000	FHIT	1.00000	0

248	chr3	60635000	60636000	0.000	0.000	FHIT	1.00000	0
249	chr3	60640000	60641000	0.000	0.000	FHIT	1.00000	0
250	chr3	60647000	60648000	0.000	0.040	FHIT	1.00000	0
251	chr3	60648000	60649000	0.000	0.040	FHIT	1.00000	0
252	chr3	60652000	60653000	0.000	0.000	FHIT	1.00000	0
253	chr3	60660000	60661000	0.040	0.000	FHIT	1.00000	0
254	chr3	60665000	60666000	0.000	0.040	FHIT	1.00000	0
255	chr3	60666000	60667000	0.000	0.040	FHIT	1.00000	0
256	chr3	60671000	60672000	0.000	0.000	FHIT	1.00000	0
257	chr3	60673000	60674000	0.040	0.000	FHIT	1.00000	0
258	chr3	60675000	60676000	0.000	0.040	FHIT	1.00000	0
259	chr3	60678000	60679000	0.000	0.040	FHIT	1.00000	0
260	chr3	60683000	60684000	0.000	0.000	FHIT	1.00000	0
261	chr3	60684000	60685000	0.000	0.040	FHIT	1.00000	0
262	chr3	60688000	60689000	0.040	0.000	FHIT	1.00000	0
263	chr3	60717000	60718000	0.000	0.000	FHIT	1.00000	0
264	chr3	60740000	60741000	0.040	0.000	FHIT	1.00000	0
265	chr3	60774000	60775000	0.000	0.040	FHIT	1.00000	0
266	chr3	60792000	60793000	0.000	0.000	FHIT	1.00000	0
267	chr3	60806000	60807000	0.040	0.000	FHIT	1.00000	0
268	chr3	60812000	60813000	0.000	0.000	FHIT	1.00000	0
269	chr3	60860000	60861000	0.000	0.000	FHIT	1.00000	0
270	chr3	71551000	71552000	0.040	0.000	EIF4E3	1.00000	0
271	chr3	78274000	78275000	0.000	0.040	ROBO1	1.00000	0
272	chr3	80273000	80274000	0.000	0.000	ROBO1	1.00000	0
273	chr3	83094000	83095000	0.000	0.000	GBE1	1.00000	0
274	chr3	83924000	83925000	0.000	0.000	CADM2	1.00000	0
275	chr3	84293000	84294000	0.000	0.040	CADM2	1.00000	0
276	chr3	85260000	85261000	0.000	0.040	CADM2	1.00000	0
277	chr3	85261000	85262000	0.000	0.000	CADM2	1.00000	0
278	chr3	85799000	85800000	0.040	0.000	CADM2	1.00000	0
279	chr3	86226000	86227000	0.000	0.000	CADM2	1.00000	0
280	chr3	88146000	88147000	0.040	0.000	CGGBP1	1.00000	0
281	chr3	94709000	94710000	0.000	0.000	NSUN3	1.00000	0
282	chr3	95460000	95461000	0.000	0.000	MTRNR2L12	1.00000	0
283	chr3	95724000	95725000	0.080	0.000	MTRNR2L12	0.48980	0

284	chr3	101569000	101570000	0.000	0.040	NFKBIZ	1.00000	0
285	chr3	111851000	111852000	0.000	0.000	GCSAM	1.00000	0
286	chr3	111852000	111853000	0.040	0.040	GCSAM	1.00000	0
287	chr3	122377000	122378000	0.080	0.040	PARP14	1.00000	0
288	chr3	150478000	150479000	0.000	0.000	SIAH2	1.00000	0
289	chr3	150479000	150480000	0.000	0.040	SIAH2	1.00000	0
290	chr3	150480000	150481000	0.000	0.120	SIAH2	0.23469	0
291	chr3	163237000	163238000	0.000	0.000	SI	1.00000	0
292	chr3	163238000	163239000	0.000	0.000	SI	1.00000	0
293	chr3	163615000	163616000	0.040	0.040	SI	1.00000	0
294	chr3	183270000	183271000	0.000	0.000	KLHL6	1.00000	0
295	chr3	183271000	183272000	0.000	0.040	KLHL6	1.00000	0
296	chr3	183272000	183273000	0.000	0.120	KLHL6	0.23469	0
297	chr3	183273000	183274000	0.000	0.040	KLHL6	1.00000	0
298	chr3	186648000	186649000	0.000	0.040	ADIPOQ	1.00000	0
299	chr3	186714000	186715000	0.080	0.160	ST6GAL1	0.66710	1
300	chr3	186715000	186716000	0.080	0.000	ST6GAL1	0.48980	1
301	chr3	186739000	186740000	0.120	0.040	ST6GAL1	0.60921	1
302	chr3	186740000	186741000	0.160	0.080	ST6GAL1	0.66710	1
303	chr3	186742000	186743000	0.000	0.000	ST6GAL1	1.00000	1
304	chr3	186783000	186784000	0.160	0.240	ST6GAL1	0.72520	1
305	chr3	186784000	186785000	0.040	0.040	ST6GAL1	1.00000	1
306	chr3	187458000	187459000	0.000	0.000	BCL6	1.00000	1
307	chr3	187459000	187460000	0.000	0.000	BCL6	1.00000	1
308	chr3	187460000	187461000	0.040	0.040	BCL6	1.00000	1
309	chr3	187461000	187462000	0.240	0.360	BCL6	0.53803	1
310	chr3	187462000	187463000	0.440	0.560	BCL6	0.57214	1
311	chr3	187463000	187464000	0.360	0.440	BCL6	0.77329	1
312	chr3	187464000	187465000	0.200	0.200	BCL6	1.00000	1
313	chr3	187468000	187469000	0.120	0.000	BCL6	0.23469	1
314	chr3	187635000	187636000	0.040	0.000	BCL6	1.00000	1
315	chr3	187636000	187637000	0.000	0.000	BCL6	1.00000	1
316	chr3	187653000	187654000	0.040	0.040	BCL6	1.00000	1
317	chr3	187658000	187659000	0.000	0.040	BCL6	1.00000	1
318	chr3	187660000	187661000	0.040	0.160	BCL6	0.34868	1
319	chr3	187661000	187662000	0.040	0.240	BCL6	0.09828	1

320	chr3	187664000	187665000	0.040	0.080	BCL6	1.00000	1
321	chr3	187686000	187687000	0.040	0.000	AC022498.1	1.00000	0
322	chr3	187687000	187688000	0.000	0.040	AC022498.1	1.00000	0
323	chr3	187693000	187694000	0.040	0.040	AC022498.1	1.00000	0
324	chr3	187696000	187697000	0.040	0.000	AC022498.1	1.00000	0
325	chr3	187697000	187698000	0.040	0.000	AC022498.1	1.00000	0
326	chr3	187803000	187804000	0.000	0.000	AC022498.1	1.00000	0
327	chr3	187806000	187807000	0.080	0.080	AC022498.1	1.00000	0
328	chr3	187957000	187958000	0.120	0.160	AC022498.1	1.00000	0
329	chr3	187958000	187959000	0.240	0.280	AC022498.1	1.00000	0
330	chr3	187959000	187960000	0.120	0.040	AC022498.1	0.60921	0
331	chr3	187960000	187961000	0.000	0.040	AC022498.1	1.00000	0
332	chr3	188222000	188223000	0.000	0.000	LPP	1.00000	0
333	chr3	188298000	188299000	0.040	0.000	LPP	1.00000	0
334	chr3	188299000	188300000	0.080	0.080	LPP	1.00000	0
335	chr3	188471000	188472000	0.120	0.240	LPP	0.46349	0
336	chr3	188472000	188473000	0.000	0.080	LPP	0.48980	0
337	chr4	50000	51000	0.080	0.000	ZNF595;ZNF718;	0.48980	0
338	chr4	51000	52000	0.120	0.040	ZNF595;ZNF718;	0.60921	0
339	chr4	54000	55000	0.080	0.000	ZNF595;ZNF718;	0.48980	0
340	chr4	290000	291000	0.000	0.000	ZNF732	1.00000	0
341	chr4	385000	386000	0.080	0.000	ZNF141	0.48980	0
342	chr4	550000	551000	0.000	0.000	PIGG	1.00000	0
343	chr4	2707000	2708000	0.000	0.040	FAM193A	1.00000	0
344	chr4	5206000	5207000	0.080	0.000	STK32B	0.48980	0
345	chr4	25863000	25864000	0.080	0.040	SEL1L3	1.00000	0
346	chr4	25864000	25865000	0.000	0.040	SEL1L3	1.00000	0
347	chr4	25865000	25866000	0.040	0.000	SEL1L3	1.00000	0
348	chr4	29657000	29658000	0.040	0.000	PCDH7	1.00000	0
349	chr4	30356000	30357000	0.040	0.000	PCDH7	1.00000	0
350	chr4	33418000	33419000	0.000	0.000	PCDH7	1.00000	0
351	chr4	33449000	33450000	0.000	0.040	PCDH7	1.00000	0
352	chr4	39348000	39349000	0.000	0.040	RFC1	1.00000	0

353	chr4	39974000	39975000	0.000	0.000	PDS5A	1.00000	0
354	chr4	40194000	40195000	0.000	0.120	N4BP2	0.23469	0
355	chr4	40195000	40196000	0.000	0.040	N4BP2	1.00000	0
356	chr4	40196000	40197000	0.040	0.000	N4BP2	1.00000	0
357	chr4	40197000	40198000	0.000	0.000	N4BP2	1.00000	0
358	chr4	40198000	40199000	0.120	0.080	N4BP2	1.00000	0
359	chr4	40199000	40200000	0.280	0.240	N4BP2	1.00000	0
360	chr4	40200000	40201000	0.080	0.080	RHOH	1.00000	1
361	chr4	40201000	40202000	0.120	0.120	RHOH	1.00000	1
362	chr4	40202000	40203000	0.080	0.000	RHOH	0.48980	1
363	chr4	40204000	40205000	0.000	0.040	RHOH	1.00000	1
364	chr4	45308000	45309000	0.000	0.000	GNPDA2	1.00000	0
365	chr4	46360000	46361000	0.000	0.040	GABRA2	1.00000	0
366	chr4	62375000	62376000	0.000	0.000	LPHN3	1.00000	0
367	chr4	62530000	62531000	0.000	0.000	LPHN3	1.00000	0
368	chr4	62911000	62912000	0.000	0.040	LPHN3	1.00000	0
369	chr4	63120000	63121000	0.040	0.040	LPHN3	1.00000	0
370	chr4	64015000	64016000	0.000	0.000	LPHN3	1.00000	0
371	chr4	65038000	65039000	0.040	0.000	TECRL	1.00000	0
372	chr4	65165000	65166000	0.000	0.040	TECRL	1.00000	0
373	chr4	65966000	65967000	0.000	0.040	EPHA5	1.00000	0
374	chr4	66827000	66828000	0.000	0.080	EPHA5	0.48980	0
375	chr4	71531000	71532000	0.000	0.040	IGJ	1.00000	0
376	chr4	71532000	71533000	0.000	0.000	IGJ	1.00000	0
377	chr4	74456000	74457000	0.040	0.000	RASSF6	1.00000	0
378	chr4	74483000	74484000	0.040	0.000	RASSF6	1.00000	0
379	chr4	74484000	74485000	0.040	0.000	RASSF6	1.00000	0
380	chr4	74485000	74486000	0.120	0.000	RASSF6	0.23469	0
381	chr4	91886000	91887000	0.040	0.000	CCSER1	1.00000	0
382	chr4	92787000	92788000	0.000	0.040	CCSER1	1.00000	0
383	chr4	113206000	113207000	0.000	0.000	TIFA	1.00000	0
384	chr4	114466000	114467000	0.000	0.000	CAMK2D	1.00000	0
385	chr4	114681000	114682000	0.000	0.080	CAMK2D	0.48980	0
386	chr4	117928000	117929000	0.040	0.000	TRAM1L1	1.00000	0
387	chr4	123637000	123638000	0.000	0.000	BBS12	1.00000	0
388	chr4	123227000	123228000	0.040	0.000	ANKRD50	1.00000	0

389	chr4	127371000	127372000	0.000	0.000	FAT4	1.00000	0
390	chr4	133455000	133456000	0.000	0.000	PCDH10	1.00000	0
391	chr4	134538000	134539000	0.000	0.040	PCDH10	1.00000	0
392	chr4	134743000	134744000	0.040	0.040	PABPC4L	1.00000	0
393	chr4	134867000	134868000	0.000	0.000	PABPC4L	1.00000	0
394	chr4	134949000	134950000	0.080	0.000	PABPC4L	0.48980	0
395	chr4	135064000	135065000	0.040	0.000	PABPC4L	1.00000	0
396	chr4	135077000	135078000	0.000	0.000	PABPC4L	1.00000	0
397	chr4	136799000	136800000	0.000	0.000	PCDH18	1.00000	0
398	chr4	136867000	136868000	0.000	0.040	PCDH18	1.00000	0
399	chr4	140236000	140237000	0.040	0.000	NAA15	1.00000	0
400	chr4	151723000	151724000	0.000	0.000	LRBA	1.00000	0
401	chr4	151950000	151951000	0.000	0.000	LRBA	1.00000	0
402	chr4	152125000	152126000	0.040	0.040	SH3D19	1.00000	0
403	chr4	157246000	157247000	0.040	0.000	CTSO	1.00000	0
404	chr4	164532000	164533000	0.000	0.000	1-Mar-19	1.00000	0
405	chr4	178732000	178733000	0.040	0.040	AGA	1.00000	0
406	chr4	178885000	178886000	0.040	0.000	AGA	1.00000	0
407	chr4	179898000	179899000	0.000	0.040	AGA	1.00000	0
408	chr4	180885000	180886000	0.040	0.000	TENM3	1.00000	0
409	chr4	181554000	181555000	0.040	0.040	TENM3	1.00000	0
410	chr4	182122000	182123000	0.000	0.040	TENM3	1.00000	0
411	chr5	436000	437000	0.000	0.000	AHRR	1.00000	0
412	chr5	3982000	3983000	0.040	0.000	IRX1	1.00000	0
413	chr5	17218000	17219000	0.040	0.000	BASP1	1.00000	0
414	chr5	17219000	17220000	0.080	0.000	BASP1	0.48980	0
415	chr5	18514000	18515000	0.040	0.000	CDH18	1.00000	0
416	chr5	22356000	22357000	0.040	0.000	CDH12	1.00000	0
417	chr5	22517000	22518000	0.040	0.000	CDH12	1.00000	0
418	chr5	24632000	24633000	0.000	0.000	CDH10	1.00000	0
419	chr5	25275000	25276000	0.000	0.040	CDH10	1.00000	0
420	chr5	25541000	25542000	0.000	0.000	CDH10	1.00000	0
421	chr5	26119000	26120000	0.000	0.080	CDH9	0.48980	0
422	chr5	26450000	26451000	0.000	0.000	CDH9	1.00000	0
423	chr5	29224000	29225000	0.080	0.000	CDH6	0.48980	0
424	chr5	29492000	29493000	0.000	0.000	CDH6	1.00000	0

425	chr5	29648000	29649000	0.000	0.000	CDH6	1.00000	0
426	chr5	51521000	51522000	0.000	0.040	CTD-2203A3.1	1.00000	0
427	chr5	83841000	83842000	0.040	0.000	EDIL3	1.00000	0
428	chr5	88177000	88178000	0.040	0.000	MEF2C	1.00000	0
429	chr5	88178000	88179000	0.040	0.000	MEF2C	1.00000	0
430	chr5	91417000	91418000	0.000	0.000	ARRDC3	1.00000	0
431	chr5	103678000	103679000	0.040	0.000	NUDT12	1.00000	0
432	chr5	123696000	123697000	0.000	0.000	ZNF608	1.00000	1
433	chr5	124079000	124080000	0.000	0.040	ZNF608	1.00000	1
434	chr5	124080000	124081000	0.040	0.000	ZNF608	1.00000	1
435	chr5	127594000	127595000	0.000	0.040	FBN2	1.00000	0
436	chr5	127875000	127876000	0.000	0.000	FBN2	1.00000	0
437	chr5	131825000	131826000	0.120	0.040	IRF1	0.60921	0
438	chr5	131826000	131827000	0.040	0.040	IRF1	1.00000	0
439	chr5	149791000	149792000	0.160	0.240	CD74	0.72520	1
440	chr5	149792000	149793000	0.040	0.080	CD74	1.00000	1
441	chr5	158380000	158381000	0.000	0.080	EBF1	0.48980	0
442	chr5	158479000	158480000	0.000	0.000	EBF1	1.00000	0
443	chr5	158526000	158527000	0.040	0.080	EBF1	1.00000	0
444	chr5	158527000	158528000	0.040	0.040	EBF1	1.00000	0
445	chr5	158528000	158529000	0.040	0.000	EBF1	1.00000	0
446	chr5	164247000	164248000	0.040	0.040	MAT2B	1.00000	0
447	chr5	164441000	164442000	0.000	0.000	MAT2B	1.00000	0
448	chr5	165932000	165933000	0.000	0.000	TENM2	1.00000	0
449	chr5	173300000	173301000	0.000	0.000	CPEB4	1.00000	0
450	chr5	179166000	179167000	0.040	0.040	MAML1	1.00000	0
451	chr5	180102000	180103000	0.040	0.000	FLT4	1.00000	0
452	chr6	392000	393000	0.120	0.080	IRF4	1.00000	1
453	chr6	393000	394000	0.080	0.080	IRF4	1.00000	1
454	chr6	141180000	141190000	0.160	0.440	CD83	0.06222	1
455	chr6	141190000	141200000	0.000	0.120	CD83	0.23469	1
456	chr6	181111000	181112000	0.000	0.080	NHLRC1	0.48980	0
457	chr6	183870000	183880000	0.000	0.040	RNF144B	1.00000	1
458	chr6	183880000	183890000	0.000	0.040	RNF144B	1.00000	1
459	chr6	195730000	195740000	0.040	0.040	ID4	1.00000	0
460	chr6	228730000	228740000	0.040	0.000	HDGFL1	1.00000	0

461	chr6	26031000	26032000	0.000	0.040	HIST1H3B	1.00000	1
462	chr6	26032000	26033000	0.000	0.040	HIST1H3B	1.00000	1
463	chr6	26056000	26057000	0.120	0.040	HIST1H1C	0.60921	1
464	chr6	26123000	26124000	0.120	0.040	HIST1H2BC	0.60921	1
465	chr6	26124000	26125000	0.120	0.080	HIST1H2AC;HIST1H2BC;	1.00000	0
466	chr6	26125000	26126000	0.000	0.040	HIST1H2AC	1.00000	1
467	chr6	26156000	26157000	0.120	0.080	HIST1H1E	1.00000	1
468	chr6	26157000	26158000	0.080	0.040	HIST1H1E	1.00000	1
469	chr6	26216000	26217000	0.040	0.040	HIST1H2BG	1.00000	1
470	chr6	26234000	26235000	0.080	0.040	HIST1H1D	1.00000	0
471	chr6	27101000	27102000	0.040	0.040	HIST1H2AG	1.00000	1
472	chr6	27114000	27115000	0.080	0.040	HIST1H2AH;HIST1H2BK;	1.00000	0
473	chr6	27792000	27793000	0.120	0.040	HIST1H4J	0.60921	0
474	chr6	27833000	27834000	0.040	0.000	HIST1H2AL	1.00000	1
475	chr6	27860000	27861000	0.000	0.080	HIST1H2AM	0.48980	1
476	chr6	27861000	27862000	0.000	0.040	HIST1H2BO	1.00000	1
477	chr6	29778000	29779000	0.000	0.040	LOC554223	1.00000	0
478	chr6	29780000	29781000	0.040	0.000	HLA-G	1.00000	0
479	chr6	29911000	29912000	0.080	0.040	HLA-A	1.00000	0
480	chr6	29927000	29928000	0.040	0.000	HLA-A	1.00000	0
481	chr6	31324000	31325000	0.040	0.040	HLA-B	1.00000	1
482	chr6	31325000	31326000	0.000	0.000	HLA-B	1.00000	1
483	chr6	31543000	31544000	0.080	0.000	TNF	0.48980	1
484	chr6	31549000	31550000	0.200	0.240	LTB	1.00000	1
485	chr6	31550000	31551000	0.040	0.040	LTB	1.00000	1
486	chr6	32440000	32441000	0.120	0.000	HLA-DRA	0.23469	0
487	chr6	32451000	32452000	0.040	0.000	HLA-DRB5	1.00000	0
488	chr6	32452000	32453000	0.080	0.000	HLA-DRB5	0.48980	0
489	chr6	32455000	32456000	0.040	0.040	HLA-DRB5	1.00000	0
490	chr6	32457000	32458000	0.000	0.000	HLA-DRB5	1.00000	0
491	chr6	32498000	32499000	0.000	0.040	HLA-DRB5	1.00000	0
492	chr6	32505000	32506000	0.040	0.000	HLA-DRB5	1.00000	0
493	chr6	32511000	32512000	0.000	0.000	HLA-DRB5	1.00000	0
494	chr6	32522000	32523000	0.040	0.000	HLA-DRB1	1.00000	0

495	chr6	32525000	32526000	0.040	0.000	HLA-DRB1	1.00000	0
496	chr6	32526000	32527000	0.000	0.000	HLA-DRB1	1.00000	0
497	chr6	32527000	32528000	0.000	0.000	HLA-DRB1	1.00000	0
498	chr6	32548000	32549000	0.000	0.000	HLA-DRB1	1.00000	0
499	chr6	32552000	32553000	0.040	0.000	HLA-DRB1	1.00000	0
500	chr6	32557000	32558000	0.000	0.080	HLA-DRB1	0.48980	0
501	chr6	32609000	32610000	0.000	0.040	HLA-DQA1	1.00000	0
502	chr6	32630000	32631000	0.000	0.040	HLA-DQB1	1.00000	0
503	chr6	32632000	32633000	0.080	0.040	HLA-DQB1	1.00000	0
504	chr6	32727000	32728000	0.040	0.040	HLA-DQB2	1.00000	0
505	chr6	32729000	32730000	0.000	0.040	HLA-DQB2	1.00000	0
506	chr6	33048000	33049000	0.000	0.040	HLA-DPB1	1.00000	0
507	chr6	34179000	34180000	0.000	0.040	HMGA1	1.00000	0
508	chr6	37138000	37139000	0.200	0.200	PIM1	1.00000	1
509	chr6	37139000	37140000	0.120	0.120	PIM1	1.00000	1
510	chr6	37140000	37141000	0.040	0.000	PIM1	1.00000	1
511	chr6	58001000	58002000	0.040	0.000	PRIM2	1.00000	0
512	chr6	67923000	67924000	0.040	0.000	BAI3	1.00000	0
513	chr6	77256000	77257000	0.040	0.000	IMPG1	1.00000	0
514	chr6	81437000	81438000	0.040	0.000	BCKDHB	1.00000	0
515	chr6	88468000	88469000	0.000	0.040	AKIRIN2	1.00000	0
516	chr6	88630000	88631000	0.040	0.080	SPACA1	1.00000	0
517	chr6	88876000	88877000	0.000	0.000	CNR1	1.00000	0
518	chr6	89323000	89324000	0.000	0.000	RNGTT	1.00000	0
519	chr6	89338000	89339000	0.080	0.000	RNGTT	0.48980	0
520	chr6	89348000	89349000	0.080	0.000	RNGTT	0.48980	0
521	chr6	89470000	89471000	0.080	0.000	RNGTT	0.48980	0
522	chr6	89471000	89472000	0.000	0.000	RNGTT	1.00000	0
523	chr6	90061000	90062000	0.040	0.040	UBE2J1	1.00000	1
524	chr6	90062000	90063000	0.040	0.000	UBE2J1	1.00000	1
525	chr6	90994000	90995000	0.000	0.080	MAP3K7	0.48980	0
526	chr6	91004000	91005000	0.040	0.040	MAP3K7	1.00000	0
527	chr6	91005000	91006000	0.120	0.280	MAP3K7	0.28902	0
528	chr6	91006000	91007000	0.040	0.120	MAP3K7	0.60921	0
529	chr6	91007000	91008000	0.000	0.040	MAP3K7	1.00000	0
530	chr6	94822000	94823000	0.000	0.040	EPHA7	1.00000	0

531	chr6	107704000	107705000	0.000	0.000	PDSS2	1.00000	0
532	chr6	112885000	112886000	0.040	0.000	RFPL4B	1.00000	0
533	chr6	118244000	118245000	0.040	0.000	SLC35F1	1.00000	0
534	chr6	121288000	121289000	0.000	0.000	C6orf170	1.00000	0
535	chr6	121489000	121490000	0.000	0.080	C6orf170	0.48980	0
536	chr6	123504000	123505000	0.040	0.000	TRDN	1.00000	0
537	chr6	127313000	127314000	0.040	0.000	RSPO3	1.00000	0
538	chr6	133785000	133786000	0.080	0.000	EYA4	0.48980	0
539	chr6	134491000	134492000	0.000	0.080	SGK1	0.48980	1
540	chr6	134492000	134493000	0.080	0.040	SGK1	1.00000	1
541	chr6	134493000	134494000	0.040	0.080	SGK1	1.00000	1
542	chr6	134494000	134495000	0.040	0.080	SGK1	1.00000	1
543	chr6	134495000	134496000	0.160	0.280	SGK1	0.49620	1
544	chr6	134496000	134497000	0.000	0.200	SGK1	0.05015	1
545	chr6	142046000	142047000	0.000	0.080	NMBR	0.48980	0
546	chr6	147860000	147861000	0.000	0.040	SAMD5	1.00000	0
547	chr6	150954000	150955000	0.040	0.040	PLEKHG1	1.00000	0
548	chr6	159238000	159239000	0.000	0.080	EZR	0.48980	0
549	chr6	159239000	159240000	0.040	0.000	EZR	1.00000	0
550	chr6	159240000	159241000	0.040	0.000	EZR	1.00000	0
551	chr6	159464000	159465000	0.040	0.000	TAGAP	1.00000	0
552	chr6	159463000	159466000	0.040	0.000	TAGAP	1.00000	0
553	chr6	161265000	161266000	0.000	0.040	PLG	1.00000	0
554	chr6	161833000	161834000	0.000	0.000	PARK2	1.00000	0
555	chr6	162712000	162713000	0.000	0.000	PARK2	1.00000	0
556	chr6	164941000	164942000	0.000	0.000	C6orf118	1.00000	0
557	chr6	168813000	168814000	0.000	0.000	SMOC2	1.00000	0
558	chr7	1898000	1899000	0.040	0.040	AC110781.3	1.00000	0
559	chr7	1963000	1964000	0.040	0.000	MAD1L1	1.00000	0
560	chr7	2080000	2081000	0.000	0.040	MAD1L1	1.00000	0
561	chr7	5568000	5569000	0.040	0.080	ACTB	1.00000	1
562	chr7	5569000	5570000	0.040	0.120	ACTB	0.60921	1
563	chr7	5570000	5571000	0.040	0.040	ACTB	1.00000	1
564	chr7	9933000	9934000	0.040	0.040	NDUFA4	1.00000	0
565	chr7	13017000	13018000	0.000	0.040	ARL4A	1.00000	0
566	chr7	13346000	13347000	0.000	0.000	ETV1	1.00000	0

567	chr7	154590000	154600000	0.000	0.000	AGMO	1.00000	0
568	chr7	163820000	163830000	0.040	0.000	ISPD	1.00000	0
569	chr7	286000000	286010000	0.040	0.000	CREB5	1.00000	0
570	chr7	408460000	408470000	0.040	0.000	C7orf10	1.00000	0
571	chr7	503490000	503500000	0.040	0.040	IKZF1	1.00000	0
572	chr7	503500000	503510000	0.080	0.040	IKZF1	1.00000	0
573	chr7	533350000	533360000	0.000	0.000	POM121L12	1.00000	0
574	chr7	577130000	577140000	0.080	0.040	ZNF716	1.00000	0
575	chr7	624750000	624760000	0.040	0.040	AC006455.1	1.00000	0
576	chr7	706690000	706700000	0.040	0.000	WBSCR17	1.00000	0
577	chr7	715530000	715540000	0.000	0.040	CALN1	1.00000	0
578	chr7	798470000	798480000	0.040	0.000	GNAI1	1.00000	0
579	chr7	806940000	806950000	0.040	0.000	AC005008.2	1.00000	0
580	chr7	815560000	815570000	0.000	0.000	CACNA2D1	1.00000	0
581	chr7	841270000	841280000	0.040	0.000	SEMA3A	1.00000	0
582	chr7	842470000	842480000	0.000	0.040	SEMA3D	1.00000	0
583	chr7	842570000	842580000	0.000	0.000	SEMA3D	1.00000	0
584	chr7	869140000	869150000	0.000	0.040	CROT	1.00000	0
585	chr7	903560000	903570000	0.000	0.040	CDK14	1.00000	0
586	chr7	933040000	933050000	0.000	0.000	CALCR	1.00000	0
587	chr7	936820000	936830000	0.040	0.000	BET1	1.00000	0
588	chr7	1026440000	1026450000	0.000	0.000	FBXL13	1.00000	0
589	chr7	1056990000	1057000000	0.000	0.040	CDHR3	1.00000	0
590	chr7	1103210000	1103220000	0.040	0.040	IMMP2L	1.00000	0
591	chr7	1105430000	1105440000	0.040	0.000	IMMP2L	1.00000	0
592	chr7	1105450000	1105460000	0.040	0.000	IMMP2L	1.00000	0
593	chr7	1105970000	1105980000	0.000	0.040	IMMP2L	1.00000	0
594	chr7	1106010000	1106020000	0.000	0.000	IMMP2L	1.00000	0
595	chr7	1106020000	1106030000	0.040	0.000	IMMP2L	1.00000	0
596	chr7	1106090000	1106100000	0.040	0.000	IMMP2L	1.00000	0
597	chr7	1106100000	1106110000	0.040	0.000	IMMP2L	1.00000	0
598	chr7	1106170000	1106180000	0.040	0.000	IMMP2L	1.00000	0
599	chr7	1106180000	1106190000	0.000	0.000	IMMP2L	1.00000	0
600	chr7	1106190000	1106200000	0.040	0.000	IMMP2L	1.00000	0
601	chr7	1106210000	1106220000	0.000	0.040	IMMP2L	1.00000	0
602	chr7	1106280000	1106290000	0.040	0.000	IMMP2L	1.00000	0

603	chr7	110629000	110630000	0.000	0.000	IMMP2L	1.00000	0
604	chr7	110631000	110632000	0.000	0.040	IMMP2L	1.00000	0
605	chr7	110632000	110633000	0.040	0.000	IMMP2L	1.00000	0
606	chr7	110636000	110637000	0.040	0.000	IMMP2L	1.00000	0
607	chr7	110637000	110638000	0.000	0.000	IMMP2L	1.00000	0
608	chr7	110638000	110639000	0.000	0.040	IMMP2L	1.00000	0
609	chr7	110639000	110640000	0.000	0.040	IMMP2L	1.00000	0
610	chr7	110641000	110642000	0.000	0.000	IMMP2L	1.00000	0
611	chr7	110650000	110651000	0.000	0.000	IMMP2L	1.00000	0
612	chr7	110651000	110652000	0.000	0.040	IMMP2L	1.00000	0
613	chr7	110666000	110667000	0.000	0.000	IMMP2L	1.00000	0
614	chr7	110671000	110672000	0.000	0.080	IMMP2L	0.48980	0
615	chr7	110677000	110678000	0.000	0.000	IMMP2L	1.00000	0
616	chr7	110679000	110680000	0.000	0.000	IMMP2L	1.00000	0
617	chr7	110680000	110681000	0.000	0.000	IMMP2L	1.00000	0
618	chr7	110685000	110686000	0.000	0.000	LRRN3	1.00000	0
619	chr7	110686000	110687000	0.000	0.040	LRRN3	1.00000	0
620	chr7	110688000	110689000	0.000	0.000	LRRN3	1.00000	0
621	chr7	110699000	110700000	0.080	0.000	LRRN3	0.48980	0
622	chr7	110700000	110701000	0.040	0.000	LRRN3	1.00000	0
623	chr7	110709000	110710000	0.000	0.040	LRRN3	1.00000	0
624	chr7	110711000	110712000	0.000	0.040	LRRN3	1.00000	0
625	chr7	110714000	110715000	0.000	0.040	LRRN3	1.00000	0
626	chr7	110727000	110728000	0.000	0.040	LRRN3	1.00000	0
627	chr7	110728000	110729000	0.040	0.000	LRRN3	1.00000	0
628	chr7	110729000	110730000	0.000	0.040	LRRN3	1.00000	0
629	chr7	110734000	110735000	0.000	0.040	LRRN3	1.00000	0
630	chr7	110737000	110738000	0.000	0.000	LRRN3	1.00000	0
631	chr7	110740000	110741000	0.040	0.080	LRRN3	1.00000	0
632	chr7	110744000	110745000	0.000	0.000	LRRN3	1.00000	0
633	chr7	110746000	110747000	0.000	0.040	LRRN3	1.00000	0
634	chr7	110747000	110748000	0.000	0.000	LRRN3	1.00000	0
635	chr7	110748000	110749000	0.000	0.000	LRRN3	1.00000	0
636	chr7	110755000	110756000	0.000	0.000	LRRN3	1.00000	0
637	chr7	110764000	110765000	0.000	0.000	LRRN3	1.00000	0
638	chr7	110767000	110768000	0.040	0.000	LRRN3	1.00000	0

639	chr7	110769000	110770000	0.000	0.040	LRRN3	1.00000	0	
640	chr7	110771000	110772000	0.040	0.040	LRRN3	1.00000	0	
641	chr7	110779000	110780000	0.000	0.000	LRRN3	1.00000	0	
642	chr7	110780000	110781000	0.000	0.040	LRRN3	1.00000	0	
643	chr7	110783000	110784000	0.000	0.040	LRRN3	1.00000	0	
644	chr7	110785000	110786000	0.000	0.080	LRRN3	0.48980	0	
645	chr7	110801000	110802000	0.000	0.040	LRRN3	1.00000	0	
646	chr7	110802000	110803000	0.000	0.040	LRRN3	1.00000	0	
647	chr7	110810000	110811000	0.000	0.000	LRRN3	1.00000	0	
648	chr7	110816000	110817000	0.000	0.000	LRRN3	1.00000	0	
649	chr7	110821000	110822000	0.000	0.040	LRRN3	1.00000	0	
650	chr7	110824000	110825000	0.000	0.000	LRRN3	1.00000	0	
651	chr7	110827000	110828000	0.040	0.000	LRRN3	1.00000	0	
652	chr7	110836000	110837000	0.040	0.040	LRRN3	1.00000	0	
653	chr7	110847000	110848000	0.000	0.040	LRRN3	1.00000	0	
654	chr7	111567000	111568000	0.000	0.000	DOCK4	1.00000	0	
655	chr7	119056000	119057000	0.040	0.000	KCND2	1.00000	0	
656	chr7	121380000	121381000	0.040	0.000	PTPRZ1	1.00000	0	
657	chr7	123887000	123888000	0.000	0.000	TMEM229A	1.00000	0	
658	chr7	125262000	125263000	0.000	0.040	POT1	1.00000	0	
659	chr7	145723000	145724000	0.000	0.000	CNTNAP2	1.00000	0	
660	chr7	148508000	148509000	0.000	0.000	EZH2	1.00000	0	
661	chr7	155127000	155128000	0.000	0.000	BLACE	1.00000	0	
662	chr7	157162000	157163000	0.040	0.000	DNAJB6	1.00000	0	
663	chr7	158684000	158685000	0.000	0.040	WDR60	1.00000	0	
664	chr8	1646000	1647000	0.000	0.040	DLGAP2	1.00000	0	
665	chr8	5558000	5559000	0.000	0.040	MCPH1	1.00000	0	
666	chr8	5612000	5613000	0.000	0.000	MCPH1	1.00000	0	
667	chr8	8602000	8603000	0.000	0.120	MFHAS1	0.23469	0	
668	chr8	8706000	8707000	0.000	0.000	MFHAS1	1.00000	0	
669	chr8	8717000	8718000	0.000	0.040	MFHAS1	1.00000	0	
670	chr8	11352000	11353000	0.040	0.040	BLK	1.00000	0	
671	chr8	14080000	14081000	0.000	0.040	SGCZ	1.00000	0	
672	chr8	14796000	14797000	0.040	0.000	SGCZ	1.00000	0	
673	chr8	16090000	16091000	0.000	0.040	MSR1	1.00000	0	
674	chr8	16187000	16188000	0.000	0.080	MSR1	0.48980	0	

675	chr8	23101000	23102000	0.000	0.040	CHMP7	1.00000	0
676	chr8	24207000	24208000	0.000	0.000	ADAM28	1.00000	0
677	chr8	29155000	29156000	0.000	0.040	KIF13B	1.00000	0
678	chr8	35657000	35658000	0.000	0.000	AC012215.1	1.00000	0
679	chr8	38759000	38760000	0.040	0.000	PLEKHA2	1.00000	0
680	chr8	54986000	54987000	0.040	0.000	LYPLA1	1.00000	0
681	chr8	60031000	60032000	0.040	0.000	TOX	1.00000	0
682	chr8	67525000	67526000	0.040	0.000	MYBL1	1.00000	0
683	chr8	77105000	77106000	0.000	0.000	ZFHX4	1.00000	0
684	chr8	78400000	78401000	0.000	0.040	PEX2	1.00000	0
685	chr8	90322000	90323000	0.040	0.000	RIPK2	1.00000	0
686	chr8	93199000	93200000	0.000	0.040	RUNX1T1	1.00000	0
687	chr8	94618000	94619000	0.000	0.040	FAM92A1	1.00000	0
688	chr8	110586000	110587000	0.000	0.040	SYBU	1.00000	0
689	chr8	126687000	126688000	0.000	0.000	TRIB1	1.00000	0
690	chr8	128748000	128749000	0.080	0.280	MYC	0.13833	1
691	chr8	128749000	128750000	0.080	0.320	MYC	0.07375	1
692	chr8	128750000	128751000	0.080	0.120	MYC	1.00000	1
693	chr8	128751000	128752000	0.040	0.080	MYC	1.00000	1
694	chr8	128752000	128753000	0.000	0.000	MYC	1.00000	1
695	chr8	137918000	137919000	0.000	0.040	FAM135B	1.00000	0
696	chr8	138274000	138275000	0.000	0.000	FAM135B	1.00000	0
697	chr8	143183000	143184000	0.000	0.040	TSNARE1	1.00000	0
698	chr8	144123000	144124000	0.000	0.040	C8orf31	1.00000	0
699	chr9	6411000	6412000	0.040	0.040	UHRF2	1.00000	0
700	chr9	6413000	6414000	0.040	0.040	UHRF2	1.00000	0
701	chr9	6414000	6415000	0.000	0.000	UHRF2	1.00000	0
702	chr9	9928000	9929000	0.000	0.000	PTPRD	1.00000	0
703	chr9	13965000	13966000	0.040	0.000	NFIB	1.00000	0
704	chr9	22824000	22825000	0.040	0.000	DMRTA1	1.00000	0
705	chr9	25260000	25261000	0.040	0.000	TUSC1	1.00000	0
706	chr9	29890000	29891000	0.040	0.000	LINGO2	1.00000	0
707	chr9	30656000	30657000	0.000	0.040	ACO1	1.00000	0
708	chr9	37003000	37004000	0.040	0.000	PAX5	1.00000	1
709	chr9	37005000	37006000	0.040	0.000	PAX5	1.00000	1
710	chr9	37024000	37025000	0.040	0.040	PAX5	1.00000	1

711	chr9	37025000	37026000	0.160	0.120	PAX5	1.00000	1
712	chr9	37026000	37027000	0.240	0.120	PAX5	0.46349	1
713	chr9	37027000	37028000	0.080	0.040	PAX5	1.00000	1
714	chr9	37033000	37034000	0.120	0.040	PAX5	0.60921	1
715	chr9	37034000	37035000	0.120	0.040	PAX5	0.60921	1
716	chr9	37035000	37036000	0.000	0.040	PAX5	1.00000	1
717	chr9	37196000	37197000	0.040	0.000	ZCCHC7	1.00000	0
718	chr9	37197000	37198000	0.040	0.000	ZCCHC7	1.00000	0
719	chr9	37293000	37294000	0.000	0.000	ZCCHC7	1.00000	0
720	chr9	37294000	37295000	0.080	0.000	ZCCHC7	0.48980	0
721	chr9	37327000	37328000	0.040	0.000	ZCCHC7	1.00000	0
722	chr9	37336000	37337000	0.080	0.000	ZCCHC7	0.48980	0
723	chr9	37337000	37338000	0.000	0.000	ZCCHC7	1.00000	0
724	chr9	37338000	37339000	0.000	0.040	ZCCHC7	1.00000	0
725	chr9	37369000	37370000	0.040	0.000	ZCCHC7	1.00000	0
726	chr9	37371000	37372000	0.080	0.080	ZCCHC7	1.00000	0
727	chr9	37372000	37373000	0.000	0.000	ZCCHC7	1.00000	0
728	chr9	37383000	37384000	0.080	0.080	ZCCHC7	1.00000	0
729	chr9	37384000	37385000	0.120	0.040	ZCCHC7	0.60921	0
730	chr9	37385000	37386000	0.040	0.000	ZCCHC7	1.00000	0
731	chr9	37387000	37388000	0.080	0.040	ZCCHC7	1.00000	0
732	chr9	37397000	37398000	0.040	0.120	GRHPR	0.60921	0
733	chr9	37398000	37399000	0.040	0.000	GRHPR	1.00000	0
734	chr9	37399000	37400000	0.080	0.000	GRHPR	0.48980	0
735	chr9	37402000	37403000	0.000	0.040	GRHPR	1.00000	0
736	chr9	37406000	37407000	0.000	0.040	GRHPR	1.00000	0
737	chr9	37407000	37408000	0.200	0.080	GRHPR	0.41743	0
738	chr9	37408000	37409000	0.080	0.000	GRHPR	0.48980	0
739	chr9	37410000	37411000	0.000	0.000	GRHPR	1.00000	0
740	chr9	37424000	37425000	0.040	0.040	GRHPR	1.00000	0
741	chr9	37425000	37426000	0.000	0.040	GRHPR	1.00000	0
742	chr9	112811000	112812000	0.080	0.080	AKAP2	1.00000	0
743	chr9	117037000	117038000	0.000	0.040	COL27A1	1.00000	0
744	chr9	119779000	119780000	0.040	0.000	ASTN2	1.00000	0
745	chr9	126232000	126233000	0.040	0.000	DENND1A	1.00000	0
746	chr9	130741000	130742000	0.040	0.000	FAM102A	1.00000	1

747	chr9	130742000	130743000	0.040	0.080	FAM102A	1.00000	1
748	chr9	132767000	132768000	0.000	0.040	FNBP1	1.00000	0
749	chr9	132785000	132786000	0.040	0.000	FNBP1	1.00000	0
750	chr9	132803000	132804000	0.000	0.040	FNBP1	1.00000	0
751	chr9	132804000	132805000	0.040	0.120	FNBP1	0.60921	0
752	chr9	134551000	134552000	0.040	0.000	RAPGEF1	1.00000	0
753	chr9	138874000	138875000	0.000	0.040	UBAC1	1.00000	0
754	chr10	3333000	3334000	0.000	0.000	PITRM1	1.00000	0
755	chr10	5707000	5708000	0.040	0.040	ASB13	1.00000	0
756	chr10	5728000	5729000	0.000	0.040	ASB13	1.00000	0
757	chr10	15393000	15394000	0.000	0.000	FAM171A1	1.00000	0
758	chr10	20796000	20797000	0.040	0.000	PLXDC2	1.00000	0
759	chr10	35424000	35425000	0.000	0.000	CREM	1.00000	0
760	chr10	56678000	56679000	0.000	0.000	PCDH15	1.00000	0
761	chr10	63440000	63441000	0.000	0.040	C10orf107	1.00000	0
762	chr10	63659000	63660000	0.040	0.000	ARID5B	1.00000	1
763	chr10	63660000	63661000	0.040	0.080	ARID5B	1.00000	1
764	chr10	63662000	63663000	0.000	0.000	ARID5B	1.00000	1
765	chr10	63720000	63721000	0.000	0.000	ARID5B	1.00000	1
766	chr10	63803000	63804000	0.000	0.000	ARID5B	1.00000	1
767	chr10	63809000	63810000	0.000	0.080	ARID5B	0.48980	1
768	chr10	63810000	63811000	0.000	0.040	ARID5B	1.00000	1
769	chr10	67907000	67908000	0.000	0.040	CTNNA3	1.00000	0
770	chr10	68474000	68475000	0.000	0.000	CTNNA3	1.00000	0
771	chr10	98510000	98511000	0.080	0.000	PIK3AP1	0.48980	0
772	chr10	101384000	101385000	0.000	0.000	SLC25A28	1.00000	0
773	chr10	108276000	108277000	0.040	0.000	SORCS1	1.00000	0
774	chr10	113473000	113474000	0.040	0.040	GPAM	1.00000	0
775	chr10	113636000	113637000	0.040	0.000	GPAM	1.00000	0
776	chr10	116458000	116459000	0.000	0.040	ABLIM1	1.00000	0
777	chr10	121623000	121624000	0.040	0.000	MCMBP	1.00000	0
778	chr10	132973000	132974000	0.040	0.000	TCERG1L	1.00000	0
779	chr10	134326000	134327000	0.000	0.000	INPP5A	1.00000	0
780	chr11	871000	872000	0.040	0.040	CHID1	1.00000	0
781	chr11	1149000	1150000	0.000	0.000	MUC5AC	1.00000	0
782	chr11	25065000	25066000	0.040	0.000	LUZP2	1.00000	0

783	chr11	25289000	25290000	0.040	0.040	LUZP2	1.00000	0
784	chr11	27216000	27217000	0.000	0.040	BBOX1	1.00000	0
785	chr11	28849000	28850000	0.000	0.000	METTL15	1.00000	0
786	chr11	29253000	29254000	0.040	0.000	KCNA4	1.00000	0
787	chr11	29900000	29901000	0.000	0.000	KCNA4	1.00000	0
788	chr11	40626000	40627000	0.000	0.000	LRRC4C	1.00000	0
789	chr11	40845000	40846000	0.000	0.000	LRRC4C	1.00000	0
790	chr11	40868000	40869000	0.000	0.000	LRRC4C	1.00000	0
791	chr11	41066000	41067000	0.000	0.000	LRRC4C	1.00000	0
792	chr11	41844000	41845000	0.000	0.000	API5	1.00000	0
793	chr11	57171000	57172000	0.040	0.000	SLC43A3	1.00000	0
794	chr11	60224000	60225000	0.040	0.080	MS4A1	1.00000	1
795	chr11	65190000	65191000	0.080	0.120	FRMD8	1.00000	0
796	chr11	65191000	65192000	0.080	0.120	FRMD8	1.00000	0
797	chr11	65266000	65267000	0.000	0.040	SCYL1	1.00000	0
798	chr11	65267000	65268000	0.120	0.040	SCYL1	0.60921	0
799	chr11	85963000	85964000	0.000	0.000	EED	1.00000	0
800	chr11	92261000	92262000	0.000	0.040	FAT3	1.00000	0
801	chr11	102117000	102118000	0.000	0.000	YAP1	1.00000	0
802	chr11	102188000	102189000	0.200	0.280	BIRC3	0.74164	1
803	chr11	102189000	102190000	0.040	0.080	BIRC3	1.00000	1
804	chr11	107497000	107498000	0.000	0.000	ELMOD1	1.00000	0
805	chr11	108781000	108782000	0.000	0.040	DDX10	1.00000	0
806	chr11	108975000	108976000	0.040	0.000	DDX10	1.00000	0
807	chr11	109066000	109067000	0.000	0.000	C11orf87	1.00000	0
808	chr11	111248000	111249000	0.000	0.040	POU2AF1	1.00000	1
809	chr11	111249000	111250000	0.120	0.160	POU2AF1	1.00000	1
810	chr11	115761000	115762000	0.000	0.040	CADM1	1.00000	0
811	chr11	118723000	118724000	0.040	0.000	CXCR5	1.00000	0
812	chr11	126496000	126497000	0.040	0.000	KIRREL3	1.00000	0
813	chr11	128390000	128391000	0.040	0.040	ETS1	1.00000	1
814	chr11	128391000	128392000	0.160	0.040	ETS1	0.34868	1
815	chr12	6554000	6555000	0.000	0.040	CD27	1.00000	0
816	chr12	8762000	8763000	0.040	0.000	AICDA	1.00000	0
817	chr12	8763000	8764000	0.080	0.040	AICDA	1.00000	0
818	chr12	8764000	8765000	0.080	0.000	AICDA	0.48980	0

819	chr12	8765000	8766000	0.040	0.000	AICDA	1.00000	0
820	chr12	9823000	9824000	0.040	0.000	CLEC2D	1.00000	0
821	chr12	11710000	11711000	0.000	0.040	ETV6	1.00000	1
822	chr12	11803000	11804000	0.040	0.000	ETV6	1.00000	1
823	chr12	14923000	14924000	0.040	0.040	HIST4H4	1.00000	1
824	chr12	16717000	16718000	0.000	0.000	LMO3	1.00000	0
825	chr12	23805000	23806000	0.000	0.040	SOX5	1.00000	0
826	chr12	25149000	25150000	0.000	0.040	C12orf77	1.00000	0
827	chr12	25151000	25152000	0.000	0.040	C12orf77	1.00000	0
828	chr12	25174000	25175000	0.040	0.040	C12orf77	1.00000	0
829	chr12	25205000	25206000	0.040	0.040	LRMP	1.00000	1
830	chr12	25206000	25207000	0.080	0.120	LRMP	1.00000	1
831	chr12	25207000	25208000	0.080	0.120	LRMP	1.00000	1
832	chr12	25208000	25209000	0.000	0.040	LRMP	1.00000	1
833	chr12	25665000	25666000	0.000	0.000	IFLTD1	1.00000	0
834	chr12	38920000	38921000	0.000	0.000	CPNE8	1.00000	0
835	chr12	48027000	48028000	0.080	0.080	RPAP3	1.00000	0
836	chr12	57496000	57497000	0.040	0.000	STAT6	1.00000	0
837	chr12	69203000	69204000	0.000	0.040	MDM2	1.00000	0
838	chr12	76202000	76203000	0.000	0.000	PHLDA1	1.00000	0
839	chr12	79270000	79271000	0.000	0.000	SYT1	1.00000	0
840	chr12	82572000	82573000	0.000	0.040	CCDC59	1.00000	0
841	chr12	84837000	84838000	0.000	0.000	SLC6A15	1.00000	0
842	chr12	86114000	86115000	0.040	0.000	RASSF9	1.00000	0
843	chr12	86115000	86116000	0.040	0.000	RASSF9	1.00000	0
844	chr12	92538000	92539000	0.080	0.080	BTG1	1.00000	1
845	chr12	92539000	92540000	0.080	0.040	BTG1	1.00000	1
846	chr12	96030000	96031000	0.000	0.040	NTN4	1.00000	0
847	chr12	110171000	110172000	0.000	0.040	FAM222A	1.00000	0
848	chr12	110980000	110981000	0.000	0.040	PPTC7	1.00000	0
849	chr12	113493000	113494000	0.080	0.000	DTX1	0.48980	1
850	chr12	113494000	113495000	0.240	0.040	DTX1	0.09828	1
851	chr12	113495000	113496000	0.160	0.080	DTX1	0.66710	1
852	chr12	113496000	113497000	0.160	0.040	DTX1	0.34868	1
853	chr12	113497000	113498000	0.080	0.040	DTX1	1.00000	1
854	chr12	113499000	113500000	0.000	0.000	DTX1	1.00000	1

855	chr12	113512000	113513000	0.000	0.000	DTX1	1.00000	1
856	chr12	115966000	115967000	0.000	0.000	MED13L	1.00000	0
857	chr12	122432000	122433000	0.040	0.000	WDR66	1.00000	0
858	chr12	122433000	122434000	0.080	0.000	WDR66	0.48980	0
859	chr12	122447000	122448000	0.000	0.040	WDR66	1.00000	0
860	chr12	122458000	122459000	0.080	0.120	BCL7A	1.00000	1
861	chr12	122459000	122460000	0.240	0.320	BCL7A	0.75361	1
862	chr12	122460000	122461000	0.120	0.280	BCL7A	0.28902	1
863	chr12	122461000	122462000	0.240	0.240	BCL7A	1.00000	1
864	chr12	122462000	122463000	0.160	0.200	BCL7A	1.00000	1
865	chr12	122463000	122464000	0.120	0.200	BCL7A	0.70194	1
866	chr12	124054000	124055000	0.000	0.080	TMED2	0.48980	0
867	chr12	127965000	127966000	0.000	0.000	TMEM132C	1.00000	0
868	chr12	131303000	131304000	0.000	0.120	STX2	0.23469	0
869	chr12	131649000	131650000	0.000	0.000	GPR133	1.00000	0
870	chr12	133306000	133307000	0.000	0.000	ANKLE2	1.00000	0
871	chr13	21913000	21914000	0.040	0.040	ZDHHC20	1.00000	0
872	chr13	32116000	32117000	0.040	0.040	RXFP2	1.00000	0
873	chr13	35498000	35499000	0.000	0.000	NBEA	1.00000	0
874	chr13	38371000	38372000	0.040	0.000	TRPC4	1.00000	0
875	chr13	38630000	38631000	0.040	0.000	TRPC4	1.00000	0
876	chr13	41156000	41157000	0.000	0.040	FOXO1	1.00000	1
877	chr13	41240000	41241000	0.000	0.040	FOXO1	1.00000	1
878	chr13	46958000	46959000	0.000	0.000	KIAA0226L	1.00000	0
879	chr13	46959000	46960000	0.040	0.000	KIAA0226L	1.00000	0
880	chr13	46960000	46961000	0.160	0.040	KIAA0226L	0.34868	0
881	chr13	46961000	46962000	0.000	0.040	KIAA0226L	1.00000	0
882	chr13	46962000	46963000	0.000	0.040	KIAA0226L	1.00000	0
883	chr13	55239000	55240000	0.040	0.000	OLFM4	1.00000	0
884	chr13	55386000	55387000	0.040	0.000	OLFM4	1.00000	0
885	chr13	55598000	55599000	0.000	0.000	OLFM4	1.00000	0
886	chr13	57222000	57223000	0.000	0.040	PRR20A;PRR20 DPRR20BPRR2 0E;	1.00000	0
887	chr13	61343000	61344000	0.000	0.000	TDRD3	1.00000	0
888	chr13	62830000	62831000	0.000	0.000	PCDH20	1.00000	0

889	chr13	63049000	63050000	0.080	0.000	PCDH20	0.48980	0
890	chr13	63157000	63158000	0.000	0.000	AL445989.1	1.00000	0
891	chr13	63214000	63215000	0.040	0.000	AL445989.1	1.00000	0
892	chr13	64802000	64803000	0.000	0.040	AL445989.1	1.00000	0
893	chr13	65637000	65638000	0.000	0.040	PCDH9	1.00000	0
894	chr13	68656000	68657000	0.000	0.000	PCDH9	1.00000	0
895	chr13	69418000	69419000	0.000	0.000	KLHL1	1.00000	0
896	chr13	70956000	70957000	0.040	0.000	KLHL1	1.00000	0
897	chr13	74542000	74543000	0.000	0.040	KLF12	1.00000	0
898	chr13	75983000	75984000	0.000	0.040	TBC1D4	1.00000	0
899	chr13	75984000	75985000	0.000	0.160	TBC1D4	0.10986	0
900	chr13	83450000	83451000	0.000	0.000	SLITRK1	1.00000	0
901	chr13	84641000	84642000	0.040	0.000	SLITRK1	1.00000	0
902	chr13	87793000	87794000	0.040	0.000	SLITRK5	1.00000	0
903	chr13	91480000	91481000	0.000	0.000	GPC5	1.00000	0
904	chr13	106081000	106082000	0.040	0.000	DAOA	1.00000	0
905	chr13	114786000	114787000	0.040	0.000	RASA3	1.00000	0
906	chr13	114916000	114917000	0.000	0.000	RASA3	1.00000	0
907	chr14	22948000	22949000	0.040	0.000	TRAJ56	1.00000	0
908	chr14	22949000	22950000	0.040	0.000	TRAJ56	1.00000	0
909	chr14	22950000	22951000	0.040	0.000	TRAJ54	1.00000	0
910	chr14	22977000	22978000	0.000	0.040	TRAJ53	1.00000	0
911	chr14	27286000	27287000	0.000	0.000	NOVA1	1.00000	0
912	chr14	28645000	28646000	0.000	0.000	FOXG1	1.00000	0
913	chr14	49407000	49408000	0.000	0.000	RPS29	1.00000	0
914	chr14	50864000	50865000	0.000	0.000	CDKL1	1.00000	0
915	chr14	54812000	54813000	0.000	0.000	CDKN3	1.00000	0
916	chr14	55348000	55349000	0.040	0.000	GCH1	1.00000	0
917	chr14	59827000	59828000	0.000	0.040	DAAM1	1.00000	0
918	chr14	63143000	63144000	0.000	0.040	KCNH5	1.00000	0
919	chr14	64194000	64195000	0.000	0.040	SGPP1	1.00000	0
920	chr14	69258000	69259000	0.240	0.200	ZFP36L1	1.00000	1
921	chr14	69259000	69260000	0.360	0.240	ZFP36L1	0.53803	1
922	chr14	78418000	78419000	0.000	0.040	ADCK1	1.00000	0
923	chr14	81685000	81686000	0.000	0.040	GTF2A1	1.00000	0
924	chr14	84420000	84421000	0.040	0.000	FLRT2	1.00000	0

925	chr14	91883000	91884000	0.040	0.000	CCDC88C	1.00000	0
926	chr14	94941000	94942000	0.000	0.120	SERPINA9	0.23469	1
927	chr14	94942000	94943000	0.040	0.200	SERPINA9	0.18946	1
928	chr14	96179000	96180000	0.160	0.120	TCL1A	1.00000	1
929	chr14	96180000	96181000	0.080	0.160	TCL1A	0.66710	1
930	chr14	101597000	101598000	0.000	0.000	AL117190.3	1.00000	0
931	chr14	102285000	102286000	0.040	0.000	PPP2R5C	1.00000	0
932	chr14	105954000	105955000	0.040	0.040	CRIP1	1.00000	0
933	chr14	106031000	106032000	0.040	0.000	IGHA2	1.00000	0
934	chr14	106042000	106043000	0.080	0.200	IGHA2	0.41743	0
935	chr14	106048000	106049000	0.040	0.040	IGHA2	1.00000	0
936	chr14	106054000	106055000	0.040	0.040	IGHA2	1.00000	0
937	chr14	106055000	106056000	0.080	0.240	IGHA2	0.24672	0
938	chr14	106056000	106057000	0.040	0.200	IGHA2	0.18946	0
939	chr14	106057000	106058000	0.000	0.080	IGHA2	0.48980	0
940	chr14	106058000	106059000	0.000	0.080	IGHA2	0.48980	0
941	chr14	106066000	106067000	0.000	0.120	IGHE	0.23469	0
942	chr14	106067000	106068000	0.000	0.120	IGHE	0.23469	0
943	chr14	106068000	106069000	0.040	0.120	IGHE	0.60921	0
944	chr14	106069000	106070000	0.040	0.200	IGHE	0.18946	0
945	chr14	106070000	106071000	0.000	0.160	IGHE	0.10986	0
946	chr14	106071000	106072000	0.000	0.160	IGHE	0.10986	0
947	chr14	106072000	106073000	0.000	0.120	IGHE	0.23469	0
948	chr14	106082000	106083000	0.000	0.000	IGHG4	1.00000	0
949	chr14	106092000	106093000	0.040	0.000	IGHG4	1.00000	0
950	chr14	106094000	106095000	0.160	0.200	IGHG4	1.00000	0
951	chr14	106095000	106096000	0.080	0.160	IGHG4	0.66710	0
952	chr14	106110000	106111000	0.080	0.040	IGHG2	1.00000	0
953	chr14	106111000	106112000	0.000	0.040	IGHG2	1.00000	0
954	chr14	106112000	106113000	0.280	0.200	IGHG2	0.74164	0
955	chr14	106113000	106114000	0.240	0.320	IGHG2	0.75361	0
956	chr14	106114000	106115000	0.320	0.200	IGHG2	0.52019	0
957	chr14	106146000	106147000	0.000	0.000	IGHA1	1.00000	0
958	chr14	106151000	106152000	0.040	0.000	IGHA1	1.00000	0
959	chr14	106152000	106153000	0.040	0.000	IGHA1	1.00000	0
960	chr14	106161000	106162000	0.000	0.040	IGHA1	1.00000	0

961	chr14	106173000	106174000	0.040	0.040	IGHA1	1.00000	0	
962	chr14	106174000	106175000	0.040	0.000	IGHA1	1.00000	0	
963	chr14	106175000	106176000	0.040	0.000	IGHA1	1.00000	0	
964	chr14	106176000	106177000	0.080	0.040	IGHA1	1.00000	0	
965	chr14	106177000	106178000	0.000	0.000	IGHA1	1.00000	0	
966	chr14	106178000	106179000	0.120	0.000	IGHA1	0.23469	0	
967	chr14	106208000	106209000	0.040	0.040	IGHG1	1.00000	0	
968	chr14	106209000	106210000	0.160	0.080	IGHG1	0.66710	0	
969	chr14	106210000	106211000	0.160	0.120	IGHG1	1.00000	0	
970	chr14	106211000	106212000	0.440	0.120	IGHG1	0.02548	0	
971	chr14	106212000	106213000	0.520	0.120	IGHG1	0.00544	0	
972	chr14	106213000	106214000	0.520	0.120	IGHG1	0.00544	0	
973	chr14	106214000	106215000	0.240	0.000	IGHG1	0.02229	0	
974	chr14	106237000	106238000	0.080	0.040	IGHG3	1.00000	0	
975	chr14	106238000	106239000	0.320	0.120	IGHG3	0.17062	0	
976	chr14	106239000	106240000	0.440	0.040	IGHG3	0.00192	0	
977	chr14	106240000	106241000	0.480	0.080	IGHG3	0.00361	0	
978	chr14	106241000	106242000	0.320	0.040	IGHG3	0.02322	0	
979	chr14	106242000	106243000	0.040	0.000	IGHG3	1.00000	0	
980	chr14	106321000	106322000	0.040	0.000	IGHM	1.00000	0	
981	chr14	106322000	106323000	0.240	0.040	IGHM	0.09828	0	
982	chr14	106323000	106324000	0.400	0.160	IGHM	0.11366	0	
983	chr14	106324000	106325000	0.320	0.120	IGHM	0.17062	0	
984	chr14	106325000	106326000	0.160	0.320	IGHM	0.32089	0	
985	chr14	106326000	106327000	0.920	0.920	IGHJ6	1.00000	0	
986	chr14	106327000	106328000	0.800	0.760	IGHJ6	1.00000	0	
987	chr14	106328000	106329000	0.680	0.800	IGHJ6	0.52019	0	
988	chr14	106329000	106330000	0.880	0.920	IGHJ6	1.00000	0	
989	chr14	106330000	106331000	0.720	0.520	IGHJ3;IGHJ4;IGHJ5;	0.24363	0	
990	chr14	106331000	106332000	0.120	0.080	IGHD7-27;IGHJ1;IGHJ2;	1.00000	0	
991	chr14	106338000	106339000	0.040	0.000	IGHD7-27	1.00000	0	
992	chr14	106350000	106351000	0.040	0.000	IGHD4-23	1.00000	0	
993	chr14	106352000	106353000	0.000	0.040	IGHD3-22	1.00000	0	

994	chr14	106353000	106354000	0.000	0.000	IGHD2-21	1.00000	0
995	chr14	106354000	106355000	0.000	0.040	IGHD2-21	1.00000	0
996	chr14	106355000	106356000	0.000	0.040	IGHD2-21	1.00000	0
997	chr14	106357000	106358000	0.040	0.080	IGHD1-20;IGHD6-19;	1.00000	0
998	chr14	106358000	106359000	0.000	0.040	IGHD5-18	1.00000	0
999	chr14	106362000	106363000	0.000	0.000	IGHD3-16	1.00000	0
1000	chr14	106364000	106365000	0.040	0.000	IGHD2-15	1.00000	0
1001	chr14	106367000	106368000	0.040	0.000	IGHD6-13	1.00000	0
1002	chr14	106370000	106371000	0.080	0.000	IGHD3-10;IGHD3-9;	0.48980	0
1003	chr14	106371000	106372000	0.040	0.000	IGHD3-9	1.00000	0
1004	chr14	106372000	106373000	0.040	0.000	IGHD2-8	1.00000	0
1005	chr14	106375000	106376000	0.000	0.000	IGHD1-7	1.00000	0
1006	chr14	106376000	106377000	0.000	0.040	IGHD6-6	1.00000	0
1007	chr14	106380000	106381000	0.000	0.040	IGHD3-3	1.00000	0
1008	chr14	106381000	106382000	0.000	0.040	IGHD2-2	1.00000	0
1009	chr14	106382000	106383000	0.040	0.120	IGHD2-2	0.60921	0
1010	chr14	106383000	106384000	0.080	0.040	IGHD2-2	1.00000	0
1011	chr14	106384000	106385000	0.040	0.040	IGHD1-1	1.00000	0
1012	chr14	106385000	106386000	0.080	0.040	IGHD1-1	1.00000	0
1013	chr14	106387000	106388000	0.040	0.080	KIAA0125	1.00000	0
1014	chr14	106405000	106406000	0.000	0.040	IGHV6-1	1.00000	0
1015	chr14	106406000	106407000	0.000	0.040	IGHV6-1	1.00000	0
1016	chr14	106419000	106420000	0.000	0.080	IGHV6-1	0.48980	0
1017	chr14	106452000	106453000	0.040	0.000	IGHV1-2	1.00000	0
1018	chr14	106453000	106454000	0.080	0.000	IGHV1-2	0.48980	0
1019	chr14	106454000	106455000	0.040	0.000	IGHV1-2	1.00000	0
1020	chr14	106494000	106495000	0.000	0.040	IGHV2-5	1.00000	0
1021	chr14	106518000	106519000	0.000	0.080	IGHV3-7	0.48980	0
1022	chr14	106519000	106520000	0.000	0.080	IGHV3-7	0.48980	0
1023	chr14	106539000	106540000	0.000	0.040	IGHV1-8	1.00000	0
1024	chr14	106552000	106553000	0.000	0.000	IGHV3-9	1.00000	0
1025	chr14	106573000	106574000	0.040	0.000	IGHV3-11	1.00000	0
1026	chr14	106574000	106575000	0.040	0.000	IGHV3-11	1.00000	0
1027	chr14	106578000	106579000	0.040	0.000	IGHV3-11	1.00000	0

1028	chr14	106579000	106580000	0.040	0.000	IGHV3-11	1.00000	0
1029	chr14	106610000	106611000	0.000	0.000	IGHV3-15	1.00000	0
1030	chr14	106641000	106642000	0.040	0.040	IGHV1-18	1.00000	0
1031	chr14	106642000	106643000	0.040	0.000	IGHV1-18	1.00000	0
1032	chr14	106691000	106692000	0.000	0.000	IGHV3-21	1.00000	0
1033	chr14	106692000	106693000	0.000	0.040	IGHV3-21	1.00000	0
1034	chr14	106725000	106726000	0.120	0.160	IGHV3-23	1.00000	0
1035	chr14	106726000	106727000	0.040	0.080	IGHV3-23	1.00000	0
1036	chr14	106733000	106734000	0.000	0.080	IGHV1-24	0.48980	0
1037	chr14	106757000	106758000	0.000	0.040	IGHV2-26	1.00000	0
1038	chr14	106758000	106759000	0.000	0.040	IGHV2-26	1.00000	0
1039	chr14	106791000	106792000	0.040	0.040	IGHV3-30	1.00000	0
1040	chr14	106804000	106805000	0.040	0.040	IGHV4-31	1.00000	0
1041	chr14	106805000	106806000	0.040	0.040	IGHV4-31	1.00000	0
1042	chr14	106806000	106807000	0.000	0.000	IGHV4-31	1.00000	0
1043	chr14	106815000	106816000	0.000	0.040	IGHV3-33	1.00000	0
1044	chr14	106816000	106817000	0.000	0.160	IGHV3-33	0.10986	0
1045	chr14	106817000	106818000	0.000	0.080	IGHV3-33	0.48980	0
1046	chr14	106829000	106830000	0.160	0.080	IGHV4-34	0.66710	0
1047	chr14	106830000	106831000	0.160	0.000	IGHV4-34	0.10986	0
1048	chr14	106877000	106878000	0.040	0.080	IGHV4-39	1.00000	0
1049	chr14	106878000	106879000	0.000	0.080	IGHV4-39	0.48980	0
1050	chr14	106967000	106968000	0.040	0.040	IGHV1-46	1.00000	0
1051	chr14	106994000	106995000	0.000	0.120	IGHV3-48	0.23469	0
1052	chr14	106995000	106996000	0.000	0.000	IGHV3-48	1.00000	0
1053	chr14	107034000	107035000	0.040	0.000	IGHV5-51	1.00000	0
1054	chr14	107035000	107036000	0.080	0.000	IGHV5-51	0.48980	0
1055	chr14	107048000	107049000	0.000	0.000	IGHV3-53	1.00000	0
1056	chr14	107049000	107050000	0.000	0.000	IGHV3-53	1.00000	0
1057	chr14	107083000	107084000	0.040	0.040	IGHV4-59	1.00000	0
1058	chr14	107084000	107085000	0.000	0.040	IGHV4-59	1.00000	0
1059	chr14	107095000	107096000	0.040	0.000	IGHV4-61	1.00000	0
1060	chr14	107113000	107114000	0.080	0.000	IGHV3-64	0.48980	0
1061	chr14	107114000	107115000	0.080	0.000	IGHV3-64	0.48980	0
1062	chr14	107169000	107170000	0.200	0.240	IGHV1-69	1.00000	0
1063	chr14	107170000	107171000	0.360	0.280	IGHV1-69	0.76241	0

1064	chr14	107176000	107177000	0.200	0.200	IGHV2-70	1.00000	0
1065	chr14	107177000	107178000	0.080	0.040	IGHV2-70	1.00000	0
1066	chr14	107178000	107179000	0.200	0.520	IGHV2-70	0.03776	0
1067	chr14	107179000	107180000	0.240	0.360	IGHV2-70	0.53803	0
1068	chr14	107183000	107184000	0.000	0.000	IGHV2-70	1.00000	0
1069	chr14	107199000	107200000	0.000	0.080	IGHV3-72	0.48980	0
1070	chr14	107218000	107219000	0.000	0.080	IGHV3-74	0.48980	0
1071	chr14	107219000	107220000	0.000	0.160	IGHV3-74	0.10986	0
1072	chr14	107221000	107222000	0.000	0.080	IGHV3-74	0.48980	0
1073	chr14	107232000	107233000	0.000	0.000	IGHV3-74	1.00000	0
1074	chr14	107253000	107254000	0.000	0.000	IGHV7-81	1.00000	0
1075	chr14	107258000	107259000	0.000	0.040	IGHV7-81	1.00000	0
1076	chr14	107259000	107260000	0.160	0.200	IGHV7-81	1.00000	0
1077	chr15	45003000	45004000	0.040	0.040	B2M	1.00000	0
1078	chr15	45007000	45008000	0.000	0.000	B2M	1.00000	0
1079	chr15	45814000	45815000	0.000	0.040	SLC30A4	1.00000	0
1080	chr15	59664000	59665000	0.000	0.080	MYO1E	0.48980	0
1081	chr15	65588000	65589000	0.040	0.000	PARP16	1.00000	0
1082	chr15	78332000	78333000	0.000	0.000	TBC1D2B	1.00000	0
1083	chr15	83227000	83228000	0.000	0.040	CPEB1	1.00000	0
1084	chr15	86226000	86227000	0.040	0.040	AKAP13	1.00000	0
1085	chr15	86233000	86234000	0.040	0.000	AKAP13	1.00000	0
1086	chr15	86245000	86246000	0.080	0.120	AKAP13	1.00000	0
1087	chr16	368000	369000	0.000	0.040	AXIN1	1.00000	0
1088	chr16	3788000	3789000	0.040	0.000	CREBBP	1.00000	0
1089	chr16	10971000	10972000	0.080	0.120	CIITA	1.00000	1
1090	chr16	10972000	10973000	0.120	0.320	CIITA	0.17062	1
1091	chr16	10973000	10974000	0.120	0.240	CIITA	0.46349	1
1092	chr16	10974000	10975000	0.080	0.120	CIITA	1.00000	1
1093	chr16	11348000	11349000	0.080	0.200	SOCS1	0.41743	1
1094	chr16	11349000	11350000	0.120	0.240	SOCS1	0.46349	1
1095	chr16	21167000	21168000	0.040	0.000	DNAH3	1.00000	0
1096	chr16	27325000	27326000	0.000	0.040	CTD-3203P2.2	1.00000	0
1097	chr16	27326000	27327000	0.080	0.080	CTD-3203P2.2	1.00000	0
1098	chr16	27327000	27328000	0.000	0.000	IL4R	1.00000	0
1099	chr16	27414000	27415000	0.040	0.000	IL21R	1.00000	0

1100	chr16	29248000	29249000	0.000	0.000	61E3.4	1.00000	0
1101	chr16	31910000	31911000	0.040	0.000	ZNF267	1.00000	0
1102	chr16	46821000	46822000	0.000	0.040	C16orf87	1.00000	0
1103	chr16	50985000	50986000	0.040	0.000	CYLD	1.00000	0
1104	chr16	64351000	64352000	0.000	0.040	CDH11	1.00000	0
1105	chr16	78398000	78399000	0.000	0.000	WWOX	1.00000	0
1106	chr16	78615000	78616000	0.040	0.000	WWOX	1.00000	0
1107	chr16	78753000	78754000	0.000	0.040	WWOX	1.00000	0
1108	chr16	78811000	78812000	0.000	0.040	WWOX	1.00000	0
1109	chr16	79988000	79989000	0.000	0.040	MAF	1.00000	0
1110	chr16	81836000	81837000	0.000	0.000	PLCG2	1.00000	0
1111	chr16	85932000	85933000	0.040	0.040	IRF8	1.00000	1
1112	chr16	85933000	85934000	0.080	0.240	IRF8	0.24672	1
1113	chr16	85934000	85935000	0.040	0.000	IRF8	1.00000	1
1114	chr16	85936000	85937000	0.000	0.000	IRF8	1.00000	1
1115	chr16	88441000	88442000	0.040	0.000	ZNF469	1.00000	0
1116	chr17	3598000	3599000	0.040	0.040	P2RX5;P2RX5-TAX1BP3P2RX5;	1.00000	0
1117	chr17	17286000	17287000	0.080	0.000	SMCR9	0.48980	0
1118	chr17	21194000	21195000	0.000	0.040	MAP2K3	1.00000	0
1119	chr17	29646000	29647000	0.000	0.000	EVI2A	1.00000	0
1120	chr17	38020000	38021000	0.000	0.040	IKZF3	1.00000	0
1121	chr17	43662000	43663000	0.040	0.000	PLEKHM1	1.00000	0
1122	chr17	56408000	56409000	0.120	0.040	BZRAP1	0.60921	0
1123	chr17	56409000	56410000	0.360	0.200	BZRAP1	0.34513	0
1124	chr17	57916000	57917000	0.040	0.080	VMP1	1.00000	1
1125	chr17	57917000	57918000	0.040	0.080	VMP1	1.00000	1
1126	chr17	62007000	62008000	0.040	0.000	CD79B	1.00000	0
1127	chr17	62008000	62009000	0.040	0.000	CD79B	1.00000	0
1128	chr17	63067000	63068000	0.040	0.000	GNA13	1.00000	0
1129	chr17	65676000	65677000	0.040	0.000	PITPNC1	1.00000	0
1130	chr17	69365000	69366000	0.000	0.040	AC007461.1	1.00000	0
1131	chr17	70083000	70084000	0.000	0.000	SOX9	1.00000	0
1132	chr17	74733000	74734000	0.000	0.000	SRSF2	1.00000	0
1133	chr17	75447000	75448000	0.080	0.000	9-Sep-19	0.48980	0

1134	chr17	75448000	75449000	0.040	0.000	9-Sep-19	1.00000	0
1135	chr17	76775000	76776000	0.000	0.000	CYTH1	1.00000	0
1136	chr17	80928000	80929000	0.000	0.000	B3GNTL1	1.00000	0
1137	chr17	80976000	80977000	0.000	0.040	B3GNTL1	1.00000	0
1138	chr18	2709000	2710000	0.000	0.000	SMCHD1	1.00000	0
1139	chr18	3600000	3601000	0.040	0.000	DLGAP1	1.00000	0
1140	chr18	12062000	12063000	0.000	0.000	ANKRD62	1.00000	0
1141	chr18	27771000	27772000	0.040	0.000	DSC3	1.00000	0
1142	chr18	28066000	28067000	0.000	0.040	DSC3	1.00000	0
1143	chr18	30349000	30350000	0.000	0.000	AC012123.1;KLHL14;	1.00000	0
1144	chr18	36806000	36807000	0.040	0.000	CELF4	1.00000	0
1145	chr18	37751000	37752000	0.000	0.040	PIK3C3	1.00000	0
1146	chr18	38672000	38673000	0.000	0.040	PIK3C3	1.00000	0
1147	chr18	42168000	42169000	0.000	0.000	SETBP1	1.00000	0
1148	chr18	51952000	51953000	0.040	0.000	C18orf54	1.00000	0
1149	chr18	52447000	52448000	0.000	0.080	RAB27B	0.48980	0
1150	chr18	52988000	52989000	0.040	0.000	TCF4	1.00000	0
1151	chr18	54653000	54654000	0.000	0.000	WDR7	1.00000	0
1152	chr18	60794000	60795000	0.000	0.080	BCL2	0.48980	1
1153	chr18	60805000	60806000	0.000	0.000	BCL2	1.00000	1
1154	chr18	60806000	60807000	0.000	0.120	BCL2	0.23469	1
1155	chr18	60809000	60810000	0.000	0.080	BCL2	0.48980	1
1156	chr18	60821000	60822000	0.000	0.040	BCL2	1.00000	1
1157	chr18	60825000	60826000	0.000	0.080	BCL2	0.48980	1
1158	chr18	60826000	60827000	0.000	0.040	BCL2	1.00000	1
1159	chr18	60828000	60829000	0.000	0.000	BCL2	1.00000	1
1160	chr18	60873000	60874000	0.000	0.040	BCL2	1.00000	1
1161	chr18	60875000	60876000	0.000	0.000	BCL2	1.00000	1
1162	chr18	60876000	60877000	0.000	0.040	BCL2	1.00000	1
1163	chr18	60983000	60984000	0.000	0.040	BCL2	1.00000	1
1164	chr18	60984000	60985000	0.000	0.240	BCL2	0.02229	1
1165	chr18	60985000	60986000	0.040	0.320	BCL2	0.02322	1
1166	chr18	60986000	60987000	0.080	0.320	BCL2	0.07375	1
1167	chr18	60987000	60988000	0.080	0.320	BCL2	0.07375	1
1168	chr18	60988000	60989000	0.080	0.280	BCL2	0.13833	1

1169	chr18	61810000	61811000	0.040	0.000	SERPINB8	1.00000	0
1170	chr18	63080000	63081000	0.000	0.000	CDH7	1.00000	0
1171	chr18	63791000	63792000	0.000	0.000	CDH7	1.00000	0
1172	chr18	63875000	63876000	0.040	0.000	CDH19	1.00000	0
1173	chr18	64643000	64644000	0.000	0.000	CDH19	1.00000	0
1174	chr18	65863000	65864000	0.000	0.000	TMX3	1.00000	0
1175	chr18	66328000	66329000	0.040	0.000	TMX3	1.00000	0
1176	chr18	70462000	70463000	0.000	0.040	NETO1	1.00000	0
1177	chr18	73767000	73768000	0.040	0.000	ZNF516	1.00000	0
1178	chr18	76515000	76516000	0.040	0.000	SALL3	1.00000	0
1179	chr18	76724000	76725000	0.040	0.000	SALL3	1.00000	0
1180	chr18	76725000	76726000	0.040	0.000	SALL3	1.00000	0
1181	chr19	1612000	1613000	0.000	0.040	TCF3	1.00000	0
1182	chr19	2476000	2477000	0.040	0.040	GADD45B	1.00000	1
1183	chr19	10304000	10305000	0.040	0.080	DNMT1	1.00000	0
1184	chr19	10305000	10306000	0.000	0.080	DNMT1	0.48980	0
1185	chr19	10335000	10336000	0.000	0.040	S1PR2	1.00000	1
1186	chr19	10340000	10341000	0.080	0.160	S1PR2	0.66710	1
1187	chr19	10341000	10342000	0.120	0.280	S1PR2	0.28902	1
1188	chr19	16030000	16031000	0.000	0.000	CYP4F11	1.00000	0
1189	chr19	16436000	16437000	0.040	0.000	KLF2	1.00000	1
1190	chr19	20889000	20890000	0.000	0.040	ZNF626	1.00000	0
1191	chr19	21073000	21074000	0.040	0.000	ZNF85	1.00000	0
1192	chr19	21092000	21093000	0.000	0.040	ZNF85	1.00000	0
1193	chr19	23841000	23842000	0.040	0.000	ZNF675	1.00000	0
1194	chr19	29256000	29257000	0.040	0.000	UQCRFS1	1.00000	0
1195	chr19	44183000	44184000	0.040	0.000	PLAUR	1.00000	0
1196	chr19	50399000	50400000	0.040	0.040	IL4I1	1.00000	0
1197	chr19	53419000	53420000	0.000	0.000	ZNF321P:ZNF816:ZNF816-ZNF321PZNF321P-ZNF321P:	1.00000	0
1198	chr20	15470000	15471000	0.000	0.040	MACROD2	1.00000	0
1199	chr20	23359000	23360000	0.000	0.000	NAPB	1.00000	0
1200	chr20	23912000	23913000	0.000	0.000	CST5	1.00000	0

1201	chr20	46131000	46132000	0.040	0.120	NCOA3	0.60921	1
1202	chr20	49127000	49128000	0.000	0.000	PTPN1	1.00000	0
1203	chr20	49648000	49649000	0.040	0.000	KCNG1	1.00000	0
1204	chr20	61607000	61608000	0.000	0.000	SLC17A9	1.00000	0
1205	chr21	21597000	21598000	0.000	0.000	NCAM2	1.00000	0
1206	chr21	23458000	23459000	0.000	0.040	NCAM2	1.00000	0
1207	chr21	24998000	24999000	0.000	0.040	MRPL39	1.00000	0
1208	chr21	26935000	26936000	0.000	0.080	MRPL39	0.48980	0
1209	chr21	35779000	35780000	0.000	0.000	SMIM11	1.00000	0
1210	chr21	38779000	38780000	0.000	0.000	DYRK1A	1.00000	0
1211	chr21	43254000	43255000	0.000	0.040	PRDM15	1.00000	0
1212	chr21	44612000	44613000	0.000	0.000	CRYAA	1.00000	0
1213	chr21	45381000	45382000	0.040	0.000	AGPAT3	1.00000	0
1214	chr21	46058000	46059000	0.000	0.000	KRTAP10-10	1.00000	0
1215	chr22	19050000	19051000	0.000	0.000	DGCR2	1.00000	0
1216	chr22	20212000	20213000	0.040	0.000	RTN4R	1.00000	0
1217	chr22	20708000	20709000	0.040	0.040	FAM230A	1.00000	0
1218	chr22	21994000	21995000	0.000	0.000	SDF2L1	1.00000	0
1219	chr22	22379000	22380000	0.040	0.040	IGLV4-69	1.00000	0
1220	chr22	22380000	22381000	0.040	0.080	IGLV4-69	1.00000	0
1221	chr22	22381000	22382000	0.040	0.040	IGLV4-69	1.00000	0
1222	chr22	22385000	22386000	0.040	0.080	IGLV4-69	1.00000	0
1223	chr22	22452000	22453000	0.000	0.040	IGLV8-61	1.00000	0
1224	chr22	22453000	22454000	0.000	0.040	IGLV8-61	1.00000	0
1225	chr22	22516000	22517000	0.000	0.160	IGLV4-60	0.10986	0
1226	chr22	22517000	22518000	0.000	0.080	IGLV4-60	0.48980	0
1227	chr22	22550000	22551000	0.160	0.000	IGLV6-57	0.10986	0
1228	chr22	22569000	22570000	0.040	0.000	IGLV10-54	1.00000	0
1229	chr22	22676000	22677000	0.040	0.000	IGLV1-51	1.00000	0
1230	chr22	22677000	22678000	0.040	0.000	IGLV1-51	1.00000	0
1231	chr22	22707000	22708000	0.040	0.080	IGLV5-48	1.00000	0
1232	chr22	22712000	22713000	0.160	0.040	IGLV1-47	0.34868	0
1233	chr22	22723000	22724000	0.000	0.000	IGLV7-46	1.00000	0
1234	chr22	22724000	22725000	0.080	0.040	IGLV7-46	1.00000	0
1235	chr22	22730000	22731000	0.040	0.040	IGLV5-45	1.00000	0
1236	chr22	22731000	22732000	0.000	0.000	IGLV5-45	1.00000	0

1237	chr22	22735000	22736000	0.080	0.120	IGLV1-44	1.00000	0
1238	chr22	22749000	22750000	0.120	0.040	IGLV7-43	0.60921	0
1239	chr22	22758000	22759000	0.080	0.040	IGLV1-40	1.00000	0
1240	chr22	22759000	22760000	0.080	0.080	IGLV1-40	1.00000	0
1241	chr22	22764000	22765000	0.120	0.080	IGLV1-40	1.00000	0
1242	chr22	23028000	23029000	0.000	0.040	IGLV3-25	1.00000	0
1243	chr22	23029000	23030000	0.040	0.120	IGLV3-25	0.60921	0
1244	chr22	23035000	23036000	0.000	0.040	IGLV2-23	1.00000	0
1245	chr22	23039000	23040000	0.000	0.000	IGLV2-23	1.00000	0
1246	chr22	23040000	23041000	0.120	0.040	IGLV2-23	0.60921	0
1247	chr22	23041000	23042000	0.040	0.000	IGLV2-23	1.00000	0
1248	chr22	23055000	23056000	0.040	0.000	IGLV3-21	1.00000	0
1249	chr22	23063000	23064000	0.040	0.000	IGLV3-19	1.00000	0
1250	chr22	23090000	23091000	0.120	0.000	IGLV3-16	0.23469	0
1251	chr22	23100000	23101000	0.040	0.000	IGLV2-14	1.00000	0
1252	chr22	23101000	23102000	0.120	0.040	IGLV2-14	0.60921	0
1253	chr22	23114000	23115000	0.000	0.000	IGLV3-12	1.00000	0
1254	chr22	23134000	23135000	0.000	0.000	IGLV2-11	1.00000	0
1255	chr22	23154000	23155000	0.120	0.000	IGLV3-10	0.23469	0
1256	chr22	23161000	23162000	0.000	0.000	IGLV3-9	1.00000	0
1257	chr22	23162000	23163000	0.000	0.000	IGLV3-9	1.00000	0
1258	chr22	23165000	23166000	0.000	0.000	IGLV2-8	1.00000	0
1259	chr22	23192000	23193000	0.080	0.080	IGLV4-3	1.00000	0
1260	chr22	23197000	23198000	0.040	0.000	IGLV4-3	1.00000	0
1261	chr22	23198000	23199000	0.160	0.040	IGLV4-3	0.34868	0
1262	chr22	23199000	23200000	0.200	0.200	IGLV4-3	1.00000	0
1263	chr22	23203000	23204000	0.000	0.000	IGLV4-3	1.00000	0
1264	chr22	23204000	23205000	0.080	0.000	IGLV4-3	0.48980	0
1265	chr22	23205000	23206000	0.000	0.000	IGLV4-3	1.00000	0
1266	chr22	23207000	23208000	0.000	0.040	IGLV4-3	1.00000	0
1267	chr22	23209000	23210000	0.000	0.040	IGLV4-3	1.00000	0
1268	chr22	23213000	23214000	0.120	0.040	IGLV4-3	0.60921	0
1269	chr22	23214000	23215000	0.040	0.040	IGLV4-3	1.00000	0
1270	chr22	23219000	23220000	0.080	0.000	IGLV3-1	0.48980	0
1271	chr22	23220000	23221000	0.080	0.000	IGLV3-1	0.48980	0
1272	chr22	23222000	23223000	0.040	0.120	IGLV3-1	0.60921	0

1273	chr22	23223000	23224000	0.320	0.520	IGLV3-1	0.25159	0
1274	chr22	23224000	23225000	0.080	0.080	IGLV3-1	1.00000	0
1275	chr22	23226000	23227000	0.120	0.000	IGLV3-1	0.23469	0
1276	chr22	23227000	23228000	0.200	0.360	IGLL5	0.34513	0
1277	chr22	23228000	23229000	0.240	0.200	IGLL5	1.00000	0
1278	chr22	23229000	23230000	0.040	0.160	IGLL5	0.34868	0
1279	chr22	23230000	23231000	0.440	0.600	IGLL5	0.39610	0
1280	chr22	23231000	23232000	0.480	0.440	IGLL5	1.00000	0
1281	chr22	23232000	23233000	0.320	0.240	IGLL5	0.75361	0
1282	chr22	23233000	23234000	0.200	0.040	IGLJ1	0.18946	0
1283	chr22	23234000	23235000	0.200	0.080	IGLJ1	0.41743	0
1284	chr22	23235000	23236000	0.320	0.080	IGLJ1;IGLL5;	0.07375	0
1285	chr22	23236000	23237000	0.240	0.200	IGLJ1;IGLL5;	1.00000	0
1286	chr22	23237000	23238000	0.040	0.160	IGLC1;IGLL5;	0.34868	0
1287	chr22	23241000	23242000	0.040	0.040	IGLJ2	1.00000	0
1288	chr22	23242000	23243000	0.120	0.040	IGLC2	0.60921	0
1289	chr22	23243000	23244000	0.080	0.040	IGLC2	1.00000	0
1290	chr22	23244000	23245000	0.000	0.040	IGLC2	1.00000	0
1291	chr22	23247000	23248000	0.280	0.160	IGLJ3	0.49620	0
1292	chr22	23248000	23249000	0.040	0.000	IGLC3	1.00000	0
1293	chr22	23249000	23250000	0.040	0.000	IGLC3	1.00000	0
1294	chr22	23260000	23261000	0.000	0.000	IGLJ6	1.00000	0
1295	chr22	23261000	23262000	0.000	0.000	IGLJ6	1.00000	0
1296	chr22	23263000	23264000	0.000	0.040	IGLJ7	1.00000	0
1297	chr22	23264000	23265000	0.000	0.040	IGLC7	1.00000	0
1298	chr22	23273000	23274000	0.000	0.040	IGLC7	1.00000	0
1299	chr22	23277000	23278000	0.040	0.040	IGLC7	1.00000	0
1300	chr22	23278000	23279000	0.000	0.120	IGLC7	0.23469	0
1301	chr22	23281000	23282000	0.040	0.000	IGLC7	1.00000	0
1302	chr22	23282000	23283000	0.080	0.160	IGLC7	0.66710	0
1303	chr22	23284000	23285000	0.000	0.000	IGLC7	1.00000	0
1304	chr22	23523000	23524000	0.000	0.080	BCR	0.48980	0
1305	chr22	23524000	23525000	0.000	0.000	BCR	1.00000	0
1306	chr22	27236000	27237000	0.000	0.000	CRYBA4	1.00000	0
1307	chr22	29195000	29196000	0.040	0.040	XBP1	1.00000	0
1308	chr22	29196000	29197000	0.040	0.040	XBP1	1.00000	0

1309	chr22	31826000	31827000	0.040	0.000	DRG1	1.00000	0
1310	chr22	32982000	32983000	0.000	0.040	SYN3	1.00000	0
1311	chr22	39852000	39853000	0.040	0.000	TAB1	1.00000	0
1312	chr22	39854000	39855000	0.000	0.000	TAB1	1.00000	0
1313	chr22	43360000	43361000	0.000	0.000	PACSIN2	1.00000	0
1314	chr22	47186000	47187000	0.000	0.000	TBC1D22A	1.00000	0
1315	chr22	47738000	47739000	0.000	0.000	LL22NC03-75H12.2	1.00000	0
1316	chr22	50336000	50337000	0.000	0.000	CRELD2	1.00000	0
1317	chrX	228000	229000	0.000	0.000	GTPBP6	1.00000	0
1318	chrX	1514000	1515000	0.000	0.040	SLC25A6	1.00000	0
1319	chrX	1611000	1612000	0.040	0.040	P2RY8	1.00000	1
1320	chrX	12993000	12994000	0.320	0.280	TMSB4X	1.00000	1
1321	chrX	12994000	12995000	0.200	0.160	TMSB4X	1.00000	1
1322	chrX	13419000	13420000	0.000	0.040	ATXN3L	1.00000	0
1323	chrX	27031000	27032000	0.080	0.040	DCAF8L2	1.00000	0
1324	chrX	32315000	32316000	0.000	0.000	DMD	1.00000	1
1325	chrX	32317000	32318000	0.000	0.000	DMD	1.00000	1
1326	chrX	33144000	33145000	0.000	0.000	DMD	1.00000	1
1327	chrX	33145000	33146000	0.000	0.040	DMD	1.00000	1
1328	chrX	33146000	33147000	0.080	0.120	DMD	1.00000	1
1329	chrX	41366000	41367000	0.040	0.000	CASK	1.00000	0
1330	chrX	42802000	42803000	0.080	0.120	MAOA	1.00000	0
1331	chrX	48775000	48776000	0.120	0.040	PIM2	0.60921	1
1332	chrX	48776000	48777000	0.080	0.000	PIM2	0.48980	1
1333	chrX	64071000	64072000	0.120	0.080	ZC4H2	1.00000	0
1334	chrX	67030000	67031000	0.000	0.000	AR	1.00000	0
1335	chrX	80238000	80259000	0.000	0.000	HMGN5	1.00000	0
1336	chrX	81172000	81173000	0.040	0.000	SH3BGRL	1.00000	0
1337	chrX	87742000	87743000	0.040	0.000	CPXCR1	1.00000	0
1338	chrX	87831000	87832000	0.000	0.000	CPXCR1	1.00000	0
1339	chrX	88263000	88264000	0.000	0.000	CPXCR1	1.00000	0
1340	chrX	88458000	88459000	0.040	0.000	CPXCR1	1.00000	0
1341	chrX	92647000	92648000	0.000	0.000	NAP1L3	1.00000	0
1342	chrX	93279000	93280000	0.040	0.000	FAM133A	1.00000	0
1343	chrX	94079000	94080000	0.040	0.000	FAM133A	1.00000	0

1344	chrX	104006000	104007000	0.040	0.000	IL1RAPL2	1.00000	0
1345	chrX	104269000	104270000	0.040	0.000	IL1RAPL2	1.00000	0
1346	chrX	106132000	106133000	0.000	0.000	RIPPLY1	1.00000	0
1347	chrX	113095000	113096000	0.000	0.040	HTR2C	1.00000	0
1348	chrX	115676000	115677000	0.040	0.000	CXorf61	1.00000	0
1349	chrX	124996000	124997000	0.000	0.000	DCAF12L2	1.00000	0
1350	chrX	125708000	125709000	0.000	0.000	DCAF12L1	1.00000	0
1351	chrX	128565000	128566000	0.040	0.040	SMARCA1	1.00000	0
1352	chrX	129643000	129644000	0.000	0.040	RBMX2	1.00000	0
1353	chrX	134903000	134904000	0.000	0.000	CT45A3;CT45A4;	1.00000	0
1354	chrX	140846000	140847000	0.040	0.000	SPANXD;SPANXE;	1.00000	0
1355	chrX	143750000	143751000	0.000	0.000	SPANXN1	1.00000	0
1356	chrX	145016000	145017000	0.040	0.000	TMEM257	1.00000	0

Table 3

#	Chromosome	Region Start	Region End	Closest Gene	Reason for Inclusion
1	chr1	2306311	2306832	MORN1	Genotyping
2	chr1	2334441	2334664	RER1	Genotyping
3	chr1	2334671	2335161	RER1	Genotyping
4	chr1	2488006	2488247	TNFRSF14	Phased Variants
5	chr1	2489111	2489330	TNFRSF14	Genotyping
6	chr1	2489726	2489973	TNFRSF14	Genotyping
7	chr1	2491206	2491455	TNFRSF14	Genotyping
8	chr1	2492036	2492175	TNFRSF14	Genotyping
9	chr1	2493051	2493333	TNFRSF14	Genotyping
10	chr1	2494241	2494376	TNFRSF14	Genotyping
11	chr1	2494556	2494745	TNFRSF14	Genotyping
12	chr1	3547350	3547715	WRAP73	Genotyping
13	chr1	3747620	3747798	CEP104	Genotyping
14	chr1	3800045	3800148	DFFB	Genotyping
15	chr1	3800155	3800363	DFFB	Genotyping
16	chr1	4472438	4472621	AJAP1	Genotyping
17	chr1	4476348	4476627	AJAP1	Genotyping
18	chr1	9784432	9784540	PIK3CD	Genotyping
19	chr1	23885407	23885541	ID3	Genotyping
20	chr1	23885582	23885938	ID3	Genotyping
21	chr1	27059146	27059321	ARID1A	Genotyping
22	chr1	27101071	27101294	ARID1A	Genotyping
23	chr1	27101401	27101613	ARID1A	Genotyping
24	chr1	27105466	27105671	ARID1A	Genotyping
25	chr1	27106311	27106523	ARID1A	Genotyping
26	chr1	27106711	27106920	ARID1A	Genotyping
27	chr1	29069531	29070185	YTHDF2	Genotyping
28	chr1	34404022	34404171	CSMD2	Phased Variants
29	chr1	35472492	35472739	ZMYM6	Genotyping
30	chr1	61553802	61554330	NFIA	Genotyping
31	chr1	72334891	72335045	NEGR1	Phased Variants
32	chr1	72335051	72335120	NEGR1	Phased Variants
33	chr1	85733207	85733640	BCL10	Phased Variants
34	chr1	85736272	85736619	BCL10	Genotyping
35	chr1	85741932	85742068	BCL10	Genotyping
36	chr1	86591437	86591909	COL24A1	Genotyping
37	chr1	107866871	107867579	NTNG1	Genotyping
38	chr1	109649126	109649304	C1orf194	Genotyping
39	chr1	109822181	109822805	PSRC1	Genotyping
40	chr1	110561141	110561757	AHCYL1	Genotyping
41	chr1	111441722	111442219	CD53	Genotyping
42	chr1	111715727	111715908	CEPT1	Genotyping

43	chr1	117078642	117078856	CD58	Genotyping
44	chr1	117086927	117087172	CD58	Genotyping
45	chr1	120457960	120459297	NOTCH2	Genotyping
46	chr1	160319283	160319532	NCSTN	Genotyping
47	chr1	181452914	181453131	CACNA1E	Genotyping
48	chr1	185833555	185833832	HMCN1	Genotyping
49	chr1	185972790	185973006	HMCN1	Genotyping
50	chr1	186062580	186062797	HMCN1	Genotyping
51	chr1	186083050	186083301	HMCN1	Genotyping
52	chr1	186143590	186143828	HMCN1	Genotyping
53	chr1	186158895	186159102	HMCN1	Genotyping
54	chr1	190067139	190068194	FAM5C	Genotyping
55	chr1	201038552	201038756	CACNA1S	Genotyping
56	chr1	203274697	203275926	BTG2	Phased Variants
57	chr1	203276207	203276586	BTG2	Genotyping
58	chr1	226923691	226925200	ITPKB	Phased Variants
59	chr1	227842646	227842718	ZNF678	Genotyping
60	chr2	1652010	1652858	PXDN	Genotyping
61	chr2	48027958	48028159	MSH6	Genotyping
62	chr2	48059883	48060051	FBXO11	Genotyping
63	chr2	48065973	48066184	FBXO11	Genotyping
64	chr2	55237198	55237610	RTN4	Genotyping
65	chr2	56149510	56150116	EFEMP1	Genotyping
66	chr2	58520800	58521222	FANCL	Genotyping
67	chr2	59821914	59822083	BCL11A	Genotyping
68	chr2	60773084	60773479	BCL11A	Genotyping
69	chr2	61118794	61118998	REL	Genotyping
70	chr2	61145504	61145785	REL	Genotyping
71	chr2	61148869	61149644	REL	Genotyping
72	chr2	61441169	61441870	USP34	Genotyping
73	chr2	61719434	61719642	XPO1	Genotyping
74	chr2	62934009	62934460	EHBP1	Genotyping
75	chr2	63217829	63218002	EHBP1	Genotyping
76	chr2	63335242	63335600	WDPCP	Genotyping
77	chr2	63631157	63631817	WDPCP	Genotyping
78	chr2	63826277	63826429	MDH1	Genotyping
79	chr2	65258145	65258367	SLC1A4	Phased Variants
80	chr2	65593035	65593153	SPRED2	Phased Variants
81	chr2	65593180	65593250	SPRED2	Phased Variants
82	chr2	77746602	77746988	LRRTM4	Genotyping
83	chr2	80801235	80801513	CTNNA2	Genotyping
84	chr2	88906681	88906861	EIF2AK3	Phased Variants
85	chr2	89127261	89127335	IGKC	Phased Variants

86	chr2	89127461	89127946	IGKC	Phased Variants
87	chr2	89128431	89128574	IGKC	Phased Variants
88	chr2	89131726	89132295	IGKC	Phased Variants
89	chr2	89140556	89140755	IGKC	Phased Variants
90	chr2	89140886	89141350	IGKC	Phased Variants
91	chr2	89157326	89157609	IGKC	Phased Variants
92	chr2	89157626	89158011	IGKC	Phased Variants
93	chr2	89158036	89158938	IGKC	Phased Variants
94	chr2	89158941	89159493	IGKJ5	Phased Variants
95	chr2	89159511	89161445	IGKJ1	Phased Variants
96	chr2	89161926	89162149	IGKJ1	Phased Variants
97	chr2	89162776	89163285	IGKJ1	Phased Variants
98	chr2	89163306	89163837	IGKJ1	Phased Variants
99	chr2	89163861	89164838	IGKJ1	Phased Variants
100	chr2	89164866	89165181	IGKJ1	Phased Variants
101	chr2	89165191	89165644	IGKJ1	Phased Variants
102	chr2	89184966	89185186	IGKV4-1	Phased Variants
103	chr2	89185196	89185704	IGKV4-1	Phased Variants
104	chr2	89196226	89196411	IGKV5-2	Phased Variants
105	chr2	89196851	89197324	IGKV5-2	Phased Variants
106	chr2	89214836	89215040	IGKV5-2	Phased Variants
107	chr2	89246681	89246772	IGKV1-5	Phased Variants
108	chr2	89246786	89246857	IGKV1-5	Phased Variants
109	chr2	89246911	89247053	IGKV1-5	Phased Variants
110	chr2	89247096	89247215	IGKV1-5	Phased Variants
111	chr2	89247526	89247628	IGKV1-5	Phased Variants
112	chr2	89247641	89247735	IGKV1-5	Phased Variants
113	chr2	89247831	89248010	IGKV1-5	Phased Variants
114	chr2	89265756	89265829	IGKV1-6	Genotyping
115	chr2	89265936	89266013	IGKV1-6	Genotyping
116	chr2	89291906	89291981	IGKV1-8	Phased Variants
117	chr2	89292131	89292217	IGKV1-8	Phased Variants
118	chr2	89442291	89442561	IGKV3-20	Phased Variants
119	chr2	89442616	89443259	IGKV3-20	Phased Variants
120	chr2	89475781	89476009	IGKV2-24	Genotyping
121	chr2	89476041	89476122	IGKV2-24	Genotyping
122	chr2	89544331	89544608	IGKV2-30	Genotyping
123	chr2	89544656	89544899	IGKV2-30	Phased Variants
124	chr2	89976276	89976426	IGKV2D-30	Genotyping
125	chr2	89986776	89987023	IGKV2D-29	Genotyping
126	chr2	89987031	89987108	IGKV2D-29	Genotyping
127	chr2	90025206	90025289	IGKV2D-26	Genotyping
128	chr2	90025296	90025378	IGKV2D-26	Genotyping

129	chr2	90025471	90025554	IGKV2D-26	Genotyping
130	chr2	90077981	90078054	IGKV3D-20	Genotyping
131	chr2	90078136	90078222	IGKV3D-20	Genotyping
132	chr2	90078251	90078335	IGKV3D-20	Genotyping
133	chr2	90121891	90122008	IGKV1D-17	Genotyping
134	chr2	90122021	90122157	IGKV1D-17	Genotyping
135	chr2	90212016	90212093	IGKV3D-11	Genotyping
136	chr2	90212196	90212278	IGKV3D-11	Genotyping
137	chr2	90249151	90249275	IGKV1D-43	Genotyping
138	chr2	90249346	90249419	IGKV1D-43	Genotyping
139	chr2	90259931	90260059	IGKV1D-8	Genotyping
140	chr2	90260181	90260258	IGKV1D-8	Genotyping
141	chr2	96809889	96810144	DUSP2	Genotyping
142	chr2	96810164	96810374	DUSP2	Phased Variants
143	chr2	100758483	100758660	AFF3	Phased Variants
144	chr2	103148733	103148948	SLC9A4	Genotyping
145	chr2	117951919	117952057	DDX18	Phased Variants
146	chr2	136872525	136872740	CXCR4	Genotyping
147	chr2	136874415	136874797	CXCR4	Phased Variants
148	chr2	136874920	136875662	CXCR4	Phased Variants
149	chr2	141245127	141245373	LRP1B	Genotyping
150	chr2	145162401	145162624	ZEB2	Genotyping
151	chr2	145187091	145187638	ZEB2	Genotyping
152	chr2	145270956	145271394	ZEB2	Genotyping
153	chr2	145275631	145275744	ZEB2	Genotyping
154	chr2	145275756	145276174	ZEB2	Genotyping
155	chr2	145278026	145278305	ZEB2	Genotyping
156	chr2	145278311	145278659	ZEB2	Genotyping
157	chr2	145692901	145693081	ZEB2	Genotyping
158	chr2	148680516	148680692	ACVR2A	Genotyping
159	chr2	169781120	169781352	ABCB11	Genotyping
160	chr2	170101185	170101401	LRP2	Genotyping
161	chr2	198950434	198951003	PLCL1	Genotyping
162	chr2	242793232	242793447	PDCD1	Genotyping
163	chr2	242794037	242794192	PDCD1	Genotyping
164	chr2	242794317	242794537	PDCD1	Genotyping
165	chr2	242794822	242795040	PDCD1	Genotyping
166	chr2	242800887	242801093	PDCD1	Genotyping
167	chr3	7620223	7620990	GRM7	Genotyping
168	chr3	16419204	16419479	RFTN1	Phased Variants
169	chr3	38180129	38180549	MYD88	Genotyping
170	chr3	38181334	38181509	MYD88	Genotyping
171	chr3	38181854	38182099	MYD88	Genotyping

172	chr3	38182194	38182407	MYD88	Genotyping
173	chr3	38182554	38182844	MYD88	Genotyping
174	chr3	49397608	49397717	RHOA	Genotyping
175	chr3	49397718	49397827	RHOA	Genotyping
176	chr3	49399903	49400084	RHOA	Genotyping
177	chr3	49405833	49406013	RHOA	Genotyping
178	chr3	49412838	49413046	RHOA	Genotyping
179	chr3	64547204	64547477	ADAMTS9	Genotyping
180	chr3	64579889	64580094	ADAMTS9	Genotyping
181	chr3	71551101	71551497	EIF4E3	Phased Variants
182	chr3	140281598	140281875	CLSTN2	Genotyping
183	chr3	164730700	164730888	SI	Genotyping
184	chr3	165548198	165548680	BCHE	Genotyping
185	chr3	176750699	176750928	TBL1XR1	Genotyping
186	chr3	176767759	176767977	TBL1XR1	Genotyping
187	chr3	176769304	176769543	TBL1XR1	Genotyping
188	chr3	176771659	176771732	TBL1XR1	Genotyping
189	chr3	183209758	183209937	KLHL6	Genotyping
190	chr3	183210258	183210544	KLHL6	Genotyping
191	chr3	183272308	183272521	KLHL6	Phased Variants
192	chr3	183273063	183273456	KLHL6	Phased Variants
193	chr3	184580663	184580872	VPS8	Genotyping
194	chr3	185146278	185146873	MAP3K13	Genotyping
195	chr3	185197923	185198317	MAP3K13	Genotyping
196	chr3	185236908	185237109	LIPH	Genotyping
197	chr3	185446223	185446389	C3orf65	Genotyping
198	chr3	185538773	185538951	IGF2BP2	Genotyping
199	chr3	185697423	185697669	TRA2B	Genotyping
200	chr3	186714604	186715001	ST6GAL1	Phased Variants
201	chr3	186782529	186782790	ST6GAL1	Phased Variants
202	chr3	186783389	186784291	ST6GAL1	Phased Variants
203	chr3	187440189	187440445	BCL6	Genotyping
204	chr3	187442669	187442920	BCL6	Genotyping
205	chr3	187443239	187443438	BCL6	Genotyping
206	chr3	187446814	187447831	BCL6	Genotyping
207	chr3	187449434	187449655	BCL6	Genotyping
208	chr3	187451284	187451667	BCL6	Genotyping
209	chr3	187460134	187460530	BCL6	Phased Variants
210	chr3	187460824	187461302	BCL6	Phased Variants
211	chr3	187461319	187461381	BCL6	Phased Variants
212	chr3	187461454	187461918	BCL6	Phased Variants
213	chr3	187461924	187462343	BCL6	Phased Variants
214	chr3	187462374	187462887	BCL6	Phased Variants

215	chr3	187462924	187462999	BCL6	Phased Variants
216	chr3	187463004	187463525	BCL6	Phased Variants
217	chr3	187463709	187463781	BCL6	Phased Variants
218	chr3	187463794	187464109	BCL6	Phased Variants
219	chr3	187619334	187619708	BCL6	Phased Variants
220	chr3	187660817	187661390	BCL6	Phased Variants
221	chr3	187957432	187957507	AC022498.1	Phased Variants
222	chr3	187957512	187957754	AC022498.1	Phased Variants
223	chr3	187957767	187958110	AC022498.1	Phased Variants
224	chr3	187958282	187958675	AC022498.1	Phased Variants
225	chr3	187958787	187959184	AC022498.1	Phased Variants
226	chr3	187959462	187959686	AC022498.1	Phased Variants
227	chr3	188299217	188299605	LPP	Phased Variants
228	chr3	188471412	188471549	LPP	Phased Variants
229	chr3	188471567	188471937	LPP	Phased Variants
230	chr4	7728456	7728661	SORCS2	Genotyping
231	chr4	40198810	40199653	N4BP2	Phased Variants
232	chr4	40199660	40199873	N4BP2	Phased Variants
233	chr4	40199990	40200211	N4BP2	Phased Variants
234	chr4	40200505	40200727	RHOH	Phased Variants
235	chr4	40200730	40201571	RHOH	Phased Variants
236	chr4	80327792	80328151	GK2	Genotyping
237	chr4	88011077	88011285	AFF1	Genotyping
238	chr4	106157604	106157813	TET2	Genotyping
239	chr4	134727698	134727916	PABPC4L	Phased Variants
240	chr4	153249285	153249507	FBXW7	Genotyping
241	chr4	154624670	154625050	TLR2	Genotyping
242	chr4	187509884	187510410	FAT1	Genotyping
243	chr4	187557779	187557985	FAT1	Genotyping
244	chr4	188924114	188924897	ZFP42	Genotyping
245	chr5	5182145	5182494	ADAMTS16	Genotyping
246	chr5	11110990	11111137	CTNND2	Genotyping
247	chr5	11236740	11236956	CTNND2	Genotyping
248	chr5	11364700	11364923	CTNND2	Genotyping
249	chr5	11397080	11397377	CTNND2	Genotyping
250	chr5	11411600	11411807	CTNND2	Genotyping
251	chr5	13864465	13864696	DNAH5	Genotyping
252	chr5	21783415	21783668	CDH12	Genotyping
253	chr5	54964698	54964921	SLC38A9	Phased Variants
254	chr5	67590966	67591183	PIK3R1	Genotyping
255	chr5	75913716	75914448	F2RL2	Genotyping
256	chr5	83258967	83259183	EDIL3	Genotyping
257	chr5	112176756	112176958	APC	Genotyping

258	chr5	124079827	124080721	ZNF608	Phased Variants
259	chr5	131825017	131825239	IRF1	Genotyping
260	chr5	135381969	135382218	TGFBI	Genotyping
261	chr5	137801487	137801637	EGR1	Genotyping
262	chr5	137801697	137801804	EGR1	Genotyping
263	chr5	140208033	140208874	PCDHA6	Genotyping
264	chr5	158527642	158528019	EBF1	Phased Variants
265	chr5	176522449	176522613	FGFR4	Genotyping
266	chr6	392760	392967	IRF4	Phased Variants
267	chr6	393090	393309	IRF4	Phased Variants
268	chr6	394815	395025	IRF4	Genotyping
269	chr6	14117992	14118654	CD83	Phased Variants
270	chr6	14131732	14132021	CD83	Genotyping
271	chr6	14133857	14133996	CD83	Genotyping
272	chr6	14135317	14135496	CD83	Genotyping
273	chr6	26020709	26020958	HIST1H3A	Genotyping
274	chr6	26032014	26032217	HIST1H3B	Genotyping
275	chr6	26045744	26046077	HIST1H3C	Genotyping
276	chr6	26056034	26056315	HIST1H1C	Genotyping
277	chr6	26056319	26056558	HIST1H1C	Genotyping
278	chr6	26123614	26123778	HIST1H2BC	Phased Variants
279	chr6	26123879	26124098	HIST1H2BC	Genotyping
280	chr6	26124544	26124640	HIST1H2AC	Genotyping
281	chr6	26124714	26124889	HIST1H2AC	Genotyping
282	chr6	26156649	26157377	HIST1H1E	Phased Variants
283	chr6	26158529	26158608	HIST1H2BD	Genotyping
284	chr6	26158739	26158835	HIST1H2BD	Genotyping
285	chr6	26197104	26197182	HIST1H3D	Genotyping
286	chr6	26197189	26197465	HIST1H3D	Genotyping
287	chr6	26216779	26216920	HIST1H2BG	Genotyping
288	chr6	26217214	26217431	HIST1H2AE	Genotyping
289	chr6	26234654	26234976	HIST1H1D	Genotyping
290	chr6	26250459	26250537	HIST1H3F	Genotyping
291	chr6	26250594	26250703	HIST1H3F	Genotyping
292	chr6	26252154	26252232	HIST1H2BH	Genotyping
293	chr6	27100079	27100185	HIST1H2BJ	Genotyping
294	chr6	27100939	27101039	HIST1H2AG	Genotyping
295	chr6	27101159	27101300	HIST1H2AG	Genotyping
296	chr6	27114004	27114216	HIST1H2BK	Phased Variants
297	chr6	27114319	27114396	HIST1H2BK	Genotyping
298	chr6	27114494	27114592	HIST1H2BK	Genotyping
299	chr6	27277284	27277495	POM121L2	Genotyping
300	chr6	27777783	27777900	HIST1H3H	Genotyping

301	chr6	27777928	27778106	HIST1H3H	Genotyping
302	chr6	27782718	27782926	HIST1H2BM	Genotyping
303	chr6	27799168	27799381	HIST1H4K	Genotyping
304	chr6	27833408	27833516	HIST1H2AL	Genotyping
305	chr6	27834968	27835075	HIST1H1B	Genotyping
306	chr6	27839658	27839805	HIST1H3I	Genotyping
307	chr6	27860479	27860659	HIST1H2AM	Genotyping
308	chr6	27860794	27860938	HIST1H2AM	Genotyping
309	chr6	27861244	27861344	HIST1H2BO	Genotyping
310	chr6	27861399	27861485	HIST1H2BO	Genotyping
311	chr6	37138284	37139559	PIM1	Phased Variants
312	chr6	37140749	37140956	PIM1	Genotyping
313	chr6	37141679	37141903	PIM1	Genotyping
314	chr6	41903611	41903834	CCND3	Genotyping
315	chr6	41904271	41904477	CCND3	Genotyping
316	chr6	41904941	41905155	CCND3	Genotyping
317	chr6	41908071	41908365	CCND3	Genotyping
318	chr6	41909196	41909441	CCND3	Genotyping
319	chr6	75965846	75966046	TMEM30A	Genotyping
320	chr6	75969006	75969288	TMEM30A	Genotyping
321	chr6	91004618	91004828	MAP3K7	Phased Variants
322	chr6	91005793	91005998	MAP3K7	Phased Variants
323	chr6	94120219	94120743	EPHA7	Genotyping
324	chr6	106534266	106534477	PRDM1	Genotyping
325	chr6	106536046	106536340	PRDM1	Genotyping
326	chr6	106543466	106543637	PRDM1	Genotyping
327	chr6	106547146	106547437	PRDM1	Genotyping
328	chr6	106552761	106552932	PRDM1	Genotyping
329	chr6	106552961	106553841	PRDM1	Genotyping
330	chr6	106554221	106554400	PRDM1	Genotyping
331	chr6	106554766	106555383	PRDM1	Genotyping
332	chr6	108040228	108040856	SCML4	Genotyping
333	chr6	108041553	108042219	SCML4	Genotyping
334	chr6	110777718	110778244	SLC22A16	Genotyping
335	chr6	134491382	134491589	SGK1	Genotyping
336	chr6	134491892	134492111	SGK1	Genotyping
337	chr6	134492132	134492333	SGK1	Genotyping
338	chr6	134492717	134492923	SGK1	Genotyping
339	chr6	134493307	134493474	SGK1	Genotyping
340	chr6	134493732	134494308	SGK1	Phased Variants
341	chr6	134494342	134494514	SGK1	Genotyping
342	chr6	134494552	134494718	SGK1	Phased Variants
343	chr6	134494722	134494795	SGK1	Phased Variants

344	chr6	134494967	134495974	SGK1	Phased Variants
345	chr6	138188483	138188650	TNFAIP3	Genotyping
346	chr6	138192338	138192683	TNFAIP3	Genotyping
347	chr6	138195963	138196172	TNFAIP3	Genotyping
348	chr6	138196803	138197021	TNFAIP3	Genotyping
349	chr6	138197108	138197313	TNFAIP3	Genotyping
350	chr6	138198193	138198407	TNFAIP3	Genotyping
351	chr6	138199548	138200525	TNFAIP3	Genotyping
352	chr6	138201178	138201404	TNFAIP3	Genotyping
353	chr6	138202138	138202494	TNFAIP3	Genotyping
354	chr6	150954420	150954823	PLEKHG1	Phased Variants
355	chr6	159238415	159238794	EZR	Phased Variants
356	chr7	2963818	2963952	CARD11	Genotyping
357	chr7	2963953	2964056	CARD11	Genotyping
358	chr7	2969593	2969738	CARD11	Genotyping
359	chr7	2976668	2976876	CARD11	Genotyping
360	chr7	2977493	2977712	CARD11	Genotyping
361	chr7	2978258	2978502	CARD11	Genotyping
362	chr7	2979398	2979601	CARD11	Genotyping
363	chr7	2983918	2984199	CARD11	Genotyping
364	chr7	2985403	2985610	CARD11	Genotyping
365	chr7	2987163	2987382	CARD11	Genotyping
366	chr7	5569095	5569200	ACTB	Genotyping
367	chr7	5569210	5569359	ACTB	Genotyping
368	chr7	80285799	80286074	CD36	Genotyping
369	chr7	82387830	82388061	PCLO	Genotyping
370	chr7	82453520	82453733	PCLO	Genotyping
371	chr7	82763800	82764050	PCLO	Genotyping
372	chr7	82784490	82784643	PCLO	Genotyping
373	chr7	106508490	106509161	PIK3CG	Genotyping
374	chr7	110545276	110545445	IMMP2L	Phased Variants
375	chr7	110697971	110698144	LRRN3	Phased Variants
376	chr7	110737411	110737634	LRRN3	Phased Variants
377	chr7	110746681	110746893	LRRN3	Phased Variants
378	chr7	110762936	110764629	LRRN3	Genotyping
379	chr7	110764636	110764981	LRRN3	Genotyping
380	chr7	119915406	119915800	KCND2	Genotyping
381	chr7	122634905	122635140	TAS2R16	Genotyping
382	chr7	140453012	140453121	BRAF	Genotyping
383	chr7	140453162	140453268	BRAF	Genotyping
384	chr7	146997183	146997422	CNTNAP2	Genotyping
385	chr7	148506318	148506416	EZH2	Genotyping
386	chr7	148506448	148506551	EZH2	Genotyping

387	chr7	148508658	148508867	EZH2	Genotyping
388	chr7	148513738	148513900	EZH2	Genotyping
389	chr7	148523533	148523743	EZH2	Genotyping
390	chr7	151943421	151943500	KMT2C	Phased Variants
391	chr8	623880	624090	ERICH1	Genotyping
392	chr8	3141724	3141942	CSMD1	Genotyping
393	chr8	4494931	4495105	CSMD1	Genotyping
394	chr8	8748687	8749284	MFHAS1	Genotyping
395	chr8	8750067	8750281	MFHAS1	Genotyping
396	chr8	18729445	18729937	PSD3	Genotyping
397	chr8	75898190	75898400	CRISPLD1	Genotyping
398	chr8	101730376	101730457	PABPC1	Genotyping
399	chr8	103663491	103664160	KLF10	Genotyping
400	chr8	104897561	104898479	RIMS2	Genotyping
401	chr8	113308014	113308283	CSMD3	Genotyping
402	chr8	113364624	113364791	CSMD3	Genotyping
403	chr8	113568994	113569205	CSMD3	Genotyping
404	chr8	116616145	116616886	TRPS1	Genotyping
405	chr8	122626847	122627163	HAS2	Genotyping
406	chr8	128492947	128493338	POU5F1B	Genotyping
407	chr8	128746807	128748893	MYC	Genotyping
408	chr8	128748902	128749969	MYC	Genotyping
409	chr8	128750367	128751183	MYC	Phased Variants
410	chr8	128752612	128753235	MYC	Genotyping
411	chr8	128754007	128754731	MYC	Genotyping
412	chr8	128754752	128756424	MYC	Genotyping
413	chr8	128756707	128756931	MYC	Genotyping
414	chr8	128756947	128757361	MYC	Genotyping
415	chr8	128757737	128757921	MYC	Genotyping
416	chr8	128764072	128764292	MYC	Genotyping
417	chr8	128951724	128951896	TMEM75	Genotyping
418	chr8	130692149	130692503	GSDMC	Genotyping
419	chr8	130760594	130761023	GSDMC	Genotyping
420	chr8	131373024	131373443	ASAP1	Genotyping
421	chr8	136569669	136569842	KHDRBS3	Genotyping
422	chr8	136659204	136659414	KHDRBS3	Genotyping
423	chr8	137101252	137101464	KHDRBS3	Genotyping
424	chr8	137528187	137528570	KHDRBS3	Genotyping
425	chr8	138849937	138850149	FAM135B	Genotyping
426	chr8	139600457	139601255	COL22A1	Genotyping
427	chr8	139601392	139601569	COL22A1	Genotyping
428	chr9	5450474	5450616	CD274	Genotyping
429	chr9	5456059	5456200	CD274	Genotyping

430	chr9	5457054	5457446	CD274	Genotyping
431	chr9	5462809	5463160	CD274	Genotyping
432	chr9	5465489	5465622	CD274	Genotyping
433	chr9	5466724	5466867	CD274	Genotyping
434	chr9	5467814	5468022	CD274	Genotyping
435	chr9	5510589	5510804	PDCD1LG2	Genotyping
436	chr9	5522484	5522636	PDCD1LG2	Genotyping
437	chr9	5534764	5535047	PDCD1LG2	Genotyping
438	chr9	5549309	5549627	PDCD1LG2	Genotyping
439	chr9	5557589	5557762	PDCD1LG2	Genotyping
440	chr9	5563119	5563251	PDCD1LG2	Genotyping
441	chr9	5569929	5570140	PDCD1LG2	Genotyping
442	chr9	13222185	13222409	MPDZ	Genotyping
443	chr9	16435498	16436307	BNC2	Genotyping
444	chr9	19957356	19958178	SLC24A2	Genotyping
445	chr9	20820916	20821095	FOCAD	Genotyping
446	chr9	20946676	20946849	FOCAD	Genotyping
447	chr9	21808814	21808891	MTAP	Genotyping
448	chr9	21808894	21808973	MTAP	Genotyping
449	chr9	21859249	21859469	MTAP	Genotyping
450	chr9	21970834	21971023	CDKN2A	Genotyping
451	chr9	21971069	21971170	CDKN2A	Genotyping
452	chr9	21974409	21974881	CDKN2A	Genotyping
453	chr9	21989304	21989976	CDKN2A	Genotyping
454	chr9	21994084	21994405	CDKN2A	Genotyping
455	chr9	22005929	22006067	CDKN2B	Genotyping
456	chr9	22006109	22006187	CDKN2B	Genotyping
457	chr9	22008649	22009012	CDKN2B	Genotyping
458	chr9	24545399	24545922	IZUMO3	Genotyping
459	chr9	24905444	24905729	IZUMO3	Genotyping
460	chr9	27950144	27950532	LINGO2	Genotyping
461	chr9	37024919	37025642	PAX5	Phased Variants
462	chr9	37025829	37025996	PAX5	Phased Variants
463	chr9	37026269	37027015	PAX5	Phased Variants
464	chr9	37033619	37033797	PAX5	Phased Variants
465	chr9	37293169	37293378	ZCCHC7	Phased Variants
466	chr9	37371494	37371879	ZCCHC7	Phased Variants
467	chr9	37384684	37384911	ZCCHC7	Phased Variants
468	chr9	37407369	37407588	GRHPR	Phased Variants
469	chr9	78686579	78686854	PCSK5	Genotyping
470	chr9	139390582	139390950	NOTCH1	Genotyping
471	chr9	139390952	139391172	NOTCH1	Genotyping
472	chr9	139402662	139402868	NOTCH1	Genotyping

473	chr10	5755066	5755273	FAM208B	Phased Variants
474	chr10	89500957	89501139	PAPSS2	Genotyping
475	chr10	89603602	89604077	KLLN	Genotyping
476	chr10	89624272	89624350	PTEN	Genotyping
477	chr10	89653752	89653825	PTEN	Genotyping
478	chr10	89653832	89653909	PTEN	Genotyping
479	chr10	89685272	89685379	PTEN	Genotyping
480	chr10	89690752	89690894	PTEN	Genotyping
481	chr10	89692737	89692810	PTEN	Genotyping
482	chr10	89692877	89692951	PTEN	Genotyping
483	chr10	89692972	89693037	PTEN	Genotyping
484	chr10	89711837	89711966	PTEN	Genotyping
485	chr10	89711982	89712058	PTEN	Genotyping
486	chr10	89717577	89717714	PTEN	Genotyping
487	chr10	89717742	89717811	PTEN	Genotyping
488	chr10	89720637	89720904	PTEN	Genotyping
489	chr10	90074239	90074419	RNLS	Genotyping
490	chr10	90537736	90538027	LIPN	Genotyping
491	chr10	90579966	90580319	LIPM	Genotyping
492	chr10	90699126	90699647	ACTA2	Genotyping
493	chr10	90773866	90774076	FAS	Genotyping
494	chr10	91092211	91092423	IFIT3	Genotyping
495	chr10	91358986	91359298	PANK1	Genotyping
496	chr10	131640289	131640505	EBF3	Genotyping
497	chr11	58978692	58978791	MPEG1	Genotyping
498	chr11	58978927	58979095	MPEG1	Genotyping
499	chr11	58979112	58979365	MPEG1	Genotyping
500	chr11	65190342	65190557	FRMD8	Phased Variants
501	chr11	65266552	65266924	SCYL1	Phased Variants
502	chr11	65267397	65267603	SCYL1	Phased Variants
503	chr11	65623422	65623506	CFL1	Genotyping
504	chr11	69346691	69346940	CCND1	Genotyping
505	chr11	102188381	102188945	BIRC3	Phased Variants
506	chr11	111234536	111235068	POU2AF1	Genotyping
507	chr11	111249311	111249530	POU2AF1	Phased Variants
508	chr11	111613196	111613432	PPP2R1B	Genotyping
509	chr11	111781036	111781641	CRYAB	Genotyping
510	chr11	111904096	111904291	DLAT	Genotyping
511	chr11	112405016	112405330	AP002884.2	Genotyping
512	chr11	112405341	112405621	AP002884.2	Genotyping
513	chr11	117101043	117101217	PCSK7	Genotyping
514	chr11	117712683	117712997	FXYD6	Genotyping
515	chr11	118754793	118755011	CXCR5	Phased Variants

516	chr11	118764838	118765408	CXCR5	Genotyping
517	chr11	118967323	118968029	DPAGT1	Genotyping
518	chr11	120127163	120127588	POU2F3	Genotyping
519	chr11	120189028	120189629	POU2F3	Genotyping
520	chr11	125472640	125472915	STT3A	Genotyping
521	chr11	128391383	128391629	ETS1	Phased Variants
522	chr11	128391648	128392132	ETS1	Phased Variants
523	chr11	129739778	129740102	NFRKB	Genotyping
524	chr11	131747549	131748030	NTM	Genotyping
525	chr11	134027789	134027980	NCAPD3	Genotyping
526	chr11	134118684	134118873	THYN1	Genotyping
527	chr11	134129469	134130211	ACAD8	Genotyping
528	chr11	134130464	134131097	ACAD8	Genotyping
529	chr11	134133389	134133972	ACAD8	Genotyping
530	chr12	6439713	6439920	TNFRSF1A	Genotyping
531	chr12	15813487	15813687	EPS8	Genotyping
532	chr12	18534682	18534856	PIK3C2G	Genotyping
533	chr12	18544037	18544241	PIK3C2G	Genotyping
534	chr12	18573807	18574017	PIK3C2G	Genotyping
535	chr12	18699197	18699459	PIK3C2G	Genotyping
536	chr12	18747397	18747562	PIK3C2G	Genotyping
537	chr12	18800762	18801046	PIK3C2G	Genotyping
538	chr12	18891267	18891560	CAPZA3	Genotyping
539	chr12	25205888	25206105	LRMP	Phased Variants
540	chr12	25206398	25206616	LRMP	Phased Variants
541	chr12	25206748	25206877	LRMP	Phased Variants
542	chr12	25207088	25207474	LRMP	Phased Variants
543	chr12	25398218	25398299	KRAS	Genotyping
544	chr12	48190731	48190983	HDAC7	Genotyping
545	chr12	49415991	49416144	KMT2D	Genotyping
546	chr12	49418306	49418550	KMT2D	Genotyping
547	chr12	49420531	49420750	KMT2D	Genotyping
548	chr12	49426451	49426592	KMT2D	Genotyping
549	chr12	49427886	49428116	KMT2D	Genotyping
550	chr12	49433331	49433507	KMT2D	Genotyping
551	chr12	49437926	49438391	KMT2D	Genotyping
552	chr12	49444391	49444595	KMT2D	Genotyping
553	chr12	49447196	49447491	KMT2D	Genotyping
554	chr12	57496552	57496735	STAT6	Genotyping
555	chr12	57498222	57498396	STAT6	Genotyping
556	chr12	57498912	57499150	STAT6	Genotyping
557	chr12	86198698	86199622	RASSF9	Genotyping
558	chr12	92537875	92538647	BTG1	Phased Variants

559	chr12	92538790	92539374	BTG1	Phased Variants
560	chr12	113495364	113496458	DTX1	Phased Variants
561	chr12	113496509	113496679	DTX1	Phased Variants
562	chr12	113496694	113496945	DTX1	Phased Variants
563	chr12	113497059	113497278	DTX1	Phased Variants
564	chr12	113515199	113515658	DTX1	Genotyping
565	chr12	113515664	113515934	DTX1	Genotyping
566	chr12	113530924	113531055	DTX1	Genotyping
567	chr12	113531319	113531531	DTX1	Genotyping
568	chr12	113531799	113531930	DTX1	Genotyping
569	chr12	113532569	113532781	DTX1	Genotyping
570	chr12	113532809	113533032	DTX1	Genotyping
571	chr12	113533099	113533237	DTX1	Genotyping
572	chr12	113534494	113534778	DTX1	Genotyping
573	chr12	122458781	122459524	BCL7A	Phased Variants
574	chr12	122460811	122461193	BCL7A	Phased Variants
575	chr12	122461316	122461882	BCL7A	Phased Variants
576	chr12	122462001	122462210	BCL7A	Phased Variants
577	chr12	122462716	122462935	BCL7A	Phased Variants
578	chr12	122463031	122463137	BCL7A	Phased Variants
579	chr13	32907206	32907376	BRCA2	Genotyping
580	chr13	32912226	32912828	BRCA2	Genotyping
581	chr13	41133662	41133842	FOXO1	Genotyping
582	chr13	41133922	41135026	FOXO1	Genotyping
583	chr13	41239682	41239755	FOXO1	Genotyping
584	chr13	41239827	41240356	FOXO1	Genotyping
585	chr13	41240362	41240788	FOXO1	Genotyping
586	chr13	46959165	46959379	KIAA0226L	Phased Variants
587	chr13	46961680	46962067	KIAA0226L	Phased Variants
588	chr13	51915233	51915552	SERPINE3	Genotyping
589	chr13	58207131	58209129	PCDH17	Genotyping
590	chr13	84453542	84455255	SLITRK1	Genotyping
591	chr13	113516229	113516436	ATP11A	Phased Variants
592	chr14	23344697	23345206	LRP10	Genotyping
593	chr14	32615405	32615617	ARHGAP5	Genotyping
594	chr14	35873671	35873838	NFKBIA	Genotyping
595	chr14	64330252	64330462	SYNE2	Phased Variants
596	chr14	69258238	69259642	ZFP36L1	Phased Variants
597	chr14	84420586	84420796	FLRT2	Phased Variants
598	chr14	96179592	96180295	TCL1A	Phased Variants
599	chr14	106048955	106049032	IGHA2	Phased Variants
600	chr14	106054695	106055541	IGHA2	Genotyping
601	chr14	106055740	106055827	IGHA2	Genotyping

602	chr14	106055910	106055995	IGHA2	Genotyping
603	chr14	106056035	106056121	IGHA2	Genotyping
604	chr14	106068705	106068911	IGHE	Phased Variants
605	chr14	106069045	106069384	IGHE	Phased Variants
606	chr14	106071060	106071135	IGHE	Phased Variants
607	chr14	106071190	106071271	IGHE	Phased Variants
608	chr14	106092380	106092608	IGHG4	Genotyping
609	chr14	106092670	106093406	IGHG4	Genotyping
610	chr14	106093435	106093575	IGHG4	Genotyping
611	chr14	106093610	106094215	IGHG4	Genotyping
612	chr14	106094235	106094479	IGHG4	Genotyping
613	chr14	106094580	106094654	IGHG4	Genotyping
614	chr14	106094675	106094915	IGHG4	Genotyping
615	chr14	106095335	106095417	IGHG4	Phased Variants
616	chr14	106095480	106095560	IGHG4	Phased Variants
617	chr14	106110675	106110814	IGHG2	Phased Variants
618	chr14	106110830	106110904	IGHG2	Phased Variants
619	chr14	106110950	106111025	IGHG2	Phased Variants
620	chr14	106111100	106111311	IGHG2	Genotyping
621	chr14	106111390	106112121	IGHG2	Genotyping
622	chr14	106112160	106112302	IGHG2	Genotyping
623	chr14	106112335	106113010	IGHG2	Phased Variants
624	chr14	106113020	106113438	IGHG2	Phased Variants
625	chr14	106113450	106113625	IGHG2	Phased Variants
626	chr14	106113695	106113901	IGHG2	Phased Variants
627	chr14	106113905	106113984	IGHG2	Phased Variants
628	chr14	106114175	106114414	IGHG2	Phased Variants
629	chr14	106174970	106175819	IGHA1	Genotyping
630	chr14	106175820	106176042	IGHA1	Genotyping
631	chr14	106176070	106176217	IGHA1	Genotyping
632	chr14	106176235	106176320	IGHA1	Genotyping
633	chr14	106176375	106176932	IGHA1	Phased Variants
634	chr14	106176985	106177069	IGHA1	Phased Variants
635	chr14	106177425	106177536	IGHA1	Genotyping
636	chr14	106211960	106212864	IGHG1	Phased Variants
637	chr14	106212870	106212948	IGHG1	Phased Variants
638	chr14	106212980	106213124	IGHG1	Phased Variants
639	chr14	106213125	106213200	IGHG1	Phased Variants
640	chr14	106213210	106213525	IGHG1	Phased Variants
641	chr14	106213660	106214042	IGHG1	Phased Variants
642	chr14	106239250	106239357	IGHG3	Phased Variants
643	chr14	106239455	106239900	IGHG3	Phased Variants
644	chr14	106239990	106240155	IGHG3	Phased Variants

645	chr14	106240170	106240815	IGHG3	Phased Variants
646	chr14	106240820	106240892	IGHG3	Phased Variants
647	chr14	106240915	106241118	IGHG3	Phased Variants
648	chr14	106241200	106241278	IGHG3	Phased Variants
649	chr14	106241345	106241627	IGHG3	Phased Variants
650	chr14	106241630	106241705	IGHG3	Genotyping
651	chr14	106241710	106241975	IGHG3	Genotyping
652	chr14	106318100	106318327	IGHM	Phased Variants
653	chr14	106322055	106322271	IGHM	Phased Variants
654	chr14	106322905	106323129	IGHM	Phased Variants
655	chr14	106323470	106323656	IGHM	Phased Variants
656	chr14	106323805	106323896	IGHM	Phased Variants
657	chr14	106324010	106324087	IGHM	Phased Variants
658	chr14	106324155	106324245	IGHM	Phased Variants
659	chr14	106324290	106324369	IGHM	Phased Variants
660	chr14	106324490	106324577	IGHM	Phased Variants
661	chr14	106324750	106325340	IGHM	Phased Variants
662	chr14	106325360	106325513	IGHM	Phased Variants
663	chr14	106325515	106325791	IGHM	Phased Variants
664	chr14	106325820	106326095	IGHJ6	Phased Variants
665	chr14	106326245	106326338	IGHJ6	Phased Variants
666	chr14	106326450	106331808	IGHD7-27	Phased Variants
667	chr14	106357890	106357967	IGHD6-19	Phased Variants
668	chr14	106380360	106380541	IGHD3-3	Phased Variants
669	chr14	106380550	106380901	IGHD3-3	Phased Variants
670	chr14	106380910	106381109	IGHD3-3	Phased Variants
671	chr14	106381275	106381351	IGHD3-3	Phased Variants
672	chr14	106381485	106381633	IGHD2-2	Phased Variants
673	chr14	106381655	106381724	IGHD2-2	Phased Variants
674	chr14	106381890	106381968	IGHD2-2	Phased Variants
675	chr14	106381990	106382161	IGHD2-2	Phased Variants
676	chr14	106382325	106382403	IGHD2-2	Phased Variants
677	chr14	106382905	106383014	IGHD2-2	Phased Variants
678	chr14	106383030	106383140	IGHD2-2	Phased Variants
679	chr14	106383980	106384142	IGHD1-1	Phased Variants
680	chr14	106384630	106384702	IGHD1-1	Phased Variants
681	chr14	106384720	106384798	IGHD1-1	Phased Variants
682	chr14	106384825	106384957	IGHD1-1	Phased Variants
683	chr14	106405615	106405963	IGHV6-1	Genotyping
684	chr14	106452660	106452748	IGHV1-2	Genotyping
685	chr14	106452755	106452907	IGHV1-2	Genotyping
686	chr14	106452940	106453023	IGHV1-2	Genotyping
687	chr14	106471395	106471476	IGHV1-3	Genotyping

688	chr14	106471510	106471609	IGHV1-3	Genotyping
689	chr14	106494090	106494168	IGHV2-5	Phased Variants
690	chr14	106494210	106494365	IGHV2-5	Phased Variants
691	chr14	106494445	106494553	IGHV2-5	Phased Variants
692	chr14	106494565	106494640	IGHV2-5	Phased Variants
693	chr14	106494650	106494806	IGHV2-5	Phased Variants
694	chr14	106518495	106518570	IGHV3-7	Phased Variants
695	chr14	106518855	106518962	IGHV3-7	Phased Variants
696	chr14	106518970	106519111	IGHV3-7	Phased Variants
697	chr14	106539175	106539315	IGHV1-8	Genotyping
698	chr14	106552365	106552502	IGHV3-9	Genotyping
699	chr14	106573315	106573414	IGHV3-11	Genotyping
700	chr14	106573445	106573524	IGHV3-11	Genotyping
701	chr14	106573540	106573645	IGHV3-11	Phased Variants
702	chr14	106573685	106574021	IGHV3-11	Phased Variants
703	chr14	106586200	106586343	IGHV3-13	Genotyping
704	chr14	106610380	106610479	IGHV3-15	Genotyping
705	chr14	106610480	106610557	IGHV3-15	Genotyping
706	chr14	106610690	106610765	IGHV3-15	Phased Variants
707	chr14	106621885	106622026	IGHV3-16	Genotyping
708	chr14	106622035	106622108	IGHV3-16	Genotyping
709	chr14	106641655	106641789	IGHV1-18	Genotyping
710	chr14	106642110	106642265	IGHV1-18	Phased Variants
711	chr14	106667545	106667628	IGHV3-20	Genotyping
712	chr14	106667675	106667750	IGHV3-20	Genotyping
713	chr14	106667805	106667882	IGHV3-20	Genotyping
714	chr14	106691755	106691904	IGHV3-21	Genotyping
715	chr14	106725295	106725442	IGHV3-23	Phased Variants
716	chr14	106725550	106725663	IGHV3-23	Phased Variants
717	chr14	106725780	106725952	IGHV3-23	Phased Variants
718	chr14	106725995	106726188	IGHV3-23	Phased Variants
719	chr14	106732970	106733077	IGHV1-24	Phased Variants
720	chr14	106733185	106733270	IGHV1-24	Phased Variants
721	chr14	106733275	106733487	IGHV1-24	Phased Variants
722	chr14	106757725	106757888	IGHV2-26	Genotyping
723	chr14	106758470	106758653	IGHV2-26	Phased Variants
724	chr14	106780610	106780752	IGHV4-28	Genotyping
725	chr14	106791090	106791169	IGHV3-30	Phased Variants
726	chr14	106805290	106805428	IGHV4-31	Genotyping
727	chr14	106805945	106806076	IGHV4-31	Phased Variants
728	chr14	106806120	106806219	IGHV4-31	Phased Variants
729	chr14	106815805	106815910	IGHV3-33	Phased Variants
730	chr14	106829685	106829757	IGHV4-34	Phased Variants

731	chr14	106829765	106829986	IGHV4-34	Phased Variants
732	chr14	106830125	106830196	IGHV4-34	Phased Variants
733	chr14	106830240	106830312	IGHV4-34	Phased Variants
734	chr14	106830315	106830884	IGHV4-34	Phased Variants
735	chr14	106831185	106831594	IGHV4-34	Phased Variants
736	chr14	106845300	106845540	IGHV3-35	Genotyping
737	chr14	106846385	106846557	IGHV3-35	Phased Variants
738	chr14	106866380	106866461	IGHV3-38	Genotyping
739	chr14	106866475	106866638	IGHV3-38	Genotyping
740	chr14	106877715	106877858	IGHV4-39	Phased Variants
741	chr14	106877930	106878498	IGHV4-39	Phased Variants
742	chr14	106878540	106878612	IGHV4-39	Phased Variants
743	chr14	106878680	106878759	IGHV4-39	Phased Variants
744	chr14	106926180	106926405	IGHV3-43	Genotyping
745	chr14	106962965	106963167	IGHV1-45	Genotyping
746	chr14	106963170	106963280	IGHV1-45	Genotyping
747	chr14	106967130	106967209	IGHV1-46	Genotyping
748	chr14	106967315	106967397	IGHV1-46	Genotyping
749	chr14	106994300	106994376	IGHV3-48	Phased Variants
750	chr14	106994430	106994534	IGHV3-48	Phased Variants
751	chr14	106994545	106994618	IGHV3-48	Phased Variants
752	chr14	106994660	106994745	IGHV3-48	Phased Variants
753	chr14	106994760	106994904	IGHV3-48	Phased Variants
754	chr14	107013035	107013204	IGHV3-49	Genotyping
755	chr14	107034665	107034845	IGHV5-51	Genotyping
756	chr14	107034955	107035097	IGHV5-51	Genotyping
757	chr14	107078455	107078631	IGHV1-58	Genotyping
758	chr14	107083565	107083726	IGHV4-59	Phased Variants
759	chr14	107083790	107083923	IGHV4-59	Phased Variants
760	chr14	107113405	107113560	IGHV3-64	Phased Variants
761	chr14	107113820	107113922	IGHV3-64	Phased Variants
762	chr14	107114095	107114238	IGHV3-64	Phased Variants
763	chr14	107136755	107136899	IGHV3-66	Phased Variants
764	chr14	107169645	107169841	IGHV1-69	Phased Variants
765	chr14	107169970	107170195	IGHV1-69	Phased Variants
766	chr14	107170220	107170472	IGHV1-69	Phased Variants
767	chr14	107170475	107170563	IGHV1-69	Phased Variants
768	chr14	107170660	107170871	IGHV1-69	Phased Variants
769	chr14	107178305	107178377	IGHV2-70	Phased Variants
770	chr14	107178415	107178869	IGHV2-70	Phased Variants
771	chr14	107178880	107179116	IGHV2-70	Phased Variants
772	chr14	107179130	107179339	IGHV2-70	Phased Variants
773	chr14	107179360	107180001	IGHV2-70	Phased Variants

774	chr14	107199020	107199094	IGHV3-72	Genotyping
775	chr14	107199095	107199173	IGHV3-72	Genotyping
776	chr14	107210955	107211159	IGHV3-73	Genotyping
777	chr14	107218755	107218891	IGHV3-74	Genotyping
778	chr14	107258910	107259078	IGHV7-81	Phased Variants
779	chr14	107259100	107259206	IGHV7-81	Phased Variants
780	chr14	107259235	107259444	IGHV7-81	Phased Variants
781	chr14	107259555	107259635	IGHV7-81	Phased Variants
782	chr14	107282770	107282884	IGHV7-81	Genotyping
783	chr14	107282945	107283018	IGHV7-81	Genotyping
784	chr15	45003678	45003861	B2M	Genotyping
785	chr15	45007718	45007927	B2M	Genotyping
786	chr15	45008463	45008603	B2M	Genotyping
787	chr15	66727354	66727536	MAP2K1	Genotyping
788	chr15	66729014	66729123	MAP2K1	Genotyping
789	chr15	66729139	66729292	MAP2K1	Genotyping
790	chr15	86312062	86312565	KLHL25	Genotyping
791	chr16	2812096	2812786	SRRM2	Genotyping
792	chr16	3779106	3779320	CREBBP	Genotyping
793	chr16	3781171	3781464	CREBBP	Genotyping
794	chr16	3781756	3781972	CREBBP	Genotyping
795	chr16	3786011	3786223	CREBBP	Genotyping
796	chr16	3786591	3786885	CREBBP	Genotyping
797	chr16	3788511	3788716	CREBBP	Genotyping
798	chr16	3789521	3789770	CREBBP	Genotyping
799	chr16	3790376	3790580	CREBBP	Genotyping
800	chr16	3794846	3794994	CREBBP	Genotyping
801	chr16	3808801	3809009	CREBBP	Genotyping
802	chr16	3817706	3817915	CREBBP	Genotyping
803	chr16	3823711	3823942	CREBBP	Genotyping
804	chr16	3824536	3824719	CREBBP	Genotyping
805	chr16	3832716	3832942	CREBBP	Genotyping
806	chr16	3900236	3900462	CREBBP	Genotyping
807	chr16	3900561	3900914	CREBBP	Genotyping
808	chr16	10971440	10973882	CIITA	Phased Variants
809	chr16	10973885	10974203	CIITA	Phased Variants
810	chr16	11348520	11349249	SOCS1	Phased Variants
811	chr16	30093722	30093935	PPP4C	Genotyping
812	chr16	33523607	33523675	IGHV3OR16-12	Phased Variants
813	chr16	81946175	81946356	PLCG2	Genotyping
814	chr16	81953055	81953307	PLCG2	Genotyping
815	chr16	81962120	81962263	PLCG2	Genotyping
816	chr16	85933003	85933569	IRF8	Phased Variants

817	chr16	85936563	85936836	IRF8	Genotyping
818	chr16	85942563	85942821	IRF8	Genotyping
819	chr16	85945108	85945330	IRF8	Genotyping
820	chr16	85946708	85946887	IRF8	Genotyping
821	chr16	85948018	85948170	IRF8	Genotyping
822	chr16	85951993	85952448	IRF8	Genotyping
823	chr16	85953683	85953837	IRF8	Genotyping
824	chr16	85954723	85954937	IRF8	Genotyping
825	chr17	5366796	5367031	DHX33	Genotyping
826	chr17	7576949	7577197	TP53	Genotyping
827	chr17	7577444	7577683	TP53	Genotyping
828	chr17	7578129	7578336	TP53	Genotyping
829	chr17	7578344	7578591	TP53	Genotyping
830	chr17	7579259	7579428	TP53	Genotyping
831	chr17	18001529	18001704	DRG2	Genotyping
832	chr17	18022119	18022791	MYO15A	Genotyping
833	chr17	40467709	40467857	STAT3	Genotyping
834	chr17	40469104	40469321	STAT3	Genotyping
835	chr17	40474309	40474530	STAT3	Genotyping
836	chr17	40474974	40475190	STAT3	Genotyping
837	chr17	40475254	40475394	STAT3	Genotyping
838	chr17	40478074	40478252	STAT3	Genotyping
839	chr17	40485844	40486132	STAT3	Genotyping
840	chr17	40489754	40489903	STAT3	Genotyping
841	chr17	40491284	40491489	STAT3	Genotyping
842	chr17	41847058	41847241	DUSP3	Genotyping
843	chr17	51900441	51900897	KIF2B	Genotyping
844	chr17	56408574	56408755	BZRAP1	Phased Variants
845	chr17	56408884	56409615	BZRAP1	Phased Variants
846	chr17	62006520	62006919	CD79B	Genotyping
847	chr17	62007105	62007279	CD79B	Genotyping
848	chr17	62007410	62007761	CD79B	Genotyping
849	chr17	62008645	62008786	CD79B	Genotyping
850	chr17	62009505	62009659	CD79B	Genotyping
851	chr17	63010240	63010308	GNA13	Phased Variants
852	chr17	63010315	63010973	GNA13	Phased Variants
853	chr17	63014313	63014461	GNA13	Genotyping
854	chr17	63049573	63049774	GNA13	Genotyping
855	chr17	63052443	63052678	GNA13	Genotyping
856	chr17	75447868	75448421	9-Sep	Phased Variants
857	chr17	78343503	78343715	RNF213	Genotyping
858	chr17	79478953	79479026	ACTG1	Genotyping
859	chr18	1477565	1477666	ADCYAP1	Phased Variants

860	chr18	6947104	6947347	LAMA1	Genotyping
861	chr18	6980464	6980680	LAMA1	Genotyping
862	chr18	13825915	13826461	MC5R	Genotyping
863	chr18	30349775	30350300	AC012123.1	Phased Variants
864	chr18	48231684	48232112	MAPK4	Genotyping
865	chr18	48327694	48327901	MRO	Genotyping
866	chr18	48512954	48513347	ELAC1	Genotyping
867	chr18	48591759	48592011	SMAD4	Genotyping
868	chr18	48593364	48593571	SMAD4	Genotyping
869	chr18	48604604	48604852	SMAD4	Genotyping
870	chr18	48703169	48703965	MEX3C	Genotyping
871	chr18	53804515	53804796	TXNL1	Genotyping
872	chr18	55274405	55274580	NARS	Genotyping
873	chr18	55319680	55319999	ATP8B1	Genotyping
874	chr18	55329690	55329857	ATP8B1	Genotyping
875	chr18	55359005	55359259	ATP8B1	Genotyping
876	chr18	56054915	56055594	NEDD4L	Genotyping
877	chr18	56063365	56063826	NEDD4L	Genotyping
878	chr18	60763829	60764032	BCL2	Genotyping
879	chr18	60764299	60764540	BCL2	Genotyping
880	chr18	60774414	60774660	BCL2	Genotyping
881	chr18	60793369	60793654	BCL2	Genotyping
882	chr18	60795829	60796006	BCL2	Genotyping
883	chr18	60806264	60806836	BCL2	Phased Variants
884	chr18	60983784	60983991	BCL2	Phased Variants
885	chr18	60984454	60986731	BCL2	Phased Variants
886	chr18	60986844	60987047	BCL2	Phased Variants
887	chr18	60987964	60988511	BCL2	Phased Variants
888	chr18	64172116	64172531	CDH19	Genotyping
889	chr18	64176241	64176518	CDH19	Genotyping
890	chr18	64239166	64239357	CDH19	Genotyping
891	chr18	65179856	65181824	DSEL	Genotyping
892	chr18	73944893	73945380	ZNF516	Genotyping
893	chr18	75683734	75684502	GALR1	Genotyping
894	chr18	77092820	77093034	ATP9B	Genotyping
895	chr18	77170715	77171032	NFATC1	Genotyping
896	chr18	77208755	77208996	NFATC1	Genotyping
897	chr18	77227415	77227661	NFATC1	Genotyping
898	chr18	77288040	77288611	NFATC1	Genotyping
899	chr18	77794425	77795130	RBFA	Genotyping
900	chr19	1376440	1376662	MUM1	Genotyping
901	chr19	6586161	6586445	CD70	Genotyping
902	chr19	6590026	6590238	CD70	Genotyping

903	chr19	6590786	6591079	CD70	Genotyping
904	chr19	8028408	8028583	ELAVL1	Genotyping
905	chr19	10334563	10335187	S1PR2	Genotyping
906	chr19	10335308	10335585	S1PR2	Genotyping
907	chr19	10340823	10341376	S1PR2	Phased Variants
908	chr19	10341833	10341984	S1PR2	Genotyping
909	chr19	12902574	12902861	JUNB	Genotyping
910	chr19	19256469	19256851	MEF2B	Genotyping
911	chr19	19257044	19257222	MEF2B	Genotyping
912	chr19	19257339	19257480	MEF2B	Genotyping
913	chr19	19257489	19257741	MEF2B	Genotyping
914	chr19	19257824	19258036	MEF2B	Genotyping
915	chr19	19258484	19258662	MEF2B	Genotyping
916	chr19	19259984	19260176	MEF2B	Genotyping
917	chr19	19261414	19261588	MEF2B	Genotyping
918	chr19	19293309	19293478	MEF2BNB	Genotyping
919	chr19	42599890	42600121	POU2F2	Genotyping
920	chr19	51525626	51525937	KLK11	Genotyping
921	chr19	51559441	51560040	KLK13	Genotyping
922	chr19	51561771	51561943	KLK13	Genotyping
923	chr19	52381611	52381786	ZNF577	Genotyping
924	chr19	52403336	52403586	ZNF649	Genotyping
925	chr19	52961146	52961224	ZNF534	Genotyping
926	chr19	52961226	52961578	ZNF534	Genotyping
927	chr19	53598586	53599055	ZNF160	Genotyping
928	chr20	23028372	23028858	THBD	Genotyping
929	chr20	25003526	25003774	ACSS1	Genotyping
930	chr20	46131072	46131213	NCOA3	Phased Variants
931	chr20	46131217	46131287	NCOA3	Phased Variants
932	chr21	18981233	18981504	BTG3	Genotyping
933	chr21	28213258	28213536	ADAMTS1	Genotyping
934	chr21	28216763	28217005	ADAMTS1	Genotyping
935	chr22	22380472	22381038	IGLV4-69	Phased Variants
936	chr22	22385622	22385767	IGLV4-69	Genotyping
937	chr22	22385777	22385898	IGLV4-69	Genotyping
938	chr22	22453287	22453502	IGLV8-61	Genotyping
939	chr22	22453527	22453608	IGLV8-61	Genotyping
940	chr22	22516707	22516785	IGLV4-60	Phased Variants
941	chr22	22516827	22517113	IGLV4-60	Phased Variants
942	chr22	22550337	22550812	IGLV6-57	Genotyping
943	chr22	22556227	22556630	IGLV11-55	Genotyping
944	chr22	22569332	22569655	IGLV10-54	Genotyping
945	chr22	22673242	22673607	IGLV5-52	Genotyping

946	chr22	22677077	22677216	IGLV1-51	Phased Variants
947	chr22	22677227	22677337	IGLV1-51	Genotyping
948	chr22	22681927	22682007	IGLV1-50	Genotyping
949	chr22	22682097	22682213	IGLV1-50	Genotyping
950	chr22	22697727	22698123	IGLV9-49	Genotyping
951	chr22	22707427	22707509	IGLV5-48	Genotyping
952	chr22	22707517	22707658	IGLV5-48	Phased Variants
953	chr22	22707742	22707823	IGLV5-48	Genotyping
954	chr22	22712077	22712496	IGLV1-47	Phased Variants
955	chr22	22712512	22712625	IGLV1-47	Genotyping
956	chr22	22723897	22724189	IGLV7-46	Phased Variants
957	chr22	22724207	22724494	IGLV7-46	Phased Variants
958	chr22	22730452	22730552	IGLV5-45	Phased Variants
959	chr22	22730607	22730756	IGLV5-45	Phased Variants
960	chr22	22730887	22730955	IGLV5-45	Phased Variants
961	chr22	22735417	22735604	IGLV1-44	Phased Variants
962	chr22	22735792	22735878	IGLV1-44	Phased Variants
963	chr22	22749602	22749701	IGLV7-43	Phased Variants
964	chr22	22749732	22749853	IGLV7-43	Phased Variants
965	chr22	22749857	22749939	IGLV7-43	Phased Variants
966	chr22	22749942	22750074	IGLV7-43	Phased Variants
967	chr22	22750092	22750342	IGLV7-43	Phased Variants
968	chr22	22758647	22759294	IGLV1-40	Phased Variants
969	chr22	22759297	22759377	IGLV1-40	Phased Variants
970	chr22	22764167	22764309	IGLV1-40	Phased Variants
971	chr22	22764367	22764450	IGLV1-40	Phased Variants
972	chr22	22764552	22764634	IGLV1-40	Phased Variants
973	chr22	22782037	22782325	IGLV5-37	Genotyping
974	chr22	22786477	22786702	IGLV1-36	Genotyping
975	chr22	22786727	22786842	IGLV1-36	Genotyping
976	chr22	22930852	22931173	IGLV2-33	Genotyping
977	chr22	22937192	22937341	IGLV3-32	Genotyping
978	chr22	22937347	22937548	IGLV3-32	Genotyping
979	chr22	23010977	23011143	IGLV3-27	Genotyping
980	chr22	23011172	23011316	IGLV3-27	Genotyping
981	chr22	23029497	23029581	IGLV3-25	Genotyping
982	chr22	23029622	23029778	IGLV3-25	Genotyping
983	chr22	23040452	23040527	IGLV2-23	Phased Variants
984	chr22	23040592	23040811	IGLV2-23	Phased Variants
985	chr22	23040852	23041365	IGLV2-23	Phased Variants
986	chr22	23047067	23047329	IGLV3-22	Genotyping
987	chr22	23055367	23055445	IGLV3-21	Genotyping
988	chr22	23055497	23055577	IGLV3-21	Phased Variants

989	chr22	23055727	23055857	IGLV3-21	Phased Variants
990	chr22	23063307	23063661	IGLV3-19	Genotyping
991	chr22	23077337	23077435	IGLV2-18	Genotyping
992	chr22	23077537	23077615	IGLV2-18	Genotyping
993	chr22	23090122	23090205	IGLV3-16	Genotyping
994	chr22	23090287	23090372	IGLV3-16	Genotyping
995	chr22	23101392	23101473	IGLV2-14	Phased Variants
996	chr22	23101532	23101605	IGLV2-14	Phased Variants
997	chr22	23101652	23101735	IGLV2-14	Genotyping
998	chr22	23114792	23114874	IGLV3-12	Genotyping
999	chr22	23114947	23115052	IGLV3-12	Genotyping
1000	chr22	23135152	23135230	IGLV2-11	Genotyping
1001	chr22	23135247	23135399	IGLV2-11	Genotyping
1002	chr22	23135437	23135521	IGLV2-11	Genotyping
1003	chr22	23154347	23154477	IGLV3-10	Phased Variants
1004	chr22	23154597	23154815	IGLV3-10	Phased Variants
1005	chr22	23161917	23162052	IGLV3-9	Genotyping
1006	chr22	23162072	23162290	IGLV3-9	Genotyping
1007	chr22	23165422	23165496	IGLV2-8	Phased Variants
1008	chr22	23165542	23165680	IGLV2-8	Phased Variants
1009	chr22	23165727	23165811	IGLV2-8	Phased Variants
1010	chr22	23192412	23192818	IGLV4-3	Phased Variants
1011	chr22	23197917	23198053	IGLV4-3	Phased Variants
1012	chr22	23198067	23198475	IGLV4-3	Phased Variants
1013	chr22	23198587	23198732	IGLV4-3	Phased Variants
1014	chr22	23198797	23198869	IGLV4-3	Phased Variants
1015	chr22	23199022	23199127	IGLV4-3	Phased Variants
1016	chr22	23199182	23199261	IGLV4-3	Phased Variants
1017	chr22	23199277	23199671	IGLV4-3	Phased Variants
1018	chr22	23213857	23214141	IGLV4-3	Genotyping
1019	chr22	23214167	23214249	IGLV4-3	Genotyping
1020	chr22	23222927	23223065	IGLV3-1	Phased Variants
1021	chr22	23223077	23223319	IGLV3-1	Phased Variants
1022	chr22	23223327	23224010	IGLV3-1	Phased Variants
1023	chr22	23227062	23227279	IGLL5	Phased Variants
1024	chr22	23227567	23227896	IGLL5	Phased Variants
1025	chr22	23227897	23228624	IGLL5	Phased Variants
1026	chr22	23229332	23229550	IGLL5	Phased Variants
1027	chr22	23229562	23229739	IGLL5	Phased Variants
1028	chr22	23230012	23231063	IGLL5	Phased Variants
1029	chr22	23231072	23231764	IGLL5	Phased Variants
1030	chr22	23231927	23232005	IGLL5	Phased Variants
1031	chr22	23232062	23232346	IGLL5	Phased Variants

1032	chr22	23232362	23232465	IGLL5	Phased Variants
1033	chr22	23232517	23232737	IGLL5	Phased Variants
1034	chr22	23234612	23235837	IGLJ1	Phased Variants
1035	chr22	23235847	23236276	IGLJ1	Phased Variants
1036	chr22	23236277	23236378	IGLJ1	Phased Variants
1037	chr22	23236387	23236526	IGLJ1	Phased Variants
1038	chr22	23236557	23236851	IGLJ1	Phased Variants
1039	chr22	23236877	23237366	IGLC1	Phased Variants
1040	chr22	23241762	23241835	IGLJ2	Genotyping
1041	chr22	23242602	23242981	IGLC2	Phased Variants
1042	chr22	23244157	23244373	IGLC2	Phased Variants
1043	chr22	23247137	23247209	IGLJ3	Genotyping
1044	chr22	23247257	23247444	IGLJ3	Phased Variants
1045	chr22	23247467	23247630	IGLJ3	Phased Variants
1046	chr22	23248182	23248404	IGLC3	Phased Variants
1047	chr22	23252687	23252824	IGLJ4	Genotyping
1048	chr22	23256362	23256504	IGLJ5	Genotyping
1049	chr22	23260267	23260399	IGLJ6	Genotyping
1050	chr22	23263507	23263653	IGLJ7	Genotyping
1051	chr22	23263872	23264263	IGLJ7	Phased Variants
1052	chr22	23278157	23278381	IGLC7	Phased Variants
1053	chr22	23282767	23282839	IGLC7	Phased Variants
1054	chr22	23282842	23282956	IGLC7	Phased Variants
1055	chr22	23523567	23524204	BCR	Genotyping
1056	chr22	23524212	23524419	BCR	Genotyping
1057	chr22	23610547	23610791	BCR	Genotyping
1058	chr22	29191136	29191455	XBP1	Genotyping
1059	chr22	29191461	29191746	XBP1	Genotyping
1060	chr22	29192006	29192215	XBP1	Genotyping
1061	chr22	29193041	29193205	XBP1	Genotyping
1062	chr22	29196261	29196547	XBP1	Genotyping
1063	chr22	41513340	41513562	EP300	Genotyping
1064	chr22	41525845	41526047	EP300	Genotyping
1065	chr22	41527440	41527664	EP300	Genotyping
1066	chr22	41536110	41536291	EP300	Genotyping
1067	chr22	41545740	41545940	EP300	Genotyping
1068	chr22	41545995	41546223	EP300	Genotyping
1069	chr22	41565485	41565650	EP300	Genotyping
1070	chr22	41566385	41566592	EP300	Genotyping
1071	chr22	41568480	41568693	EP300	Genotyping
1072	chr22	41569600	41569814	EP300	Genotyping
1073	chr22	41572225	41572436	EP300	Genotyping
1074	chr22	41572800	41573022	EP300	Genotyping

1075	chr22	41573300	41573515	EP300	Genotyping
1076	chr22	41574255	41574486	EP300	Genotyping
1077	chr22	41574685	41574904	EP300	Genotyping
1078	chr22	47570209	47570414	TBC1D22A	Phased Variants
1079	chrX	1584324	1585521	P2RY8	Genotyping
1080	chrX	1655789	1656029	AKAP17A	Genotyping
1081	chrX	12993264	12993539	TMSB4X	Phased Variants
1082	chrX	12993544	12994173	TMSB4X	Phased Variants
1083	chrX	12994289	12994397	TMSB4X	Phased Variants
1084	chrX	12994444	12994514	TMSB4X	Phased Variants
1085	chrX	33146106	33146490	DMD	Phased Variants
1086	chrX	35820576	35821268	MAGEB16	Genotyping
1087	chrX	70347816	70348034	MED12	Genotyping
1088	chrX	70612661	70612778	TAF1	Genotyping
1089	chrX	73962123	73963110	KIAA2022	Genotyping
1090	chrX	86772953	86773345	KLHL4	Genotyping
1091	chrX	90026453	90026652	PABPC5	Phased Variants
1092	chrX	100610984	100611308	BTK	Genotyping
1093	chrX	119509280	119509492	ATP1B4	Genotyping
1094	chrX	141291052	141291326	MAGEC2	Genotyping
1095	chrX	141291357	141291566	MAGEC2	Genotyping
1096	chrX	153997383	153997622	DKC1	Genotyping

Table 4

#	Chromosome	Region Start	Region End	Number of 50bp bins	Gene	Mean frac DLBCL with PV	Mean frac GCB with PV	Mean frac ABC with PV	Mean frac PMBCL with PV	Mean frac cHL with PV	ranksumP ABCvsGCB	ranksumP PMBCLvsDLBCL	ranksumP cHLvsDLBCL
1	chr22	23227063	23237340	135	IGLL5	0.184	0.158	0.224	0.242	0.088	0.00000	0.00003	0.00000
2	chr18	60763830	60988465	104	BCL2	0.111	0.165	0.029	0.056	0.004	0.00000	0.00000	0.00000
3	chr14	106239251	106241954	49	IGHG3	0.193	0.155	0.251	0.105	0.032	0.00000	0.00000	0.00000
4	chr14	106092381	106095531	51	IGHG4	0.179	0.155	0.217	0.136	0.056	0.00000	0.00000	0.00000
5	chr6	37138285	37141880	36	PIM1	0.073	0.039	0.124	0.068	0.000	0.00000	0.00251	0.00000
6	chr22	22758648	22764603	22	IGLV1-40	0.064	0.098	0.013	0.102	0.000	0.00000	0.46986	0.00001
7	chr2	89161240	89165610	66	IGKJ1	0.144	0.134	0.160	0.140	0.109	0.00000	0.00006	0.36296
8	chr14	106829686	106831586	30	IGHV4-34	0.077	0.049	0.121	0.100	0.012	0.00000	0.10144	0.01432
9	chr2	89158619	89160190	32	IGKJ5	0.307	0.286	0.339	0.350	0.219	0.00000	0.28398	0.00000
10	chr22	23222928	23223998	22	IGLV3-1	0.266	0.300	0.215	0.429	0.208	0.00000	0.00000	0.22589
11	chr14	106211961	106214011	39	IGHG1	0.229	0.197	0.277	0.131	0.035	0.00000	0.00000	0.00000
12	chr14	106329751	106330201	10	IGHJ5	0.320	0.261	0.410	0.375	0.148	0.00000	0.24822	0.00000
13	chr3	187957433	188471931	54	LPP	0.080	0.102	0.046	0.168	0.062	0.00001	0.00027	0.00345
14	chr2	89160890	89161190	7	IGKJ2	0.151	0.096	0.236	0.116	0.062	0.00001	0.02569	0.00086
15	chr6	134491383	134495968	64	SGK1	0.039	0.053	0.018	0.075	0.001	0.00002	0.58192	0.99403
16	chr6	150954421	150954821	9	PLEKHG1	0.067	0.049	0.094	0.063	0.000	0.00002	0.11666	0.00114
17	chr2	89246682	89247982	18	IGKV1-5	0.031	0.023	0.043	0.097	0.024	0.00003	0.01798	0.00005
18	chr8	128746808	128764273	164	MYC	0.037	0.047	0.021	0.039	0.001	0.00003	0.00000	0.86966
19	chr22	23040453	23041334	17	IGLV2-23	0.051	0.073	0.018	0.088	0.005	0.00003	0.77724	0.04594
20	chr2	89160240	89160540	7	IGKJ4	0.259	0.225	0.311	0.241	0.130	0.00003	0.04157	0.00006
21	chr22	22516708	22517100	8	IGLV4-60	0.084	0.117	0.034	0.078	0.022	0.00003	0.17854	0.01628
22	chr12	122458782	122463132	48	BCL7A	0.091	0.106	0.068	0.173	0.041	0.00005	0.00033	0.01552
23	chr14	107178306	107179990	33	IGHV2-70	0.224	0.242	0.195	0.182	0.115	0.00006	0.00002	0.00004
24	chr2	89160590	89160840	6	IGKJ3	0.185	0.137	0.258	0.135	0.109	0.00006	0.00291	0.00284
25	chr22	22730453	22730938	7	IGLV5-45	0.069	0.108	0.011	0.107	0.019	0.00010	0.70241	0.37522
26	chr22	23248183	23248383	5	IGLC3	0.164	0.236	0.055	0.113	0.035	0.00014	0.00837	0.00072
27	chr2	89127262	89158569	66	IGKC	0.089	0.077	0.107	0.164	0.041	0.00022	0.00008	0.04625
28	chr9	37293170	37384885	18	ZCCHC7	0.055	0.075	0.025	0.069	0.002	0.00023	0.36871	0.42872
29	chr14	106732971	106733441	9	IGHV1-24	0.036	0.060	0.000	0.090	0.000	0.00026	0.33149	0.77291
30	chr2	89184967	89185677	15	IGKV4-1	0.103	0.133	0.057	0.133	0.078	0.00035	0.83189	0.36813
31	chr2	59821915	60773435	12	BCL11A	0.035	0.053	0.008	0.089	0.000	0.00075	0.19138	0.80319
32	chr20	46131073	46131277	5	NCOA3	0.071	0.102	0.025	0.025	0.009	0.00085	0.00670	0.02848
33	chr22	23165423	23165766	6	IGLV2-8	0.045	0.022	0.079	0.083	0.043	0.00090	0.90873	0.01148
34	chr8	8748688	8750268	17	MFHAS1	0.033	0.051	0.004	0.055	0.000	0.00099	0.48925	0.69644
35	chr19	52961147	52961549	9	ZNF534	0.029	0.018	0.044	0.063	0.000	0.00113	0.75367	0.44231
36	chr9	16435499	16436299	17	BNC2	0.034	0.049	0.012	0.077	0.000	0.00119	0.51920	0.84956
37	chr22	23264173	23282921	11	IGLC7	0.041	0.061	0.011	0.131	0.000	0.00129	0.00884	0.29860
38	chr14	106318161	106325773	50	IGHM	0.181	0.175	0.190	0.139	0.024	0.00192	0.00000	0.00000
39	chr22	23235813	23235973	4	IGLJ1	0.059	0.033	0.100	0.266	0.000	0.00225	0.00168	0.05724
40	chr16	11348521	11349221	15	SOCS1	0.108	0.126	0.080	0.292	0.046	0.00303	0.00000	0.07342
41	chr16	10971441	10974194	56	CIITA	0.072	0.084	0.054	0.289	0.082	0.00307	0.00000	0.00000
42	chr5	138644666	138864666	5	DNAH5	0.034	0.056	0.000	0.088	0.000	0.00408	0.40676	0.90937

43	chr6	27777784	27778862	6	HIST1H3H	0.041	0.025	0.067	0.042	0.000	0.00488	0.21081	0.62256	
44	chr22	23192413	23214234	46	IGLV4-3	0.061	0.074	0.042	0.162	0.025	0.00501	0.00000	0.65960	
45	chr14	106330251	106330601	8	IGHJ4	0.166	0.143	0.200	0.180	0.043	0.00606	0.43909	0.00002	
46	chr14	106877716	106878731	18	IGHV4-39	0.050	0.064	0.028	0.059	0.053	0.00685	0.08333	0.00000	
47	chr10	90773867	90774067	5	FAS	0.042	0.066	0.005	0.038	0.000	0.00715	0.19681	0.45229	
48	chr22	22723898	22724466	12	IGLV7-46	0.057	0.081	0.021	0.094	0.000	0.00728	0.81618	0.00596	
49	chr5	137801488	137801798	6	EGR1	0.031	0.052	0.000	0.167	0.000	0.00799	0.01126	0.75859	
50	chr22	23242603	23244358	13	IGLC2	0.139	0.164	0.100	0.163	0.094	0.00835	0.72971	0.51511	
51	chr22	22930853	22931153	7	IGLV2-33	0.030	0.021	0.043	0.045	0.000	0.00870	0.55261	0.56841	
52	chr14	106325852	106329701	73	IGHJ6	0.474	0.471	0.478	0.470	0.362	0.00948	0.02862	0.00000	
53	chr3	185697424	185697624	5	TRA2B	0.040	0.059	0.010	0.075	0.000	0.00954	0.90180	0.48859	
54	chr6	26056539	26056539	11	HIST1H1C	0.059	0.079	0.027	0.017	0.000	0.00967	0.00022	0.00680	
55	chr3	71551102	71551452	8	FOXP1	0.015	0.006	0.028	0.031	0.011	0.00999	0.57172	0.00116	
56	chr3	187440190	187661368	137	BCL6	0.106	0.116	0.089	0.126	0.044	0.01002	0.04210	0.00007	
57	chr11	128391384	128392103	15	ETS1	0.061	0.059	0.065	0.021	0.000	0.01042	0.00001	0.00039	
58	chr13	46959166	46962031	13	KIAA0226L	0.034	0.029	0.042	0.067	0.000	0.01112	0.97915	0.84801	
59	chr11	118754794	118765389	17	CXCR5	0.035	0.029	0.044	0.077	0.000	0.01378	0.40303	0.93788	
60	chr17	62006521	62009656	27	CD79B	0.041	0.039	0.044	0.083	0.002	0.01401	0.66941	0.59741	
61	chr1	2334442	2335149	15	RER1	0.019	0.016	0.023	0.088	0.000	0.01514	0.02024	0.00677	
62	chr8	139600458	139601543	20	COL22A1	0.031	0.043	0.011	0.078	0.000	0.01532	0.28495	0.48626	
63	chr1	34404023	34404123	3	CSMD2	0.073	0.104	0.025	0.042	0.000	0.01556	0.06834	0.05288	
64	chr6	26216780	26216880	3	HIST1H2BG	0.040	0.066	0.000	0.063	0.000	0.01575	0.79954	0.58401	
65	chr19	52381612	52381762	4	ZNF577	0.032	0.053	0.000	0.063	0.000	0.01627	0.93639	0.94029	
66	chr11	65266553	65267598	13	SCYL1	0.030	0.045	0.008	0.048	0.003	0.01646	0.43210	0.34042	
67	chr22	23029498	23029739	5	IGLV3-25	0.085	0.108	0.050	0.113	0.043	0.01712	0.97583	0.80122	
68	chr9	78686580	78686830	6	PCSK5	0.035	0.052	0.008	0.073	0.000	0.01813	0.77106	0.87235	
69	chr14	106048956	106056101	25	IGHA2	0.071	0.071	0.072	0.180	0.007	0.01828	0.00255	0.02269	
70	chr14	69258239	69259639	29	ZFP36L1	0.088	0.103	0.065	0.159	0.013	0.01945	0.03212	0.00000	
71	chr5	75913717	75914417	15	FRL2	0.030	0.044	0.010	0.108	0.000	0.01980	0.01754	0.55332	
72	chr14	106926181	106926381	5	IGHV3-43	0.038	0.056	0.010	0.038	0.000	0.01981	0.22178	0.96725	
73	chr6	27782719	27782919	5	HIST1H2BM	0.032	0.052	0.000	0.000	0.000	0.02014	0.01525	0.81176	
74	chr2	100758484	100758634	4	AFF3	0.037	0.025	0.056	0.078	0.033	0.02064	0.69126	0.04169	
75	chr8	136569670	137528538	22	KHDRBS3	0.029	0.041	0.011	0.065	0.000	0.02090	0.60391	0.32890	
76	chr6	392761	395016	15	IRF4	0.035	0.031	0.042	0.021	0.000	0.02146	0.00420	0.95404	
77	chr8	3141725	4495082	9	CSMD1	0.034	0.051	0.008	0.076	0.000	0.02188	0.57834	0.96296	
78	chr14	106330651	106331101	10	IGHJ3	0.057	0.075	0.030	0.150	0.009	0.02210	0.00851	0.25752	
79	chr16	30093723	30093923	5	PPP4C	0.034	0.023	0.050	0.050	0.000	0.02254	0.59983	0.95843	
80	chr12	92537876	92539341	28	BTG1	0.058	0.057	0.059	0.074	0.012	0.02452	0.27041	0.12731	
81	chr17	5366797	5366997	5	DHX33	0.022	0.010	0.040	0.025	0.000	0.02494	0.30467	0.19851	
82	chr22	22697728	22698078	8	IGLV9-49	0.041	0.035	0.050	0.047	0.000	0.02532	0.32166	0.47874	
83	chr22	23256363	23256463	3	IGLJ5	0.059	0.082	0.025	0.042	0.000	0.02682	0.15950	0.08878	
84	chr5	176522450	176522600	4	FGFR4	0.037	0.025	0.056	0.063	0.000	0.02722	0.79786	0.74613	
85	chr13	113516230	113516430	5	ATP11A	0.050	0.069	0.020	0.113	0.000	0.02729	0.27017	0.10654	
86	chr14	106331551	106331651	3	IGHJ1	0.046	0.033	0.067	0.104	0.029	0.02734	0.59010	0.16336	

87	chr2	117951920	117952020	3	DDX18	0.033	0.055	0.000	0.063	0.000	0.02815	0.98381	0.97542
88	chr14	107210956	107211156	5	IGHV3-73	0.046	0.033	0.065	0.113	0.000	0.02872	0.30080	0.42892
89	chr12	6439714	6439914	5	TNFRSF1A	0.038	0.056	0.010	0.050	0.000	0.02933	0.46779	0.82988
90	chr2	136872526	136875621	28	CXCR4	0.105	0.101	0.113	0.100	0.025	0.03071	0.00337	0.00000
91	chr3	165548199	165548649	10	BCHE	0.012	0.008	0.018	0.081	0.000	0.03118	0.04749	0.00098
92	chr4	188924115	188924865	16	ZFP42	0.033	0.046	0.014	0.066	0.000	0.03190	0.74698	0.62135
93	chr20	25003527	25003727	5	ACSS1	0.032	0.049	0.005	0.138	0.000	0.03215	0.03660	0.87436
94	chr14	106994899	106994899	11	IGHV3-48	0.041	0.036	0.048	0.125	0.043	0.03245	0.00471	0.00001
95	chr16	3779107	3900912	82	CREBBP	0.035	0.043	0.022	0.070	0.001	0.03490	0.47515	0.61294
96	chr2	89544332	89544880	11	IGKV2-30	0.029	0.042	0.009	0.091	0.000	0.03816	0.14785	0.41409
97	chr5	112176957	112176957	5	APC	0.028	0.046	0.000	0.088	0.000	0.03821	0.23210	0.50694
98	chr3	185146279	185198274	20	MAP3K13	0.022	0.033	0.006	0.103	0.000	0.03855	0.00439	0.01617
99	chr11	129739779	129740079	7	NFRKB	0.037	0.030	0.046	0.054	0.000	0.03877	0.49619	0.72943
100	chr12	86198699	86199599	19	RASSF9	0.035	0.047	0.017	0.066	0.000	0.04167	0.79797	0.81991
101	chr12	15813488	15813638	4	EPS8	0.035	0.025	0.050	0.031	0.000	0.04189	0.24118	0.93977
102	chr2	63826278	63826428	4	MDH1	0.017	0.008	0.031	0.203	0.000	0.04203	0.00443	0.12932
103	chr14	107083566	107083891	7	IGHV4-59	0.040	0.054	0.018	0.179	0.043	0.04206	0.00035	0.00040
104	chr22	22735843	22735843	6	IGLV1-44	0.059	0.079	0.029	0.073	0.000	0.04311	0.62445	0.18113
105	chr12	18891268	18891518	6	CAPZA3	0.012	0.005	0.021	0.125	0.000	0.04368	0.00589	0.00868
106	chr14	106174971	106177526	44	IGHA1	0.117	0.117	0.116	0.125	0.027	0.04581	0.05495	0.00009
107	chr13	58207132	58209982	40	PCDH17	0.038	0.047	0.024	0.092	0.000	0.04705	0.03043	0.23893
108	chr6	26156650	26157350	15	HIST1H1E	0.064	0.077	0.045	0.008	0.000	0.04776	0.00000	0.00658
109	chr8	75898191	75898391	5	CRISPLD1	0.012	0.007	0.020	0.050	0.000	0.04779	0.61717	0.01894
110	chr9	37024920	37033770	38	PAX5	0.059	0.060	0.059	0.107	0.015	0.04840	0.84733	0.06185
111	chr17	18001530	18001680	4	DRG2	0.015	0.008	0.025	0.031	0.000	0.04924	0.70570	0.06008
112	chr10	91092212	91092412	5	IFIT3	0.026	0.016	0.040	0.050	0.000	0.05027	0.89626	0.41400
113	chr2	56149511	56150111	13	EFEMP1	0.030	0.029	0.031	0.115	0.000	0.05115	0.00217	0.49133
114	chr6	26032015	26032215	5	HIST1H3B	0.030	0.046	0.005	0.013	0.000	0.05360	0.05680	0.72269
115	chrX	1584325	1655990	29	P2RY8	0.031	0.041	0.016	0.093	0.001	0.05546	0.01173	0.29622
116	chr4	187509885	187557980	16	FAT1	0.028	0.039	0.013	0.094	0.000	0.05661	0.05492	0.36536
117	chr5	11110991	11411801	24	CTNND2	0.031	0.040	0.016	0.060	0.000	0.05690	0.95068	0.19315
118	chr14	106110676	106114376	65	IGHG2	0.213	0.210	0.217	0.147	0.049	0.05698	0.00000	0.00000
119	chr1	4472439	4476599	10	AJAP1	0.030	0.026	0.035	0.031	0.000	0.05889	0.10905	0.59078
120	chr1	110561142	110561742	13	AHCYL1	0.019	0.018	0.021	0.058	0.000	0.05908	0.58438	0.01312
121	chr14	106725296	106726174	14	IGHV3-23	0.099	0.111	0.080	0.027	0.000	0.05952	0.00000	0.00001
122	chr1	111715728	111715878	4	CEPT1	0.022	0.016	0.031	0.047	0.000	0.06085	0.91905	0.26127
123	chr11	118967324	118968024	15	DPAGT1	0.032	0.044	0.013	0.046	0.000	0.06151	0.19789	0.69126
124	chr2	55237199	55237599	9	RTN4	0.047	0.060	0.028	0.063	0.000	0.06231	0.41805	0.17702
125	chr11	111781037	111781637	13	CRYAB	0.025	0.037	0.008	0.082	0.000	0.06377	0.11838	0.14383
126	chr14	106573316	106574003	13	IGHV3-11	0.041	0.054	0.021	0.082	0.007	0.06792	0.84332	0.93964
127	chr18	48231685	48232085	9	MAPK4	0.022	0.020	0.025	0.021	0.000	0.07104	0.07945	0.10112
128	chr2	62934010	63217980	14	EHBP1	0.030	0.042	0.013	0.080	0.000	0.07190	0.51773	0.62080
129	chr22	22677078	22677289	5	IGLV1-51	0.046	0.066	0.015	0.113	0.000	0.07234	0.37625	0.20872
130	chr7	119915407	119915757	8	KCND2	0.038	0.053	0.016	0.039	0.000	0.07723	0.12619	0.48614
131	chr22	23154348	23154798	8	IGLV3-10	0.024	0.020	0.028	0.102	0.000	0.07866	0.03037	0.15798

132	chr6	26045745	26046045	7	HIST1H3C	0.030	0.026	0.036	0.045	0.019	0.08101	0.47189	0.03046
133	chr10	131640290	131640490	5	EBF3	0.040	0.036	0.045	0.100	0.000	0.08357	0.26942	0.76490
134	chr1	109822182	109822782	13	PSRC1	0.027	0.038	0.012	0.072	0.000	0.08367	0.51165	0.24502
135	chr17	18022120	18022770	14	MYO15A	0.039	0.036	0.043	0.085	0.000	0.08686	0.51095	0.37846
136	chr16	85933004	85954924	56	IRF8	0.037	0.047	0.024	0.065	0.012	0.08712	0.41154	0.04982
137	chr2	89986777	89987085	7	IGKV2D-29	0.024	0.021	0.029	0.045	0.000	0.09053	0.66530	0.22260
138	chr2	90249152	90249397	5	IGKV1D-43	0.040	0.033	0.050	0.063	0.009	0.09076	0.87053	0.96927
139	chr2	242793233	242801088	24	PDCD1	0.047	0.048	0.046	0.083	0.000	0.09248	0.64737	0.01000
140	chr6	27100080	27100180	3	HIST1H2BJ	0.033	0.027	0.042	0.060	0.029	0.09735	0.05014	0.09524
141	chr7	110545277	110698122	8	BMP2L	0.004	0.002	0.006	0.063	0.000	0.10148	0.15804	0.00010
142	chr1	111441723	111442173	10	CD53	0.027	0.038	0.010	0.100	0.000	0.10715	0.04221	0.30553
143	chrX	70612662	70612762	3	TAF1	0.007	0.000	0.017	0.063	0.000	0.10731	0.45417	0.02634
144	chr21	18981234	18981484	6	BTG3	0.020	0.033	0.000	0.073	0.000	0.10744	0.29340	0.11987
145	chr14	107113406	107114196	10	IGHV3-64	0.015	0.013	0.018	0.050	0.000	0.10843	0.86649	0.00490
146	chr22	22380473	22385883	18	IGLV4-69	0.044	0.054	0.029	0.073	0.000	0.10860	0.97247	0.18279
147	chr9	5510590	5570130	34	PDCD1LG2	0.026	0.028	0.024	0.057	0.000	0.11075	0.98596	0.05983
148	chr1	27059147	27106912	29	ARID1A	0.035	0.043	0.023	0.073	0.006	0.11182	0.58280	0.43378
149	chr13	32907207	32912827	17	BRCA2	0.013	0.013	0.013	0.088	0.000	0.11539	0.00502	0.00005
150	chr18	48703170	48703920	16	MEX3C	0.022	0.023	0.022	0.059	0.000	0.11749	0.74407	0.02655
151	chr1	203274698	203276558	33	BTG2	0.131	0.129	0.133	0.133	0.012	0.11791	0.01136	0.00000
152	chr8	128492948	128493298	8	POU5F1B	0.022	0.035	0.003	0.047	0.000	0.11971	0.87638	0.11243
153	chr6	27834969	27835069	3	HIST1H1B	0.043	0.038	0.050	0.042	0.000	0.12081	0.31080	0.40430
154	chr22	23010978	23011307	7	IGLV3-27	0.045	0.059	0.025	0.045	0.000	0.12123	0.15843	0.35845
155	chr1	117078643	117087128	10	CD58	0.022	0.021	0.023	0.025	0.000	0.12266	0.14627	0.06157
156	chr14	106380361	106381326	17	IGHD3-3	0.040	0.040	0.040	0.022	0.010	0.12443	0.00226	0.54240
157	chr12	49415992	49447447	47	KMT2D	0.029	0.031	0.026	0.097	0.000	0.12454	0.00102	0.09879
158	chr22	22782038	22782288	6	IGLV5-37	0.051	0.066	0.029	0.052	0.000	0.12900	0.22779	0.08945
159	chr8	18729446	18729896	10	PSD3	0.036	0.048	0.018	0.100	0.000	0.12911	0.49227	0.67922
160	chr14	106552366	106552466	3	IGHV3-9	0.020	0.011	0.033	0.063	0.000	0.12919	0.69275	0.24178
161	chrX	35820577	35821227	14	MAGEB16	0.021	0.032	0.005	0.080	0.000	0.13076	0.08392	0.03514
162	chr16	81946176	81962221	13	PLCG2	0.027	0.028	0.027	0.058	0.000	0.13686	0.98920	0.29436
163	chr22	22712078	22712594	11	IGLV1-47	0.050	0.063	0.032	0.108	0.000	0.13854	0.36497	0.04398
164	chr3	16419205	16419455	6	RETN1	0.050	0.046	0.054	0.063	0.000	0.14045	0.43890	0.10024
165	chr11	111613197	111613397	5	PPP2R1B	0.026	0.039	0.005	0.000	0.000	0.14058	0.02490	0.46424
166	chr14	106331151	106331501	8	IGHJ2	0.048	0.047	0.050	0.102	0.027	0.14335	0.33135	0.15651
167	chr1	226923692	226925192	31	ITPKB	0.044	0.053	0.031	0.139	0.000	0.14412	0.00007	0.03739
168	chr6	27100940	27101260	5	HIST1H2AG	0.024	0.020	0.030	0.038	0.000	0.14525	0.54138	0.28737
169	chr10	91358987	91359287	7	PANK1	0.021	0.019	0.025	0.107	0.000	0.15224	0.01412	0.10864
170	chr14	32615406	32615606	5	ARHGAP5	0.020	0.033	0.000	0.100	0.000	0.15384	0.16273	0.16433
171	chrX	119509281	119509481	5	ATP1B4	0.016	0.013	0.020	0.088	0.000	0.15508	0.23890	0.07712
172	chr18	77794426	77795126	15	RBFA	0.014	0.014	0.013	0.075	0.000	0.15602	0.08296	0.00029
173	chr10	89624273	89720888	32	PTEN	0.015	0.016	0.013	0.023	0.000	0.15663	0.04633	0.00000
174	chr14	64330253	64330453	5	SYNE2	0.006	0.003	0.010	0.025	0.000	0.15837	0.74245	0.00357
175	chr9	24545400	24905695	17	IZUMO3	0.030	0.039	0.016	0.037	0.000	0.15955	0.10765	0.43759

176	chr5	54964699	54964899	5	SLC38A9	0.002	0.000	0.005	0.013	0.000	0.16320	0.46997	0.00144	
177	chr8	101730377	101730427	2	PABPC1	0.015	0.008	0.025	0.000	0.000	0.16445	0.26379	0.18377	
178	chr8	131373025	131373425	9	ASAP1	0.030	0.040	0.014	0.028	0.000	0.16655	0.98650	0.59884	
179	chr22	23101393	23101730	6	IGLV2-14	0.048	0.044	0.054	0.073	0.022	0.16893	0.83695	0.56495	
180	chr1	109649127	109649277	4	C1orf194	0.047	0.045	0.050	0.078	0.022	0.17014	0.88867	0.40591	
181	chr11	65623423	65623473	2	CFL1	0.025	0.041	0.000	0.031	0.000	0.17060	0.58174	0.54924	
182	chr22	22707428	22707793	7	IGLV5-48	0.035	0.047	0.018	0.071	0.000	0.17227	0.95304	0.82874	
183	chr14	106331701	106331801	3	IGHD7-27	0.026	0.022	0.033	0.125	0.000	0.17412	0.05590	0.56584	
184	chr14	96179593	96180293	15	TCL1A	0.050	0.050	0.050	0.071	0.000	0.17445	0.59106	0.01278	
185	chr22	23063308	23063658	8	IGLV3-19	0.031	0.029	0.034	0.039	0.000	0.17496	0.31060	0.64225	
186	chr17	7576950	7579410	24	TP53	0.040	0.051	0.023	0.107	0.000	0.17822	0.03641	0.51953	
187	chr2	148680517	148680667	4	ACVR2A	0.025	0.037	0.006	0.031	0.000	0.18073	0.41320	0.38140	
188	chr19	10334564	10341984	35	SIPR2	0.064	0.077	0.044	0.104	0.002	0.18105	0.40386	0.00014	
189	chr6	108040229	108042204	27	SCML4	0.025	0.026	0.023	0.060	0.005	0.18315	0.54097	0.01195	
190	chr6	27277285	27277485	5	PQM121L2	0.042	0.039	0.045	0.050	0.000	0.18414	0.38135	0.41604	
191	chr3	186714605	186784290	33	ST6GAL1	0.084	0.091	0.072	0.087	0.018	0.18556	0.01425	0.00007	
192	chr19	12902575	12902825	6	JUNB	0.053	0.052	0.054	0.010	0.000	0.18604	0.00259	0.04452	
193	chr14	107199021	107199172	4	IGHV3-72	0.045	0.041	0.050	0.000	0.000	0.18636	0.00860	0.27305	
194	chr11	102188382	102188932	12	BIRC3	0.104	0.123	0.075	0.104	0.043	0.18760	0.23061	0.02703	
195	chr1	185833556	186159096	32	HMCN1	0.021	0.023	0.018	0.074	0.000	0.18799	0.04332	0.00092	
196	chr12	18534683	18801013	30	PIK3C2G	0.017	0.020	0.013	0.054	0.000	0.18947	0.52931	0.00001	
197	chrX	100610985	100611285	7	BTK	0.021	0.021	0.021	0.116	0.000	0.18957	0.01363	0.10957	
198	chr18	64172117	64239317	19	CDH19	0.023	0.032	0.009	0.072	0.002	0.19120	0.37384	0.02195	
199	chr2	1652011	1652811	17	PXDN	0.045	0.054	0.031	0.092	0.000	0.19342	0.57240	0.03398	
200	chr11	111904097	111904247	4	DLAT	0.037	0.049	0.019	0.016	0.000	0.19688	0.06546	0.70963	
201	chr22	22556228	22556628	9	IGLV11-55	0.039	0.038	0.039	0.111	0.000	0.19910	0.04960	0.53925	
202	chr2	103148734	103148934	5	SLC9A4	0.024	0.036	0.005	0.063	0.000	0.20039	0.78808	0.29891	
203	chr2	48027959	48028159	5	MSH6	0.012	0.010	0.015	0.000	0.000	0.20189	0.09865	0.01894	
204	chr4	134727699	134727899	5	PABPC4L	0.012	0.010	0.015	0.150	0.000	0.20189	0.02007	0.01894	
205	chr11	134027940	134027940	4	NCAPD3	0.047	0.061	0.025	0.078	0.000	0.20429	0.99130	0.21830	
206	chr2	77746603	77746953	8	LRRTM4	0.026	0.037	0.009	0.047	0.000	0.20711	0.60835	0.35208	
207	chr1	160319284	160319484	5	NCSTN	0.044	0.039	0.050	0.025	0.000	0.21582	0.05416	0.28073	
208	chr18	65179857	65181807	40	DSEL	0.021	0.029	0.009	0.073	0.000	0.21609	0.19591	0.00018	
209	chr15	45003679	45008564	12	B2M	0.035	0.046	0.017	0.031	0.007	0.21616	0.04427	0.31773	
210	chr1	29069532	29070182	14	YTHDF2	0.043	0.052	0.030	0.040	0.006	0.21620	0.03795	0.84925	
211	chr4	80327793	80328143	8	GK2	0.030	0.041	0.013	0.117	0.000	0.21872	0.01766	0.70075	
212	chr5	158527643	158527993	8	EBF1	0.052	0.064	0.034	0.055	0.000	0.22009	0.11870	0.13982	
213	chr1	3747621	3747771	4	CEP104	0.025	0.037	0.006	0.109	0.000	0.22034	0.26105	0.39687	
214	chr2	48059884	48066174	9	FBXO11	0.014	0.015	0.014	0.063	0.000	0.22199	0.44292	0.00401	
215	chrX	33146107	33146457	8	DMD	0.059	0.059	0.059	0.359	0.082	0.22404	0.00000	0.00004	
216	chr6	26124545	26124865	6	HIST1H2AC	0.051	0.063	0.033	0.010	0.000	0.22855	0.00394	0.11588	
217	chr14	106791091	106791141	2	IGHV3-30	0.045	0.041	0.050	0.063	0.000	0.24046	0.72117	0.43844	
218	chr3	183209759	183273414	23	KLHL6	0.036	0.036	0.036	0.052	0.006	0.24437	0.12177	0.41139	
219	chr17	79478954	79479004	2	ACTG1	0.005	0.000	0.013	0.125	0.043	0.24604	0.05674	0.01689	

220	chr22	47570210	47570410	5	TBC1D22A	0.030	0.043	0.010	0.175	0.000	0.24818	0.00334	0.70762
221	chr6	27799169	27799369	5	HIST1H4K	0.022	0.033	0.005	0.038	0.000	0.24870	0.54640	0.19851
222	chr2	65258146	65258346	5	SLC1A4	0.018	0.030	0.000	0.050	0.000	0.25016	0.78384	0.08170
223	chr14	106586201	106586301	3	IGHV3-13	0.033	0.027	0.042	0.021	0.000	0.25073	0.17545	0.97542
224	chr6	26158530	26158790	4	HIST1H2BD	0.030	0.041	0.013	0.016	0.000	0.25147	0.13295	0.69509
225	chr14	106691756	106691856	3	IGHV3-21	0.053	0.066	0.033	0.042	0.000	0.25208	0.23957	0.18828
226	chr10	90579967	90580317	8	LIPM	0.035	0.035	0.034	0.047	0.000	0.25854	0.32941	0.85606
227	chr7	82387831	82784641	19	PCLO	0.035	0.044	0.022	0.049	0.000	0.25896	0.17138	0.85294
228	chr22	23090123	23090338	4	IGLV3-16	0.030	0.041	0.013	0.063	0.065	0.26082	0.88005	0.00186
229	chr2	89475782	89476114	7	IGKV2-24	0.044	0.042	0.046	0.125	0.000	0.26354	0.03650	0.25182
230	chr2	90122892	90122155	6	IGKV1D-17	0.030	0.041	0.013	0.083	0.000	0.26708	0.50393	0.47148
231	chr14	107034666	107035056	7	IGHV5-51	0.038	0.049	0.021	0.071	0.000	0.26981	0.83901	0.54622
232	chr6	26217415	26217415	5	HIST1H2AE	0.024	0.023	0.025	0.038	0.000	0.26983	0.53539	0.29891
233	chr14	84420587	84420787	5	FLRT2	0.000	0.000	0.000	0.025	0.000	0.27098	0.90753	0.00089
234	chr4	40198811	40201559	49	RHOH	0.062	0.068	0.053	0.028	0.015	0.27123	0.00000	0.12156
235	chr14	106539176	106539276	3	IGHV1-8	0.040	0.038	0.042	0.063	0.000	0.27246	0.79783	0.70059
236	chr5	83258968	83259168	5	EDIL3	0.022	0.033	0.005	0.063	0.000	0.27662	0.67082	0.19851
237	chrX	70348017	70348017	5	MED12	0.022	0.033	0.005	0.075	0.000	0.27662	0.58460	0.19851
238	chr18	48512955	48513305	8	ELAC1	0.026	0.027	0.025	0.102	0.000	0.27685	0.05340	0.35208
239	chrX	12993265	12994487	23	TMSB4X	0.098	0.108	0.083	0.177	0.057	0.27705	0.03023	0.53439
240	chr19	6586162	6591037	17	CD70	0.052	0.064	0.035	0.121	0.000	0.27742	0.02768	0.05558
241	chr9	13222386	13222386	5	MPDZ	0.018	0.016	0.020	0.050	0.000	0.27845	0.92556	0.10149
242	chr19	8028409	8028559	4	ELAVL1	0.037	0.049	0.019	0.094	0.000	0.28231	0.39328	0.68881
243	chr17	63010241	63052644	28	GNA13	0.033	0.035	0.029	0.051	0.005	0.29192	0.20921	0.55174
244	chr6	75965847	75969257	10	TMEM30A	0.017	0.018	0.015	0.063	0.000	0.29877	0.61973	0.01289
245	chr2	61118795	61149620	27	REL	0.024	0.030	0.014	0.053	0.006	0.29909	0.79282	0.00093
246	chr8	103663492	103664142	14	KLF10	0.032	0.034	0.029	0.103	0.000	0.29943	0.04753	0.77217
247	chr7	122634906	122635106	5	TAS2R16	0.040	0.036	0.045	0.050	0.000	0.30121	0.42497	0.50451
248	chr7	106508491	106509141	14	PIK3CG	0.043	0.044	0.041	0.058	0.000	0.30584	0.28865	0.12742
249	chr19	1376441	1376641	5	MUM1	0.053	0.066	0.035	0.063	0.000	0.30591	0.40617	0.10207
250	chr10	90074240	90074390	4	RNLS	0.012	0.012	0.013	0.141	0.000	0.30697	0.04146	0.05611
251	chr17	56409585	56409585	19	BZRAP1	0.107	0.116	0.095	0.122	0.050	0.31066	0.24386	0.00835
252	chr18	48327695	48327695	5	MRO	0.034	0.033	0.035	0.088	0.000	0.32051	0.36874	0.94107
253	chr2	90212017	90212247	4	IGKV3D-11	0.000	0.000	0.000	0.063	0.000	0.32488	0.18259	0.00295
254	chr3	164730701	164730851	4	SI	0.000	0.000	0.000	0.031	0.000	0.32488	0.89232	0.00295
255	chr18	75683735	75684485	16	GALR1	0.025	0.026	0.023	0.055	0.000	0.32688	0.88862	0.08570
256	chr10	90699127	90699627	11	ACTA2	0.022	0.030	0.009	0.074	0.000	0.32826	0.22549	0.05225
257	chr7	146997184	146997384	5	CNTNAP2	0.020	0.030	0.005	0.063	0.000	0.33654	0.72508	0.12531
258	chr10	90537737	90537987	6	LIPN	0.021	0.022	0.021	0.063	0.000	0.33950	0.63054	0.15262
259	chr8	116616146	116616846	15	TRPS1	0.033	0.042	0.020	0.088	0.000	0.34027	0.10857	0.96046
260	chr6	14117993	14135468	27	CD83	0.061	0.069	0.049	0.146	0.006	0.34145	0.00006	0.25221
261	chr14	106610381	106610741	6	IGHV3-15	0.036	0.046	0.021	0.042	0.000	0.34253	0.25513	0.68243
262	chr14	106962966	106963269	7	IGHV1-45	0.023	0.023	0.021	0.036	0.000	0.34439	0.45188	0.16111
263	chr6	27833409	27833509	3	HIST1H2AL	0.017	0.027	0.000	0.042	0.000	0.34503	0.82367	0.13637
264	chr7	2963819	2987364	44	CARD11	0.047	0.055	0.035	0.075	0.000	0.34677	0.68708	0.00272

265	chr11	134118685	134118835	4	THYN1	0.017	0.016	0.019	0.094	0.000	0.35301	0.26225	0.10870	
266	chr14	107258911	107282996	17	IGHV7-81	0.031	0.040	0.019	0.088	0.026	0.35469	0.15903	0.00092	
267	chrX	73962124	73963074	20	KIAA2022	0.020	0.028	0.009	0.103	0.000	0.35514	0.00284	0.00632	
268	chr3	185236909	185237109	5	LIPH	0.022	0.033	0.005	0.038	0.000	0.35786	0.57454	0.20093	
269	chr3	64547205	64580090	11	ADAMTS9	0.028	0.030	0.025	0.091	0.000	0.35888	0.08153	0.38328	
270	chr14	106405616	106405916	7	IGHV6-1	0.028	0.037	0.014	0.098	0.000	0.36129	0.28061	0.53891	
271	chr11	117712684	117712984	7	FXYD6	0.035	0.035	0.036	0.045	0.000	0.36200	0.39501	0.93264	
272	chr8	130692150	130760995	17	GSDMC	0.029	0.037	0.018	0.051	0.000	0.36490	0.59248	0.38946	
273	chr22	22749603	22750309	14	IGLV7-43	0.021	0.022	0.018	0.067	0.000	0.36721	0.26604	0.01881	
274	chr22	23135153	23135508	7	IGLV2-11	0.020	0.021	0.018	0.098	0.000	0.36740	0.03964	0.07222	
275	chr6	26234655	26234955	7	HIST1H1D	0.042	0.044	0.039	0.018	0.000	0.36781	0.01092	0.23508	
276	chr11	112405017	112405578	12	C11orf54	0.029	0.037	0.017	0.099	0.000	0.36795	0.03866	0.51208	
277	chr1	2488007	2494707	36	TNFRSF14	0.035	0.042	0.024	0.082	0.000	0.37037	0.15033	0.73903	
278	chr18	48591760	48604805	16	SMAD4	0.019	0.020	0.016	0.035	0.000	0.37088	0.36837	0.00422	
279	chr18	55274406	55274556	4	NARS	0.015	0.025	0.000	0.047	0.000	0.37631	0.84014	0.07298	
280	chrX	90026604	90026604	4	PABPC5	0.015	0.025	0.000	0.031	0.000	0.37790	0.70713	0.06008	
281	chr8	623881	624081	5	ERICH1	0.020	0.020	0.020	0.025	0.000	0.38591	0.34374	0.13521	
282	chr18	1477566	1477666	3	ADCYAP1	0.043	0.055	0.025	0.000	0.000	0.38723	0.02764	0.48180	
283	chr12	48190732	48190982	6	HDAC7	0.043	0.041	0.046	0.021	0.000	0.38786	0.03107	0.34087	
284	chr14	106381486	106383981	18	IGHD2-2	0.029	0.032	0.025	0.059	0.024	0.39142	0.82914	0.00001	
285	chr5	135381970	135382170	5	TGFB1	0.034	0.030	0.040	0.038	0.000	0.39274	0.28309	0.98151	
286	chr3	184580664	184580864	5	VPS8	0.006	0.007	0.005	0.075	0.000	0.40112	0.15248	0.00357	
287	chr14	106805291	106806190	8	IGHV4-31	0.038	0.041	0.034	0.117	0.000	0.40201	0.02655	0.49158	
288	chr22	23077338	23077588	4	IGLV2-18	0.025	0.025	0.025	0.063	0.000	0.40450	0.82223	0.42774	
289	chr11	134129470	134133940	40	ACAD8	0.027	0.034	0.016	0.063	0.000	0.40456	0.61602	0.02024	
290	chr1	190067140	190068190	22	FAM5C	0.028	0.035	0.017	0.077	0.000	0.40678	0.18209	0.12955	
291	chr19	52403337	52403537	5	ZNF649	0.026	0.026	0.025	0.075	0.000	0.41027	0.52307	0.41005	
292	chr15	66727355	66729281	10	MAP2K1	0.035	0.044	0.020	0.069	0.000	0.41169	0.93852	0.81159	
293	chr6	94120220	94120720	11	EPHA7	0.024	0.027	0.020	0.119	0.000	0.41348	0.00251	0.10186	
294	chr20	23028373	23028823	10	THBD	0.044	0.052	0.030	0.075	0.009	0.41401	0.97196	0.91852	
295	chr19	42599891	42600091	5	POU2F2	0.038	0.049	0.020	0.125	0.000	0.41703	0.03149	0.68257	
296	chrX	86772954	86773304	8	KLHL4	0.026	0.035	0.013	0.086	0.000	0.41822	0.64743	0.29530	
297	chr9	37407370	37407570	5	GRHPR	0.046	0.056	0.030	0.113	0.000	0.42725	0.84925	0.34749	
298	chr9	20820917	20946827	8	FOCAD	0.015	0.016	0.013	0.078	0.000	0.43273	0.41122	0.00842	
299	chr6	91004619	91005994	10	BACH2	0.051	0.061	0.038	0.100	0.017	0.43292	0.62927	0.61655	
300	chr9	139390583	139402863	17	NOTCH1	0.038	0.045	0.028	0.140	0.000	0.44217	0.00038	0.66264	
301	chr14	106452661	106453601	7	IGHV1-2	0.020	0.021	0.018	0.080	0.000	0.44604	0.33603	0.09047	
302	chr6	26020710	26020910	5	HIST1H3A	0.036	0.036	0.035	0.000	0.000	0.44876	0.01256	0.96541	
303	chr9	27950145	27950495	8	LINGO2	0.022	0.031	0.009	0.117	0.000	0.45177	0.00957	0.11783	
304	chr7	80285800	80286050	6	CD36	0.013	0.022	0.000	0.135	0.000	0.45506	0.00452	0.01644	
305	chr18	13825916	13826416	11	MC5R	0.035	0.043	0.023	0.085	0.000	0.45807	0.35320	0.85391	
306	chr9	5450475	5468015	33	CD274	0.026	0.029	0.020	0.049	0.000	0.46045	0.38390	0.02293	
307	chr3	185446224	185538924	8	IGF2BP2	0.019	0.027	0.006	0.102	0.000	0.47564	0.05373	0.03579	
308	chr1	3800046	3800353	7	DFFB	0.042	0.044	0.039	0.107	0.000	0.47590	0.23069	0.43666	
309	chr22	23055368	23055828	7	IGLV3-21	0.034	0.035	0.032	0.107	0.000	0.47614	0.19555	0.90440	

310	chr6	27114005	27114545	9	HIST1H2BK	0.023	0.031	0.011	0.021	0.000	0.48388	0.09402	0.14560
311	chr14	107013036	107013186	4	IGHV3-49	0.020	0.029	0.006	0.109	0.000	0.48557	0.05983	0.17265
312	chr22	22453288	22453563	6	IGLV8-61	0.053	0.055	0.050	0.083	0.000	0.48567	0.96231	0.04559
313	chr14	106357891	106357941	2	IGHD6-19	0.000	0.000	0.000	0.000	0.000	0.48646	0.45288	0.03556
314	chr16	33523608	33523658	2	IGHV3OR16-12	0.000	0.000	0.000	0.125	0.022	0.48646	0.05020	0.02436
315	chr7	151943422	151943472	2	KMT2C	0.000	0.000	0.000	0.125	0.000	0.48646	0.10655	0.03556
316	chr22	23114793	23115048	5	IGLV3-12	0.018	0.026	0.005	0.000	0.000	0.49420	0.05467	0.09497
317	chr2	80801236	80801486	6	CTNNA2	0.017	0.025	0.004	0.146	0.000	0.50036	0.00472	0.03774
318	chr22	23161918	23162288	8	IGLV3-9	0.036	0.039	0.031	0.063	0.000	0.50251	0.65174	0.76665
319	chr12	113495365	113534745	80	DTX1	0.058	0.065	0.047	0.075	0.000	0.50409	0.06246	0.00000
320	chr11	65190343	65190543	5	FRMD8	0.050	0.049	0.050	0.038	0.009	0.51163	0.10472	0.60740
321	chr14	106967131	106967366	4	IGHV1-46	0.022	0.033	0.006	0.063	0.000	0.51321	0.66087	0.32094
322	chr12	25205889	25207439	21	LRMP	0.038	0.041	0.033	0.080	0.027	0.51555	0.36573	0.00948
323	chr14	106780611	106780711	3	IGHV4-28	0.036	0.038	0.033	0.125	0.000	0.51984	0.19368	0.92185
324	chr11	125472641	125472891	6	STT3A	0.046	0.055	0.033	0.052	0.000	0.52125	0.24640	0.20117
325	chr11	69346692	69346892	5	CCND1	0.024	0.026	0.020	0.113	0.000	0.52233	0.04449	0.30659
326	chr13	51915234	51915534	7	SERPINE3	0.035	0.044	0.021	0.152	0.000	0.53028	0.03239	0.74664
327	chr5	21783416	21783666	6	CDH12	0.020	0.022	0.017	0.083	0.000	0.53207	0.16100	0.13344
328	chr12	25398219	25398269	2	KRAS	0.015	0.025	0.000	0.000	0.000	0.53308	0.26379	0.18377
329	chr1	85733208	85742033	19	BCL10	0.021	0.025	0.016	0.056	0.000	0.53493	0.60987	0.00831
330	chr1	107866872	107867572	15	NTNG1	0.013	0.015	0.010	0.063	0.000	0.53686	0.17297	0.00018
331	chr1	86591888	86591888	10	COL24A1	0.029	0.036	0.018	0.075	0.000	0.53874	0.54478	0.46033
332	chr18	30349776	30350276	11	KLHL14	0.033	0.036	0.030	0.091	0.000	0.53960	0.49213	0.94697
333	chr14	106641656	106642261	7	IGHV1-18	0.023	0.026	0.018	0.063	0.019	0.54851	0.55397	0.01550
334	chr17	78343504	78343704	5	RNF213	0.014	0.016	0.010	0.038	0.000	0.54949	0.86764	0.04664
335	chr1	120457961	120459261	27	NOTCH2	0.036	0.039	0.031	0.053	0.000	0.55999	0.22789	0.63380
336	chr17	40467710	40491485	39	STAT3	0.034	0.040	0.023	0.059	0.000	0.56418	0.51376	0.71754
337	chr9	19957357	19958157	17	SLC24A2	0.027	0.031	0.022	0.063	0.000	0.56498	0.75617	0.22788
338	chr3	38180130	38182805	29	MYD88	0.045	0.053	0.033	0.073	0.000	0.56578	0.70668	0.03867
339	chr18	73944894	73945344	10	ZNF516	0.018	0.025	0.008	0.056	0.000	0.56926	0.67544	0.01359
340	chr7	140453013	140453254	5	BRAF	0.012	0.020	0.000	0.075	0.000	0.56966	0.30182	0.01894
341	chr6	159238416	159238766	8	EZR	0.050	0.057	0.038	0.016	0.000	0.57311	0.00246	0.08463
342	chr18	77092821	77093021	5	ATP9B	0.008	0.010	0.005	0.075	0.000	0.57396	0.16232	0.00549
343	chr22	23523568	23610748	22	BCR	0.038	0.045	0.028	0.097	0.000	0.57399	0.04814	0.27043
344	chr22	22673243	22673593	8	IGLV5-52	0.027	0.035	0.016	0.117	0.000	0.57479	0.00701	0.30927
345	chr4	88011278	88011278	5	AFF1	0.014	0.016	0.010	0.038	0.000	0.57733	0.89980	0.03303
346	chr11	131747550	131748000	10	NTM	0.029	0.036	0.018	0.119	0.000	0.57801	0.02773	0.42832
347	chr2	90077982	90078316	6	IGKV3D-20	0.025	0.033	0.013	0.031	0.000	0.57996	0.26904	0.32350
348	chr2	96809890	96810360	10	DUSP2	0.063	0.066	0.060	0.006	0.000	0.58190	0.00002	0.00216
349	chr2	89265757	89265987	4	IGKV1-6	0.010	0.012	0.006	0.047	0.000	0.59812	0.84325	0.02299
350	chr19	53598587	53599037	10	ZNF160	0.024	0.031	0.013	0.063	0.000	0.60291	0.98122	0.12855
351	chr2	63335243	63631808	22	WDPCP	0.026	0.033	0.016	0.091	0.000	0.60661	0.01199	0.09457
352	chr9	21808815	21859450	9	MTAP	0.019	0.026	0.008	0.042	0.000	0.61688	0.80480	0.03120

353	chr6	27860480	27860895	7	HIST1H2AM	0.030	0.033	0.025	0.045	0.000	0.61920	0.45404	0.60865
354	chr6	27839659	27839759	3	HIST1H3I	0.036	0.038	0.033	0.021	0.000	0.62267	0.15955	0.75106
355	chr6	26252155	26252205	2	HIST1H2BH	0.015	0.016	0.013	0.063	0.000	0.62577	0.55784	0.18377
356	chr19	19256470	19293460	41	MEF2B	0.040	0.045	0.032	0.091	0.000	0.62683	0.04274	0.29098
357	chr14	107169646	107170861	21	IGHV1-69	0.091	0.098	0.082	0.107	0.029	0.63032	0.38178	0.00266
358	chr8	113308015	113569195	15	CSMD3	0.013	0.020	0.003	0.046	0.000	0.63047	0.85436	0.00010
359	chr22	22550338	22550788	10	IGLV6-57	0.042	0.049	0.030	0.131	0.017	0.64049	0.04005	0.29687
360	chr4	153249286	153249486	5	FBXW7	0.026	0.026	0.025	0.038	0.000	0.64551	0.50853	0.39977
361	chr11	120127164	120189629	22	POU2F3	0.027	0.033	0.018	0.091	0.000	0.64824	0.02013	0.09628
362	chr12	57496553	57499113	13	STAT6	0.046	0.054	0.035	0.072	0.013	0.65115	0.71967	0.94722
363	chr22	22937193	22937499	7	IGLV3-32	0.018	0.026	0.007	0.063	0.000	0.65348	0.49810	0.05644
364	chr6	138188484	138202489	64	TNFAIP3	0.024	0.028	0.018	0.035	0.004	0.65552	0.00591	0.00002
365	chr8	138849938	138850138	5	FAM135B	0.020	0.023	0.015	0.038	0.000	0.65643	0.70665	0.12531
366	chr14	107218756	107218856	3	IGHV3-74	0.073	0.082	0.058	0.104	0.058	0.66142	0.98960	0.26299
367	chr14	23344698	23345198	11	LRP10	0.059	0.063	0.052	0.034	0.000	0.66215	0.00576	0.01137
368	chr14	106866381	106866595	5	IGHV3-38	0.032	0.033	0.030	0.163	0.000	0.66584	0.01626	0.86538
369	chr1	3547351	3547701	8	WRAP73	0.024	0.027	0.019	0.063	0.000	0.66789	0.68610	0.19690
370	chr21	28213259	28216964	11	ADAMTS1	0.028	0.036	0.016	0.108	0.012	0.67094	0.03930	0.06299
371	chr2	169781121	169781321	5	ABCB11	0.016	0.023	0.005	0.125	0.000	0.67664	0.00990	0.06041
372	chr22	41513341	41574886	72	EP300	0.031	0.037	0.022	0.067	0.000	0.67996	0.51033	0.09373
373	chr18	56054916	56063816	24	NEDD4L	0.016	0.020	0.009	0.031	0.000	0.68133	0.24138	0.00093
374	chr14	106845301	106846536	9	IGHV3-35	0.055	0.064	0.042	0.097	0.000	0.68499	0.76566	0.05591
375	chr14	107136756	107136856	3	IGHV3-66	0.030	0.038	0.017	0.021	0.000	0.68512	0.22171	0.79848
376	chr22	23047068	23047318	6	IGLV3-22	0.043	0.049	0.033	0.042	0.014	0.68905	0.16524	0.80319
377	chr22	22786478	22786803	7	IGLV1-36	0.040	0.047	0.029	0.080	0.000	0.69080	0.82010	0.41665
378	chr8	122626848	122627148	7	HAS2	0.030	0.033	0.025	0.063	0.000	0.70243	0.90117	0.66520
379	chr5	131825018	131825218	5	IRF1	0.026	0.030	0.020	0.138	0.000	0.70868	0.00725	0.42851
380	chr22	23252688	23252788	3	IGLJ4	0.020	0.022	0.017	0.021	0.000	0.71377	0.39782	0.24178
381	chr14	107078456	107078606	4	IGHV1-58	0.050	0.053	0.044	0.063	0.000	0.71737	0.53128	0.17192
382	chr4	154624671	154625021	8	TLR2	0.017	0.020	0.013	0.125	0.000	0.72168	0.00257	0.03397
383	chr2	89196227	89215037	19	IGKV5-2	0.024	0.028	0.017	0.036	0.007	0.73228	0.12196	0.02080
384	chr18	55319681	55359256	17	ATP8B1	0.028	0.031	0.024	0.044	0.000	0.73256	0.29761	0.29755
385	chr1	61555803	61554303	11	NF1A	0.030	0.033	0.025	0.097	0.000	0.73331	0.11994	0.58902
386	chr10	89603603	89604053	10	KLLN	0.024	0.028	0.018	0.044	0.000	0.73666	0.57207	0.12653
387	chr22	23247138	23247609	9	IGLJ3	0.165	0.169	0.158	0.153	0.048	0.73794	0.02871	0.00093
388	chr11	117101044	117101194	4	PCSK7	0.042	0.049	0.031	0.016	0.000	0.73868	0.05815	0.47968
389	chr6	27861245	27861450	4	HIST1H2BO	0.037	0.045	0.025	0.031	0.000	0.74033	0.21815	0.85767
390	chr2	61441170	61441870	15	USP34	0.025	0.028	0.020	0.042	0.000	0.74279	0.23146	0.11749
391	chr11	111234537	111249512	16	POU2AF1	0.030	0.034	0.023	0.105	0.008	0.74326	0.02352	0.08875
392	chr5	5182146	5182446	7	ADAMTS16	0.038	0.044	0.029	0.107	0.000	0.75162	0.19189	0.54007
393	chr14	106667546	106667856	6	IGHV3-20	0.021	0.025	0.017	0.063	0.000	0.75404	0.64784	0.15262
394	chr2	145162402	145693052	53	ZEB2	0.041	0.046	0.032	0.048	0.008	0.76200	0.00643	0.47223
395	chr14	106494091	106494768	12	IGHV2-5	0.027	0.034	0.017	0.063	0.014	0.76623	0.78849	0.01259

396	chr2	65593036	65593213	4	SPRED2	0.057	0.061	0.050	0.250	0.033	0.77068	0.00195	0.40243
397	chr2	141245128	141245328	5	LRP1B	0.010	0.016	0.000	0.088	0.000	0.77497	0.10161	0.00830
398	chr22	23241763	23241813	2	IGLJ2	0.030	0.033	0.025	0.094	0.000	0.77602	0.38252	0.80404
399	chrX	153997584	153997584	5	DKC1	0.042	0.046	0.035	0.075	0.000	0.77946	0.93861	0.49207
400	chr10	5755067	5755267	5	FAM208B	0.016	0.020	0.010	0.000	0.000	0.77955	0.06988	0.04606
401	chr1	35472693	35472693	5	ZMYM6	0.016	0.020	0.010	0.025	0.000	0.77955	0.46246	0.04606
402	chr6	26250460	26250695	5	HIST1H3F	0.028	0.033	0.020	0.013	0.000	0.78052	0.07461	0.50252
403	chr3	176750700	176771710	17	TBL1XR1	0.020	0.024	0.013	0.051	0.003	0.78556	0.88935	0.00559
404	chr18	77170716	77288591	29	NFATC1	0.038	0.043	0.031	0.082	0.000	0.78831	0.61891	0.47180
405	chr13	41133663	41240784	49	FOXO1	0.025	0.031	0.016	0.042	0.000	0.78900	0.09626	0.00465
406	chr8	128951725	128951875	4	TMEM75	0.042	0.049	0.031	0.016	0.000	0.78980	0.05059	0.43332
407	chr22	22681928	22682198	5	IGLV1-50	0.020	0.026	0.010	0.088	0.000	0.79643	0.39142	0.12531
408	chr2	89976277	89976377	3	IGKV2D-30	0.066	0.071	0.058	0.125	0.000	0.79654	0.28677	0.06295
409	chr14	106757726	106758621	8	IGHV2-26	0.026	0.033	0.016	0.039	0.000	0.80101	0.48691	0.27328
410	chr1	2306312	2306812	11	MORN1	0.028	0.034	0.018	0.102	0.000	0.80151	0.03618	0.25568
411	chr14	106384031	106384926	9	IGHD1-1	0.039	0.046	0.028	0.132	0.024	0.81269	0.00673	0.00968
412	chr8	104897562	104898462	19	RIMS2	0.030	0.036	0.021	0.099	0.000	0.81294	0.04875	0.36772
413	chr10	89500958	89501108	4	PAPSS2	0.025	0.029	0.019	0.047	0.000	0.81562	0.75051	0.38140
414	chr1	201038553	201038753	5	CACNA1S	0.034	0.033	0.035	0.113	0.000	0.82537	0.08167	0.99310
415	chr13	84455243	84455243	35	SLITRK1	0.034	0.039	0.026	0.073	0.000	0.82863	0.60871	0.95353
416	chr22	23263508	23264123	9	IGLJ7	0.062	0.069	0.050	0.042	0.000	0.84212	0.02446	0.00290
417	chr5	140208034	140208834	17	PCDHA6	0.026	0.031	0.019	0.051	0.000	0.84499	0.73711	0.13168
418	chr1	23885408	23885899	10	ID3	0.015	0.020	0.008	0.081	0.000	0.84648	0.06666	0.00452
419	chr14	106518496	106519064	7	IGHV3-7	0.035	0.040	0.029	0.054	0.000	0.84779	0.54879	0.79096
420	chr9	22005930	22009000	13	CDKN2B	0.031	0.035	0.025	0.038	0.000	0.85460	0.20627	0.52500
421	chr11	58978693	58979345	11	MPEG1	0.032	0.036	0.025	0.080	0.000	0.85627	0.50475	0.70735
422	chr1	227842647	227842697	2	ZNF678	0.010	0.016	0.000	0.156	0.000	0.85664	0.04034	0.09510
423	chr6	106534267	106555367	60	PRDM1	0.031	0.036	0.023	0.065	0.000	0.86083	0.99103	0.15072
424	chr2	198950435	198950985	12	PLCL1	0.021	0.027	0.013	0.094	0.000	0.86126	0.14473	0.05072
425	chr18	6947105	6980665	10	LAMA1	0.027	0.033	0.018	0.094	0.000	0.86312	0.22629	0.28027
426	chr6	26197105	26197462	8	HIST1H3D	0.021	0.027	0.013	0.000	0.000	0.86864	0.00995	0.09168
427	chr19	51525627	51525927	7	KLK11	0.028	0.033	0.021	0.089	0.000	0.87219	0.14799	0.45199
428	chr2	61719435	61719635	5	XPO1	0.012	0.016	0.005	0.000	0.000	0.87795	0.09496	0.02531
429	chrX	141291053	141291534	10	MAGEC2	0.019	0.023	0.013	0.081	0.000	0.88059	0.07959	0.02755
430	chr14	35873672	35873822	4	NFKBIA	0.035	0.041	0.025	0.000	0.000	0.88119	0.02331	0.96205
431	chr2	89442292	89443217	19	IGKV3-20	0.042	0.047	0.036	0.148	0.050	0.88608	0.00002	0.00006
432	chr1	72334892	72335098	5	NEGR1	0.014	0.020	0.005	0.025	0.000	0.88638	0.51822	0.02712
433	chr1	9784433	9784533	3	PIK3CD	0.007	0.011	0.000	0.083	0.000	0.89151	0.14993	0.02634
434	chr2	170101186	170101386	5	LRP2	0.032	0.036	0.025	0.100	0.000	0.89564	0.18901	0.76737
435	chr7	110737412	110764944	51	LRRN3	0.019	0.024	0.011	0.086	0.002	0.90183	0.00080	0.00000
436	chr3	7620224	7620974	16	GRM7	0.032	0.038	0.023	0.078	0.000	0.90333	0.28646	0.77891
437	chr22	22569333	22569633	7	IGLV10-54	0.031	0.037	0.021	0.063	0.000	0.90702	0.86839	0.77523
438	chr17	75447869	75448419	12	9-Sep	0.031	0.037	0.021	0.036	0.000	0.90976	0.14194	0.64487
439	chr7	148506319	148523734	19	EZH2	0.019	0.025	0.011	0.082	0.000	0.91143	0.05741	0.00268
440	chr14	106621886	106622095	5	IGHV3-16	0.024	0.030	0.015	0.063	0.000	0.91521	0.67996	0.28737

441	chr1	181452915	181453115	5	CACNA1E	0.032	0.036	0.025	0.025	0.000	0.91767	0.14135	0.76209
442	chr2	58520801	58521201	9	FANCL	0.029	0.035	0.019	0.069	0.000	0.92005	0.73186	0.57669
443	chr19	51559442	51561922	16	KLK13	0.032	0.038	0.023	0.113	0.000	0.92076	0.04033	0.89701
444	chr16	2812097	2812747	14	SRRM2	0.056	0.062	0.046	0.045	0.000	0.92192	0.02154	0.01164
445	chr6	41903612	41909397	26	CCND3	0.041	0.047	0.033	0.058	0.000	0.92504	0.14949	0.21095
446	chr14	106068706	106071241	16	IGHE	0.118	0.124	0.108	0.215	0.158	0.92648	0.00059	0.00060
447	chr6	110777719	110778219	11	SLC22A16	0.027	0.033	0.018	0.034	0.000	0.92796	0.19315	0.23193
448	chr9	21970835	21994385	37	CDKN2A	0.027	0.031	0.020	0.039	0.000	0.92888	0.04082	0.03393
449	chr2	90025207	90025522	6	IGKV2D-26	0.012	0.016	0.004	0.031	0.000	0.92990	0.73921	0.01161
450	chr4	7728457	7728657	5	SORCS2	0.034	0.039	0.025	0.038	0.000	0.93035	0.30875	0.99310
451	chr7	5569056	5569356	6	ACTB	0.048	0.055	0.038	0.208	0.007	0.93481	0.00069	0.95055
452	chr3	140281599	140281849	6	CLSTN2	0.036	0.038	0.033	0.031	0.000	0.94099	0.11813	0.72422
453	chr2	89291907	89292182	4	IGKV1-8	0.020	0.025	0.013	0.047	0.022	0.94155	0.86146	0.00511
454	chr22	23260268	23260368	3	IGLJ6	0.043	0.049	0.033	0.063	0.000	0.94574	0.74604	0.48180
455	chr14	106815806	106815906	3	IGHV3-33	0.059	0.066	0.050	0.063	0.043	0.94598	0.41907	0.10857
456	chr6	26123615	26124080	9	HIST1H2BC	0.031	0.036	0.022	0.028	0.000	0.95616	0.07091	0.75304
457	chr3	49397609	49413039	18	RHOA	0.030	0.035	0.022	0.045	0.000	0.95622	0.26281	0.40030
458	chr22	29191137	29196512	28	XBP1	0.032	0.039	0.022	0.085	0.003	0.95630	0.05799	0.16891
459	chr14	106471396	106471580	4	IGHV1-3	0.007	0.012	0.000	0.141	0.000	0.95914	0.00935	0.01524
460	chr17	41847059	41847209	4	DUSP3	0.032	0.037	0.025	0.094	0.000	0.96078	0.74050	0.94029
461	chr17	51900442	51900892	10	KIF2B	0.035	0.039	0.028	0.088	0.000	0.96080	0.24029	0.71768
462	chr15	86312063	86312563	11	KLHL25	0.032	0.037	0.025	0.074	0.000	0.96521	0.83987	0.74482
463	chr18	53804516	53804766	6	TXNL1	0.036	0.041	0.029	0.115	0.000	0.96529	0.95667	0.84317
464	chr5	67590967	67591167	5	PIK3R1	0.018	0.023	0.010	0.075	0.009	0.97792	0.39415	0.02207
465	chr5	124079828	124080678	18	ZNF608	0.026	0.031	0.019	0.063	0.000	0.98245	0.74836	0.14794
466	chr2	90259932	90260232	5	IGKV1D-8	0.034	0.039	0.025	0.163	0.000	0.98690	0.17514	0.96394
467	chr2	88906682	88906832	4	EIF2AK3	0.059	0.066	0.050	0.063	0.000	0.98750	0.34568	0.07429
468	chr4	106157605	106157805	5	TET2	0.018	0.023	0.010	0.075	0.000	0.99542	0.34309	0.09635

Table 5

Reference Coordinates	Nearest Gene	Percent Non-Reference	Total Non-Reference Bases	Plus Strand Oligonucleotide	SEQ ID NOS:
chr8:128,750,550-128,750,699	*MYC*	0	0	CGACTACGACTCGGTGCAGCCGTATTTCTACTGCGACGAGGAGGAGAACTT CTACCAGCAGCAGCAGAGCGAGCTGCAGCCCCCGGCGCCCAGCGAGG ATATCTGGAAGAAATTCGAGCTGCTGCCCACCCCGCCCCTGTCCCCTAG	1331
chr8:128,750,550-128,750,699	*MYC*	2.5	4	CGACTACGACTCGGTGCAGCCGTAGTTCTACTGCGACGAGGAGGAAAACT TCTACCAGCAGCAGCAGAGCGAGCTGCAGCCCCTGGCGCCCAGCGAG GATATCTGGAAGAACTTCGAGCTGCTGCCCCACCCCGCCCCTGTCCCCTAG	1332
chr8:128,750,550-128,750,699	*MYC*	5	8	CGACTACGACTCGGTGCAGCCGTAGTTCTACTGCGACGAGGAGGAAATACTT CTACCAGCAGCAGCCGCAGAGCGAGCTGCAGCCCCTGGCGCCCAGCGAGG GTATCTGGAAGAACTTCGAGCTACTGCCCCACCCCGCCCCTGTCCCCTAG	1333
chr8:128,750,550-128,750,699	*MYC*	7.5	11	CGACTACGACTCGTTGCAGCCGTAGTTCTACTGCGACGAGGAGGAATACTT CTACCAGCAGCAGCCGCAGAGCGAGCTGCAGCGCCTGGCGCCCAGCGAGG GTATCTGGAAGAACTTCGAGCTACAGCCCACCCCGCCCCTGTCCCCTAG	1334
chr8:128,750,550-128,750,699	*MYC*	10	15	CGACTACGACTCGTTGCAGCCGTAGATCTACTGCGACGAGGAGGAAATACTT CTACCTGCAGCAGCCGCAGAGCGAGCTGCAGCGCCTGGCGCCCAGCGAGC GTATCTGGAAGAACTTCGAGCTACAGCCCACCCCGCCCCTTGTCCCCTAG	1335
chr8:128,750,550-128,750,699	*MYC*	12.5	19	CGACAACGACTCGTTGCACCCGTAGATCTACTGCGACGAGGAGGAATACTT CTACCTGCAGCAGCCGCAGAGCGAGCTGCAGCGCCTGGCGCCCAGCGAGC GTATCTGAAAGAACTTCGAGCTACAGCCCACGCCGCCCTTGTCCCCTAG	1336
chr8:128,750,550-128,750,699	*MYC*	15	23	CGACAACGACTCGTTGCACCCGTAGATCTACTGCGACGAGGAGGAATACTT CTACCTGCAGCAGCCGCAGAGCGAGCTGCAGCGCCTGGCGCCCAGCGAGC GTATCTGAAAGAACTTCGAGCTACAGCCCACGCCGCCCTTGTCCCCTAG	1337
chr3:187,443,281-187,443,430	*BCL6*	0	0	GCTCACCTGTACAAATCTGGCTCCGCAGGTTTCGCATTTGTAGGGCTTCTCT CCAGAGTGAATTCGAGTGTGGGTTTTCAGGTTGGCTGGCCGGTTGAACTGG GCCCCACAGATGTTGCAACGATAGGGTTTCTCACCTATTACCAAGAA	1338
chr3:187,443,281-187,443,430	*BCL6*	2.5	4	GCTCACCTGTACAAATCTGCCTCCGCAGGTTTCGCATTTGTAGGGCTCCTCT CCAGAGTGAATTCGAGTGTGGGTTTTCAGGTTGGCTGGGCGGTTGAACTGG GCCCCACAGATGTTGCAACGCTAGGGTTTCTCACCTATTACCAAGAA	1339

chr3:187,443,281-187,443,430	*BCL6*	5	8	GCTCACCTGTACAAATCTGCCTCCGCAGGTTTCGCCTTTGTAGGGCTCCTCT CCAGAGTGAATTCGAGTGTAGGTTTTCAAGTTGGCTGGGCGGTTGAACTGG GCCCCACGGATGTTGCAACGCTAGGGTTTCTCACCTATTACCAAGAA	1340
chr3:187,443,281-187,443,430	*BCL6*	7.5	11	GCTCACCTGTACAAATCTGCCTCCGCCGGTTTCGCCTTTTTAGGGCTCCTCT CCAGAGTGAATTCGAGTGTAGGTTTTCAAGTTGGCTGGGCGGTTGAACTGG GCCCCACGGATGTTGCAACGCTAGGGTTTCTCACCTATTTCCAAGAA	1341
chr3:187,443,281-187,443,430	*BCL6*	10	15	GCTCACCTGTACAAGTCTGCCTCCGCCGGTTACGCCTTTTTAGGGCTCCTCT CCAGAGTGAATTCGAGTGTAGGTTTTCAAGTTGGCTGGGCGGTTGAACTGG GCTCCACGGATGTTGCAACGCTAGGGATTCTCACCTATTTCCAAGAA	1342
chr3:187,443,281-187,443,430	*BCL6*	12.5	19	GCTCACCTGGACAAGTCTGCCTCCGCCGGTTACGACTTTTTAGGGCTCCTCT CCAGAGTGAATTCGAGTGTAGGCTTTCAAGTTGGCTGGGCGGTTGAACTGG GCTCCACGGCTGTTGCAACGCTAGGGATTCTCACCTATTTCCAAGAA	1343
chr3:187,443,281-187,443,430	*BCL6*	15	23	GCTCACCTGGACAAGTCTGCCTCCGCCGGTTACGACTTTTTAGGGCACCTCT CCAGAGTGAATTCGAGTGTAGGCTTTCAAGTTGGCTGGGAGCTTGAACTGG GCTGCACGGCTGTTGCAACGCTAGGGATTCTCACCTATTTCCAAGAA	1344
-	-	-	-	**Minus Strand Oligonucleotide**	-
chr8:128,750,550-128,750,699	*MYC*	0	0	CTAGGGGACAGGGGCGGGGTGGGCAGCAGCTCGAATTTCTTCCAGATATC CTCGCTGGGCGCCGGGGGGCTGCAGCTCGCTCTGCTGCTGGTAGAA GTTCTCCTCCTCGTCGCAGTAGAAATACGGCTGCACCGAGTCGTAGTCG	1345
chr8:128,750,550-128,750,699	*MYC*	2.5	4	CTAGGGGACAGGGGCGGGTGGGCAGCAGCTCGAAGTTCTTCCAGATATC CTCGCTGGGCGCCAGGGGCTGCAGCTCGCTCTGCTGCTGGTAGAA GTTTTCCTCCTCGTCGCAGTAGAACTACGGCTGCACCGAGTCGTAGTCG	1346
chr8:128,750,550-128,750,699	*MYC*	5	8	CTAGGGGACAGGGGCGGGGTGGGCAGTAGCTCGAAGTTCTTCCAGATACC CTCGCTGGGCGCCAGGGGCTGCAGCTCGCTCTGCTGCTGGTAGAA GTATTCCTCCTCGTCGCAGTAGAACTACGGCTGCACCGAGTCGTAGTCG	1347
chr8:128,750,550-128,750,699	*MYC*	7.5	11	CTAGGGGACAGGGGCGGGGTGGGCTGTAGCTCGAAGTTCTTCCAGATACC CTCGCTGGGCGCCAGGCGCTGCAGCTCGCTCTGCTGCTGGTAGAA GTATTCCTCCTCGTCGCAGTAGAACTACGGCTGCAACGAGTCGTAGTCG	1348
chr8:128,750,550-128,750,699	*MYC*	10	15	CTAGGGGACAAGGGCGGGGTGGGCTGTAGCTCGAAGTTCTTCCAGATACG CTCGCTGGGCGCCAGGCGCTGCAGCTCGCTCTGCTGCTGGCAGGTAGAA GTATTCCTCCTCGTCGCAGTAGATCTACGGCTGCAACGAGTCGTAGTCG	1349
chr8:128,750,550-128,750,699	*MYC*	12.5	19	CTAGGGGACAAGGGCGGCGTGGGCTGTAGCTCGAAGTTCTTTCAGATACG CTCGCTGGGCGCCAGGCGCTGCAGCTCGCTCTGCGGCTGCTGCAGGTAGAA GTATTCCTCCTCGTCGCAGTAGATCTACGGGTGCAACGAGTCGTTGTCG	1350
chr8:128,750,550-128,750,699	*MYC*	15	23	CTAGGCGACAAGGGCGGCGTGGGCTGTAGCTCGAAGTTCTTTCAGATACGC TCGGTGGGCGCCAGGCGCTGCAGCACGCTCTGCGGCTGCTGCAGGTAGAA GTATTCCTCCTCGTCGCAGTAGATCTACGGGTGCAACGAGTCGCTGTCG	1351

chr3:187,443,281-187,443,430	*BCL6*	0	0	TTCTTGGTAAATAGGTGAGAAAACCCTATCGTTGCAACATCTGTGGGGCCCAG TTCAACCGGCCAGCCAACCTGAAAACCCACACTCGAATTCACTCTGGAGAG AAGCCCTACAAATGCGAAACCTGCGGAGCCAGATTTGTACAGGTGAGC	1352
chr3:187,443,281-187,443,430	*BCL6*	2.5	4	TTCTTGGTAATAGGTGAGAAACCCTAGCGTTGCAACATCTGTGGGGCCCAG TTCAACCGCCCAGCCAACCTGAAAACCCACACTCGAATTCACTCTGGAGAG GAGCCCTACAAATGCGAAACCTGCGGAGGCAGATTTGTACAGGTGAGC	1353
chr3:187,443,281-187,443,430	*BCL6*	5	8	TTCTTGGTAATAGGTGAGAAACCCTAGCGTTGCAACATCCGTGGGGCCCAG TTCAACCGCCCAGCCAACTTGAAAACCTACACTCGAATTCACTCTGGAGAG GAGCCCTACAAAGGCGAAACCTGCGGAGGCAGATTTGTACAGGTGAGC	1354
chr3:187,443,281-187,443,430	*BCL6*	7.5	11	TTCTTGGAAATAGGTGAGAAACCCTAGCGTTGCAACATCCGTGGGGCCCAG TTCAACCGCCCAGCCAACTTGAAAACCTACACTCGAATTCACTCTGGAGAG GAGCCCTAAAAAGGCGAAACCGGCGGAGGCAGATTTGTACAGGTGAGC	1355
chr3:187,443,281-187,443,430	*BCL6*	10	15	TTCTTGGAAATAGGTGAGAATCCCTAGCGTTGCAACATCCGTGGAGCCCAG TTCAACCGCCCAGCCAACTTGAAAACCTACACTCGAATTCACTCTGGAGAG GAGCCCTAAAAAGGCGTAACCGGCGGAGGCAGACTTGTACAGGTGAGC	1356
chr3:187,443,281-187,443,430	*BCL6*	12.5	19	TTCTTGGAAATAGGTGAGAATCCCTAGCGTTGCAACAGCCGTGGAGCCCAG TTCAACCGCCCAGCCAACTTGAAAGCCTACACTCGAATTCACTCTGGAGAG GAGCCCTAAAAAGTCGTAACCGGCGGAGGCAGACTTGTCCAGGTGAGC	1357
chr3:187,443,281-187,443,430	*BCL6*	15	23	TTCTTGGAAATAGGTGAGAATCCCTAGCGTTGCAACAGCCGTGCAGCCCAG TTCAAGCTCCCAGCCAACTTGAAAGCCTACACTCGAATTCACTCTGGAGAG GTGCCCTAAAAAGTCGTAACCGGCGGAGGCAGACTTGTCCAGGTGAGC	1358

Table 6

Name	Sequence	SEQ ID NOs.
TNFRSF14_chr1:2488006-2488106	TCTCTTCTGGCCCACAGCCGCAGCAATGGCGCTGAGTTCCTCTGCTGGAGTTCATCCTGCTAGCTGGGTTC CCGAGCTGCCGGTCTGAGCCTGAGGCATG	1
TNFRSF14_chr1:2488106-2488206	GAGCCTCCTGGAGACTGGGGGCCTCCTCCCTGGAGATCCACCCCCAAAACCGACGTCTTGAGGCTGGTGA GCCCCCGAGCCTCCTCTCCGTCTGCTCGCA	2
TNFRSF14_chr1:2488206-2488306	GATCCCAGTTCTGACCCCAGGGCCTCCCACAGATCTCTTCCCCATGCCCCTGTCCTGGCCGTTGCTGGCTC CGGCGTCCAGCCCGTCCCCTGCTGCCTGG	3
CSMD2_chr1:34404022-34404122	CCATGTTGCTGGCTTACTTGGCATTTCCCATGATCTCACACTGCTGGCTTATTTGGCATTTCCCATGATCCC CTGCTGCTGGTTTACTTGGCATTCCCTA	4
CSMD2_chr1:34404122-34404222	TGATCCCATGTTGCTGGTTTACTTAGCATTTCCCATGATCCCATGTTGCTGGCTTACTTGGCATTTCCCATG ATACCATGTTGCTGGCTTACTTGGCATT	5
NEGR1_chr1:72334891-72334991	ATAGATTAGAGGAAGGAATTCTAGATGAAATTAAGTAAATGAGTTATTTAAGTCAACTAATACAAGTCCT CAAAACTTTGATTATATAGAGAGCTAAACT	6
NEGR1_chr1:72334991-72335091	GATAAATATAGACAAATATAGTGAGCCTATAAATTAAAGCTATACTATGATGAAAAAATAAATGAATAAT TGTGAAATAGCCAAAAATACTAAAATACAG	7
NEGR1_chr1:72335051-72335151	AATGAATAATTGTGAAATAGCCAAAAATACTAAAATACAGCTATAAGGTTAAAAATAAATCTGAATAAAA AATGTAGGAGGGAAAAGTGATTACCTTACC	8
BCL10_chr1:85733207-85733307	GACATGCATCAAATGTAAACAAATGATTACAGCCATTTTATAAAAAGTCATATTCTTTAAAACATTTTTTG TCATCATTAAAAATTAAAAGGCAATAAAG	9
BCL10_chr1:85733307-85733407	TGTCATTGTCGTGAAACAGTACGTGATCTTAAGGGAAGAAACATCTCACTAGAGTTTGCACAAGTTCCTT CTTCTTCTAACTGTAGATCTGGTGGCAAAG	10
BCL10_chr1:85733407-85733507	GAGGAGCCCCTGGGTCCCCAGGTCTGGGAAGTGTAGTTGAAGAGAAGATGGTATTTTCAGTTCTGCCTAC TTCTAGAACAGGCAAATTCAGAGAAGAATT	11
BCL10_chr1:85733507-85733607	AGTAGAAAAAAAGGGCGTCGTGCTGGATTCTCCTTCTGGATGGTACATGACAGTGGATGCCCTCAGTTTT TCAGAGAAATTACTCTCATCTGAATTTGAT	12
BCL10_chr1:85733607-85733707	CTGGAGAGGTTGTTCGTGGCTCCATCTGGAAAAGGTTCACAACTGCTACATTTTAGTCCTACAATAAAATT ATTCAGATGTAAATGAAAAAGTAACTAAA	13
BTG2_chr1:203274697-203274797	ACCCGAGACCTCTCACTGAGCCCGAGCCGCGCGCGACATGAGCCACGGGAAGGGAACCGACATGCTCCC GGAGATCGCCGCCGCCGTGGGCTTCCTCTCC	14
BTG2_chr1:203274797-203274897	AGCCTCCTGAGGACCCGGGGCTGCGTGAGCGAGCAGAGGCTTAAGGTCTTCAGCGGGGCGCTCCAGGAG GCACTCACAGGTGAGCGCATGCCGAGGGGCC	15
BTG2_chr1:203274897-203274997	TGGCGCCACCGGGGGTCGGCCCCATCCCTGCCAGGGCCGTCTTTCTTCTACTCCTGCGGCAGGGTGACCC ACGGGAGCAGCTTTGGGACTCGGTGGCCCT	16
BTG2_chr1:203274997-203275097	CCTCCGACCCCCGGGGCGGCCCGCAGTCCCCAGTTTCCTGGGTCCTCCTCCCCAGCCCTGTGCTCGGGTCT CGGCCGTGGCGGTTCTGATGGGGCGCGCC	17
BTG2_chr1:203275097-203275197	CCTCTACGCTCTCGGAGGCGCAGACCCTGGTCCTGGAGTGCCAGCCCGAGTCCCCAGCTTATGCCCCTGTC TCATTACGGGCTCGTCTCCCTCGCTGGAC	18

BTG2_chr1:203275197-203275297	CCTCGAGATCTTAAGACCCTCGATGGATGTTGTTGCGGGCCGCCCGGTCGGCCGAGGGGTCCCGATGAGG GAAGAAGGTGCAGTCGAGCCTTTTCAACAA	19
BTG2_chr1:203275297-203275397	TTTGGAGTCCCAGTGCGGTTCTTCCTGCCGGTCGGGGTGCGCTGTGCCTGGGGTAGTCCACTGGTTGCTGA CTGGCTTCAAGTTGGAATTTGGGCCCCCT	20
BTG2_chr1:203275397-203275497	TTGTGTTATCTTTGGTTCCCCTTAGCCATCTGCCACCTATTGTGGTAGGGAGGAGAGCCTCGTAGCTCGTG ACCCTGCCGTGCGGGCCTTCAAGTTGGGA	21
BTG2_chr1:203275497-203275597	GGTGAAGAGATAAGCAGCCCGCTCGCTGGCTGGGGAGAGACCTCTCTCCCAGCTGTTTCTAGCTGGTTAC TGTCAGTTTTGGGAAGCGATAGCCATCTCG	22
BTG2_chr1:203275597-203275697	GAACGCACCCACACAGACCCTGCCTTCTGAGGAAAAACAGATGTTTCATCAAAACAACCCAGTTTTCACTC CCTTAGGCACTGCTAAGGAAGGTTCTCTGA	23
BTG2_chr1:203275697-203275797	CTCTTCTGAAGGAAGCAGAGGGAACACAGGGTGGGAGGTCCAGTGACTTGCTGTGGACCCAACACAATGTTG GCAGCCTTCCTGGCCCTGAAACTTCAGCTC	24
BTG2_chr1:203275797-203275897	ACAGGTCTCCAGAGGCCCTGCCTGGACATGCCAGTCCCAGTCACACCCTTCCCTTGCTTTGGGGGTGTGCC AAAAGCAATACACTGGCCACTAGAGAGTA	25
BTG2_chr1:203275897-203275997	CCCTAGAGGCTCTAGAATCCCCCTCCCAACACGCACACACACACACACACTCTCTCTCTCACACACACA CACTCAGTCACACACACACACACACAC	26
ITPKB_chr1:226923691-226923791	CTTTCAGATCTTTCGCAGCGTCCCAACAGGGCAAAGGCTCCAGCATTCTGCCAGAAGGAATTCCCGCCTCC ACATTCCCGGTCCCCGGCTGTGCTGAGGG	27
ITPKB_chr1:226923791-226923891	GCTGCCCCCAAGCAAGCCCAGCGTTGGGGACCCTCCCTCCACTCTGTCGGAGAGCTGCCAACGGCCCCCCG CCCACGGGGGCCCCACTTCGGGCCTCCTCA	28
ITPKB_chr1:226923891-226923991	GGGCCTACGGAGGCCAGGGCCCTGGGCAGCCTGGACCAGCTCAGGGAATCAGAGGACTCTGCGGCTTTGC ACGCTCACAGTCGTCTCCTCTGGCCTTTTGC	29
ITPKB_chr1:226923991-226924091	CCACTTCAGGCTCCCCAGAGCCCGGCATGCCACAGGGCAGATATCCTTTCCCCATCTTCCCAGGGGGTTCT CCATCGCGGGGCCCGCCCCTTTCTGGGGC	30
ITPKB_chr1:226924091-226924191	TGGGCTTGTCTCACTGCCCAGAAACTGCCCCTGCCTCTCCACCAGGGGCCTCTGGGGGCTGCAGGTCCTCAA GCTCACGGGCTCTCCCAGACGGCTCAGTG	31
ITPKB_chr1:226924191-226924291	AGGGCAAGATCCTGTGGACCGGTGTGGCCCAGTGGATGTAACTCTCGCTGCCACTTCCGTGGCCATCGTTA AGCTAGCTCCGAACAGCCCCAATGAGGGAG	32
ITPKB_chr1:226924291-226924391	CTAGGCAGCTCCGAGTTCCCGGGGTAGGAGAGCCCCTTTTGTCAATTTCCATAGCTGTGGGGTGAGCCACA GCGGGGACTGGCAGGGATACCCTTCTCCAT	33
ITPKB_chr1:226924391-226924491	CCTTACAAAAGCGGATGGACCCTGAGCCTCTGATCCTGTAGGGGCAGCCCGGCGGGAAGAGGTGGCATT CCTTTCTTCACCTGCGAGGAGCATAGGCTG	34
ITPKB_chr1:226924491-226924591	GGCCCTCCTTTCCTCCCGGAGTCGGTTCCTGAAGTCTCTGGACATTGCTCCCCCCCAGGACTTTGTCCTCCG TTCCTCGCTCCGGGCGCCCTGAACCAGGA	35
ITPKB_chr1:226924591-226924691	CCCTTCCAGGGGGGCTGACTGCTGCTGCGGAAGGGGCACGGGGAGGGCGAGCGAGCCCTGCCCAAACGCG GGCTGCGCGGGCGCTTGAATGGCGGAGCTCTG	36
ITPKB_chr1:226924691-226924791	TGCCTGGATGTGCGCCTCAAACATGCCCACTTTCTGGTTCACCTGCACGTTCTGCAACTCGCGCTGCAAGA TCCGCAGCTTCCTCTTGGCCTCCTCCGGC	37

ITPKB_chr1:226924791-226924891	CCTGGCGGGGAGAGGGTACCGGCTGCCACCACCTGCTGCCGGTCCCCTCGCAGGCGACCAGCCCAACTTG GGCTGCTCACGCTACTGCCGCTGCTGCCGC	38
ITPKB_chr1:226924891-226924991	TGCCACTGCCCGCTGCTACTATTCAGCCTGCGCCGGCCGCTCCGCCAGCCCCCCGGGGCTCCGGGGCTCCTCG GGGGACAGCGACTCGGCTGGGGGGAAGAG	39
ITPKB_chr1:226924991-226925091	GAAAGAGGCGCCTCTCCCGGGGCTGAAAACGCTGCCGGGGCTCAGCACTGCCCTCCTCGGGGGCGGGGG CGTCTCGCTGCCACTGGGCCCCGGGCCGCCG	40
ITPKB_chr1:226925091-226925191	CCGCTCTTCATCTCGTTGGCGCTATTCATGATCACCAGGCTATTGAGCGCATAGCAGTACACAGCCATAGT ACTGGGTCCCCGCGCTGCCCGCCGCGG	41
ITPKB_chr1:226925191-226925291	CTCCCGCTCCTGCTCCGCCGCCGGCGCCTCCTCCCGGCGCTCCCGGCTCAGCCCCGGAGGCCCGGCAG CCGCGGCTCCGCGCGCAGATGGGGCGGCA	42
SLC1A4_chr2:65258145-65258245	AAGTGCGAAGGAAGTGTCAGGCTGGATGTCAAAATGAACACCTTGGAGAACTGGATGATGGAACAGACG GTAAAAATCAGCTAAACATCAGAGAAAATGG	43
SLC1A4_chr2:65258245-65258345	AGGAAGAGGTCAAAACTGTGAACAGGAACTAGAAGAAAGTGTAGCAGAAAAAGACTTGTCACAAACTTC GAGAGATTTGGAGAAAATGATGTCAAAACAC	44
SLC1A4_chr2:65258345-65258445	ATCTTCCTCAAGCCCATGCTGAGTATCTCTGATTTGGTTAATTTCTTGGTAAGTGTTCCAAGTACAGACAA CAAAGCAGAAAAGCACTGATTACAGGGAA	45
SPRED2_chr2:65593035-65593135	TATGCAGAATGATCCTTCAGATCATGTGAACGCTATAATTAAATGTTGCTACCAAATCCCCACTACCCTTT CTCCCACCTAGAAAAAGTTTAATGCATGAA	46
SPRED2_chr2:65593135-65593235	TTCAGTATGAGCAAATTGTGATTTATAAAAACAAACAAACAAACAAACAAAACCCACCCTATTCAC TCCGTAGGGGAATAAAGCTTTCTTGCATTA	47
SPRED2_chr2:65593180-65593280	AACAAACAAAACCCACCCTATTCACTCCGTAGGGGAATAAAGCTTTCTTGCATTAAGTCACGCATCATGG GGGTAGGAAAAAAAGCACAGTACTGAAAGAA	48
EIF2AK3_chr2:88906681-88906781	GTGAAGTGATCCAAATGTAGCCCAGAGATCCTAAAGAAAAAAACGATGCTCATGTGTTACAAAAACAAAATT TTAAGGCAATCAGTGAGGAATCACAGACAA	49
EIF2AK3_chr2:88906781-88906881	ATTTCCTTAGTGCTTTTATCAAGGTTGAATCTGAATATAAATTACTAGAGGAAAGCAAATCAGATTTCACA TCTGAAAATTAAAAACAAAATTCTTAGCT	50
IGKC_chr2:89127261-89127361	AGGCAACAAAATGAGATCCTGTCCCTAGAAAACATTTCAAAAAATTAACAGCATGGTGACGCACACTTGT AGCCCTAGCTACTTGGGAGGCTGAGTGGGA	51
IGKC_chr2:89127461-89127561	AAGAACTTAAGCAGACTAGGATATAAAGTATAGGAGCGTATTGTGTACAGGAACGGGAAATACTGTTTCC TGGATCTTTTGTTTCACTTACGCACACACC	52
IGKC_chr2:89127561-89127661	CACACCCGCCAGTAGTGTACCAGGTTGCGATGGAAATCTCTCTCTTTCTGTGGATGAGTTTGTGGAAGCCC TTGCTCCAGCATGCCCTCCTTCCTGCCCA	53
IGKC_chr2:89127661-89127761	CCCCTGGACCATTCCTTCCCTTCACAGCACTGTCCCATGGGTAGGCCACAGCCCAGGCACAGGCCCCAGCCT GGCGGCTGCAGCAGGAGCCCCATCCCAGG	54
IGKC_chr2:89127761-89127861	GCCTGAGGGGCCATGCGGGGGTCTGGGTGGGAGTGGGAACCGCTGAGGAAGGTGAAGGGAAATATGGTG AGATGACAGGCCCCGCTGTCAGGGAGAGTGGG	55
IGKC_chr2:89127861-89127961	AGGAGCCCTGGAGTGCCCTACCTCTGTGGGGCTGGAACTCCCTGTATCCGAGCTAGGGTCTTCCACACGC ATGCTACTACCCCAAGTGCCACAGCTGGAG	56

IGKC_chr2:89128431-89128531	TCATCTCCCACTGGATAACAGTGTTGTCGGGAACTTCCATCCAGCACTGGCGGACACTCCCGTCGCAGCTG CTCCTGACTGAGCAAGTCATTTAAGGGGG	57
IGKC_chr2:89128531-89128631	TCCTTGGCACTCATAAGCACTCACAGAATGGGGCTGGCAGTGCGCCCGGCCTCCCTGGGATGGGTCCAGA ATGGTAGGAAGCGCAGTCCCGGGAGGGACCC	58
IGKC_chr2:89131726-89131826	ACTGCTTAGAGCTCTCAGCCCTAGATGGCGTATCACAGTTAATGCTCTATAAAACCCATCATGGCTTTTCC CTAGTAAGCCTCAAATCGCTGCAAGCAAG	59
IGKC_chr2:89131826-89131926	GCTTCATATATGAGAGTTTCTGCTGTCTCCTGGAGCCATCTCACCCAAAGCCACTGACTCTGGGAGACCAG CCCAGGCCACAAACCAGCAAAGCACCAGT	60
IGKC_chr2:89131926-89132026	TATAGTTAGAGCTGCATTATAAAGTGGCCAGAGGACATTTCTTTGCAGTGAGATGTGTATCGTGAACGTT TGGGGCCTGTGCTCGCCTAGTCCTCATCTT	61
IGKC_chr2:89132026-89132126	TGCTTTTCTAGGTACACAAAGCCATCCCATGGCTGCAAATGTTAGCTGGGCTGGGCTCCCTACTTGCCTCA AGCCCCTTCATAGACCCTTCAGGCACATG	62
IGKC_chr2:89132126-89132226	CTTTTCTCTGGACGTTTACAGACAGGTCCTCAGAGGTCAGAGCAGGTTGTCCTAGGGAGCAGGGAGGCTT CCTAGGGAGGTCAGACTCCAAATAGTGGAT	63
IGKC_chr2:89132226-89132326	ATGGCAAAAAATGCAGCTGCAGACTCATGAGGAGTCGCCCCTGGGCTGCCACTAGGGCTCCCACAGTGTGCG CTGCCAACCTGCTGCCCGTGCCAGAAACTCT	64
IGKC_chr2:89140556-89140656	CAACTGTGCCCCTGCACTGTTAGGGCCCTTGTCAAAACAACACATTTCTCAGTGATTCTGAGACTCTTTCTC TTATCTATAGAAGTCATAACTCAAGAGTA	65
IGKC_chr2:89140656-89140756	AAATCATACCAATATTTTACATAAACCCTAGAATTTTTATAGATCTATTATTTCTTTTTAGAGTACATATTG GAAGTAACTTCACAAGGAACATTTTCTT	66
IGKC_chr2:89140886-89140986	TCTGGTCAAACCACTCCACAAATAAGTGGACTGATCCTCTTGACTCTATGTGTAAGTGCCCATTGTGTGT GCACAGAGCTGGTGAGAACCGCCATGGTG	67
IGKC_chr2:89140986-89141086	CTAGGTGGGGGTGGTGTTGGTGGAGTTGGACTAGATTATCTGGGATCATGCGAAATGGAAATTCATTTCT AGCTGGCTGGCTTCAGAAGGTGCCATCTCC	68
IGKC_chr2:89141086-89141186	TATTTTTATATGAAGCGGTGCTTTGGAACTCAGGGCAACGAAGGGGTGGGTGTGCTGCACAAGGACAGCAGA AGAGTGAGCTGACTGGTCCCTGAAATCGCA	69
IGKC_chr2:89141186-89141286	GTTGGAAAGTGGATTACCAGTGCAGTAGAACTCTTCACGGAGGCCTGGACCATCAGGTCTAATGGTGTTG TTCCAGGTGGGTGGTCATGTGGAGCAAAAA	70
IGKC_chr2:89141286-89141386	TATTTGAAATCAGCGAGCACGTACCTGAGAGATGACTTTTCCACTTGGGCTAGTCTCTTGATATTTCTGGT CCTGTTTCTTCATCTGTAAACTGGGTTAG	71
IGKC_chr2:89157326-89157426	AAGGAGACCAAGAAGCGTATTTAAAATCTTGATGTTTTGAGTTTCTTCCTAGCTTCCCCCTATTCCTTAAT AAAGTTCTAAATTGTTTTGTTGGAGCTCT	72
IGKC_chr2:89157426-89157526	TTGCAGCCATTCTGAGGGCTTTGCATGCTTTTCTGACCTTGCAGTAAACTCAATGCTTTAGGCAAAGAATG GCCACGTCATCCGACCCCCTCAGAGTTTA	73
IGKC_chr2:89157526-89157626	GAATTCAGAACAGGTCTGAAGAAGACCAGGCAGCGGCTGAGTCAAGGAAAGCCTCCGTCCGCTTTTTATTT CCCCTGTGCCTCTTCCAGGACTGTGCTGGG	74
IGKC_chr2:89157626-89157726	ATAACAGGCTCCCGGGGGTTACTTTGGCTGGGCTAAAACCTCCCTGCAGAGCAGGCCCTGAGCCC TGCCTCTGCGCCTGGGTGGTGTCAGCCCT	75

IGKC_chr2:89157726-89157826	CCACCTTCTGACTGTTCCAGCAACTCTCTAAGCCCTCCCAAAGGCCTCAAGGCCTGTAACCATATGCAGCA ATTTTCAGCCATACCAGGAGAGGTCAACT	76
IGKC_chr2:89157826-89157926	GTAATCTTGGCCACCTGCCTAAGAGGAAGTGGCTAGCTTCACTTCTGACCCTCAGCAACTGCCAGGTGGC CTCTTGGAAATCCCCCCTCTGGGGGATTCCA	77
IGKC_chr2:89157926-89158026	CCCGTTGGGTGGGAGAGCAGTAGTTAAAATGTAAAATAAGAATCTTTTGCTGGGAGAAGTCAACAGATAG GGAGAAGTCAGCTGATAACAGAAATAGTTT	78
IGKC_chr2:89158036-89158136	TAAAACTAACTTCACTGTTAACCAAGCAGTTCAACATGAAAGACTGAATCTCTTATGTTTAATATTTTCTT CTCTTTTAATCTTCATAACTAATTTTTTT	79
IGKC_chr2:89158136-89158236	CAGATAATTGTATAAAATAACCATGGTAGCAAAAATAATGTGATCACTGGAAAATAAGCAGGGAAAAACA TGCTATGAAGATACTCCTATCTGGGTGAATT	80
IGKC_chr2:89158236-89158336	CTTGATAGCTTTACATTTTTTCATCTGGCATTTAAACATTAAACAGTTAATGTATTTGACATGAAAATTATT TCAAGTTATCTTATTAGTTTTTAATAGAGT	81
IGKC_chr2:89158336-89158436	TTAAAAAGTGTTTAAAAGAGTTTTCAAAAGGCTCTAAAATCATTTTGAAATAGTTTAAAACAGTTTTTGAAT CGTTGTAAGTTAGTTTTTAATAGAGCTTTA	82
IGKC_chr2:89158436-89158536	AAAAGGCCCTAAAATAGTCCTATCAAGTTGTTGCAGACCAAAATAATCTCCTTAAATATCACTTTTGAGAT CAGCTGGGGTAAACGACAGCAACACAATG	83
IGKC_chr2:89158536-89158636	ACAAATCATTAAACTATTTTAGAGATTATGAAATTAAAATACTCAGATTAAAATTTTCCTATCACAGAATT AAGGTACTGGAAAATATGTTTTAAGTTTTT	84
IGKJ5_chr2:89158636-89158736	ATTAATCACATTGCTATAGGTTTAGATATTTTGTACAACTGAAATAAAATCACACACTGGCAGCTACATTT TTGAAAGTTAAAAACATGGTCACGAATAT	85
IGKJ5_chr2:89158736-89158836	ATCTTATTTTAAAATCAGTTAATATACCTTAATGGTATTTAATGCCAAATTCAAAGTGAATTGATCAAGCC CTCAGTGGCCAGGTCATGGGTGTGATTTT	86
IGKJ5_chr2:89158836-89158936	TACTCTGAAAGAATTACATATTTCTTTCTTTTGGTTGAGCTTTTGTTATTTAAATACATTTGATGAGAGG ATATTGAAATAATTAAATAGCACTGAAAA	87
IGKJ5_chr2:89158936-89159036	AAAAAAAGCTTTAAATTATTTACAATCCCCTAATGGAAATTTTCACTAATGAGATATCATAAATGAATGTGA ATTTTATTTCTGAAATCTCTAATAAATCA	88
IGKJ5_chr2:89158941-89159041	AAGCTTTAAATTATTTACAATCCCCTAATGGAAATTTTCACTAATGAGATATCATAAATGAATGTGAATTTTT ATTTCTGAAATCTCTAATAAATCAGTCTT	89
IGKJ5_chr2:89159041-89159141	CTCCCTGGTTTTCCCAGCTCAGCGCCCATTACGTTTCTGTTCTCTTTCCCTTAGTGGCATTATTTGTATCAC TGTGCATCAGGAAAGCTGGCTACGGCAG	90
IGKJ5_chr2:89159141-89159241	CATCAATCGGGCAGACACAGGGTGGCCACGGCCACTAGCGGCAAGGCGGCTGCCCCAAGAGCGCGGTGG CATGGCCACCAAAGCCACTCAATCGAGAAAG	91
IGKJ5_chr2:89159241-89159341	ACCGCGGCTCTGTCTACAGCTCGCGGTGCCACGGCCTTCTTGGCAGAATAAAAAATGTAGACAAGTAATAA CAGAGGATAATGAAAGAACATACTCTTTAA	92
IGKJ5_chr2:89159341-89159441	AATATTTCCTATTTTTTTCACAGACCCACGGTCATTAAAAAAATGCAATTATTTACTTTTTTTCATTTAAACA CATTTCTTTGAGATTGAGCTTTTGGGAA	93
IGKJ5_chr2:89159441-89159541	TAACCACCTTTCCACCATTACAATAAGAGATAATTTCACGTTTAGTCTAATGTACAAAATTGGATTTTTTAAA AAATGAGCTCTATCTGTGAAGCCCTTATT	94

IGKJ5_chr2:89159511-89159611	AAAATGAGCTCTATCTGTGAAGCCCTTATTCCTATAGAATGTGTCTTTTTGAGTTTATTACTTATTACAGA CTCTAAAAACAACATTGCTGCTGATTTTTC	95
IGKJ5_chr2:89159611-89159711	AAGTAAGCTGCCTCTTCTACATAGCAAATAGGTACACTTCACTTTTCCCTGATTTTTCTTAGGGCGTGCTA TTGATTTTTATTGTTGTCTGACAAAATAA	96
IGKJ5_chr2:89159711-89159811	TTTATCAAACAAAAGGGAGAAAGACTAAAAAATGTATTTTTCCACTTTTCTGTATCATGCATAATCAGCAA CAACCAATACAATATTTGGCAAGAGTGAA	97
IGKJ5_chr2:89159811-89159911	CAAAAATAAATTTACTTTTGCTCCTTAGAAATACAAGGGTTCCTTTTTAGTTACACTTTTTTTTTTTTACTTT GTGTCATTCAGTTTAGAGCAATTTAATC	98
IGKJ5_chr2:89159911-89160011	TTTTTTTCTCCAAATCCATTTTTGAAGCTGAGTTTAACTTTTGCAACCCATGGCAAATCTTAAATGCCCTCA TTTACCAATCTTTACCAAACTCCTATTT	99
IGKJ5_chr2:89160011-89160111	AAGCCTCTAAAAGTCAATACTGGCCATCAGACCCAAATTTCAGAAGACAATAGTGAAAAATTACTTACGT TTAATCTCCAGTCGTGTCCCTTGGCCGAAG	100
IGKJ5_chr2:89160111-89160211	GTGATCCACAGTGTTAACTTAATTACTTTCCCCTTAACAAAAATCTCTTTTCGCTGTTAATATCACTAACCT GACCGATGCAGAGAAAATCTTGCAATTG	101
IGKJ4_chr2:89160211-89160311	AGATGCCTCACTTAACTGGCTAGCGCTTGGCTGTTCCTTAAGATGAACTAATTTTCTATCCCTTACTCATC TGACTTTTTGAAAGAATCTGGTACTCTTT	102
IGKJ4_chr2:89160311-89160411	GGAATTGACCTGAGCTAATATCTCAAACACAAAAACGCTCCAAATTTAAAACCTTATAAGAAAAAAGCATT AGGAAAGTGCACTTACGTTTGATCTCCACC	103
IGKJ4_chr2:89160411-89160511	TTGGTCCCTCCGCCGAAAGTGAGCCACAGTGAGGGATCTCACCCTTTCCCCTCAACAAAAACCTCTCTTTGA AGCCAATCATATGAGATAGGCTGCTTGTT	104
IGKJ4_chr2:89160511-89160611	CAGAGAAAAATCTAGCTATTTCTTCCCCATTTCCCCCATGAATCCTATTCTCCTCTCAAACCCAATGATTC GTCTATTTGCTCAGCTTTTTTAAGTTCATT	105
IGKJ3_chr2:89160611-89160711	TTCTGGTGTCCTGCTATTTACTTCTGGGTCACCAGGTTTATTCAACCAAAATATCACAAAAACTTGCACAAA TGATACAATGGCACTAAAATCTCACGAAT	106
IGKJ3_chr2:89160711-89160811	AATTGAGACAGATGTACTTACGTTTGATATCCACTTTGGTCCCAGGGCCGAAAGTGAATCACAGTGATTC GTCTTAACTTTTCCCCTTTACAAAAACCTCC	107
IGKJ3_chr2:89160811-89160911	CTGAAAGCTCAGCAAGCCTCTTTCCCCCAATGAAGTTATTTTGATTTAGAAATCTTAAAAATTAGCCACAA GCTAGCGTCCTGTGGAACAATTTCCCCTC	108
IGKJ2_chr2:89160911-89161011	CTCTGTACCTAACCTGGGAATGAAGTTTGTTAGATCCCTGGCATCCGACTAATGAAAATCCACACAAAAGG AACACAAAGTAAACTAATTAGCAACAGTGA	109
IGKJ2_chr2:89161011-89161111	AGAATCAGTGGAAAAAAGTACTTACGTTTGATCTCCAGCTTGGTCCCCTGGCCAAAAGTGTACACACAAT GGTTCCTCTTAACTTCCCTCCTATACAAAA	110
IGKJ2_chr2:89161111-89161211	ACTCCCTTTCTGACAATTGACCAAGGCTCTGTCCAGAACATGTTATGTTCCCCAGGACATTTCTGAAGCTA TTACTTAGACAAGTTATTCTCACCCAATG	111
IGKJ1_chr2:89161211-89161311	ACTGAATCTTGCTTGCTCTTCAAAGAAAATGTGCAATCAATTCTCGAGTTTGACTACAGACTTATCTTTAT CTTTTCCCTGAAGGATATCAGAGGCTGAT	112
IGKJ1_chr2:89161311-89161411	TGCAGAGTCACCTTATAGATCACTTCATAGACACAGGGAACAGAAGACACAGACAACTGAGGAAGCAAA GTTTAAATTCTACTCACGTTTGATTTCCACC	113

IGKJ1_chr2:89161411-89161511	TTGGTCCCTTGGCCGAACGTCCACCACAGTGAGAGCTCTCCATTGTCTTGCTGAACAAAAACCCTTCTCAC CAAAGGGGAACAGAGTCCTGGGTCAGCTG	114
IGKJ1_chr2:89161926-89162026	ATCAACTTAAGGCTCATAACTTTGAAATGCATTTTGAAATGTAGCTCCAGATGGTATACGAAACCAAAGT GAAGACTAATAGAGTAGAAAAGTAGACTTT	115
IGKJ1_chr2:89162026-89162126	ACTTGGTTGGTTTGTCTGTTTTCACAGCACAGGAAGAGCTCAGCTCTTACTGAGCTGGACCAGGCGCATG CCATCTTTGGAGCTGCCATGGAGTCCCAGT	116
IGKJ1_chr2:89162126-89162226	GTTCCATAGTGTTTCCATAGTAATCTCATCAACAACACTGAAGACCTTTTCAGTATTTTCTTTTGAGTCCA GCTCCATTTTTGCAGCCTTGTATCTCTCT	117
IGKJ1_chr2:89162776-89162876	CCGCGCCCAGCCGAGTGCCTGTTTATTTTTACCTGCTTTCAGATTCTCTTCTACCCTTCTAAATTATAAGCT GTTTGATGTTTTTATTTGCCCTGTATTTG	118
IGKJ1_chr2:89162876-89162976	GGAGGCTCCGTCCAGTATCTTTACTTAGCAAATGCTTAACAAACATTTTCAGAATAAATAAAAAAAAATA CCTAATTGAAAGTCAATAATAGATCAGAGA	119
IGKJ1_chr2:89162976-89163076	TGCTATCATAGACCAAAGACTAATACTGACTGCCACAACAGTAACTTTTACAACAGAAATCATAACTACA ATTCTAAAGATTAGGGGTAGGTTTATTTGA	120
IGKJ1_chr2:89163076-89163176	TTCTGTCACTGGCAGCTTTGCTAGTTGCCTTGAATAGCAGAATTAGCATTTGGTCTCACCAGAAGATGAGG AAGGAGAGGGATCAAGTTAGAGGTGGAGA	121
IGKJ1_chr2:89163176-89163276	GTTAACATTGGCAAGTGAAATTTAATGTGCAAAATAGCTGACCAAGGGCATAGTCCTTTTTTAAGGGGA CACAAAGTGATTTTCTCTGCAGACATACAC	122
IGKJ1_chr2:89163276-89163376	GCAATACCAATCATAAAGGGTGACATTTATTGAGCACTTACTAAGTGCCAGACATTGTACATGGATCATC ACATTTAATTATTCCCAAGACTCTATGAAC	123
IGKJ1_chr2:89163306-89163406	TGAGCACTTACTAAGTGCCAGACATTGTACATGGATCATCACACATTTAATTATTCCCAAGACTCTATGAACT AGGAACTAATATTATCCCCTACTTTGTAG	124
IGKJ1_chr2:89163406-89163506	GTGCAAAAAACTTGAGGGCAGAGAGGTCAAGGAACTGGCTTATGGCAGTAAGTGGCAGAGCTGTGACCTA AACTCAGATCCCATGTTTTTAACTGAACTAT	125
IGKJ1_chr2:89163506-89163606	ATGCAGATTATACTCCAGGAGTAAAGTCACTCAACGGAAGCAACAAGCGTGACAGGGAATGCTGGGATG GGGGAAGGTAAAAGGAACTCCTTAGACTGGG	126
IGKJ1_chr2:89163606-89163706	ATAAGTGTGTACAGACGTATGTATAAGACTACACATGGAAATATTGTTTAAAGAGTGAAAAATAACTAAA ATCCTCATTAATAGGAGTTTGGTTAAACTG	127
IGKJ1_chr2:89163706-89163806	TGCTAGAGCTTTACAATGTAGCACAAAGCAGACATTAAGGGGAAGACGTAGACTTCTATATAGTTACGTG GAAGGTGTTTGTGAAAATGCAGGTCACTGA	128
IGKJ1_chr2:89163806-89163906	AGAGTATGTGTGGTGAGATATCATGATCCCATCTACATTGAATATATATGTATATAAATACGGGCTGAAT TTTAAAAGACATAAATTGTGCTTGGTAGTT	129
IGKJ1_chr2:89163861-89163961	AAATACGGGCTGAATTTTAAAAGACATAAATTGTGCTTGGTAGTTATCTCCTGGGATTGCAGAGGAGGAA CAATGACACTTTATGCCATCTCCTCCTACT	130
IGKJ1_chr2:89163961-89164061	CTTCTGTATGGTGATGTGAATATATTCATTTTATAGTTTTTAGAAATAATAAAACTGTACTAATTTTGAAA AACAGTAAACTCTGACATTGCCTATTAGC	131
IGKJ1_chr2:89164061-89164161	ATTCTCGATATTCCTGTGCAATGCATAAACATAACTTTTTAAAAGATATGTACACACATGTGTGAGTTTTC TTTGTCAAATACTTTTCTATAATCTTTAA	132

IGKJ1_chr2:89164161-89164261	ATCAAGCATGCCAAAAAGGTAAAAGCTTTCCTGTTTCAGTGTAGGAGATAGTCGTCTGCAAAGGAAAGAG ATGTAGGGGATAGAAACAGGAATGAAAAAG	133
IGKJ1_chr2:89164261-89164361	ATGACTGAGCTGTTCGAGGGACTTATGTTCCTAAGTGAGCTAATTGGAAATCTAATATGAACAGTGCAAC CGAATAACTATTGTAAAGCAGTATTTGTAA	134
IGKJ1_chr2:89164361-89164461	ACAATAAAAGATGATTATCATAAGTACCATTGTTGCAAAAACTATTTTATTGATCACATGCAGTGGTGATC TGTAGGAATGATTGTTGTGATGTTTGCTG	135
IGKJ1_chr2:89164461-89164561	TAACATAAAATGAAACATGGGAAGTGGCTGAGATCTTTAGGATGTGTGGTTCATTTTTTGAAAGCAAA TGTTGTCTCAGAAGCATCTGTGAGACTCTG	136
IGKJ1_chr2:89164561-89164661	CCAGGATCCACCGTTCTACAAAATATCTGTGATGGACATTGATAAGATTGATCTGTTGAGGAAAGGCAAG GTGTCAGTAAGATAGTCTGAGAGCTTCTTG	137
IGKJ1_chr2:89164661-89164761	GATTTCATGTAAAAGAGTGCTGGAAATAGAATTTCTTGGGGAACATTCCAACTAACTCATCACTGAAGGT GCTTTACATTGAACCCTCAGCAAAGTTAGA	138
IGKJ1_chr2:89164761-89164861	TTATCAGAAAAAAAATATAAACTGCTGTGAGGGGACAGGAAGGAAAGTCAGGGAGGGAGGGGGCAA GGAGAGAAAGAGCGAGAGAGGAGAGAAAGA	139
IGKJ1_chr2:89164866-89164966	AGAGAGGAGAGAGAGCACAAGTACACACTTCAATGCACACATCTATAAATCATCCTGAAAACTACTGATA AATTATTTTAGCAATGTTCCTCAGATGTAA	140
IGKJ1_chr2:89164966-89165066	CATTTCAAGAAATATCATTTTTGCTTTTTATTTGGCATAAATTTACTAGCCAATTTAGGAAGTTCCCCTCACA TCAGTAACATACAGTACATCACCCAGTA	141
IGKJ1_chr2:89165066-89165166	TGTCAGAGGACACAATGGCATAAGTTTGCCTTTTGCAAGGTTTGAGGGATGGCCATTTCCCTACCTGACTC AGGAAAGTCTGTAGCTGATATCCATCTTC	142
IGKJ1_chr2:89165166-89165266	AAGTTTGTGGTTCTTTCTCTCTATATATATTTGAGCTCAGCAGTCATGCTGGAGTCCAGAGTAGGTGAT TCTTTCTGCTTTAGCTTGACTCCTCCTTA	143
IGKJ1_chr2:89165191-89165291	TATATATTTGAGCTCAGCAGTCATGCTGGAGTCCAGAGTAGGTGATTCTTTCTGCTTTAGCTTGACTCCTC CTTAAGATTGTAACTCTCTCAGTTTTACA	144
IGKJ1_chr2:89165291-89165391	TTTTTTGTCAGACGTAAGCTGACATTCCACAAGGAGAGGAGGAAATTCTGTGGTTCACATCCAGTGGTGC TTGGAACCTGATTGGTTGTCATTCTTCCAG	145
IGKJ1_chr2:89165391-89165491	CTAGTTTGTCACGAGTGGATATCTGTCCTGGATTCCCAAGGATCAAGGCTGCCCCATTAGCCAGGAAGTA GGGAGATAGAGGAGGTCACTTGAGAAAGAG	146
IGKJ1_chr2:89165491-89165591	CTGCTTCTTTGCCGCCTCCAGGTTGTGTCTGTTTCCTCTCTATATCTGAAGACAGATGTGCTGGCAGAAGCA AAGTCCTTTGTCCGGCCACGTGCAAATGC	147
IGKJ1_chr2:89165591-89165691	ATGGGACATAAATATGAACAGAGATTCTTGTCCCACTCTAGAAAATGTAGATGTTCATCTTGTTTCCAAG GGGACAGTAAGGCTGCAGGTGTTTTTTGAC	148
IGKV4-1_chr2:89184966-89185066	CTTTTGTACTCACTGGTTGTTTTTGCATAGGCCCCTCCAGGCCACGACCAGCTGTTTGGATTTTATAAACG GGCCGTTTGCATTGTGAACTGAGCTACAA	149
IGKV4-1_chr2:89185066-89185166	CAGGCAGGCAGGGGCAGCAAGATGGTGTTGCAGACCCAGGTCTTCATTTCTCTGTTTGCTCTGGATCTCTG GTGAGGAATTAAAAAGTGCCACAGTCTTTT	150
IGKV4-1_chr2:89185166-89185266	CAGAGTAATATCTGTGTAGAAATAAAAAAAATTAAGATATAGTTGGAAATAATGACTATTTTCCAATATGG ATCCAATTATCTGCTGACTTATAATACTAC	151

IGKV4-1_chr2:89185196-89185296	ATTAAGATATAGTTGGAAATAATGACTATTTCCAATATGGATCCAATTATCTGCTGACTTATAATACTACT AGAAAGCAAATTTAAATGACATATTTCAA	152
IGKV4-1_chr2:89185296-89185396	TTATATCTGAGACAGCGTGTATAAGTTTATGTATAATCATTGTCCATTACTGACTACAGGTGCCTACGGGG ACATCGTGATGACCCAGTCTCCAGACTCC	153
IGKV4-1_chr2:89185396-89185496	CTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCA ACAATAAGAACTACTTAGCTTGGTACCAGC	154
IGKV4-1_chr2:89185496-89185596	AGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGTCCCTGACCG ATTCAGTGGCAGCGGGTCTGGGACAGATTT	155
IGKV4-1_chr2:89185596-89185696	CACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACTC CTCCCACAGTGCTTCAGCCTCGAACACAA	156
IGKV4-1_chr2:89185696-89185796	ACCTCCTCCCCATACGCTGGGCCAGTAGGTCTTTGCTGCAGCAGCTGCTTCCTCTGCACACAGCCCCCAAC ATGCATGCTTCCTCTGTGTGTTGGGGAGG	157
IGKV5-2_chr2:89196226-89196326	AATACATGAAAACAACTACCGAAATGTTATGAAATTATAGTTTAGTAGAACTAACAAGTGCATTAATGCA AAAGAAAAGTAGGGCTCAGTAATCAGGGAA	158
IGKV5-2_chr2:89196326-89196426	CCAAGTGTGCATTGTAAAAGTGCAGCCTCTCTAACACTGGGTTTCATCACAAGTAACAGAACAGGATGCC TGATGCAGGGAAAAAAAGAAAGGCAATTGTT	159
IGKV5-2_chr2:89196851-89196951	GATCTCTGGTAAGAGAAACACTTCCTCTCCTCTGTGCCACCAAGTCCCCTGCATATCCACAAAAAATAATAT ATTTTCATAAGGAATTGATTTTCCTCATT	160
IGKV5-2_chr2:89196951-89197051	CTCTGCAAATATGATGCATTTGATTTATGTTTTTTACTTTGCTCCATAATCAGATACCAGGGCAGAAACGA CACTCACGCAGTCTCCAGCATTCATGTCA	161
IGKV5-2_chr2:89197051-89197151	GCGACTCCAGGAGACAAAGTCAACATCTCCTGCAAAGCCAGCCAAGACATTGATGATGATATGAACTGGT ACCAACAGAAACCAGGAGAAGCTGCTATTT	162
IGKV5-2_chr2:89197151-89197251	TCATTATTCAAGAAGCTACTACTCTCGTTCCTGGAATCCCACCTCGATTCAGTGGCAGCGGGTATGGAACA GATTTTACCCTCACAATTAATAACATAGA	163
IGKV5-2_chr2:89197251-89197351	ATCTGAGGATGCTGCATATTACTTCTGTCTACAACATGATAATTTCCCTCTCACAGTGATACACCCTGTTA CAAAAACCTCCAAGTTCTCTCAGTGGGAT	164
IGKV5-2_chr2:89214836-89214936	GCCCTCTGTCCTGGAGACACGGCCAAGGAGGCTGGAGACTGGGTCAGCACAATGTCCCCATTGCAGCCTG AAATGATAAAGACAGATAAAATTATATCAGA	165
IGKV5-2_chr2:89214936-89215036	TATACTGAGACTGTCTCCCCATGTAGGCCATTGGTGACACTTGTAACCACAGTCATATGCAACATCTTG AGTAACCAGAAAAACAAAAGATAACTGGGGG	166
IGKV5-2_chr2:89215036-89215136	AACTTACAACCTACAATGAGTGCCCTAAATCCAACAACCAAGAATCCAGAGACACAAAAAACACAATGATGC CCACATGAGTTTGCCCGATGTTTCCCTATA	167
IGKV1-5_chr2:89246681-89246781	TACCAACACCATCAGAGTGTGGCTGCATCTGAGGACCACTCTCAGCTGATAGAGGCATCAGGAGGAGCAG CTGGGGCAGCCCTGCCTCACACATCTGCTT	168
IGKV1-5_chr2:89246786-89246886	GGGGTTTATGTTCGGGTGTGTAACACTGTGGGAGAATAACTATTATACTGTTGGCAGTAATAAGTTGCAA AATCATCAGGCTGCAGGCTGCTGATGGTGA	169
IGKV1-5_chr2:89246911-89247011	GCCGCTGAACCTTGATGGGACCCCACTTTCTAAACTAGACGCCTTATAGATCAGGAGCTTAGGGGCTTTCC CTGGTTTCTGCTGATACCAGGCCAACCAG	170

IGKV1-5_chr2:89247011-89247111	CTACTAATACTCTGACTGGCCCGGCAAGTGATGGTGACTCTGTCTCCTACAGATGCAGACAGGGTGGAAG GAGACTGGGTCATCTGGATGTCCACATTTGG	171
IGKV1-5_chr2:89247096-89247196	GGATGTCACATTTGGCACCTGAGATTGGAAATAGAAACACAAATATTCATACTATTGATCATATTATAGG AAGACTTCCCTGAATAACCAGGCAGTACTG	172
IGKV1-5_chr2:89247196-89247296	AGCACACTGGGCTGAGTAAATTCCTAGTGTTCTCCTTCCTTACCTGGGAGCCAGAGCAGCAGGAGCCCCA GGAGCTGAGCGGGGACCCTCATGTCCATGC	173
IGKV1-5_chr2:89247526-89247626	GGGACTATTTTATTATGAGAAACAATTTTTTAGGTATTTTTTTGAGAATTTTAAATATTCCTCAGGAGCCGA TAGAGTAATGTATTTCATTGGTGTATCAG	174
IGKV1-5_chr2:89247626-89247726	GATTATTTAGGAGAAATATTCTTGTTTGTAGGAAACACATAGTAAAATGTTAGATGGTAGGATTCTCAAGT CTTCAAAAGACTCTCATAAGATTCCGGGTA	175
IGKV1-5_chr2:89247641-89247741	TATTCTTGTTTGTAGGAAACACATAGTAAAATGTTAGATGGTAGGATTCTCAAGTCTTCAAAAGACTCTCA TAAGATTCCGGGTAGGGAAGGGGGTAATT	176
IGKV1-5_chr2:89247831-89247931	TGTAAGTATTAGGTAATGGTGTTATTGCCTTTGTTCTTACTAGTATTAGATCAAGCAATTTATTACAGATAT ACAAAGATGATACCGTGTTGTCTCCATGC	177
IGKV1-5_chr2:89247931-89248031	ATGCAGCACTCACAGATCCACCACTATCAAGAACTGCAGGTCTCTTTAATACCCAGAGACTAAATGAGGT GCACCTTATTCTTGTTTTGGGTACCTTCAT	178
IGKV1-8_chr2:89291906-89292006	TTGGGTGTGTAACACTGTGGGAGGGTAACTATAATACTGTTGACAGTAATAAGTTGCAAAATCTTCAGAC TGCAGGCAGCTGATGGTGAGAGTGAAATCT	179
IGKV1-8_chr2:89292131-89292231	CTGACTCGCCCGACAAGTGATGGTGACTCTGTCTCCTGTAGATGCAGAGAATGAGGATGGAGACTGGGTC ATCCGGATGGCACATCTGGCACCTGAGATT	180
IGKV3-20_chr2:89442291-89442391	CTTTCCCCTGGAGACAAAAGACAGGGTGCCTGGAGACTGCGTCAACACAATTTCTCCGGTGGTATCTGAGA TTGGAAATAAAACAGAAAAGTCACCCATGT	181
IGKV3-20_chr2:89442391-89442491	AATCTAAATCAAACCCATTGTCTTCCCAGAAGAGCCAGAATTATTGCTTTATATTGAGCTTTAATTATTGT ATTGACTGAGCAGAGTTGCCAGGTAACAG	182
IGKV3-20_chr2:89442491-89442591	GACTTGAGAGGGGTTTTCACTGACATGCAAAACCATCCCATGTTCCCCTCACCTGGGAGCCAGAGTAGCAG GAGGAAGAGAAGCTGCGCTGGGGTTTCCAT	183
IGKV3-20_chr2:89442616-89442716	AGCTCTTCTCCAGAGCTCTGACCCAGGCATTGATATGGGCTCTGGACTGCAGGGCGGCTGGGAGGGACAT GCAAAGCAGCTGGGGCGGGTGCTGGGCTTG	184
IGKV3-20_chr2:89442716-89442816	CAGCTGCAGAGACAATCTGCCTCCCCTTTCTGCTCTCAGCAGCCCATGCCCAGGTGATCAGGGCCAGAAAA GGCCGTTGGCTCAGTCTGAGGGTAGAACTT	185
IGKV3-20_chr2:89442816-89442916	CTCCCCTGCGGCCACAGAATTTAACCCCTGTGTCCTCTTGTCTCACCATCACCTAGATTGAGCCACACAGAAT GTTTGGTACAAGTCTGTTAGAAACAAAAT	186
IGKV3-20_chr2:89442916-89443016	AGAAGGCTGTGGTTTCATTTTTCTCTTTCTGCTCCAACTTGTGCCCAGTCAGCTCCCTAAATGCATGATGG ATCAGGTTGAAAGGAAGAGTCTATTACAA	187
IGKV3-20_chr2:89443016-89443116	CTTTATCTTCCGGATATACTTGTATTTACTTGTTAGTGATCTTTCCTGAGGGTCCAGAAGCTGTCTCATTCT TTGCAGAAATTAAAAGAGTAACATTCAA	188
IGKV3-20_chr2:89443116-89443216	TTAACCTCAGCACTGTGGGTGTGAGGACTTTCACAACTGCACAGATAAGTGAGACCTGGGCTCCAAATCC TCAGGGTAGTGATACCATTTCCCTAAAGAC	189

IGKV3-20_chr2:89443216-89443316	AGAAGATGGTTTTGTCCATGCAGGCAAAGAACTATTTCTTGGGTGATCCTCTAAACTATCCAGTCTTTTTA TTCTGTATAGCTGGTATAGTTTACCCTTA	190
IGKV2-30_chr2:89544656-89544756	GGCTATATATGTATTTGTTCATATTTCAAAAATACACAGTTTCAAAATGGAACTCAAGGGATCCAAGGCTC AAAGGGGTCTCCAGAAGACCCCACACCAT	191
IGKV2-30_chr2:89544756-89544856	CCCCTTTCTGTGTCAGTCTTCCCCAGAGCACAGATCCTTGTTTCTGCTTGAATCTTCCTCACTCTCACAGAT CTGATCATCACATGCCCCCACTCTGGAGG	192
IGKV2-30_chr2:89544856-89544956	ACAACATGTGCATGTCCAATACAGGAAAGGAACACACATAGGAGTGTAGTGAGACCCCCAGAGATCACT GTTGTTAGAGGCAGTGGGGCCCCAGAACTCA	193
DUSP2_chr2:96810164-96810264	GGAGCAGCAGCGGGTGGAGACCCCATGGGCTGGCCGAGACAAGAGGAACTCCTCAGCCAGTCCTCCTGAC CTGAGACAGGTCTCAGGAATGTGCGGAGGAC	194
DUSP2_chr2:96810264-96810364	ACACCGGGACATACATTTCCCTTCATGCTCCCAACATACACATGCAAACATACACAGACCCATACAGGCA CGCGCGAGCAGCCATGCCCCACCCCCTCCC	195
DUSP2_chr2:96810364-96810464	CCAACACACACGTATAAAAGTGTGTGTATATGGGCAAACTGCTCGCATCCCCAAATGGCAGGCTCTTT CCCTAGAGGCGCCCAGTCCGCGCGGGAG	196
AFF3_chr2:100758483-100758583	AAGCTCACTCACTGGGGCCATTGACTGGGATCCAGTCTGTGGCCATGTCATGGTTTCTATTTTTGAGGTTA TAGCTAATGAGCAACATGAGGTTAAGACA	197
AFF3_chr2:100758583-100758683	CACTTTTCATAAGGCCCCAGCCAGCATCATAAATATGTGTGTGAGCATGTTCACACTCAGGTTATGTCTTC TTTATGTGCACCCTCTACCACACACACAC	198
DDX18_chr2:117951919-117952019	GCCAAGAACCACGACTCTCTAATTTTACTTCCCAGCAGGTATTCAGTGCATAAATAGTTCCTACTTAGAAGT ATCATATTTGCCCAAACACACAAGGTGATAC	199
DDX18_chr2:117952019-117952119	CCAAAATGAGGTAAGTTTCCTGTTTTCTCAGTGAGATCTTTTGTTGTTGTTGTTGTTTTGTTG TCGATGTTGTTGTTTTTGGTTTTTGGTCT	200
CXCR4_chr2:136874415-136874515	CCGGGTCGTCCAGCCCCGGGCCGCCGGCTGCCCACTACACCCACGCCAACCGCCCGCAAGCAGCGGCTG CAGGGGCTCCGGCTGGGCGACACGGCCAGGCT	201
CXCR4_chr2:136874515-136874615	CTGTCCCACAGGGTGCTGGGGAGCGACTGGGCGGCTCCGGCCGAGCGTCTTTGAATTGCGCGCCGCTGC AGGAAACCAAAAAACTCCCTAGCAAGAGGGT	202
CXCR4_chr2:136874615-136874715	TTCAAAAGGTTTCTGGAAACCACCGACGGTTAAACATCACAACTGGACTCGGAGAGAGCCAAACGGTTTC CCCACTTGCACCTGCCAGTCTTCGCGGCGG	203
CXCR4_chr2:136874715-136874815	CGACCTGGCAGCCCAGGTGCGGTCTTAACCGCCCCCGCCCCCTCACCCCGTACCCGCTCCTATCCCCGGAGC GCAAATCTCAGGGCTGGCAGCTGCGCGGT	204
CXCR4_chr2:136874920-136875020	GGAAGGTTTTCCCCCTCAAACCCAAAGCGCGCGGGCGGATCAACTCCTAGCTGCTGCCACCACTCGATCC CCTCAGAGGATCGGGCGCGGTGGGTCCACCC	205
CXCR4_chr2:136875020-136875120	GCCTCTCCCGCCCTCTGCCTACTGTGCTGGGAGACTGGCACAGCTCCGTCGGCCGCACAGAGTTTAACAA ACACGCACCCAGTGTCAAGAACAGTCACCA	206
CXCR4_chr2:136875120-136875220	GGCGCTTAACCCCGAAGTTAAAGCGGGCGCAATCTCCTCCTGGGAACTCAGCCCAGGCACGCCGCCCTCC GCCTCTAAATTCAGACAATGTAACTCGCTC	207
CXCR4_chr2:136875220-136875320	CAAGACATCCCCGCTTCCCCAAGGAAGAGACCGGTGGTCTGAGTCCCGAGGCAGCGCGGCACGCCTTCTCT GCACTTGTGCACAGAATGTTCTTACGTTTG	208

CXCR4_chr2:136875320-136875420	CAAACAGCGTGCAAGCCGCCGCGCGGCGGGACTCAAGGGGGAGACACATGCAGCCACTGGAACGCTC TTTCCAGTCGTTTCTCCTCGACTCACAGAGA	209
CXCR4_chr2:136875420-136875520	AAAAGATTCCAATCCTGCTCCCCCCCCACCCACCCGCACTATATAGGCATGGTCAAGAAAACTCCTTTCGG TGACCCTTTTTTGGAGTACGGGTACCTCC	210
CXCR4_chr2:136875520-136875620	AATGTCCTGGCCGCTTCTGCCCGCTCGGAGAGGGGCTGCGCTCTAAGTTCAAACGTTTGTACATTTATGAC AAAGCAGGTTGAAACTGGACTTACACTGA	211
CXCR4_chr2:136875620-136875720	TCCCCTCCATGGTAACCGCTGGTTCTCCAGATGCGGTGGCTACTGGAGCACTCAGGCCCTCGGCGTCACTT TGCTACCTGCTGCCGCAGCCAACAAACTG	212
RFTN1_chr3:16419204-16419304	CCCATTGCTGACATACTTACTCCCTGAGAGTGGCTCTTCATGCACCTCCAAGGGGTTGCTCTCCGGTCCAT CCAGTGTCTTGCTCACCCCCTGTGGTGAA	213
RFTN1_chr3:16419304-16419404	AGTTCTCCACCATCTCCCTCTCCGGAGGGTGAGCTGGGCTGCTTGGCGAGGGGCACCTCCCCTCTGGGGC CTGAGCTGGGCTCTGGGCTTTGGTTTCTCC	214
RFTN1_chr3:16419404-16419504	CAGCCGGAGCACTGCACACATCCCCCAGTCCCCGGTTTCTCATTCTCCAGTGACGCGTGATCCCCACGTGCG TTTTTTGCATCTCTGGCATCCTCGGTGCT	215
EIF4E3_chr3:71551101-71551201	ATTTGCAGGTTATATCCTGGATGGTGGCACCGACAGCGCCTGGAACACAGAAGGTTGGGAGGCGTGACGCT CATCAGGAAGGCTCTTTTGGGGAGCCAGGA	216
EIF4E3_chr3:71551201-71551301	AGAGTCCCCCAGAAGCCCACTTGGCACCCTATCTATAACAAGTTGCTCTTTAAGAATCATGGGAACTCCA GAATCATTTTCACAAATACCTTCCACTCAT	217
EIF4E3_chr3:71551301-71551401	GATTCAATTAAATGGCAGAAAACACAAACCTTCCGTTCCCACTGGCAAACTGGGTCTAGCTAACTGAGCA CAGCTAGCACAAGGCAGGCCCCCTGCTAGC	218
EIF4E3_chr3:71551401-71551501	AGGGCAAGTGGCGGCCCGGTCCCCAAGGCCCAGGGGAGCCTCTGCAGCTCCCTGGAAGGACGGTCAAGT GAACAGAGAGCTGGCTGCCATCTGGGTTCTT	219
KLHL6_chr3:183272308-183272408	ATGAGATCACCAGTTTATCGTAACTAGAGGCCTCTCCCATCTAAAGCATCTTTGTAACTGCTTTCCCTTTC CCCACACTGCCTACACACATAAAGAAGCCCC	220
KLHL6_chr3:183272408-183272508	TAATTTGTAACAAGTCATTTGACAACTCCAGAAGAGGGGCCACATCCTTTTTCTCTATGTCTGTTGATTAA CAAAGACAACATTATGTTTCCAACACCAG	221
KLHL6_chr3:183272508-183272608	TCAGACCAAGGGGGAAAAAAAGTCCCCATGACTTCAGTAATTTTCCATCCTTTGGAACAAGGAAATATACA CAAAAGGTTTACTATAGAATGTAAGCATTG	222
KLHL6_chr3:183273063-183273163	AACTGTTCAAGATTGGGCTCTCACACTAACACACCTCTTCCTTGCAACTTGCACCCAATTTGACTCTGGTC CTAGGCATGCTGACCTGAAATAGTTGCTG	223
KLHL6_chr3:183273163-183273263	GCTGCGGCAAGCACCACGCGGTGGCAGGAGAATTCCTGAATGTCCACACACAAGATGACATCTGTCAGAG CGTTTTCCATTCGCAGGGTTTCCAGGCCAT	224
KLHL6_chr3:183273263-183273363	TCTGAAGAATTAAGGAGAGTCCCGCGTCGTCAAATTTGACCTTTTCCCCATTTAAGATCTCGACCAAGTCT CCTGTTTTCTGGGAGGGCTCATCTGTAGA	225
KLHL6_chr3:183273363-183273463	AGGTGCCAGGGGCCCTTCCAAACTCTTCTCGACCACATCACCCATGGTCCAGGCGCCCCTTTGTCCTGCCA TCAACATCGAGACTGAAGGAGCGCCCAAG	226
ST6GAL1_chr3:186714604-186714704	CCTTCCTGTTGGCCACTACATACGTGTCCCCCGCTTCTTGCCCCTCTCTGCTTGGGTCCCTGCTACACTGGT ATCCTGCACTTTCCACCTTGTATTGCCA	227

ST6GAL1_chr3:186714704-186714804	GTTTGTTTCCAAGGCCATCTCCACTTTGAGCTTGTTCATGACCACCTCACACAGCACACTTGGTCTGTGTG GTGGTTTGAGGGGTTCTGTCTGTACACTG	228
ST6GAL1_chr3:186714804-186714904	TGCTTTGGCTGTGTTGGAGGCGGGCAGGTGGGAAGGAAGAAATGTATTCTTGGGGAGATTTGTTTTTAGA GACATGAGACATGGAAAAATAGTTAAGTAAT	229
ST6GAL1_chr3:186714904-186715004	AATATAATATGGGAGGCATGGACTATCAGAGGAGGCAGGCAGGACTGCCCAACCTCCTCACTGGGCACGT TACGCTACTTCCTCCTGACCTCTATAGTCC	230
ST6GAL1_chr3:186782529-186782629	CTATCATTGCCCTTTCTTACCTTGATATCCTAAAAAGCTGGTGGTCTGTCTTCTCTATCTTTTGTCCTGGTC AGTTATCCTAACTATTTTGTGTCTGTTT	231
ST6GAL1_chr3:186782629-186782729	CTGTGGATTAGTAAACGGGGTCCCCACCCCCACTCCACAAGGAGAACATCTGGCACCCAGAAGTCACTGA GAGAATAGCTGTTGCTTTGGTAGAATTCTG	232
ST6GAL1_chr3:186782729-186782829	CCTCTGAGTGGCTTGTTCTTTTCCCAGACGGAGAGGTCTCCTGACAGCAGCTCTCTTCTTTTTCTTTTTTTT TTTTTTTGAGACAGAGTTTTGCTCTTGC	233
ST6GAL1_chr3:186783389-186783489	CTCCTGTACCCTGTGGCCTGAGAGAGGAGACAATGGGACAAGAAGACCCAGTGGCTTCCTTGGAAGCTT TTGTGCTAGCTGGAGAGAGAAGACCTACTT	234
ST6GAL1_chr3:186783489-186783589	CCTATATGCCTAGCAACAGTCCACACTGACTGGCAACCAGGACATTTCCAGATTACTCAGTGGGGC TTATCTTGAAATAATAGTTGATGCCATTTG	235
ST6GAL1_chr3:186783589-186783689	TTAAATATATTATATACCATCTAAGGGTCTTACATGCCTTCTCTCATTTGATCTTCATGGCAAACCCTGT GAGGTATGACCACCAACCACCATTTTAC	236
ST6GAL1_chr3:186783689-186783789	CTCAGAACTCAGGCTCCCAGAGTTTAAGTTGCTCACAGGAGCCCAGAAAGTAAGCGACAGAGGTGGGATT TGGTTCTAGGTGTTTGCCACCAGCACTTTA	237
ST6GAL1_chr3:186783789-186783889	AATCACCAAAGCTTTCTGGAAGCTCCAACTTTTCTTCTCAAGATACTGAAAGACAGGTATCTGGATGGGTT GGCAGGGCGGGTGGGAGGTGGGCGAGATT	238
ST6GAL1_chr3:186783889-186783989	TCCATCAACAACGGGTCTAAAACCAGCGATGGTGAGCTGGGTGATTTTGATGGAACCCCTGCCATACAGT CTATTAATATCATAATTGGAGCTAAAATTT	239
ST6GAL1_chr3:186783989-186784089	AATCATGATGGCAATCATGAGTTCTGGGGCTTCTTGATTTGGGCCAGCAGACACAGTCTCAGTCACTAGTT CTCCGAATCAGAGAAAGGATGCCTTCAGG	240
ST6GAL1_chr3:186784089-186784189	CTGTGTCTTCACATGGCTTTTCCTCTGTGCGTGGTGGAAAGAGAGAGCTCTGCGGGTCTCTTCTTGTTGTA AGGACACTGGCCCCATTGGATTAGGGCCC	241
ST6GAL1_chr3:186784189-186784289	CACCACATGACACATTTAATCCTAATTACCTCCCTCACAGCCCTATTTCCAAACAGGGTATTAGTCACATT AGGGATTAGGGCTTCAACATAGGAATTCT	242
ST6GAL1_chr3:186784289-186784389	GGGGGCACACAATTCAGTCTATAACAGAGGGAAAACAGATTTGAGAAGAAAAAAGTCCAAAATATGCAC AGTGGTAATATCTGAAGATGTGCGTGCGTGC	243
BCL6_chr3:187460134-187460234	TCAAGGGCTCAGCAAACGACAACTTAAGCATTTAGAGTCCCATCCCTATCCACCAAACCCAGAATAAGTT AGTCTTTCAAGAAAGCATTGGTATAAAAC	244
BCL6_chr3:187460234-187460334	CCTTCAAAACTGAAAAGAAGAAAGGGGCAATTGGAGAATTCCCACTTTTTCTGGCTGTCTCCTTCAAGTC GCCCAGTTTTTTATGAACAGCATCTAGCCTT	245
BCL6_chr3:187460334-187460434	ACTGTCACTATCAACAACCCTTAAAACTAGCCAATGCTTCGGCCTCTAGTATTGGAAAGTCTTCCAAATAG GATACTGGAAACTTCTATTTATAAGCTTG	246

BCL6_chr3:187460434-187460534	GGGTGGCGGGCGGCGGGAGGTGGAGAGAGAGTTGCCATCTACAGGTTTCTATTTTGGCCTGAAGAC TCAACTGCAGTCATTAGAGTAAGGAATGCC	247
BCL6_chr3:187460824-187460924	TTATTTATTAAAACCACACACACCTTGCAAAGAAAAAGGGAAACTGGCAGTCTCTGTAGAGGAAGCCGGT GGCATCGCTCAGAGCCACACAAACTGTATTTTC	248
BCL6_chr3:187460924-187461024	TAAACAGCCCTTTCCCTGGTTCCCTCTCCTGCCCCACTTTTTTAAAATCCAGACTGTAAAAAACACATC TACTGACACTCACTTTACTTTAAAAAAA	249
BCL6_chr3:187461024-187461124	GAAGAGAAAAAGTAAAGCGTTACAAGACTTTCCTCCTGGAAACTATAAACTGAAAAAAAAAAATCCATAAA AGATTAAATCCTGGCCGGTTGTGGGGTGGCG	250
BCL6_chr3:187461124-187461224	GGGGCCGGCGGGGAGGGGGGCGCGGAGTGGAGATTGGCTCTCTGAGGTGGTCAGGGGCCCTGTGACAGCT TGGGACTTTCAGCACCTGGTTTGGGGTCATT	251
BCL6_chr3:187461224-187461324	TATCTGCTCAACTGTCAGGACCCCCCACCCCCAAACCCCAGCCACCAACACAACCATCGTAGAAGGGAAC ACAACACAGAGGGTCTTTTTTTCATTTTTTT	252
BCL6_chr3:187461319-187461419	TTTTTAAAAAATCGGTTTGTGTTTTTGTTTTCCATGGGGGAGCTTTAAAACTCATTATTGCAACACT AGTTCCATTTTTCGCCAGGGTTCCAATAA	253
BCL6_chr3:187461454-187461554	CAAGACATTTACCACGGTCACTACATCCGGCAGCGGGGTGGCCCCTAGCTCCTGCTGCCCCCCCGGCCCTTT CTCCCCGCCCCGCCCCCGGAGCTCAGCCGA	254
BCL6_chr3:187461554-187461654	TTTCTGAGGCTCCAACTCTACCCACTCCCTCCCCGGGCCGCCGGCGCCTTCCCCCATTCTTACTCCC TCGAGGAGAGCCACAGGTTGCAAATCCA	255
BCL6_chr3:187461654-187461754	ACCAACCTCGCAATCTATTTTTGCAAAATCACTCACAAAGATCTCCCTTTCGGCCCGCCCGCTCCTCC CGCGCCGGGTCCCCTCAGCCACGGCCACA	256
BCL6_chr3:187461754-187461854	AAGTGCCCTTCTCTCCTCCTGAGTCTTGCACATAAGGAACGCGGGCTGGGGCTCTGTTCGTTCTTTCTCCTC GCCCAAGGTAAGGACCTCGGGAATCTGAA	257
BCL6_chr3:187461854-187461954	GCCTGGCGTCCACTACGCTCAGGCCCGCAGTTCCCTTTTTTACAGAGCTTGCACCATGGGAAAAAAATAAAA TAAAATTTAGGAAAGGGAGGCAACAGCCAT	258
BCL6_chr3:187461924-187462024	TAAAATTTAGGAAAGGGAGGCAACAGCCATTGGGAGCCAACACAGAGTCACGCAGCGCCCAAAATACAA ACACCGCAGCGGCCAGAAATCCCGCCACCTT	259
BCL6_chr3:187462024-187462124	TCTCGTTCTCCCAGGCTGTCCTGTCGAGGTTCCCTGAGTCCCCCCCGCACACTGAAAGGCATCGCAGGTGCA GTGCGCACCCCCTTTCCCACCCACCCCAAG	260
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BCL6_chr3:187462224-187462324	AAGTGTTCAACATCCCCGCCCCCAAGCTCCCCAAAACACAGGGGCAGGGAACACCAAAACACTCGGCTCT CATTAGGAAGATCACGGCTCTGAAAGGAAA	262
BCL6_chr3:187462324-187462424	TAGTAGACACGATACTTCATCTCATCTGGATTTATGACCAAAAAAACAAAAAACCCAAAGAGTTC GCTTGCATTTTTTCCTTCCAAATCTCGGTT	263
BCL6_chr3:187462374-187462474	AACAAAAAACCCAAAGAGTTCGCTTTGCATTTTTTCCTTCCAAATCTCGGTTCGGCTCGAAGGCAGGGAATCT AAAAGACCGAGGCCGATGGAAGAGAGCCA	264
BCL6_chr3:187462474-187462574	GCGGGGCGAGCGAGCGGGCAGCCTCCCTTTTTGCCTCCCGGAGTTACCCAGAAGGACAGGGGAAGGGAA GGAAGAAGAGGCGAGGAAAAAAGAGGAGGGAG	265

BCL6_chr3:187462574-187462674	GGAAGCGGAGGCCAGGAGCGACGGAGCAAGGAAAGCAGTTTGCAAGCGAGAAAAGAGGGAAAAAACAC AGCCGCACGAATCCAGAGAGATCACAAGCCGT	266
BCL6_chr3:187462674-187462774	ACGCAAGCAGCAGAAAAGAGCGAGGCGCGAGCGCGTCCTCTCCGCGGTCTGGGGCCAGACAGCC CCCAGACTAGCCCGAATCACCCCCCCAAGCAC	267
BCL6_chr3:187462774-187462874	TGTCTCGTCCTCTCTGCTCCGGCCGCCCCTAATTCCCCTCCTTCCTCTCCTCCTTTCCAAAAACC AAAACAACACAAGGGAGGGTGGCAAAAG	268
BCL6_chr3:187462874-187462974	CCTCCCCCAAACCGGCCGATTCACTCAAAGACAACAATAATAATAAATACATAACAATCTATATCCTA TGGTGGGAGAGACGTGGGACTAATCTTCGG	269
BCL6_chr3:187462924-187463024	ACATAACAATCTATATCCTATGGTGGGAGACGTGGGACTAATCTTCGGCATTTATTTTAACACCTGACA GCTAGAATAAATAAATATATACATTTATA	270
BCL6_chr3:187463004-187463104	AATAAATATATACATTTATATCAATAGATACACATAGAAAACTTGGAGCCAAAGCATTTGGCAAAGAGCGG AAAAAAAAAGAATTAAAAGGTAAAATAATG	271
BCL6_chr3:187463104-187463204	ATCATGAGCAGCGGCGGCGGCACCAGCGGCAACAGCGGCGGCGGCAGTAGCAGCAGCAGCAGC GGCGGCAGCAACAGCAATAATCACCTGGTGT	272
BCL6_chr3:187463204-187463304	CCGGCCTTTCCTAGAAACTTCTTGCATCACCACTTCTAAGAACCCCAGTTCTAAGAATCAACAGAGCTCAA TTCTCGGAATTTGAGCTTCGGACTTTACC	273
BCL6_chr3:187463304-187463404	ACTGCTACGTGGCAGGGAGGAGTTGGTGTCAGCTCTCCGAGATTTTTACTGCCCCTGGCCAACCAAAAAG CCCTCAAAGCCACACAAGATTTTTTTCACTGGC	274
BCL6_chr3:187463404-187463504	CGGCATATTTCGAGGTCCTCATAAGCAGAGCGTCTCGGATTTGGAGGTTCCGGTTCGAGGCTCGAGGGGC CTGAAGGTGGCTCTCCCTCCCCGGGCCCAA	275
BCL6_chr3:187463504-187463604	GACGATGGTATGGCCTGCTCCGCCACCATCACGTGGGCTCCTCCTCTGTGACGTCGGCGCCTTCGCTGTAG CAAAGCTCCGGCCTCTGGAATTCTGAGAAC	276
BCL6_chr3:187463709-187463809	GCACAAAAGGGAGCGAGAGGTTTGAACCACTGGGAAAAAGTATGTTATATATAGTAGGGTTAGAGAGG CGAGTAAGAGAAAAATAAAATAAAAATAAAACA	277
BCL6_chr3:187463794-187463894	AAAATAAAATAAACATCACAGCTCTTTCCAACTAGAATATTAGGCACCACGAGAAAAAATATTTGCCAAGC AGTTTTCGGTGGGTTCATTTGCTTTATTTT	278
BCL6_chr3:187463894-187463994	TATTTAGGACAGGGGTTTTTGCTGTTGTTCTGGGTTTTTTTCTTTCTGGTGTGGTGGCTTGGGATTTTTGGT TTCTGTATTTTGATGGTTTATGGATTTT	279
BCL6_chr3:187463994-187464094	TGCTTCTGATTTTTTGCCTTTTGCAAGTTTGTGGTGTTACGTAAATCACAGGATCGGCATCGGTTGGATTT TTTTGTACGTGCCTTTTCTTTCCCTATCT	280
BCL6_chr3:187464094-187464194	AATCCCTCAAGCGTTTTTAAAGATGTATTATTTCAATACTAATACTATTGAAAGAAGCTTAAATTTTTGGCC ATATGTAACAATCCCAGCCCCCACTTTTT	281
BCL6_chr3:187619334-187619434	ATTATCATCATCACCACCAACATCCTCTGCCCTGGAGACCAAGAGAATTCAAACAGGTCAGCACCTCTAA TTGCTGTATAGAACATTGACCCTACTGTCT	282
BCL6_chr3:187619434-187619534	CCCAGTTCCTGAGGATGGTGTGATAATAATACATCTCAGAGTTCTGTAGTTTCTTCACCACTGTGCAGGTG TGGTTGGTGGGAGCAATGCCCTGGATGGA	283
BCL6_chr3:187619534-187619634	TAAGCCAAGCTCTTGTGTCCTGGCAGATAAACAAGGTGAACCCTCAATCCGTGTAGCAGGAGTTTCCAGA CAAACTCACTTTGCATGGAAGGACACTAAC	284

BCL6_chr3:187619634-187619734	CCTTCCAGGTGCATGGAAATATTTTGTAGTTTTTACTGTCTCCCCCTTCCTCCACTGCCTCATCTTTTTTTGT TTTTTCCCCTGTGAGACTATTTGCTCTG	285
BCL6_chr3:187660817-187660917	CCTTTCCAACACTGGCCTGCCTTAGGGACTCACCGTCTGCACTCCGCCTGCACAGGTGGAACTGAGTTCAG ATGAGGGAGAATTGCTTTCCATTGTTCAG	286
BCL6_chr3:187660917-187661017	TAGGCTTTTTGTAATTTCTAGTTTTGCTTACCTTTCCTACTCACCACACACACAAAACAGTGTGAGCTTTCT CATTCTAGTGCATAAACACAGGTCGGTC	287
BCL6_chr3:187661017-187661117	AATACCCACAAGTGTTCCAAAAGGTGAGCTGGCATTGCTGCCCAACTGGGCATTATAGTCCCTTCTGTCCC TGCCCATCAGGCTTGCCTTCCTCGGCAAC	288
BCL6_chr3:187661117-187661217	CTTTCTAGCTTTGAATTGTACTGTGACTCCTTCTCACGGACCACTCCCGGAGACTGGTGAAAGTTGGGCCCA TTCTTGAAGCCTCTGCTTCTAAATCATGT	289
BCL6_chr3:187661217-187661317	TTTCCATAAAGTCTCCCTCATCGTGCTTGCTTCCACCTTCTCCTATTTGGAATTACTGGTGGGCTCTTCCAC TGTCCCATAGCAAGTGTTCTATACATTC	290
BCL6_chr3:187661317-187661417	TGAAGGCACATTTGAATATATACTTTGTCATGGTTGCTTGGAACCATGTCGTCTTTTCCAAGTAGGCTGTG AACATTCAGTGGCATGGATCATACCGTGC	291
AC022498.1_chr3:187957432-187957532	CCCATTGTTCAAAGAAAGGCATTATGGAGTCTCCAAAAGCCATTGGCAGGTGGTGTCTGTGACTTCCTTA GCCTGGAAATAAACAAATAAACAAGCACAA	292
AC022498.1_chr3:187957512-187957612	AAACAAATAAACAAGCACACAAATTAGAAGTCTTTGCCCTATTACTGCACTATTAGTATTGATTGCGCAACA TCATGCAAAAAGTCACTTTAATTTATCTGG	293
AC022498.1_chr3:187957612-187957712	CAGGTCCTATGTAAACACCAATACAGTCAAGAGGGCTTGGATGGGTATTTGCTTTCATTTCTAATGAAATT TCAGGCCTCTAGGGTAGGATATTCAAAATT	294
AC022498.1_chr3:187957712-187957812	GGTAGATCATTTGCAATTTATTTTATCCCAAACACCTCACTTTACAGTCAGAGAAACTGAGGCCCAGAGA AGTAAAATGAGTTGCTCAAGGTCTCAGAGA	295
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AC022498.1_chr3:187957867-187957967	GTTCATGGAGCTGGCAGATGGATACATCTGTGACCTGGGATGATGGAGAGACTGCTGGACCCTTCAGAGG ATCTCATCTCAAGGTGGGGTTTATGTGTAA	297
AC022498.1_chr3:187957967-187958067	ATGATATCTGTGTTTCATTTTCCTTTCATAAACTAATTTAAAAATCCTTTTGGTATCAAATTTTAAGCCA AAAAGTAGTGAGGGGGAACATGGGTAGG	298
AC022498.1_chr3:187958067-187958167	AATAGCTTACAGCTTGCCTAACAAGGTTGTTGACTGCATAAGAGTCAGGAGTTTTGGGTAAGAGTGTGTG TGTGTGTGTGTGTGTGTGTGTGTGAG	299
AC022498.1_chr3:187958282-187958382	CGTACTGAATTTGACTGCTTTATTTTGTAGGGAAGGAAACTGATGTGCCTAGAGTAGTTGAGAGCTTTATT CAAACTCATTCCACTGTTATTGAGTAGTT	300
AC022498.1_chr3:187958382-187958482	AGGATATTAGACCAGCAACATATTTGGGTAGAAACTTTCATATATAAAAAAGCGTAATCATAACTATCCAAT CATGTCAACTAGTAAGGCTGCTCAGGTGGG	301
AC022498.1_chr3:187958482-187958582	ATAACACATCAACCTTCTTTGGGATTCTTCCCTCAGACATGGTTTTGGTGGGAGGAGCATGGCAAGGGAG GGGCGAGCTCCAAATGCAGGGCTGCTCTGT	302
AC022498.1_chr3:187958582-187958682	CCTCGGCGACCTGAGCAGACACACGAGCAGAGATCAGAGACACTCTTAGTGAATGAACCTCCCTATTGGC TATATTAAAGTAATGCTCTGAAAAAGTTCC	303

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AC022498.1_chr3:187958887-187958987	GAGGGTTAATGTTCCACGTAGTGGCTGCAAGAATGATAAGTGGTCATGGGGATAGCCTGACACTCTAGGA GCAGAAGGTGGTGGGTATGGATAGAACTAC	305
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AC022498.1_chr3:187959087-187959187	ACTGGGTATAAACGCCTGTCCGCTGTGTGCTGGACAGCCCCAGACACCCTCGGCAGCCTGCTGTGTTTGT GTGAGACATGCTGTGTTAGGGATTTAAGCA	307
AC022498.1_chr3:187959462-187959562	ACAGCTTTCTCATCTACATGGACAACCTATTTTTAAAGAATCTTCAGAGAGTCGTTGACTTTGTTATAACT ACTACTATATACGTAATTTCAGATGATAG	308
AC022498.1_chr3:187959562-187959662	AATTGAAAAATTTAACTTGTTTTTCTAGAAAGAGTTTATTTTCCCTATAACTTCAAAGAGTAATGGTGGGGA GTAGGACATTCTGAAAATAAGAAGAAACA	309
AC022498.1_chr3:187959662-187959762	TGTCAAATGAATTTCTGACTTCCAGCTAGGCATATGGAATAAAGGTCTTTATTCCAGTGACCTCTGCTCAT TGGAAAACTTTGGGCTGGTAGATTTCATG	310
LPP_chr3:188299217-188299317	TCTCTTGCATTCTTAACTTGCAATTTAGTACTGTTTATATTCTGCTTGAAGGTTAGAGACATTCGACTAAA TGGTCTTTTCTCCACATTGCTGTCATTCA	311
LPP_chr3:188299317-188299417	TTAATGTCCTGGTCCTGGACTTTACTCATTGACCACAGGACAAGTGGCTCAACTCTCTCCTGCCACTACCC AGGCTGTTAGTCCTGTTGGGAGGCTCAGG	312
LPP_chr3:188299417-188299517	GCCCAACTCACTCATCTGTAACTCTCATCTCCATTCAGCTGCAGCCTCTACAGCCCCTGGTTATACCCTGG ATCTTATCATTGCTTCGCTCTATTTTACC	313
LPP_chr3:188299517-188299617	TCCTAAATCGTAAAAATTAAAACCAGCCTCGGAACACAACCCCTCATTCTTCCAGCACTCTCTCTCATTCA GGTAACTCCTATTCTACTTTTCTTCAGCA	314
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LPP_chr3:188471512-188471612	TCCTAGTGGCAGTCATTGATCCTTTTCTTGTTGCGAGTGTTTGAGTGTGGGTGTGTGAGTGTGTATATG TATTTGTAGAGGGAAAAACAAGAGAGAGG	316
LPP_chr3:188471567-188471667	TGTGAGTGTGTATATGTATTTGTAGAGGGAAAAACAAGAGAGAGGGAAACAGACATTGGAGCCACCTTTC CCCCACTAGCCACGTACCTGTTGAACCTTC	317
LPP_chr3:188471667-188471767	AAGCCTCTCTATAGAATCAGATATACACAAGCACAGTGACAGAACTACATGTGTCCTACAGTCCAGCTTT TAAGATATGATAAAAAACTCTTGTATTCACA	318
LPP_chr3:188471767-188471867	GAGCTAAATGGCAATAACCATAGGAGATTGCATATTGCTACATTATGTAAAGACAGAGTCCCAAGAAAAT AGTGAGAACTCAGTTTGATGTATGATGTGA	319
LPP_chr3:188471867-188471967	TATGTGATATCTTACTTTACATGGCTAACAGTTGACATTCTTTGTGGATTCTATATTGTCTAAGGCTACAG AAGAGCCATATGATAAATTCATCGGCAAC	320
N4BP2_chr4:401988810-401988910	CAGTGAAAAAGGCTTGGGCCGCTTTTGTTTTCACCTGCTTTTGTTGAACAAATTTGATTTCCGGAGTCAGTC ATTTTACTGTCAAGACATTTCTTCGGCAT	321
N4BP2_chr4:401988910-401990010	TCTGCAACAGGTAAGGATTTTGCTTCCTTAAAAGTATTTTCTTTGGTGTCAAAAAGAAAATTTTTCTAATTTTA TTTAGCTTTTACTCTAGGCCAAACATCGT	322

N4BP2_chr4:40199010-40199110	AATGACTCTGAGCTACCTGCTGTAAGGTGTAGAATCAATTTACAGGGGACGGGGGTCGGGGGGGTGAG TGTTGCTTTGATATTCACTGCCCCTCACCAC	323
N4BP2_chr4:40199110-40199210	AGTCCTAACAAGATTTTTGAAACATGAAAAGTTACAATAGTTGGCTTTTTGGTTTTCCAGATATTCTAGAG AATGCATATGCTTGTGACTGTGGCTGAGC	324
N4BP2_chr4:40199210-40199310	TCAACTGTATGGGTAGTTTAAATACTACCCAAGGTTTGATGAAGTAAATCTAAAGATGCTCTAAGTTGTG CAAATATGAATTTTTAAAGTTGTCTAGTTCA	325
N4BP2_chr4:40199310-40199410	GAAAAGAAACAGAACCGAAGTCTAAATGATGTAGATTTCAATCTGGAATTTCTAGCTTGTGTTTTTCACCT ATTGCCAATGTTAATGACCATTTCCCAAA	326
N4BP2_chr4:40199410-40199510	AGTGCTCTATGATGTATAACATGTATTTTTTAATTAAATTTAATCTTTCTTCTGAGGTGGTTTGATTTGGAG ATATGCTACCGAGGTACCAGTCAGTAGCC	327
N4BP2_chr4:40199510-40199610	TGAGTTGTAACTAAACAAAGTTTGGGAAATCACCGGTTTTAGGTGCTTTACTAAATGAAAGTTGCCATTG ACGTATTCAAGCAGGCAACAAGTAGTTGGT	328
N4BP2_chr4:40199610-40199710	GTCCCCTTATTGGTTCTAAGCTGGTGCCGTGGAGGATATAAGAGAAATATTTTAAAAATCTCTACTTTGAA GGACCCTATAATCTGGTAGTTGTGATAAG	329
N4BP2_chr4:40199660-40199760	TTTAAAAATCTCTACTTTGAAGGACCCTATAATCTGGTAGTTGTGATAAGAAGTAAAATTTAGGAAGCAA TGCAAGATGAGAATTCAGTGATGAGTGGGG	330
N4BP2_chr4:40199760-40199860	CAGCACAGGCTTGAAGAGTTCTGTGAATTCCATGGAGAGGGGGCCTGGGGGCAAACTGGAGTTGTCAGGAA GATCTGGGCTTTGGAAGAATGCGAAGTGTCG	331
N4BP2_chr4:40199860-40199960	GTAGAAGGAGAAGGGGCAGGTGATTTCAGACTGGGAGGACCTTGTGGGCAAAGGCACAAAGGCGAGACT GACCTGGAGATGATAAGGCCAGTTGAAGAGA	332
N4BP2_chr4:40199990-40200090	ACATTGCAGGAAATCAGATTAGACAGTTAGGGTGTGGACACAAAAGCGAGGACCTTGCAGGCACTGGGG AGAAGTGACCCCCATTCAATAGTCCTTGGTCT	333
N4BP2_chr4:40200090-40200190	CCTTCTGCCCTGCGGCTGCGCTTCCTCGGCTCTCACGGCACCAGCAGAATTCCATGTGAGAGGGAGCTTGT CGAGCGTGGCCTCTTCCCACTTGGGGCTG	334
N4BP2_chr4:40200190-40200290	CTTTCTGCATCCCTGTGCCTGGCTGTGGGCCTCCATTTGCCCTCTACTGTCTTCCCTTAGGACATCATTTAT GCAGAGAAAGGTTCGTGTGTGGCTCGGGGT	335
RHOH_chr4:40200505-40200605	GGACGTTGTTTAGAGAGTCAGTAGATCATAATAATTCAGACACTTTTTTTTCTGGACCATAAAATATCTGAA CCCATATAATAACAAACATACAGCACGGT	336
RHOH_chr4:40200605-40200705	GAATAAGAACCCAACTTTTGAGCCAGATCACTTTGCATGGAATCCCCATTCTATCATTCTATTTCTGG GCTGTGGGAACCTCAGACAAGTTACTTAA	337
RHOH_chr4:40200705-40200805	CTTCTTCAATGCTCAGATTAAAAAAAAAAATTCACAAAATATCTCTAATAACAGTAATAATAACTGAAAAT ACCTACCTCAGAGGGTTGTCGTAGAGATCA	338
RHOH_chr4:40200730-40200830	AAAATTCACAAAATATCTCTAATAACAGTAATAATAACTGAAAATACCTACCTCAGAGGGTTGTCGTAGA GATCAAATGAGATAAAAATATGTAAAGCAT	339
RHOH_chr4:40200830-40200930	GTAGCCTAGTGCCTGACTGAAAAAAAAAAATCTCTCAATAGATGCAACTCTTATGATTCTTATTAAGGACTTG GCTATTGCCACAAATGAAGGTGTTATGAG	340
RHOH_chr4:40200930-40201030	CCCTGGCTTAAGAGCAAGAAGCCTGCAAAGCTAACTCTCCTAATCCCAACATTCCTTTCCAGGGAAAGTA GGGTGACAGGTGGAGGCTGGGAATTAACGT	341

RHOH_chr4:40201030-40201130	TTTTTGAGCACCAAATATGGACAAGGCACAGGGGTTGGGTGTTTTTCTAGTGAGAATACATATGAAAGAA GGAAAACAAACTTGGAAAACCGCTATTTTAA	342
RHOH_chr4:40201130-40201230	GCCATTTGGTAACAGTTTCTCTAGCTTATGAGATGAGAGAGGTCCTCTCAGTATCCGCTGCATTACTTGTG GGCCTCCTTGGTTGACGTCCGCTCTCTGAA	343
RHOH_chr4:40201230-40201330	CGCTTGGGGTGGAATTCTAGAGGTGCTTTTCATTAGAGGCAGAGAGCATGACCTTTCTTCCTTGCCCAGTT TAAATTAAATTATTTTATCTTACAATGTG	344
RHOH_chr4:40201330-40201430	TTAATTTTAGTGCTAGCAAGGCACAGCTAAAATTCCATTTCTACTTAGGAGTGGGGATCATTGTGGCAGT GAGTGCTTATTTGGGTTTGGGATGCTTGGA	345
RHOH_chr4:40201430-40201530	TCTGGGTGAAAGCCAGGATTAAAAAGCATCCTCCTTCCCCATTCCACTCTCTAGGTTATAAATATTTTTTT GGATTAAAAGCCTCCTTTAAAAAAATGCA	346
RHOH_chr4:40201530-40201630	AATCCACCTGGCATGTTAATTGTGCAGGGGATTCCTAATTATGTGTGCAGATGACGTGAGTCACACGGTG ATAGTGTTCCTTCTAGAGTCCCACTGGTGT	347
PABPC4L_chr4:134727698-134727798	ACTAGGCCGTTCATCCTGTGTAATTTGAAAATATGTCACACGTGGTGATGAGAATCTATTTGAGGAACATG GGCAGTTTGAAATAAATATATGCAATGTATG	348
PABPC4L_chr4:134727798-134727898	ACTAGTTTATATAATGAAAGGAAGTATTTAAAAAGATAGAATGACATAGACTAATCTAATTGAGAAATAT GAAAGTCTAACAGAAATGATTGCTTGTGAA	349
PABPC4L_chr4:134727898-134727998	ATTTTATGAAGAAATCCACAGATAAATTCTCCACCTTGATCTATGTAATCCGAAATTTAGATGTTAAAAAT ATGTTGATTCTGAAAATTTATATTTTATTC	350
SLC38A9_chr5:54964698-54964798	TTTGGTATGAATAGGTCAAAACAAGTCACCATTAACTGACAGGAAGCACAGAATTCTCAATTTAGTTTTG GCAAAGACATTATTTTATAAATATGAGTTT	351
SLC38A9_chr5:54964798-54964898	TTAAATGATTCTTATGAAGAAACTAGCACCAAAGTGAATGCACTCTGCAAATAACTCCCAGCTTCTCTGA ATTTCAAAAGCAGCCACTAAATATTATTAG	352
SLC38A9_chr5:54964898-54964998	CAAATCAATTTAGCTGAAAGCGATGAATTACAGAAGTAAATCTTTAGGTACAAAGTAGACAGCTGACACA CATGTAGCATATACACACTAGTGATCTGCC	353
ZNF608_chr5:124079827-124079927	TTCCTTCTTTACCAACATAGAGTTTCCCATGAGCCCTGAATCCGGGGCACTTTTGCTAACTTCCCCTGCAG CGGCGACGCTGCCACTCCCAGTGCCCCCG	354
ZNF608_chr5:124079927-124080027	CAGTGGAAGGGGCTCGCGCCACCTCCATTGCTCTTGGCCCCAAAGCCATAGAGGTGCCCCCCGGAAGGGG CCTGGCTGCCACTGCCATTCTGGTGGCCCT	355
ZNF608_chr5:124080027-124080127	GAAGCAGGTCGTGCTTGTCCTTCCTGGATTTCCCCGCATCCTTATCCCGCTTGGCGCCTCGGCTGCTCTGG CTTTTACCTGGCTTCTCCTCTTTGCTTTT	356
ZNF608_chr5:124080127-124080227	CCCACAGGAGCCTGCCCCCGCGGTGGCGGCAGAGGTGCTGGTGCTGGTACTATTGCTGTTTGGGTTGCCG CTGCCGCCGCTGCTCACACTTTGACCCAGC	357
ZNF608_chr5:124080227-124080327	GCTGAATTCATGCCAGTTGCCTCTCCAGGGCGCCCTTGGACTTCCTGCCTCTTGCCAGTGCTGCTGATCTC GGGAATCCCATACAAGGCAGCAGAAGGCA	358
ZNF608_chr5:124080327-124080427	GAGATTTATTAGCATCCTTAGAAGTTTTACTCCTTTTCACTTTTGATTTGCTGGTCTCTTTGTGTGAATTCC CCTGGGGAGCAGAGGCCTGAACAGAAGC	359
ZNF608_chr5:124080427-124080527	AAATTTTAGGCCATCAGCTAAGGCTGCGGTAGCACCAGCCCCACTGGAGGCCGGACCTCCACAATCCTTG GAGTTGCTGCTACTAGTGGTGGTGGTGGAA	360

ZNF608_chr5:124080527-124080627	TTATTCATCTCAAATTTCTGTCTGTCCTTCTCCAAATCAGCGTCCAAATCAATTATTAAATTTCCAACCCCG ATTTCCCAATCATCGCCACTGTCATAAG	361
ZNF608_chr5:124080627-124080727	TATCAACTGTATTTGGATCCACACCTTTCCTGCAGTAGAAATGTTCACTGACATCCTGAAGATGAGCTCT CTAGAATAAAAATCCGATGAACTTTTCTT	362
EBF1_chr5:158527642-158527742	TTCCTCAGGAATTTGAGCTGGGGATCTGCATCCTGGCCATTGCAGTCCTTTAGCATCCTCGCCGCGCCCTG AGCGCGCTGGAGGCTCGCAGGCTGCGCCC	363
EBF1_chr5:158527742-158527842	TCCCAGGGCTGATGCCCGCGTCCTGCTCCGCCGTTCTGGGACGTCGGGGACAAAAAGTGGAGGAGACGGGA GAGCCCGGGCAGAAAAAGCAGGACGCGCGTC	364
EBF1_chr5:158527842-158527942	CCAGGTGCCCACCTCTTCGCTTTGAGGCGGGGGCGGTGGGATGGAATATGGGTGCGCGAGGTCGGGGCTG GTAACTCTCGGAGGGGCACGGCCTCCACGC	365
EBF1_chr5:158527942-158528042	TGGGAGGGATGAATGGACGCTGGGCCCCGGCAAATGAGGCGCTGTGGGTCCCCAGGAAGTGGGGGTACCA GGCTCTACTCCCCACCCCGGCCTCTGAAACGC	366
IRF4_chr6:392760-392860	GGCCAGGAGGGGTGGCGGCTGGGTGGGGAGAGAGGGTGCAAGACGAGCGGCGCGTGTCGGGAGCCTTTG GGCTGCCGGTGCCTTACAGGAGAGCAGGCGG	367
IRF4_chr6:392860-392960	GTAGGAGCCTTCGCGGGGGCCGAGCTCGGAAGGCGGACGGCTGTGCCCCGCCCAGGGGATGCGCCCGGGC CGGCCGCGAAGGTGCCTTCTTCCGCGGGCCC	368
IRF4_chr6:392960-393060	GGACGACCCTGACACGGCACGCGCGCTTCGCAGCCTCAAAGACTCCGGGGCCTCGTGGTCACTGGCGC AGGGGATCGGGGCGGGGTGCCCGGAGTGCG	369
IRF4_chr6:393090-393190	CCCGCAGTGCAGAGCAGAGCGGCGGAGGACCCCGGGCGCGGGACGGCACGCGGGGCATGAACC TGGAGGGCGGCGCCGAGGCGGAGAGTTCGG	370
IRF4_chr6:393190-393290	CATGAGCCGCGGTGAGCTGCGGCAACGGGAAGCTCCGCCAGTGGCTGATCGACCAGATCGACAGCGGCAA GTACCCCGGGCTGGTGTGTGGGAGAACGAGAG	371
IRF4_chr6:393290-393390	AAGAGCATCTTCCGCATCCCCTGGAAGCACGCGGGCAAGCAGGACTACAACCGCGAGGAGGACGCCGCG CTCTTCAAGGTCTCCGGCCTCGGGAGCCGGC	372
CD83_chr6:14117992-14118092	CCCGCGCGCCACAGCTCTGCAGCTCGTGGCAGCGGCGCAGCGCTCCAGCCATGTCGCGCGGCCTCCAGCT TCTGCTCCTGAGCTGCGGTAGGGCTCGCGA	373
CD83_chr6:14118092-14118192	GCGCCTGTCTCGCCTGTCGCCCCCCGCCCCTCCACGACACCCCCTCCCGTCGGTCGCTTGCTCACGACGCG CTCTCTCTTTCTTGTAGCCTACAGCCTGG	374
CD83_chr6:14118192-14118292	CTCCCGCGACGCCCGGAAGGTGAAGGTGGCTTGCTCCGAAGATGTGGACTTGCCCTGCACCGCCCCCTGGGA TCCGCAGGTTCCCTACACGGTCTCCTGGGT	375
CD83_chr6:14118292-14118392	CAAGGTAGGTGCTGCGATACCCACGGGCTGGGGTTTGGTGGGCTCATTTGAAGACAGCAGGAACCATCTTC CCCTAGGCTGGCGACCCTCTGTGGCCA	376
CD83_chr6:14118392-14118492	GGTGGGGGCGAGGGGCGTCTCCCGCAGCTGAACTTGGAGTACCCAGCCTCCGGTCGGCGCCTCCCCCCACCC CATCCGCATCCAGGTACAGGGCCGAATTAG	377
CD83_chr6:14118492-14118592	GTTTTGCTCTCCGCAGACCTCAATCCCCTTCCTGTCACTGAAGGTGGCCTGAGATGAATGATCCACTTAAG ATGTTTTGGAAGGGCAGAGACTCTCATTT	378
CD83_chr6:14118592-14118692	GGATTAATTCTGGAGGCCACCTGTGGTTGTGGGCCAGGCAGGTCAGGAAGAAAGCAACAGGGACCTAGAT TTGGGCATTGGACAGGGGGAATGTCTCCAGA	379

HIST1H2BC_chr6:26123614-26123714	CTCTCCAGTTCCTATATTCTAATACCCCTCCGCCGCCAAATAAAATTTGGCGTCTGGCCACAGCTCTTTTA GTGGGTATCTGGGTGGCTCTTAAAAGAGC	380
HIST1H2BC_chr6:26123714-26123814	CTTTGGGGTTAGGTGTTAAGACGCTTACTTGGAATGTTTACTTGGAGCTGGTGTACTTGGTGACGGCCTTG GTGCCCTCCGACACGGCGTGCTTGGCCAG	381
HIST1H1E_chr6:26156649-26156749	CTCCGGCCCCTGCCGAGAAGACTCCCGTGAAGAAGAAGGCCCGCAAGTCTGCAGGTGCGGCCAAGCGCA AAGCGTCTGGGCCCCCGGTGTCCGAGCTCAT	382
HIST1H1E_chr6:26156749-26156849	TACTAAAGCTGTTGCCGCCTCCAAGGAGCGCAGCGGCGTATCTTTGGCCGCTCTCAAGAAAAGCGCTGGCA GCCGCTGGCTATGACGTGGAGAAGAACAAC	383
HIST1H1E_chr6:26156849-26156949	AGCCGCATCAAGCTGGGTCTCAAGAGCCTGGTGAGCAAGGGCACCCTGGTGCAGACCAAGGGCACCGGC GCGTCGGGTTCCTTCAAACTCAACAAGAAGG	384
HIST1H1E_chr6:26156949-26157049	CGGCCTCTGGGAAGCCAAGCCTAAGGCTAAAAAAGGCAGGCGCGGCCAAGAAGCCAGCAGGAG CGGCGAAGAGCCCAAGAAGGCGACGGGGGC	385
HIST1H1E_chr6:26157049-26157149	GGCCACCCCCAAGAAGAGCGCCAAGAAGACCCCAAAGAAGGCGAAGAAGCCGGCTGCAGCTGCTGGAGGC CAAAAAAGCGAAAAAGCCCGAAAAAGGCGAAA	386
HIST1H1E_chr6:26157149-26157249	GCAGCCAAGCCAAAAAAGGCGCCCAAGAGCCCAAAGCAGTTAAACCCAAGGCGGCTAAA CCAAAGACCGCCAAGCCCAAGGCAGCCAAGC	387
HIST1H1E_chr6:26157249-26157349	CAAAGAAGGCGGCAGCCAAGAAAAAGTAGAAAGTTCCTTTGGCCAACTGCTTAGAAGCCCAACACAACC CAAAGGCTCTTTTCAGAGCCACCCACCGCTC	388
HIST1H1E_chr6:26157349-26157449	TCAGTAAAAGAGCTGTTGCACTATTAGGGGGCGTGGCTCGGGAAAACGCTGCTAAGCAGGGGCGGGTCT CCCGGGAACAAAGTCGGGGAGAGGAGTGGGA	389
HIST1H2BK_chr6:27114004-27114104	CTCCTTAGCCAGACTCGATTACAAGCACTGCATGCATTACTCAGTGTGATAAGATCATGATAAATCCCTTTA AAAAGATCGCCCCGAATTTAAGCCTGGATT	390
HIST1H2BK_chr6:27114104-27114204	AGGAACACGTGTTTACAGCTCTAATATCGATAATTTAAGTGGCTCTTAAAAGAGCCTTTGGGGTTGGGCT TTAAGACGCTTACTTGGCAAGTTTACTTAG	391
HIST1H2BK_chr6:27114204-27114304	CGCTGGTGTACTTGGTGACGGCCTTGGTGCCCTCGGACACGGCGTGCTTGGCCAACTCCCCGGGCAGCAG CAGGCGCACGGCCGTCTGGATCTCCCTGGA	392
PIM1_chr6:37138284-37138384	CCCCGGCTCCGGCTCCTGCGGCAGCTCCTCTGGGCACCGTCCCTGCGCCGACATCCTGGAGGTTGGGATG CTCTTGTCCAAAATCAACTCGCTTGCCCAC	393
PIM1_chr6:37138384-37138484	CTGCGCGCCCGCGCCCTGCAACGACCTGCACGCCACCAAGCTGGCGCCCGGTGAGAGCACCCCCCCGCCTCC GGCCCGGGGATGCCGGGGCCGCGCCGGGATC	394
PIM1_chr6:37138484-37138584	TCCTGGGTGGGGAGCTGGCGGCTCGCGGCCGGCACTGAGTCCCCGTGCTTCCCCCTTTCCTAGGCAAGG AGAAGGAGCCCCCTGGAGTCGCAGTACCAGG	395
PIM1_chr6:37138584-37138684	TGGGCCCGCTACTGGGCAGCGGCGGCTTCGGCTCGGTCTACTCAGGCATCCGCGTCTCCGACAACTTGCC GGTGAGTGGGCGCCCCCGCGGTGGGGAGGGC	396
PIM1_chr6:37138684-37138784	GCGCCGGGCGGGGGGCGCACGGGCGTGCTTTAGCCCGGACGAGGGAAGGAACCCTGGGCTTC CAGGTGGCCATCAAACACGTGGAGAAGGACC	397
PIM1_chr6:37138784-37138884	GGATTTCCGACTGGGGAGAGCTGGTGAGTGCCCTGCAGGAGCGACCCCCCAGGATGAGTGGGTGGGGTGA GGGGCGCCCCCGACTCCCGCCCTAACGCGC	398

PIM1_chr6:37138884-37138984	CCCCTCGGCCCCTGCAGCCTAATGGCACTCGAGTGCCCATGGAAGTGGTCCTGCTGAAGAAGGTGAGCTCG GGTTTCTCCGGCGTCATTAGGCTCCTGGAC	399
PIM1_chr6:37138984-37139084	TGGTTCGAGAGGCCCGACAGTTTCGTCCTGATCCTGGAGAGGCCCGAGCCGGTGCAAGATCTCTTCGACT TCATCACGGAAAGGGGAGCCCTGCAAGAGG	400
PIM1_chr6:37139084-37139184	AGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCACTGCCACAACTGCGGGGTGCTCCA CCGCGACATCAAGGACGAAAACATCCTTAT	401
PIM1_chr6:37139184-37139284	CGACCTCAATCGCGGCGAGCTCAAGCTCATCGACTTCGGGTCGGGGGCGCTGCTCAAGGACACCGTCTAC ACGGACTTCGATGGTGAGCCAGGCCCGGGA	402
PIM1_chr6:37139284-37139384	GGGAGCTGCCCAGGTGACTCGGCCCGGCCCAGTCCGGAGGCCTCGGCCAGTCTCCCGCGCCAGCC TTTTGTAAAGGTCATTGGGCCGCCTGGCTC	403
PIM1_chr6:37139384-37139484	GATGCTAGCCGGGGTGGGACGCAGGAGAGCCTCCCAGCGTAGTAAAGCCGGGGATTTTCAGCCAGCTGA ACCTGTAATGTTTCTGGCATGATTTTATTCT	404
PIM1_chr6:37139484-37139584	TCAAGTGGAATTCAGTTAGTTCCAGGCTTTCCCGATGAATAAGAGGTTGTGGGCAACCGGCGGTAGCCCA GATTTTTCTAAAGTCTGACCCAGTTTCCCC	405
MAP3K7_chr6:91004618-91004718	CTCTAAACAGACAAAAAGCAAAATATCTCATTAGGCATCATCTCCGCCAAGGTTCCCACTAGGCAGGAAAG GATTTTTATCTAAAGTAATTACCCTTTTTA	406
MAP3K7_chr6:91004718-91004818	GTTAAATACACTCAACAGATGAAATTTACAGAGAGTGAGAGACTGCAGCACTAGACAGCGAAGGTGAAA ACCAGGAACGCCGCGTCTCGCCGCCCGCGGG	407
MAP3K7_chr6:91004818-91004918	CCCGCCGGGAGACTGCGGGTCCGTCTCGGCGGGTGGGGCGCCCCGGTCCCTCTCGTTCCTGGAGGCCACA GGTCACGGCGACGGCGGTGACCGGGAGAGC	408
MAP3K7_chr6:91005793-91005893	CGGGTCTGACAGCTGCTGCGGCTCGCGCGGACGCGCGCCTCCTGCAGCCCGCCCTCCCCATGCCTGACTT ATTACTCTCTGCTCCTCCTCCCTCCTCTGCTGT	409
MAP3K7_chr6:91005893-91005993	TCCAAAACACCCTTCGACGCCAGCAAAATACAATGCGCCTCGGCCGCCGTAAACAGCCGGGAGGGAGAG CACACATTCGGCGCGCGGCCGGCCGCTC	410
MAP3K7_chr6:91005993-91006093	GGCTCCCACCCCCTTCCCGTTCCTAGAAAATGCCATAAAAGCGGGCAGGGCGCGGGAGGGCGGCTGCGC GCCCGGCGCCGGGCTCCCTTCCCGCGCC	411
SGK1_chr6:134493732-134493832	TATGAAACAGCCAGTGCTACGTCTCCTTATACCAAAACTGGTAGCCTGAAGAGCTCTCAGGCTTACCTAT AAACGATGTTCAGTGAATGCAGGTAGCCC	412
SGK1_chr6:134493832-134493932	AAGGCACTGGCTATTTCAGCAGCATAGAAACGAGCCCGTGGTTCCAGGAAGCAGCGTTCCCTCTGGAGAT GGTAGAACAACTGCAGGAGACAGAACAAAG	413
SGK1_chr6:134493932-134494032	TCATTCTGGGTTGCAAATGAATTTAATTAGTTTTGACATACACAGCAAAAGAACAACTGCAGGAAGTGGC CCCAAGTAATCTATTAACTATAAACCTGAC	414
SGK1_chr6:134494032-134494132	AGGTTGAAGGAAATGCTAATTCTGGTAACATTCTCCCCACCAAAAAATCTTTGAAAACTTTTTTCTCAAACT AAAACAAAGCAGGCTGTGCAGAGACACTA	415
SGK1_chr6:134494132-134494232	AGAGTTGACTTCTATCCCCCCTGCTCACCTCTCCACCATTAATGTAGTCTAGGACAAAGTACAATTTGTCA GCAGTCTGGAAAGAAGTGAAGGCCCAC	416
SGK1_chr6:134494232-134494332	CAGGAAAGGGTGCTTCACATTCTTCAACAGAACATTCCGCTCCGACATAATATGCTTCTCCTAGGAAAAT GACGATTCAGATTTAGTGGCATGTTTCAAC	417

SGK1_chr6:134494552-134494652	GAGGACATGAAGGAAGTGTACCAAAAGATCTTCAGATTTGAAATTACCTTTCCAAAACTGCCCTTTCCGA TCACTTTCAAGAAGTGAAAGTCAGATGGTT	418
SGK1_chr6:134494652-134494752	TAGCATGAGGATTGGACGACGGGCCAAGGTTGATTTGCTGAGAAGGACTTGGCTAGAAAAAAAAAAAAAA GAATTTCTTTTAATACCATTGCTTCAAAGGA	419
SGK1_chr6:134494722-134494822	AATTTCTTTTAATACCATTGCTTCAAAGGAAGACATCTATAACATAAACGATGTAGAAAATGTTACATCTA CAAATGACTGATGCAAATGACCATACATC	420
SGK1_chr6:134494967-134495067	AATAAAATAATACTCTGACTCAATACTTAAATATTTATATCACTTGTTATGCCATAATGAAGCATTCCTGC CTTGATACTAATTTCTAGAAATGCTATTT	421
SGK1_chr6:134495067-134495167	TAATCCATTAATGTAGGAATACTAACTGACTCCCTTACAGTTCTCCACAGATGCACGGCACATACAAAAA CTTACTGGAGGAGAAGGGTTGGCATTCATA	422
SGK1_chr6:134495167-134495267	AGCTCAGGCTCCTGAGGTTGGGAGATCTTCAAGATGGACTGAACTTCAGGGCTGCAGGGAATAAAGGGC ACGATTTAGAATCCAGCTCGCCACTAGGGGG	423
SGK1_chr6:134495267-134495367	CACACCAACATCAAAAGTGAGTTTCTGGCTCTACCGACTTCTACCCGGATAAATTCACTGTTTAAACTGAAA ATACCCCAATACATTAGTCAGTTAAAGAA	424
SGK1_chr6:134495367-134495467	AATAATAAAACCCCATTAAATACAGAAATAAGGATTGTTGCTCATGGAGAAAGGCCGTGAATTCGGCCAAC ACGAACCATTTATCTTACATCTCCAGTTCA	425
SGK1_chr6:134495467-134495567	AGCCAAATCAGCAAATTAACTTTAATGTTTAAAATGTGTCAAATATATTAGAATTTAAGGAGAAATGAGA TCCCCACCCCAGAAGAAGTCTTCGCCTTCC	426
SGK1_chr6:134495567-134495667	CGATAAACGCCGTGATGAGAATGTTTACCGCTGGCAAATTCAAACTATACTAGTTATTTCCTCAAATCCGG TCAAACTTACTGTTTGCATGCATAGGAGT	427
SGK1_chr6:134495667-134495767	TATTGGCAATCTTCTGAATAAAGTCGTTCAGACCCATCCTCCTCTGCTTCATGAAAGCTGTGGATGAAGGA GGAGAAATAAAGAAACGTTTAGACCGCTT	428
SGK1_chr6:134495767-134495867	CATAACGTCCGGCGCCACACACACTAATCTGATCCGGGACTTTCAAAAAATTTCCACTTTGCGTCTCCTGG AGCAGAAGTCCCGCAAGATTCCTGCACTC	429
SGK1_chr6:134495867-134495967	ACCGATGAGAATTGCCACCATGCCCCTCATCCTGGAGTAAGTGAGGGTGCCCTTAGCAGCCTCAGTTTTC ACCGTCATCACCACCGCGGGGAGACAGAAA	430
SGK1_chr6:134495967-134496067	GACGTTAGCGCTCAAAGACCGGCTCGGCGTATGCTGCGCCAGGCCGCCGCTCGGCCTTATAAAAAAGGC ACCGCCGCGGGGGCCGGGGCCTGCGCGCAG	431
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EZR_chr6:159238515-159238615	CAATTCAAGTCCATGGCTAACCTTCTGTTAGAGACAGAAAATTCTGCTGCAGCCAGCAAGTTTGCTGGTGT ACAGGGCACCGCTTCATGGGCCTAGTAGGA	438
EZR_chr6:159238615-159238715	AGCGAAGCTGAAAGGCAACTTCCGAAAGCCAGTCTCCTCTCCCAAACGCCCTTTAATATCTCCCCAGTTG GATCTGGGGCGCCTGTGGTTTCGGACCCTT	439
EZR_chr6:159238715-159238815	AGGAGCTCTGAGAACTGGTGTGTGGTCGGAAGCCATCTGAGTCTCCCTGTGATTTGGACTTTTTAAGA AACTTCTAAGTTGTATTACTATACCCTTTA	440
IMMP2L_chr7:110545276-110545376	TTCCCTTGTCATATGACTTCCATCCTCAGCACTACAAATATTATCATTAATGTTTAAATCATTGTCAAGTCTG TGATTGCCTTAGAGATTTATTAAGAATA	441
IMMP2L_chr7:110545376-110545476	ACATGCTAGGATTAGGAAAGTTTAACTTTTTACCATCCTTAAAATTAGATTTTTGAAAACTGTCTTATCCC CATTAAAGAAAAAAATAAAAAGGATGAAT	442
LRRN3_chr7:110697971-110698071	TATACATACCTGCACATATATACAGCATATGTATATGTCTGTATTATAATGAAAGATTATC CACATTTTGTTCTTTAGGATCTTCAGCAG	443
LRRN3_chr7:110698071-110698171	CTCTCTTCCCATCACAATAGAAAGGCCTGAGCTAACATTTCCATTTCTGCAAAAGGCAGATTTTGTTCAAT TAAAAATTATAATGCCTTAAATTTCCACA	444
LRRN3_chr7:110737411-110737511	GACATTTAAGAGACTTCGTTTTCACTGTGATAAACAGGTTTGATTTGGACTTATAACTTTTTTCTAAAATT ATCAAATTAATAACGACTATATAATGAAATA	445
LRRN3_chr7:110737511-110737611	GAGGCAAATATTTTAGAGGATTCATTCCTTGGGGTAACATTTGTTCTATAATTTATAGTCTCATAATGTTG AGAGATTAAAGCATTTAAATAACATTGTC	446
LRRN3_chr7:110737611-110737711	AACTAACTTTCAGCTTACCTTTCTTAAGGAAAAAAAACAAAAAAATGTTAAAAATAGACATGTATTTTTC AAACATACAATTCATGTTTTTTATGTCATTA	447
LRRN3_chr7:110746681-110746781	AAGAGATGTGAGGGACTTATAAATAATATTAAGATAACAGGAATTAAAGTCTCGGTGTGTGAAAATACTG TATATCTAGGATGCACACATAAAAAACTGCCCT	448
LRRN3_chr7:110746781-110746881	TACAGATCTTGCAGGGAAAAGTACCTGACTATACTGTATAAGACTTCTGCTGTACCATTTAATCATACCAA AAAAAATGGAATCAACACACACAAATAGATT	449
LRRN3_chr7:110746881-110746981	TCTTTTCCACTGTTCTCAATTTAAAAATAATTGGAGAAATGTGTGCTTTGTTTAGAAGAGTAAAGGAAAAC ATTCATTCAATAGTACCATGCAGAATGAT	450
KMT2C_chr7:151943421-151943521	CAGAAAAATAGAAAGATTATCATCGGATTTGGGAATCAAAGACAGCTCAGCAAAATACTAGGACATGGC TCATATAAGATGGAATAAGCCTGGAAATACA	451
MYC_chr8:128750367-128750467	CTTTAGGGGATAGCTCTGCAAGGGAGAGGTTCGGGACTGTGGCGCGCTGCGCCAGGTTTC CGCACCAAGACCCCTTTAACTCAAGACTGC	452
MYC_chr8:128750467-128750567	CTCCCGCTTTGTGTGCCCCGCTCCAGCAGCCTCCCCGCGACGATGCCCCTCAACGTTAGCTTCACCAACAGG AACTATGACCTCGACTACGACTCGGTGCA	453
MYC_chr8:128750567-128750667	GCCGTATTTCTACTGCGACGAGGAGGAGAACTTCTACCAGCAGCAGCAGAGCGAGGCTGCAGCCCCCG GCGCCCAGCGAGGATATCTGGAAGAAATTC	454
MYC_chr8:128750667-128750767	GAGCTGCTGCCCACCCCGCCCCTGTCCCCTAGCCGCCGCTCCGGGCTCTGCTCGCCCTCCTACGTTGCGGT CACACCCTTCTCCCTTCGGGGAGACAACG	455

MYC_chr8:128750767-128750867	ACGGCGGTGGCGGAGCTTCTCCACGGCCGACCAGCTGGAGATGGTGACCGAGCTGCTGGGAGGAGACA TGGTGAACCAGAGTTTCATCTGCGACCCGGA	456
MYC_chr8:128750867-128750967	CGACGAGACCTTCATCAAAAACATCATCATCCAGGACTGTATGTGGAGCGGCTTCTCGGCCGCCGCCAAG CTCGTCTCAGAGAAGCTGGCCTCCTACCAG	457
MYC_chr8:128750967-128751067	GCTGCGCGCAAAGACAGCGGCAGCCCGAACCCCGCCCGCGGCCACAGCGTCTGCTCCACCTCCAGCTTGT ACCTGCAGGATCTGAGCGCCGCCGCCTCAG	458
MYC_chr8:128751067-128751167	AGTGCATCGACCCCTCGGTGGTCTTCCCCTACCCTCTCAACGACAGCAGCTCGCCCAAGTCCTGCGCCTCG CAAGACTCCAGCGCCTTCTCTCCGTCCTC	459
MYC_chr8:128751167-128751267	GGATTCTCTGCTCTCCTCGACGGAGTCCTCCCCGCAGGGCAGCCCCGAGCCCCTGGTGCTCCATGAGGAG ACACCGCCCACCACCAGCAGCGACTCTGGT	460
PAX5_chr9:37024919-37025019	GCTCCCCATCTGTCCCCACAGTTGCTCCTTGGCTGAGCCAAGGGCTTGCTCACCTCTCAGAGCATTGCCCT AACTGGTTTGTTTTGGGCTTACATTGCAA	461
PAX5_chr9:37025019-37025119	GATCAGGTCCTCCCCAGAGCCAGGCTGGAGTCCGAGGCAGAAAAGGCTGTGGAGGGCACTGGGGTCACC ACAGACTGGAAACCGGTTGGGCGCAGGCCCC	462
PAX5_chr9:37025119-37025219	AAACCTTGAGGAATCGTTTGGGCTGGGACCAGAACAGGGGGCTCCTCTGCACAGAGCTCCCCCACCGCTTT GGTGGATTACTTCAGACTCAGAAAATTGAC	463
PAX5_chr9:37025219-37025319	ACAAAGAGAAACTGACCTGCCCGCAGCCAGCCCTGGCTGCCTACACAAGCTTTCCCCTGCTTGCCAGGCC ACTCAGCACTGCGTGGCAGACACGGACATG	464
PAX5_chr9:37025319-37025419	CTCGCCCCGGGAAGCTCACCTTCACTCCAGCCGGGTCTCTGCTGCCTTTGTTAAATAGGGGACCTGCGGCT AGGAAAGCTGGATCCCAGGCTGTTGGGAT	465
PAX5_chr9:37025419-37025519	GGGGGGAGCCGGGGTGGAGGACCAGGCATGGGGACGGCTCCTAGCCCGGGAGCAACTCCCTGACCTGA AGCCCGCAGAGACCCCGAGCGGCACCCGAGC	466
PAX5_chr9:37025519-37025619	CGAGGCTGCCGAAGCCTGTCACCTTCCTCCAGCCTGGCTCTGCAGCAAACAGAAAGGAAACGCGATTCGT TCCACTTGGAATTTCCTTGAAATCTCCGAA	467
PAX5_chr9:37025619-37025719	TCTAATCCGGCGTTAACTCACCGTGAGAGGAGCGCTCATCTCACAGGAGGCTGTGGTAATGGGTGAATTG GCAGGATCCCCTGCGGGCCAGGCAGCCAGGC	468
PAX5_chr9:37025829-37025929	TTTTCGTTTCTTATCCTCTTTTTTTAAAGGGAGAAGCCATGAGAAAAGGCGTCCTGCAGAGAAGGACCC AATGGGGTCTTTAAGGGTCTCTGTATGAAC	469
PAX5_chr9:37025929-37026029	TGGCCGGCTCCTAAGCAGAAGCTGAACTCAGAAAACCGCTACTTCCTTGATTTTTTCAAAGCCCCCCTCCTCAA CTCCAGGACGCCTTTGGAGCCCTAGCCCC	470
PAX5_chr9:37026269-37026369	TGTCGCCGCCGGAGCCTTGAAAGGCTGCAGCTCGCTGCCCAAGCTACGCGTTGCCGGAGGCGGGATTCCC AGGTGCCTCAGCCCGGGCGGCAAGTGCGT	471
PAX5_chr9:37026369-37026469	TGTTTCAGGTCCCCTGCCTGGGATCCCTGCACTTTGCAAAGTTAGCTGCGCGGCTGCAGAGGTCCGAGATC CTTCCGGCCTTAGTACCTGACCCACGGTC	472
PAX5_chr9:37026469-37026569	CGGCACCCCCAACCCGGTCCCGGCGGGAGAGTGAGAAGCGAGCTCGCCGCCTACTTACTATGCATGGA TGCAAACGGGTCGTGCTTACAGTGTATTTC	473
PAX5_chr9:37026569-37026669	CATCGGGGCGCTCCAGACTGCAGGCCGGCCCACGCCGCCTCCCGGCGCCAAGGGGCTGCCCCAGGGCG GATAGGGAGCCTCGCCACCAGGCCAGCAC	474

PAX5_chr9:37026669-37026769	TGTGCGAGCTGGGCTCAGAAAACACTGCTGGAGCTTCGGGGTCTCTCTCAGAGCCTCCCTGCTGGAGACC GCCCGGAGCTGCGCGGAGAGGCGGGAAATG	475
PAX5_chr9:37026769-37026869	GTGCTAGCGCACACCCGGGCTAGGAGCGGGTGCCCAACTCCGGCTGGCTTCCCTCCCTGGCTGGCTCAAGCA GCAGCTCCGGGGCCCAGCCCGGGGTAGCTGC	476
PAX5_chr9:37026869-37026969	GGCCAAGGCGCCCGCGGCTTCGGGGGCATAGCGTAGGGGCCCGCCTCCGGGACAGCCAGCAGCCCCCGG CCCCAGGAAGGAGCAGCTTTGAGGAGGCCGC	477
PAX5_chr9:37026969-37027069	CGGAACAATCGGCCCTTGACTTCACTCAGGGGGCGGAGAGACCCGGGGGCTGCCAGGCTGGTTCCGCGGC CTCGATGCTTCTGAGGTCCCTCCTCGACCC	478
PAX5_chr9:37033619-37033719	CACACAGGCAAACAACTTTTGGACACAAACTCATATATTTTTACATCTTTTAAAAATACATATACTGTAAT GAACACACTGAGTCCCTTATATAAACACA	479
PAX5_chr9:37033719-37033819	CAGGCCCTAACTTGCAGACCCCCGGAAGGACGCCAGCGTGAACATTCAGAAACAGAGAAAAACACAGAC AAACTCACAGATATTTGGACTGATGCAGAAG	480
ZCCHC7_chr9:37293169-37293269	ACAGTTTGAAGTGTGAGCCTGAACATGTTTGATCTAAGGTCTGGAGGAAGATGTGAAGCAAATCTGACCT AAAAAAAATTATAGGAAAAAAGCAAATTGT	481
ZCCHC7_chr9:37293269-37293369	TCTGGATTTTGTTTCACCAAGGAACAAGTAAGCAGAGAACCAGACACTGGAGAAAAAAAAGGAGTCAGGAA GTAGACAAGGAAATGTTTAAAAGAAATAATAG	482
ZCCHC7_chr9:37293369-37293469	GATAACTGAAAGAATGTAGCTTCCAGATTGCTAGCTATCAGCAGATAGATAGAAACTTTTATACAGCCTT TAAATCTTCCCTAGAAACCTTTTTTAAAAGT	483
ZCCHC7_chr9:37371494-37371594	CAAGGGCCTGCCAGGATGAGAACGGGCAAACCTGGCCAAGGTGACCCCATTAGGGACTACCCTCCTAGG GACAGCACTCAGGGCCGTTCCCAATCACCCC	484
ZCCHC7_chr9:37371594-37371694	GGATTTCCTGTCCTGCTCGTCTCCTGCCACACCTCCTTTTGATCTACCCCCAAGACACCCCTACCTTTTTAT TCTGTGAAAATTTACTCATGCTGTGGGC	485
ZCCHC7_chr9:37371694-37371794	CCTGCTGGAAATGCCCTCCTACTGTTTCCCCAAACCCCGTCAGAAATTCCACGGGGAAACTCCCTTCCCTT CTGCTGCAGGCACCGTCACTGTGTCTCTC	486
ZCCHC7_chr9:37371794-37371894	AGCTCTGCCCCCCAGCCTCTGAGTACCACCTTATCCTAGCCCTTAGCTACTGGCTTGTCATTGTCTCTTTAC GTTCTCAGCCTCCCACAGAAGCCTGGGA	487
ZCCHC7_chr9:37384684-37384784	AGGCACACTCGCCCCTGGTCTCCAAGGCTCTGGGTCCTCAGACTGGCTGAGTACTGGGGACCAAGGTCAC CCAAGAAGCCCTGAGTGGCCCTCTTGAGGG	488
ZCCHC7_chr9:37384784-37384884	TTAGCAGAGCTTCTCTCTGTCCAAGACAGGTCAGGCTCTCTCCCCTGGCCCCCAGCTCCACCGTCACTCAGA GGAGTGGCCTAAACAAACGCTGCAGGTGA	489
ZCCHC7_chr9:37384884-37384984	GGCTCCCGAGCCCCTGACATGGATGTTTATGGAAGAGGACTCTTGGCATCAGCACCTGGGCAAGGTGGGT AGAGGCAGGAGTGGGCAAATGGGAAAGTCT	490
GRHPR_chr9:37407369-37407469	GGAGAGCCGTTTGAGATTCACCAGGTGAATGAACCCCCGGTTTTTTTCTGGGTAACAGGTCGAATGTGAAT TACTTATTTTCACAAGCTCTTGACATGTTC	491
GRHPR_chr9:37407469-37407569	CGTCAAATTGCTGTTCCCCAAAGAGTGGACTCTGGTGACATATAAGTGTGTGGGACCATTGCATCTTACCC CAGAGATCCACTCCTGATCTGGCATTATT	492
GRHPR_chr9:37407569-37407669	CAAAATCTGCTGAATTCAAAACGATCCTGTACTTCCTGCTCACCAGGTCTGAAAAGAAAAAAGAAAAAAG AAGAAGGAAAGACTACACCTGACAAAAGAC	493

FAM208B_chr10:5753066-5755166	TTCACGGTTTCTCTTTAGTTTTATCTGAAATACATTTGTAAGCTTAGGGTGCAATTTGGATTAAAACAGTT	494
	TTCTTTAGTGTCAATAATGGCCTTTACTA	
FAM208B_chr10:5755166-5755266	GAGTGAATGGATATTTTTCCATTCTGGATTATCGTTTAATCGAAACTTTGTTCCTGTGGAAATTTTTCTG	495
	GTTTAAGTTATTTGATTTGGGAGATAAAT	
FAM208B_chr10:5755266-5755366	CATGTAACTTAATAAACTTTGGCATCCTGGTTAACTGAAATTGCTTCATTCAATATTTGAAGACTGAAATC	496
	TGTATTGTTGCCTGTACCTAAATTATGGG	
FRMD8_chr11:65190342-65190442	GGACAGACAGGGAGAGATGACTGAGTTAGATGAGACGAGGGGGCGGGCTGGGGGTGCGAGAAGGAAGC	497
	TTGGCAAGGAGACTAGGTCTAGGGGGACCACA	
FRMD8_chr11:65190442-65190542	GTGGGGCAGGCTGCATGGAAAATATCCGCAGGGTCCCCCAGGCAGAACAGCCACGCTCCAGGCCAGGCT	498
	GTCCCTACTGCCTGGTGGAGGGGGAACTTGA	
FRMD8_chr11:65190542-65190642	CCTCTGGGAGGGCGCCGCTCTTGCATAGCTGAGCGAGCCCGGGTGCGCTGGTCTGTGTGGAAGGAGGAA	499
	GGCAGGGAGAGGTAGAAGGGGTGGAGGAGTC	
SCYL1_chr11:65266552-65266652	GGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGTTTTTTTCTCTTTGAAAGATAGAGATTAATACAACT	500
	ACTTAAAAAATATAGTCAATAGGTTACTAA	
SCYL1_chr11:65266652-65266752	GATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAAAAATATGAAGACTT	501
	AGAAGAGTAGCATGAGGAAGGAAAAGATA	
SCYL1_chr11:65266752-65266852	AAAGGTTTCTAAAACATGACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAGAA	502
	AATTGAGAGAAAGGACTACAGAGCCCCGAA	
SCYL1_chr11:65266852-65266952	TTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAATGAAGGTGACTTAAACAGCTTAAAGTTTAGTTT	503
	AAAAGTTGTAGGTGATTAAAATAATTTGAA	
SCYL1_chr11:65267397-65267497	TTGGAGAAGTATAGAAGATAGAAAAATATAAAGCCAAAAAATTGGATAAAATAGCACTGAAAAAAATGAGG	504
	AAATTATTGGTAACCAATTTATTTTTAAAAGC	
SCYL1_chr11:65267497-65267597	CCATCAATTTAATTTCTGGTGGTGCAGAAGTTAGAAGGTAAAGCTTGAGAAGATGAGGGTGTGTTTACGTAG	505
	ACCAGAACCAATTTAGAAGAATACTTGAAG	
SCYL1_chr11:65267597-65267697	CTAGAAGGGGAAGTTGGTTAAAAATCACATCAAAAAGCTACTAAAAGGACTGGTGTAATTTAAAAAAAA	506
	CTAAGGCAGAAGGCTTTTGGAAGAGTTAGAA	
BIRC3_chr11:102188381-102188481	TGGTGTAAGAGATGTGCCAGCGGCTGGCCGAGGGGGCGCTTAGGGCTAGAGCCCGGGGCGCTGCAGAGGT	507
	TGAGAGTCAGTGGGTGGGGCGCAGTTATCAA	
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	CCAGTGGAATTGTGAAGTTGTGGCATTTTG	
BIRC3_chr11:102188581-102188681	ATTCGGTTGCCAAGAGTTATCACTGGGCCTTTGCAGGTGCCAAATAAATTTCAGGACAGAGCCTAAGGCA	509
	GAGCTCTGGCACAGGAAGGAAGTAAAACGT	
BIRC3_chr11:102188681-102188781	TTAATGAGCAAATGGACGCATGTTTCCAAGCGGTGGTAGGAAGACAGCAGTTTTTGGTTGTCTTCCTGGT	510
	GATCAGCATGGAAACCTAGTAGTGCTCTTA	
BIRC3_chr11:102188781-102188881	CTCTGATCAATACATTGTCGAAGGCATGTACCTGATGCTAACGTAACAATAAATATTAAATATTGACTTTAT	511
	TTGCTATTATTTATTGCTAACATTAAGTA	
BIRC3_chr11:102188881-102188981	CTGCTACCTGCTATGTGCTAGGTTTGTCTCTGAAGACTTTACATGTATTTTTCACGTTTAATTATCATAATC	512
	TTAAGAAGCAGGTACCATAATTATCTCC	

POU2AF1_chr11:111249311-111249411	GGGAAAAAGAATGACGAAAGGCAAGACAGTGGAGCAAGTGAGGACACGCTTCACCGAGCCAGATCTCCA CTCCTCCCAGGGTATCCACAGGGACAAGTCA	513
POU2AF1_chr11:111249411-111249511	CACCTGGCAGAAAGCTAAGTCACTCAGCTAGAAACAGGCCCCAGGGAATTCAACAGAAGGCTGAAGAGCC ACTGCTTATGGAAATAAAGCCCCCTCCTGTAA	514
POU2AF1_chr11:111249511-111249611	AGAACTGCATGGCTTTTCCCTCCCAACCCCAAACCCATCCCACATCTGGCTTTGTTGTGTGAATCATAAA CTGCCCTTTTCTTCACCACAGTGATTCATG	515
CXCR5_chr11:118754793-118754893	AATCCTCTCCCACTGTGGATCTGTAAAATCTAGACAGGTCAGTCAGCTCCCGCCCTTTAAGAGTTTATTTT CCATTCTGTGGAAGAAGCAGATAAGGAGA	516
CXCR5_chr11:118754893-118754993	GCTGCTGTCCTTAGGAGACATCCTTTAGAGGAAGCTGGAAGACACGGGTTCAGGCCCTGCATCCTCCTCT GAGTTGCTATGTGACTGGGAACAGGATACT	517
CXCR5_chr11:118754993-118755093	TCACCTCTCCATTCTTTCTCTCCTTTTCTCTTAGGGTCGGAATATGGAACTAGACAGGAAAAGTACTTTGGA GGTTTTCTTACCGTAAGGAGGCTGGCATT	518
ETS1_chr11:128391383-128391483	GGGCCCTCCACCCAGCCTCAGTTCTATGGGGACGTGGAGTCAGGCGATGATGTCCTCTGAGGCAGCGTC CATCTCCCCTTAACATTAAGGAATAAGGCC	519
ETS1_chr11:128391483-128391583	AGAGGGTTCTCGCTCATTTGGGAAAATAAAAAAAGCAGGAATGGGGCGCTGGAAATTCTATAAGCTTTTC CCCACCACTCACAAAAAACACAGCTGTGAAA	520
ETS1_chr11:128391583-128391683	ATAAATACCACCCCCCAAACCAAGGGTCTAGGGCCACCAACAGTCCTCCTCCTCCTCCTTCT CCTCCTCGTCCTCCAGATCCAGCTGCCAA	521
ETS1_chr11:128391648-128391748	CCTTCTCCTCCTCGTCCTCCAGATCCAGCTGCCAACAGCATCCCCCGCTCCTGAAGAAATGCACCGCCCAG AAGGGAACGGCGAAAGGGGGAAGAAGTCC	522
ETS1_chr11:128391748-128391848	AGGGGACCCCCGGCCTCTGGCCGAGAGCTTGGGTGGGGGCCTCGGCCGTCGCCACTCACCCGGGGAGGG GAAAAGCTCCAGATCGACTTTTTCCGTCTTG	523
ETS1_chr11:128391848-128391948	ATGATGGTGAGAGTCGGCTTGAGATCGACGGCCGCCTTCATGGTGCCAGGAGTGGGGGGACGTACGGGAT GGTAGCAAGTTTGCAGTTACTGTTGTTTTC	524
ETS1_chr11:128391948-128392048	TTTTTAATGAGGATTAGTAACAGGGGGAAGGGGGACGGGGGAAATCCGACTTTCTTCCCAAAAATCTCAAA TTCCCGCTGCCTTTCTTTCCCCCGCGCCCG	525
ETS1_chr11:128392048-128392148	GACGGTGCGCCCGGCACTCCAGGGGAAGTTGGCACTTTGCGGCGAAGTGAGCGCGCTCGGGTCCCAGC CTCGCCCGCGCCGCGCCCGCTCCTCCTGCC	526
LRMP_chr12:25205888-25205988	GAGTGAGTAGCAAATATTCATTTATGACCCAGTTTTTTGTCCACCCTCAGGCGGGGCATAGGACTACAGAC ATTTTTCTAGATTACAGCTAGGATATTATT	527
LRMP_chr12:25205988-25206088	CCTGAGTTTATGACAATGAAATGGTTTGAGAAGGCAATATTGTGGGGCTTTCAGAGAGGTTTGCTGAGTG GCTAGGTGCATGCATGGGTTTAACCATTAA	528
LRMP_chr12:25206088-25206188	CTTCCCTTTTTGCCTTTTTATTATAAGCTGGTTTTTGTCTGTGGCTGTTTTTTTCTTTTAAAATTAATTAAAAAC TTCTCAAAATTTCTAAAAGTAAACAAG	529
LRMP_chr12:25206398-25206498	GCATTCTCTACATACATCTACATACATATTTTGCATTTTAAAAAATTGGAATATATTTGTCATTTTTTCTGTATTA CCCAAAAGTATATAAAACAGTTACCAGAG	530
LRMP_chr12:25206498-25206598	ATTTATGTGAGAAGACAGTTGTCACATTACAGATGTCAGATTAGCTATAAAAATTGTTTCATTCTAGAAACC TAATATGGTAAAAATAAACCTTACTTATT	531

LRMP_chr12:25206598-25206698	TAGCCATTTATCAGACAATTGCTTTTGTTCAGCCAGTTTCTTGTTCTAGCAGTATAAATATTCTTTTTATAG AAAGTTACTTGGTTTTGAGAAATAAACAT	532
LRMP_chr12:25206748-25206848	ATAAGCTTAAGGTAGGCTAGAGATGAAAAATTTCAGACTTGTGTTTGTTTTGGATTTATTGTACCCTTTCT ACTATTATCTGAGAAAGCTATTTTAGGAGT	533
LRMP_chr12:25206848-25206948	TTAAGAAATAGTCTAGTTTTAAAATAGCAATGGTTTGCCGGACACAGTGGCTCACCCCTGTAATCCCAGC ATTTTGGGAGGCCGAGGTGGGCAGATTGCT	534
LRMP_chr12:25207088-25207188	GAATTTGCCAGTTTTCAATATTCTGATTCACTCTGTTAAGCTAGTAAGGCAGTCTTTAAATTACACAGTCT GTGTGTTATTTTACTACTGCTCAGAGGC	535
LRMP_chr12:25207188-25207288	ATTGGAGAAGGTTCCCTTGTGATTAGAACTGTTCATGTTGAGACATGAATCATAAGGCATTCCAAAGTTG GTTTAAGGTGTGTCTGCTTTAGACACTGTG	536
LRMP_chr12:25207288-25207388	CCCAGGACTATTCTTTTTGCTCCAGTTTTTGCCTTTTGATTAAATCAATATTATACCTGAGTTTTATAAACTAC TAAGAATTTGTTCCCCTTCCTCACTGTG	537
LRMP_chr12:25207388-25207488	ATTTTCTTGCAGTATTTTCTTAGAAGAGTCAACTTTAATAACTTACCCCAAAGTGCACGTTCTTGATATTA TGAACTTGCTATTGTTGTCTTCCCAGTTT	538
BTG1_chr12:92537875-92537975	TATTGTAGTTTTTGGAAGGGCTCGTTCTGCCCAAGAGAAGTTCCTCCTTACAGCTGATTCGGCTGTCTACC ATTTGCACGTTGGTGCTGTTTTGAGTGCT	539
BTG1_chr12:92537975-92538075	ACCTCCTGCTGGTGAGGCTTCATACAGCACACAGATGGAGCCATCCTCTCCAATTCTGTAGGACACTTCAT AGGGGTCAACCCAGAGTGTGAGTTCACTT	540
BTG1_chr12:92538075-92538175	GGGAGAAGCCTGAACAGCTCCTGACTGCTCAGTCCAATCCGCTGTGCTGCCTGTCCAATCAGAGGATCCA TTTTATGGTTGATGCGAATACAACGGTAAC	541
BTG1_chr12:92538175-92538275	CCGATCCCTTGCATGGCTTTTCTGGGAACCAGTGATGTTTATAATGTTCTATAGAAGAAAAGAAGAACAG AGAAACAACGCTTAGGATCGTTAGCTCCCA	542
BTG1_chr12:92538275-92538375	CTGCGGATTCCTCCTACCCCAGGCTCCTTTGAGGAGCGAAAAATGAAAAACTATCAACTTTTTAAAATGTCCA GGATTGCATCCGTTGTTGTGCATGTGCGG	543
BTG1_chr12:92538375-92538475	GGATGGAAAAAGCGGGCAGGGTTTTAGAAATAACACAGTAGTACCGGACAAAACAATCTCCAGGAACCA ACCGGTTGAGCCGCCAAAACAGGAATCAGGC	544
BTG1_chr12:92538475-92538575	GCGCAGCCTCGGCCAGTCGGGAAGCCACTGGCACCTATGGCCAGGCGAGAAACTGTTTACTTTCTCCACC CCACCCCAGATGCACACAATGGAGTTGATG	545
BTG1_chr12:92538575-92538675	GCTTTGGAGATGAGAAGCGCCACCGGACTGTTAACCCCGAAGGGAAGAAAAACAAGCAACCCTAAACCA CGCTCTGGGCAGGGCTGTTAATTGTGCCGGT	546
BTG1_chr12:92538790-92538890	ACGCAACGGTTGGAGGGGCTGAGGAAAGGGACGTCGAACCCACCCCAGCCCCACGGCTCCTTTGTCCC CAAATCCGCCGACGGTCCTCGGACCGCAGC	547
BTG1_chr12:92538890-92538990	TCCCGCCTCGGTGGGCTTAAGTTTCTTTGTTGTGCGTGTTGTCTTCTCCTCTCCGTTTTGCCAGCTGGGGGG AAGGGGGCGCCCTCCGTCCAGCCCCTAA	548
BTG1_chr12:92538990-92539090	AGCCTCGCGGGGAACCGCTGTTAGCGGCCACCCAGCGCAACCACACCGGTCCCGCGGCGGGCCCAAGC GCGACCGGCCCCGGGGCGCTGCCGAGGTTCC	549
BTG1_chr12:92539090-92539190	CGCAGCCCCGACGGCCGGACTCTGACCCAGGGATGTGGGGCCCGCGTCCCTCCGACGCCCTCGCCCTGCT CACCTGCCAGCAGCTCCTGCAGGCTCTGGC	550

BTG1_chr12:92539190-92539290	TGAAGGTCTGCAGCTGTCGCTCGCTCGTGAGCCCCTTGGTGCGGAGAAACTTGGAGATGAAGGACACGGC GGCGGCGATCTCTCGCCTATCATGGTGGCGGC	551
BTG1_chr12:92539290-92539390	CCGGGTGTAGAAGGGATGCATGGGGGCGGCGTGCGGGGGCGGCCCGGGGCTGGGGCTCGGCGGCGC GGCCCCGACGGCGGAGCAGCCACCCCCGGGCT	552
DTX1_chr12:113495364-113495464	ACGCCGCACCCCTCCCCCGTGCGTTCTGCGGCCACCCAGGCCTTCCAGGACACCGTGGAGAGGGAACAAG GGGGCAGGGACGCCCCCTTCGGCAGGAGCC	553
DTX1_chr12:113495464-113495564	GTCGGAGAAGGGGGCCCAGACCGGAGGGAGGCGAGAAGCCCCACTGAAGCCGGGCGCAGGGTCTGGGA CGCAGTTGGGAGTGCAAAGGGCTGGCTGAGAG	554
DTX1_chr12:113495564-113495664	CCGCAGGAGCAGCAGGCTGTGGCCCAGGCCTCCTGGGTGACAGGCCCTGTCTGGCGGGGAAGAGGGACC AAGAGACAACACGGAAGAGGGCTGGACCTCGA	555
DTX1_chr12:113495664-113495764	ACAGGGGCGGCTGCCTCACTCCCTACCTGAGCCAGCCGAGGGGGCCAAGGACTTTAGAGCTGTTTCCTCC GGCATAAGAGAGACACTTGCTTTCCAGGGC	556
DTX1_chr12:113495764-113495864	AGCACCCTTTATCGGAGAAGGCTCTACAGGGAAGGGGTCTTTGCAGCCTGGATGGCCATCCCACATTCCT TTAACGGAGGTCTCTAGGCCTCAGAGAGAA	557
DTX1_chr12:113495864-113495964	CCCAGAGTTAGAAAGGAGGCCAGACGGTCCTTGCTGTCCCCCTGGGGAGAGGAAGTTGCCGCCTGCTG CCAGGCCCAGGAGGAGCTGGGCCTGCAATA	558
DTX1_chr12:113495964-113496064	GTGGGGGACCTGGCCCCTGAGGCAGTGGCGGCCATGTCACGGCCAGGCCACGGTGGGCTGATGCCTGTG AATGGTCTGGGCTTCCCACCGCAGAACGTGG	559
DTX1_chr12:113496064-113496164	CCCGGGTGGTGTGGGAGTGGCTGAATGAGCACAGCCGCTGGCGGCCCTACACGGCCACCGTGTGCCA CCACATTGAGAACGTGCTGAAGGAGGACGC	560
DTX1_chr12:113496164-113496264	TCGCGGTTCCGTGGTCCTGGGGCAGGTGGACGCCCAGCTTGTGCCCTACATCATCGACCTGCAGTCCATG CACCAGTTTCGCCAGGACACAGGTGAGCAG	561
DTX1_chr12:113496264-113496364	ACACCCACCCCATGCCACCCGCCCCGCCGAGCCATCACTACCTTGCAGCGTAGGATGCTGAAAATCCCAG TAAATCTGCTGATGCCAAATCCCTTCCCA	562
DTX1_chr12:113496364-113496464	TCTCCCTGCCTCACCTCCAGAAAAACAGGGCAGTCTAACCTTGTCCAGTTTAAGACTTGGATTCCAATGCA GCCTCTGAGCAAGCTGTAGGGCCTTGAGC	563
DTX1_chr12:113496509-113496609	GGGTAGATCAATATCTCTCACAGCTGAGTGAGGATTAAATAAAATTGTGCTCACTGAGCACAGAACCTAG AACAGCAGTAGCATGGGATTGTAGAATAAG	564
DTX1_chr12:113496609-113496709	GGCTTTACATGCACTTCCTCATTTGATTTTTCCCAAGAATCACAGGCAGTAAGTCTGTGTATTGTTGTATT ATTATGAGTCCCATTTTATAGATGAAGAA	565
DTX1_chr12:113496694-113496794	TTTATAGATGAAGAAACCGAGTCTCCCAGAAGCTGAGTGATTTAAACTCAGAGCTGGGATTTAAACCCAG GCGGTTGAGTTCCAGAACCAAAGTTCTTAA	566
DTX1_chr12:113496794-113496894	CTGGTATCCTATACTGGCTCCAAGTGTTGGTTTGTGGGGTGGAGTCGTGCTGGTGGTAATTAATTGGGGA TGGGGGGCGTTGGTGGTTGATGGTGGGG	567
DTX1_chr12:113496894-113496994	TGAGGTGGCAATGATGGAGGAGACAGTGTTAGCGGTTGTGTTGGTGGTGACTCAGTGATAGTATTGATGG TGGTGGGGTCTTGGTGACAATGGAGGGATG	568
DTX1_chr12:113497059-113497159	TGTTGGTGACATTGATAGTTGTTGGTGGTGCTGGGAAGTGGTGTGATGGGGGTGGTGATGATGGAGA AAATGAGAGAATGATGTTGGTGGCAGTCTT	569

DTX1_chr12:113497159-113497259	CGTGGCCATGTGGTGTGGCTGGTAGCCCTGTGTGTGGCTGTTACTTAGTGGTATTGGTGATCCTGTTGTGG TTGTAATGATGGTGATGTTGATGGTTGCG	570
DTX1_chr12:113497259-113497359	TTGGTGGTAATGTGATGGCTGATGATGGAGATAAAATCGATGAGGTCCCACTCTCAGGCCTACTCTCTTTT GTTCTGGAGATTTGTCATCGTTGGGGAGA	571
BCL7A_chr12:122458781-122458881	TGAAATGGCTGCTGTCGGGCTGTCATCTCCAGGCCCGGGGCGCTGACATTTGGGCCACTCTCGGTCTCCCT CTTCATTCTGGGCGCGCATTAGCTCTGGT	572
BCL7A_chr12:122458881-122458981	CCGGCCGGTTCCGCTGCAGCTGAACAGCAAGATGCGGCACCCAGGTTACCCTGATCATCGCAGATTTCTC CCCGGGGCTCTGTTCTGAGGCCTCAAAAGT	573
BCL7A_chr12:122458981-122459081	GCTCCTTGTAGATGGGACCAGGGGTCATTTGGGCAGTAGCAGCGCCTGGTCTCAGTCTGGTACTGAAGTC AGGAATGGCTTAAGGTGAAATCGTGGTCCT	574
BCL7A_chr12:122459081-122459181	CTGGTGAAGCTCAGCGAAGACCCCCTCGCCTTGTTTATGACAAGAGAACTTCTGGGGGCGGGAGGAAGAG TCCCTGTTACGATGCTGATCATCATTGAGC	575
BCL7A_chr12:122459181-122459281	TTTTGCTGAGCAGAAAAACTCTTTAGTACTCAAGGTCGAGAGTCTCTGGTGGTCTGCCTGGCACCAGGCAC CTTCCTACAACCCTAGTTTTCCAAAAGGAC	576
BCL7A_chr12:122459281-122459381	AAAGCCTGGGGCAGGCGACGTCCTAGCTCGCATTTGAACAGGGCCGCGGGCCAGCAGAGATGCGCGATG CCCAACTCTTTCCAAGAGCACCTCGCGTCCC	577
BCL7A_chr12:122459381-122459481	GAACCGGTGCCTTCAACTCGGAGAAGTCAAGAGACCCGCAAGAAACTTGCACGACTGCACCCGGCCGCGC GCTCTGGGGGGCTGGGCAGGGGCAGCTGGGC	578
BCL7A_chr12:122459481-122459581	TGGCTCCCGGGGAACGCGACCCCCCCGCGCCCCGCAGACCGGCTGTCTCCCATGGACCCCTCGGCACCTG CAGCCTCCGAGGAAGGGTCAGCGCGCGTGT	579
BCL7A_chr12:122460811-122460911	GGGGGGCTCGGGCCAGCCGATGTTTTTGGCCAGAAGCCGTTCGTCCTGGGCCGCGGCTGCCTCTCCACAC CGGGAGCTCGTGTTTGTTTTTGCGGAGGGAG	580
BCL7A_chr12:122460911-122461011	CTGTTGTTTTTGTTCTCTGCACCGGGGAGAGGGGGACTTGGTGGCGGCCGTGGTTTTTCGGGATCAC ATTAGCGTCCGCCGGCGTGGCCCGGTCGA	581
BCL7A_chr12:122461011-122461111	CATTAAGGGGATCGAACCTTTCCGCGGCCTCGTCGGGGTCTGCTCGGAATCGGCCCCCTGGGCCAGGCCCG AGGCGCAAGCAGATCGCCAGGTTGGGTCAG	582
BCL7A_chr12:122461111-122461211	AGTTGTTGAAAACTCCCCCGCTGCCTGATTTCAACTTTATTATTTTTTTCCCACGCCTTCACTGGGGTCCCGG AGGGAGAGGAGCCGCCGCAACGCTGGCT	583
BCL7A_chr12:122461316-122461416	AGTAGCGCCTCGGTCTCTAAAAGCCACTGGGGGCGAGCCTCCGGTGTGGCGGTGTCACAAGTTAGCTGTC CTTTCTGAGTCAAACCCAACAAAAAAAGGCA	584
BCL7A_chr12:122461416-122461516	AGAGGAAAATCAATAAAGTCCACGTGCTCCCGGCCTCCTATGGAAAGGGCTGGCTGCGATGGCCGGGATG CCCGGCCCGTGGGCTGGGTTTGGCTCCAGTG	585
BCL7A_chr12:122461516-122461616	GGACAAAGAATTTTCAGAACCGTGAGAAGGGGAGGCTTTCCAAAGTTGAGATCCAAGTCGTCGGTGTCTC GGGAGCTCCCCCTGGTACACAGGGTGCCCGG	586
BCL7A_chr12:122461616-122461716	TGCCCGACTGGAGCCATTTAAAAATGGCAGAAACAGCTGCAGGCCAACACACACACGCTGGAAAACAAC CCGCAGCCCCCCTCTACTGTGGGATTCCCCGC	587
BCL7A_chr12:122461716-122461816	GGGAAGCCCGGAGTTGCTCCCCTCCTTGCCTCAGCCCCTGTGCAAAGAAAGAACTGGTGTCTGTGCCTGG GTCCCTTCTGTCGCCGGCCTGGAGGTTGGG	588

BCL7A_chr12:122461816-122461916	AAACAGCCGGCAAGCCGCCTTTCTCTGCTCGAGGAGGCGTGGTGGGGCCTCCTACTCCAGGTTCCCGGCT GGACAGAGGCTCCTGCACCCTGACCAGCTGC	589
BCL7A_chr12:122462001-122462101	GGAGGCCTTCCAGCCCCGCTGACCCCGCGGGGACCAGGCCTGTAGTTGGAGCTTGAGGGGCTGTACCTCTG CGCCTCCCTGGGTTTGGGGAAACAACACAT	590
BCL7A_chr12:122462101-122462201	CGTGTCCTCTGAAGACCTCAGGCTTTGGGATCTCATGGTCCAGCTTCCAGTTCACTTCGTTGCCGCGACCT TGGGCATATCATTGTCACTTCTCTAACCA	591
BCL7A_chr12:122462201-122462301	TGGTGACCCGGGGTTTTGTGCTTGCTTCCAGGTCCCCTCGGGTTATTGAGGACGATTGAGGTCATGCCTC CGAGAGCACCGCGCCCTGGGCGCAGGAGG	592
BCL7A_chr12:122462716-122462816	AATGCAAATTTAACAGGGCACCCTGTATTTTACCCAGAGGGAAGCCGAAGTGTTTGGCAGATCATTTGGC CCCATGAGCCTTGGGTGGGTTTCTCCTCAG	593
BCL7A_chr12:122462816-122462916	CCCTAGTGACCCCTAAAATTACCCCCCCCGACCCACCCACTGTCCCCTGATGCTTCCCCCACCCCCGGAAAA AGCTGTGGCCTCCCTCTCATTTGGGGCAG	594
BCL7A_chr12:122462916-122463016	GCTGCCTCCTGTTCTCTTTTTCTGGTGTTTCAGCAAGGCAGGCCAGTGGAGGTGAGGTGACCAGAAGATG GCTAAAGGGAAAACAAAAATGGTGGGCCTCT	595
BCL7A_chr12:122463031-122463131	CCAGGGTTTGGGGGCCCTGTGCTGTGGAGGAGAAGACCCCAGGGCGATGGTAGGAGACGAAAGCTT GGGCTGCAGCGTAAGCTTGGAGGCCCGCTGC	596
BCL7A_chr12:122463131-122463231	GGTGGCTCACGCCTGTAATCCCAGAGCTTTGGGAGGCTGAGACAGGAGGATTGCTTGAGCCCAGGAGTTT GAGACCAGCCTGGGTCTCAAACCAAAAAAA	597
KIAA0226L_chr13:46959165-46959265	TAAATATAATTTTAACGCCAATCTGAGAAAAATGACTTATTAGCTGTGTGATTTTGAGCAATGCTCTTAAC CTCCCCCATGAAGGATGGTGTGAGAACGA	598
KIAA0226L_chr13:46959265-46959365	ACAGAATTGTAGCACGTGTATCAGTCTGGTACACAATGTCCTATGAAGGTTAGCTTTATTATCACCATCAT TATTATTGCAGAAAGACTTTCAGTTCAGA	599
KIAA0226L_chr13:46959365-46959465	ATAAGACAGCACAGTTACAGAGACCTGGTTTTATTTTCCAGCTTCTTAACTGAGTCATCTTTCAGCTCCTT TTAATTAAAAAGAAAAAAACAATCAGAGAT	600
KIAA0226L_chr13:46961680-46961780	TCAAAGACCTGGCAGAAATGACTTCCCAACCCCAGATGCCCCCAGCAGCAGTATTTAGCAGTCATACAAT TGCCTGAAATGAAGAATGAGTAATCTGGAT	601
KIAA0226L_chr13:46961780-46961880	GAGTCGGCCCTGAAATCGACCTGCAACTTACCCGGAACGTGAGCTGTCTCTCTCTGACCTCTGGCTGCTGC TTCACCTGGAGTCTGAGTCCGACTCATGT	602
KIAA0226L_chr13:46961880-46961980	AGCACTTCACTGTCCGCGTTAGTTTAGCCTTCACTGTCAGCAACTCGTCACCTTGTCCTCTTGCAGCGAAG GTTTGGAATCCCATCACGGGTGTGCAGTG	603
KIAA0226L_chr13:46961980-46962080	GTTAGTCCTGAGATCATGGTGGTGCTAGGAGAACCTGCCAACCAATACAGAAAGTTGTCACGAATAGAAA CCTAAGCTCTGGCCGGGTGCGGGTGGTTCAA	604
ATP11A_chr13:113516229-113516329	AGATATACTGTTCTAGACATGTGTCTGAAAGGAATCCTGCAAATTCTGTCTTATTGAACAGGCATAAGGT GTCACGTCAGGCGTAAGGTGTCACAGCAGG	605
ATP11A_chr13:113516329-113516429	CGTAAGGCGTCACGTCAGGCGTAAGGTGTCACAGCAGGCGTAAGGCATCACGTCAGGCGTAAGGCGTCA CGTCAGGCGTAAGGTGTCACAAGCTCGGTGA	606
ATP11A_chr13:113516429-113516529	ACGTCAGGGGTGTGCCTTGTGTTCTCTGTTCGTTGCTTTCAGAAGCAGCAGCATGTGGCAGCATCTCTGTG CCTATGACGATATTGCAGTGAATATGAGA	607

SYNE2_chr14:64330252-64330352	AATTGTACATTTCAACAACATAAATAAGCTGTTCAAGACTGTCTCCCATGCCTCCAAAACAAATAAAAAC CCCCCACAACTCAAATGCATATAAGCTGTT	608
SYNE2_chr14:64330352-64330452	ACTATAGTATAATGGTGAGTTATAGCCAGTGTATGATGGGATTGTTGATAGAATAATGCATATTAGAGCT TTTAGTTCAAAAAATTTGAGATAGTGATTCA	609
SYNE2_chr14:64330452-64330552	GAAAGAAAAAAAGGAATGATTATCATGAATTCTGTTTATTAGAATTCTGTTTATTAAAGAGTTAAAGATA TGTTTTATTTTTTTTATCTTTATTATCATTA	610
ZFP36L1_chr14:69258238-69258338	AATTCTAATGTTGGTCCCTTAGGATCAGCAGGGGGGGGACCGGGAATCTGTAACTGCAACCACCCCACCGA GAGGATTACAGGAACCCAGTCGAGAGCTGG	611
ZFP36L1_chr14:69258338-69258438	TTCCCAACAATGAGGTTCATTTAAAAAGTCGTGAGGGGGGGAGGGGGGCCAAAGAAAGAAATAGATCAAA GAGCGGGAGAGTCGAGAAAAAGAAGGAAGAAA	612
ZFP36L1_chr14:69258438-69258538	TGTTGGGGAGCGCTGGCAGCCGGGCTGGCAAGTGGAGTTTGGGAATGTGCAGGGAGGGGAAGGAAGCTGA AAAATTCAAACTTTTTTAAATGCTACTCTTCA	613
ZFP36L1_chr14:69258538-69258638	GCTCCTCGGCGTCCCTGCACCCCAACCCTGCAGCCCTGGGGCGTTGGCAGCTGCACCAACAGGAGCAGCA AGCTGGGAAAACAGAGCAACATGACCCGAC	614
ZFP36L1_chr14:69258638-69258738	GTGTTAAGAGAAGGCAAAACACTTCAGCAATTAAAAAGTAGCCCAGCAGCTTCACCCTTTCAAATTGGGA GGGGGAGGTTGGAAAGAAATTTAACAACAT	615
ZFP36L1_chr14:69258738-69258838	CCATAGACTTTTGCTATGTACATTTAAACCGCAGTCCTGGAACATTCCGAGTTTAAAACTTGCTTTTTTCAA CACTGGCTGACAAGCAACATGTTTTAAGG	616
ZFP36L1_chr14:69258838-69258938	AGCCCCCCATTAAATCCTTACTCGCGGGACTCTCGAGTTCAAGCCAGCATTTTGTCGCCACCTCCCCCCCC AACCCCGCCCGCAATCGATGAGCCGCAAT	617
ZFP36L1_chr14:69258938-69259038	GCCTCGGCAACACAGGTAAGCGGGTCAACCTGAATGCCTCTTTCACCCCAAAGTTTGCTGCACGATCGGC TATCGCGGGAAGAAGCCCCAACGGAGCTAGG	618
ZFP36L1_chr14:69259038-69259138	GCGGACTCAAGCCCCCACTGCAAACTTGTTCTGCAACATCTTTTTGAATCACAACTTGGCCTTTCTTCCTCG CATATCCCCAGCTCCCCCCCAAAGAGTGGA	619
ZFP36L1_chr14:69259138-69259238	GGAAAACATTGTCCCGAGACTCACTTCCCCGAGGGGACCTCCCCAACCCCACGGGTGGGTAATGCC GCTGGACAGACCTAGGGCGCAGACTGGGAA	620
ZFP36L1_chr14:69259238-69259338	CCCGATCAGACCAGCAAACCTGGGATCCAGCAGCACGTTACGTAAAACAGGATCGCCCAAAACTTGTCCC AATCCCAGCCCCTCCCCCCCGAAGCCCCCCGGG	621
ZFP36L1_chr14:69259338-69259438	CTGCCCTGCCAGGCAAACTTCGCCCCTCAAAACCCTGGCCTCCAGATTCACATGTAATCCCCGCCAGCAAC TGTTGAAACTCAAAGGGTGGGAAGGACGG	622
ZFP36L1_chr14:69259438-69259538	GGCCAAATTCCTTCAAACTTGGGAGAAATGCCGGAGGAGAAAGAAGAATCATCTCGCTGCACCACTTTCCCC ATTGCCTTCCAAGACCCAAACTTTTGGGGG	623
ZFP36L1_chr14:69259538-69259638	TTCTTTCTTAAGGCAAAAGAAAAAGACTTTTTGAAAAGCAAATGCTCCGCCCCCCTTTACCTTGCATAAAAA CTTCGCTCAAGTCGAAGATGGTGGCAGAC	624
ZFP36L1_chr14:69259638-69259738	ACGAGGGTGGTGGTCATCCTGTGCGTTCGGCGCGAGCCCAGGGGCGAGGATCTGGTGTGTCGCGAAGGTCCC GGTGCGGGGAAGGCGCAGCCTCTCCTGTCT	625
FLRT2_chr14:84420586-84420686	TTATTTTTTTATATTAAGATTTATTCTAAATTTTGATTCTTCTAAAATATAGTATATATTTAGTATATATATA ATGCACCTCTCTTACCTAATGATCATTT	626

FLRT2_chr14:84420686-84420786	CTAAATAATCATAACAACATCGAGTAAAAACTATGTAATAACACATATTATTATTAAGATAAGTATAAGAA ATATAATAATAAATTGTCCCTGTTCTAAAA	627
FLRT2_chr14:84420786-84420886	GGTAATTATATAATGCTGAATGTGTCAGAGGCATTCGAACCAGAGTGACTCCATTTTGAGTGAGGGCTAG GAAAATGAGGCTGAGACTTGCTGGGATGCA	628
TCL1A_chr14:96179592-96179692	TTTAATTTTTATGCTTTCTTCAGTGTATGTTTGGAGAGAGTTTGAACATTTTTTGACTCTTTTTCATTGAGT AAATCCAAATACTTGTAAAAGACTTATC	629
TCL1A_chr14:96179692-96179792	TATTTCTTTAACAAAAAACTTAACATGGATTAAGGACCCATCTTAAGGCATCACACATTAAAAAAAGTCAAT ATTGATTCAATACCGGCGCTTATACTACGA	630
TCL1A_chr14:96179792-96179892	CATCACTTGTTAAATTTGTTTTCTAAATAAAGCCCAGAGGTAGTGGAAAAATACTTCACACTCTAGGCCAGT GTTTGCTATGCCTGGTTGACCCTAAACTG	631
TCL1A_chr14:96179892-96179992	TTGAGGGTTCTTTTTAAAAATACAGATTTCTGGGACCCACCTGAGATGATTCCGATAATCGGCCATATGGA TGAGTCACTTAGAGATACCCATTTTTAAG	632
TCL1A_chr14:96179992-96180092	GATTAGGACCCCGAAGCCCAGAAAATGCCTGCTGTAGTCAACATTATAGTCACACTCCACAGGCACTGGG TCCACCCCTTTGACCGACATTCCCTTTGCGG	633
TCL1A_chr14:96180092-96180192	TTTTCCCACCCTTCTTCCCTGCCTGGAGAACTCCTATTCATCCTCCAGAGCCCGGCTCAAAGTGGCTTCATC TGTGGGGATCCTCCCCTGCCCCATAGTGA	634
TCL1A_chr14:96180192-96180292	GTGCTCCTTGAGTCCTCGCCCTTCCTAGGGCATCCCAAGCTCCCAGGGGCTGCCCCTGCTGCCTCGCCATC CGCTCCAAAGCTGGCTGTACCTCGATGGT	635
TCL1A_chr14:96180292-96180392	TAAGGGCAGCCAGGCGTGCTGCTTCTCGTCCAAATACACGAACTTCTCCCAGGCCCACAGGCGGTCCGGG TGGTCGGTGACTGCCTCCTCCCGAGTGTCGGG	636
IGHA2_chr14:106048955-106049055	AGGAATCAGATTTCAAAATGAATATGTATAAGAAAAGAACCGGGGATCAGTGATCAGGAACAGGGATCC ATGATCTGGTCCAGGGCTCAGCGGTCAGGAA	637
IGHE_chr14:106068705-106068805	CCCTGGCCTGGAGTCCCAAGTCCCCAGCCCATCCTGCCCCCTGGAGCCCCAGTTTAGCTTGGTCTTGAAGTCT GCTCTAGGTACCCCCAAAATCACAGTATC	638
IGHE_chr14:106068805-106068905	CAGCCCCGCTCTGCCCACCGGGACAGCCAAGTTCAGCTGAGACTGGCCTACCGGGGGAGTCGCCCTCTGA AGTTCACTCTAAGCCAGCCTGGTTCAGCCT	639
IGHE_chr14:106068905-106069005	GGCCCAGGTCAGCCCAGGACCTCCCCCTTGCAGGCAGCAAACTCTTATTTCAGTCCAGCCAGCTCAACCAG CTTGCTTCTGACTCAGCTCCTCTTAGCCAG	640
IGHE_chr14:106069045-106069145	TTAGCTCAGCAAAGCTGGACCTAAAGTAGCCACCTCACCCCAGCTTCATCCAGATGAATACAGTCCAGAT CAGCTTAGTCAGTTAAGCCTAGCCTAGCTA	641
IGHE_chr14:106069145-106069245	GTTAAATCCAGTTACGACCAGCTCAACTAATCCTGCTCAGGCCTGCTCAGCCCAGCCCAGCTGAACCCAGT TTAGCCGAGGCCAGGCCAGCCCAGCTGAA	642
IGHE_chr14:106069245-106069345	TACAGTTGCCCAGTCTAGCTCAGCCCAGTCCAGCACTGCCCAGTTTAGCTGAGCTCAGCCTGGCCCAGCCC AGCTCATATCAGCCCATCTCAGCTGAACC	643
IGHE_chr14:106069345-106069445	AGTTTGACCCAGTCTAACCCAACCCCGCTCAGCTGAACCCAGCCCAGCCCAGCCCAGCCAAACCC AGTTTAGCCTAGCTCAGCTCAGCCCATTTC	644
IGHE_chr14:106071060-106071160	CCTGTCCTAGGGGTGGCAGGCAGTCTGCACCCAGCCTAGCCCTGCCCAGCGTGGGGTCTCTGACCTTCTTG GTCTTGGGCCCAGCCAAGATTCCCAGCCC	645

IGHE_chr14:106071190-106071290	TTCTAGCTTTCCTGTGTCCCCATGCAGGGAAGGGATGCCTAGAGTCCACGCAGTGACCAAGAAGCTTGGT TGATGCTGTGAGGGTGGCCCCAGGAGTCCCC	646
IGHG4_chr14:106095335-106095435	CACCTGCTGTCCTTGGTCCTGGCTGAGAGGAGGGCCCTACGGCCAGCTCTGCTGACCCTGCCCCTGGGCTCT GGTGATGCTGCCGGCCTGGACAAGCCCCT	647
IGHG4_chr14:106095480-106095580	GAGCTCAGGTCGGTCGTGCCCATCCTGGCATCACCCCACAGCCGGTTCTGCCGCATCCCGTCATGTTCCTC GTGCTCCCAGCCCCGGTCGTCCTGGAGGCC	648
IGHG2_chr14:106110675-106110775	TGAGCATGAGTGGGGCGGGCAGAGGCCTCCGGGTGAGGAGACAGATGGGGCCTGCCTTGCTGCCCTGGG CTGGGGCTGCACAGCCGGGGTGCGTCCAGGC	649
IGHG2_chr14:106110775-106110875	AGGAGGGCTGAGCCTGGCTTCCAGCAGACACCCTCCCTCCCTGAGCTGGCCTCTCACCAACTGTCTTGTCC ACCTTGGTGTTGCTGGGCTTGTGATCTAC	650
IGHG2_chr14:106110830-106110930	ACCAACTGTCTTGTCCACCTTGGTGTTGCTGGGCTTGTGATCTACGTTGCAGGTGTAGGTCTGGGTGCCGA AGTTGCTGGAGGGCACGGTCACCACGCTG	651
IGHG2_chr14:106110950-106111050	GGACTGTAGGACAGCCGGGAAGGTGTGCACGCCGCTGGTCAGAGCGCCTGAGTTCCACGACACCGTCACC GGTTCGGGGAAGTAGTCCTTGACCAGGCAG	652
IGHG2_chr14:106112335-106112435	TGCTACACTGCCCCTGCACCACCTCCACTCAGCTTCATTGTGCTGGTGGGCCCTGGCTCCTGGCAGCCCATCT TGCTCCTTCTGGGGCGCCAGCCTCAGAGG	653
IGHG2_chr14:106112435-106112535	CCTTCCTGCCTAGGGTCCGCTGGGGCCAGCCCTGGGACCCTCCTGGTCTCAAGCACACATTCCCCCTGCAG CCACACCTGCCCCTGCCTGAGAGCTCAGC	654
IGHG2_chr14:106112535-106112635	CCCGAGCCCTGGAATGCCTTCCCTTCTCCATCCCAGCTCACCCTTGCCAACTGCTCAGTGGGATGGGCTCA CACTCCCTTCCTGGCACCAGGAGGCTGCA	655
IGHG2_chr14:106112635-106112735	CTGCACTTTCACCAGCCCTCAGCTGTCTGCTGCCAGCAACTACCCAGCTCCTGCCAAAATCTAGGAGCTGA GTGATGCCTCCCACCGGCCCTGCTCACCT	656
IGHG2_chr14:106112735-106112835	GTGGTTGCCTTGCCCTGAGCTCTAGTGCCTGTCCCCTGCTCGTCCTGCCTCCCACCGGCCCTGCTCACCTG TGGCTGCTCTGCTCTGATTCCCTGAGGCT	657
IGHG2_chr14:106112835-106112935	AAGCCTCAGTCCTGCTCACCTTCTGATGCTCTCCTCTGTCCCCTGAGCTCCAGGGGCTGTCCCCTGCTCGT CCTGCCTCCTACCTGCCCCTGCTTACCTG	658
IGHG2_chr14:106112935-106113035	AGGGTGCTCTGCCCTGGTGCTCTGAGCTCCAGGGGCTGTCCCCTGCTCCTCCTGCTTCCTACCAGCCCCTG CTCACCTGTGGCTGCTCTGCCCTGGTCCC	659
IGHG2_chr14:106113020-106113120	CTCTGCCCTGGTCCCCTGAGCTCCAGGGGCTTCCCCCTGCTCTTCCTGCCCCCACCAGCCCCTGTTCACCTT CAGATGCCCCTCCCCTGGTCCCCTGAAGT	660
IGHG2_chr14:106113120-106113220	CCCAGAGCTGCCCCCTGTTCCTCCTGCCTCCCACCAGCCCGTGCTCACCTGCCGCTGCTCTGCCCTGGTCC CGAGTTCCAGGGGCTGCACCCTGTTCGCC	661
IGHG2_chr14:106113220-106113320	CACCTCCCACTAGCCATGCTCAGCTCTTGATGCTCTGTCCTGGTCCCCTGAGCTCCAGGAGCTGTCCCCTA CTCGTCCTGCCACCCACCAGCCCCTGCTC	662
IGHG2_chr14:106113320-106113420	ACCTGAGGCACCTGAGGCTGCTCTGCCCTGGTCCCCTGAGCTCCAGGGTCTTCCCCCTGCTCATCCTGCCT CCCACCTGCCCTTGTTCACCTTCAGTTGC	663
IGHG2_chr14:106113420-106113520	TCTGCCCTGGTCTGCTGAGCTCCAGGAGGTGCCCCCCTGCTCCTTCTGCCCCCACCTGCCCTGCTCACCTGT GGCTGCTCGGTCCTGGTACCCTGAACTCC	664

IGHG2_chr14:106113450-106113550	GCCCCCTGCTCCTTCTGCCCCCACCTGCCCTGCTCACCTGTGGCTGCTCGGTCCTGGTACCCTGAACTCCA ATGCCTGCCCCCCTGCTCACTCTGCCCCTCC	665
IGHG2_chr14:106113550-106113650	CTCAACCCGGGCAGCAATGTCACTCAGGTCACTGTTGCCCCCCCTGCCTGTCCTGGCACCCCTCTGTCCAGGT TTGGGCTGTTTTTCTGGCCTCATTTTTGT	666
IGHG2_chr14:106113695-106113795	TGTCCAGTCAGGTCTCCCCAACAGAGCCCCTTGCCCTTGCCCATGTGCCCCCTCCTGGGTGAGCTCCCAGAT CCTCCCGTCCCCTGCACTGCTCCTCTGCTCTG	667
IGHG2_chr14:106113795-106113895	GAAGCCTCTCCAGAACCTCAGCTCCTCAGTGGCCTCTGCTCTGGGTCAGCTCCCTGAACGCACGGAG CCTCACCCCTCCCCCTCGCCCCAGGCCTGCT	668
IGHG2_chr14:106113895-106113995	GCACTCTGGGCCTTTCTGGGCCTCCCTGGACTCTTCCCTCCTCCCCATCTGTGCACTCAGCACAGCTCTCCCC TCCACTCCGCTGCTGACCACAGCCCTGC	669
IGHG2_chr14:106113905-106114005	CCTTTCTGGGCCTCCCTGGACTCTTCCCTCCCATCTGTGCACTCAGCACAGCTCTCCCCTCCACTCCGC TGCTGACCACAGCCCTGCTCCCCCGCCAG	670
IGHG2_chr14:106114175-106114275	CCCACGGCCAGCACTGCTGACCCTGCCCTGGGCTCCAGTGATGCTGCTGGCCTGGACAAGCCCCTCCGTTC ACCTGGGGCCTCTCCTCCTCCCTCGTTCT	671
IGHG2_chr14:106114275-106114375	ACTGCCTCCCTCAGCTCAGGTGGGTCCTGCCCATGCTGGCATCACCCCCACGGCCGGCTCTGCCCGCATCCCGT CAGGTTCCTCGTGCTCCCCAGCCTGGTCGT	672
IGHG2_chr14:106114375-106114475	CATGGAGGCCTCAGTCAGCCTCTGGTGTGTCCTGCCCTGTTGGCTTGGAAGCCCCTGCCCACGGTCCCCGT CATCTTGCACTGGGTGGGCGTTGGTGCCT	673
IGHA1_chr14:106176375-106176475	AGCTCAGCCCAGCCTAGTCCAGCCCAGCCCAGCACAGGTCAGCCCAGCTTAGCTTAGCCCAGGTCAGTCC AGCTCAGCTCAGTCCACTTAAGCTCACCCA	674
IGHA1_chr14:106176475-106176575	GGTCAGCTCCGTCCAGCTCAGCCCAGCCTAGCCCAGCCCAACACAGGTCAGCCCA GCTCAGCCTAGCCCAGCCCAGCTCAGCACA	675
IGHA1_chr14:106176575-106176675	GGTCAGACCAGCTCAGTACAGCTCAGGTCAGCCCAGACCAGTCCAACCCAGCCCAGCGCAGTCCAACCCA GCCCAGCTCAGCTCATCCAAGCCTAGCTCA	676
IGHA1_chr14:106176675-106176775	GCTCAGCCCAGCCCAGGTCAGCCTAGCCCAGCCGAACCCAGCTCAGCCCAGGTCAACCCAATTCAGCTCA GCTCAGCCCAGGTCAACCCAACCAAGCTCA	677
IGHA1_chr14:106176775-106176875	GCTCAGCCTAGCCCAGTCCAGCCTCAGCCCAGCTCAGCTCCAGTCCAGCTCAATCCACCTAAGCTCAC CCAGCTCAGCCCAGTCTGGCTCAGCTTAG	678
IGHA1_chr14:106176875-106176975	GTCAGCCCAGCCCAGCCTAGCCCAGATCAGTCCAGCTTAGCCCAGCCCAGGTCAGCCCAGGCCCAGGTCAG CCCAGCTCAGCTCAGCCCAGCCCAGCTCAG	679
IGHA1_chr14:106176985-106177085	CCCAGCCCAGCTCAGCGCAGCCCAGCCTAGCTCACCCCCAGCCAGGTCCAGCTTAGCCCAGCTCAGCCCAG CCCAACTCAGCTCAGCCCAGCTCAGCCCAA	680
IGHG1_chr14:106211960-106212060	TCTGAGCTCCAGGGGCTGCCCACCTGCTCCTCCTGCTTCCCACCGGCCCTGCTCACCTGCAGCTGCTCTGC CCTGGCTCCCTGAGGCTGAGCCTCAGTCC	681
IGHG1_chr14:106212060-106212160	TGCTCACCTTCTGATGCTCTCCCCTTGTCCCCTGAGCTCCAGGGGCTGACCCCCTGATCTTTCTGCTTCCTAC CTGCCCCTGCTCACCTGTGGCTGCTCTG	682
IGHG1_chr14:106212160-106212260	CCCTGATCCCCTGAGCTCCAGGAGCTGCCTCCTGCTCTTCCTGCCCCACCTGCCCCCTGCTCACCTGCAG ATCTGCCCTGGCTCTCTGAGGTCCAGGGG	683

IGHG1_chr14:106212260-106212360	CTGCCCCCTGCTCGCCCACCTCCCACCAGCCATGCTGACGTTGTGATGCTCTGCCCTGGTCTCCTGAGGTC CAGGGGCTGTCCCCCTGCTTATTCTGCCTC	684
IGHG1_chr14:106212360-106212460	CCACCTGCCCCTTCTCACCTGAGGCTCTTCTGCCCTGGTGCTCTGAGCTCCAAAAGCTGCCCACTTGCTCC TCCTGCTTCCTACCAGCCCCTGCTCTCCT	685
IGHG1_chr14:106212460-106212560	GTGGATGATCTGCCCTGGCTCTCTGAGCTCCAGGGGCTGCCCACCTGCTCCCATGCTTCCCACCTGCCCC TGCTGACCTGCGGCTGCTCTGCCTTGGCT	686
IGHG1_chr14:106212560-106212660	CCCTGAGCTCCAGGAGCTTCCCCCTGCTCATCCTGCCCCCCACTGGCCCCTGTTCACCTTCAGATGCCCTC CCTGGTCCCCTGAAGTCCAGGAGCTGCCC	687
IGHG1_chr14:106212660-106212760	CCTGTTCCTCCCGCCTCCCACCAGCCCGTGCTCACCTGCGGCTGCTCTGCCCCTGGTCCCCTGAGTTCCAGG GGCTGCCCCCCTGCTCGCCCACCTCCCACT	688
IGHG1_chr14:106212760-106212860	AGCCATGCTCACCTCCTGATGCTCTGTCCTGGTCCCCTGAGCTCCAGGGGCTGCCCCCTGCTTGCCCATCT CCCACTAGCCATGCTCACCTTCTGATGCT	689
IGHG1_chr14:106212860-106212960	CTGCCCTGGTCCCCTGAGCTCCAGGGTCTTCCCCCTGCTCATCCTGCCGCCCACCAGCCCCTGCTCACCTG AGGCTGCTCTGCCCTGGTCCCCTGAGCTC	690
IGHG1_chr14:106212870-106212970	CCCCTGAGCTCCAGGGTCTTCCCCCCTGCTCATCCTGCCGCCCCACCAGCCCCTGCTCACCTGAGGCTGCTCT GCCCTGGTCCCCTGAGCTCCAGGAGGTGC	691
IGHG1_chr14:106212980-106213080	TTCTGCCCCCACCTGCCCTGCTCACCTGTGGCTGCTTGGTCCTGGTCCCTGAGCTCCAATGCCTGCTCCCTG CTCACTCTGCCCCTCCCTCAACCCGGGCA	692
IGHG1_chr14:106213080-106213180	GCAATGTCACTCAGGTCACTGTTGCCCCCCTGCCTGTCCTGGCACCCTCTGTCCAGGTTTGGGCTGTTTTT CTGCCCTCATTTTTGATTTTTGCAGCACTT	693
IGHG1_chr14:106213125-106213225	CCTCTGTCCAGGTTTGGGCTGTTTTTCTGCCCTCATTTTTGATTTTTGCAGCACTTGGCGTGTTCCCTATGCT GTGGAGCAGCCCCCAGTGTCCAGTCAGGT	694
IGHG1_chr14:106213210-106213310	AGTGTCCAGTCAGGTCTCCCCAACAGAGCCCCTTGCCCCTTGCCCATGTGCCCCTCCTGAATGAGCTCCCGG ATCCTCCTGTCCCCTGCACTGCTCCTGCTC	695
IGHG1_chr14:106213310-106213410	TGGAAGCCTCTCTGGAACCTCAGCTCCTCAGTGGCCTCTGCTCTGCTGGGTCAGTTCCCTGAACGCACGGA GCCTCAGCCCCTTCCCCTCGCCCCAGGCCT	696
IGHG1_chr14:106213410-106213510	GCTGCACTCTGGGCCTTTCTGGGCCTCCCTGGACTCTTCCCTTCCCTCCCGCCCGTGCACTCAGCACAGCTCT CCCCTCCTCTCCACTGCTGACCACAGCCC	697
IGHG1_chr14:106213510-106213610	TGCTCCCCGCCAGCAGGTGCCCCAACCCCATCAGCTGGCTCTGAGCCCAGCCCCTGTGCCTCCCCTGTCCC TGCCTCTGCCTCTGGGCTCCTTGGCTTCC	698
IGHG1_chr14:106213660-106213760	ACCTGCTGTCCTTGGTCCTGGCTGAGAGGAGGGCCCCACGGCCAGCACTGCTGACCCTGCCCTGGGCTCC GGTGATGCTGCCGGCCTGGACACAAGCCCCTC	699
IGHG1_chr14:106213760-106213860	CGTTCACCTGGGGCCTCTCCTCCCCTCGCTCTGCTGCCTCCTGAGCTCAGGTCGGTCGTGCCCATCCCTG GCATCACCCCACGGCCGGCTCTGTGCCGCAT	700
IGHG1_chr14:106213860-106213960	CCAGTCATGTTCCTCGTGCTCCCAGCCCGGTCGTCCTGGAGGCCTCAGTCAGCCTCTGGTGTGTCCTGCCC TGTTGGCTTGGAAGCCCCTGCCCACCGGTC	701
IGHG1_chr14:106213960-106214060	CCCGTCGTCTCGCACTGGGTGGGCATCGGTGCCTGAAGGCTGCCCACCTCCCCCCGTGCTGGCTCCGCTTGG GCCTCCATGTGGGGCCGGCCTCGACCCCA	702

IGHG3_chr14:106239250-106239350	CACTGCACTTTCACCAGCCCTCAGCTGTCTGCTGCCGGCAACTACCCAGCTCCTGCCAAAGTCTAGGAGCT GCGTGCTGCCTCCCCACCGTCCCTGCTCAC	703
IGHG3_chr14:106239350-106239450	CTGTGGCTGCTCTGCCCTGGTGCTCTGAGCTCCAGGAGATGCCCCCTGCTCCTCCTGCCCCCCCACCTGCCC CTGCTCACCTGCAGCGGCTCTGCCCTGT	704
IGHG3_chr14:106239455-106239555	GAGCTCCAAGAGCTGCCCCCTGCTCCTCCTGTCCCCTGACCCTGCTCCTGTTTGCCTATGGCTGCTCTGCC CTTGTCCCCTGAGCTCCAGGAGCTGCCCC	705
IGHG3_chr14:106239555-106239655	TGCTCATTCTGCCGCCCACCTGCCCCTGTTCACCTGTGGCTGCTCTTCCCTGGTCCTCTGAGCTCCATGAGC TGCCCCTTGCTCCTCCTGCTTTCCACCA	706
IGHG3_chr14:106239655-106239755	GCCCCTGCTCACCTACCGATGATCTTCCCCGGCTCTCTGAGCTCCAGGGGCTGCCCACCTGCTACCCCTGC TTCCCACCAGCCCTGCTTACCTGCAGCTG	707
IGHG3_chr14:106239755-106239855	CTCTGCCCTGGCTGGCAGAGCTGCAGAAGCTGCCCCCTGCTCTGCAACCTCCCACCGGCCCTTCTCATCTT CTGATGTTCTCCCCTGTTCCCTGAGCTCC	708
IGHG3_chr14:106239855-106239955	AGGAGCTGCCCCCTACTCGTTCTACCTCCCACCAACCCGTGCTCACCTGCGACTGCTCTGCCCTGGTCCCC TGAGCTCCAGGGGCTGCCCCCTGCTCGCC	709
IGHG3_chr14:106239990-106240090	TGCCCTGATCCCCTGAGCTCCAGGACTGCCCCCTGCTCGTCCTGCCCCTCACCTGCTCACCTGAG GCTGCTCTGCCCTGGTCCCCTGAGCTAAA	710
IGHG3_chr14:106240090-106240190	GGGGCTGCCCCCTTACTCATCCTGCCTCCCACCAGCCCCTGCTCACCTTCTGATGCCCTCCCCTGGTCCCCTG AGCTCCAGGGGCTGCCCCCTGCTCGTCC	711
IGHG3_chr14:106240170-106240270	GGGCTGCCCCCTGCTCGTCCTGCCTCCCACCAGCCCCTGCTCACCTGCAGCTACACTGCCCTGGTTCCCCTG AGCTCCAGGAGCTGCCACCTGCTTGTCCT	712
IGHG3_chr14:106240270-106240370	GCCTTCCACCAGCCCCCTGCTCACCTGCAGCTACACTGCCCCTGGTTCCCCTGAGCTCCGGGGAGCTGCCCGCCTG CTTGTCCTGCCTCCCCACCAGCCCCCTGCTC	713
IGHG3_chr14:106240370-106240470	ACCTGTGGCTACACTGCCCCTGGTGCCCCTGAGCTCCAGGAGCTGCCCCCCTGCTTGCCCATCTTCCACTGAGC CCTGCTCACCTGCAACTGCTCTGCCCTGG	714
IGHG3_chr14:106240470-106240570	CTCTATGAGCTCCAGGGGCTGCCCCCCTGCTGGTCCTGCCTCCCACCTGCCCTGTGGCTGCCTC CTCACCTGTGGCTGCTCTGCCCCTGGTCCC	715
IGHG3_chr14:106240570-106240670	CTGAGCTCCAGGGTCTTCCTCCTGCTCATCCTGCCCCTCCACCGGCTCCTGTTCACCTTCAGATGCTCTCCCC GTGGTCCCCCTGAGCTCCAGGAGCTGCCC	716
IGHG3_chr14:106240670-106240770	CCTGTTCTTCCTGCCTCCCACCTGCCCCTGTGCACCTGTGGCTGCTTGGTCCTCCCTGAACTCCAATGC CTGCCCCCTGCTCACTCTGCCCCTCCCTC	717
IGHG3_chr14:106240770-106240870	AACCTGGGGCAGCAACGTCACTCGGTCCACTGTTGCCCCCCTGCCTGTCCTGGCACCCTCTGTCCAGGTTT AGGCTGTTTTTTCTTGCCTCATTTTTGTTT	718
IGHG3_chr14:106240820-106240920	TGGCACCCTCTGTCCAGGTTTAGGCTGTTTTTCTTGCCTCATTTTTGTTTTTTGCAGCACTTGGCGTGTTCCC TATGCTGTGGAGCAGCCCCAGTGTCCAG	719
IGHG3_chr14:106240915-106241015	TCCAGTCAGGTCTCCCCAACAGAGCCCCTTGCCCTTGCCCATGTGCCCCCTCCTGGATGAGCTCCCGGATCC TCCCGTCCCCTGCACTGCTCCTGCTCTGGA	720
IGHG3_chr14:106241015-106241115	AGCCTCTCCAGAACCTCAGCTCCTCAGTGGCCTCTGCTCTGCTGGGTCAGTTCCCTGAACGCACGGAGGCCT CAGCCCCTCCCCTCGCCCCAGGCCTGCTG	721

IGHG3_chr14:106241115-106241215	CACTCTGGGCCTTTCTGGGCCTCCCTGGACTCTTCCCTCCTCCCGCCCGTGCACTCAGCACAGCTCTCCCCT CCTCTCCGCTGCTGACCACAGCCCTGCT	722
IGHG3_chr14:106241200-106241300	GACCACAGCCCTGCTCCCGGCCAGCAGGTGCCCCAACCCCATCAGCTGGCTCTGAGCCCAGCCCCTGTGC CTCCCCTGTCCCTGCCTCTGCCTCTGGGCT	723
IGHG3_chr14:106241345-106241445	GCTCTGCTCCCAGCTCACCTGCTGTCCTTGGTCCTGGCTGAGAGGAGGGCCCTACGGCCAGCTCTGCTGAC CCTGCCCTGGGCTCCGGTGATGCTGCCGG	724
IGHG3_chr14:106241445-106241545	CCTGGACAAGCCCCTCGGTTCACCTGGGGCCTCTCCCTCCTCCCTCTCTGCTGCCTCCTGAGCTCAGGTC GGTCATGCCCCATCCTGGCATCACCCCATG	725
IGHG3_chr14:106241545-106241645	GCTGGCTCTGCCCCATCCCGTCATGTTCCTCACACTCCCAGCCCCGGTCGTCCTGGAGGCCTCAGTCAGCCT CTGGTGTGTCCTGCCCTGTTGGCTTGGAA	726
IGHM_chr14:106318100-106318200	GGGTAGAGCCCCACCTCGTGGCCTGCAAGCCAGCCAGCCCCTGCCGGTCGAGAAGGAAGCCTGTGTGTGAGA GCACACAACTGGAGGCCGGCGGGGAAGAGA	727
IGHM_chr14:106318200-106318300	AACACGTGCCAACAGGCCACCGCAGGCCAGGACCCCAGACCCGGAGGCAGCGCCCCTTTGAGTTCCTCTCT CTGGTCTCCGATGTTCTTCTGTTGGGATCA	728
IGHM_chr14:106318300-106318400	TTTCACCTACAGGCAACAGAGACAGTGTGAAATGCTTTCCCTGTGGTCGGGAAGGGAGCCGGGGGCAGAG ATGACCCAGTGGGGTGGTGTGGGGGCCTCCG	729
IGHM_chr14:106322055-106322155	CTTTGCACACCACGTGTTCGTCTGTGCCCTGCATGACGTCCTTGGAAGGCAGCAGCACCTGTGAGGTGGCT GCGTACTTGCCCCCCTCTCAGGACTGATGG	730
IGHM_chr14:106322155-106322255	GAAGCCCCGGGTGCTGCTGATGTCAGAGTTGTTCTTGTATTTCCAGGAGAAAGTGATGGAGTCGGGAAGG AAGTCCTGTGCGAGGCAGCCAACGGCCACG	731
IGHM_chr14:106322255-106322355	CTGCTCGTATCCGACGGGGAATTCTCACAGGAGACGAGGGGGAAAAGGGTTGGGGCGGATGCACTCCCT GAGGACCCGCAGGACAAAAGAGAAAGGGAGG	732
IGHM_chr14:106322905-106323005	ACTCCAGCTACCCTGAAGTCTCCCCAGGCAGACAACCCAGGCCTGGGAGTGAGTATAGGGAGAGGGTGGGT GTGATGGGGAACGCAGTGTAGACTCAGCTGA	733
IGHM_chr14:106323005-106323105	GGCTATCCATCTATGTCCAACAAGATCATGAAGATTGGCCCAGTGCCATGTCCTCCAGTTCATCCCAGCCC AGGCCAGCTCAATCCAGTTCATCCCAGCC	734
IGHM_chr14:106323105-106323205	CAGGCCAGCTCAATCCAGCCCAGCCCACCCCAGCTCAGCAAAGCCAAGCTCAGCTCAGCCCAACT CAGATGAGCTCAGACCAGCTCAGCCCAGCC	735
IGHM_chr14:106323470-106323570	CAGCTCAGCTCAGCCCAACCCAGCCCAGCTCGCTCAACCTTGCTCGGCTCAGCTTAGCCCAGCCCAGCCCA GCTCAATCCAGCCTGGCTCAGCCCAGCCC	736
IGHM_chr14:106323570-106323670	AGCCCAGTTTGGCTCAACCCAGCTTGGCTCAGCCCAGGTCAGCCTGGCTCAACTCAGCCCAGCCCAGCCC AGCTCTGCTCAACCCAGCTCTGCTCAACTC	737
IGHM_chr14:106323805-106323905	AGCCCAGCTCATCCCAGCTCAGCCCAGCCCAGCCTAGCTTAGCTCAACCCAGCTCAGCTCAGTTCAGCTCA GCCCTGCTCAGCACAGCACAGCAGAGCCC	738
IGHM_chr14:106324010-106324110	AGCCCGGATCGGCTCAACCCAGCTTAGCTCAGCCCAGGTCAGCCCAGCTTAACTCAGCCCAGGTCAGCCC AGCTTAACTCAGCCCAGCCCAGCCCAGCTC	739
IGHM_chr14:106324155-106324255	TCAGCCCAGTTCAGCCCAGCTCAGCCCAGCCTAGCTTGGCTCAACACAGCTCAGCTCAGCCAGCC CAGACCAGCTCAGCTCAGCCCAGTCCAGCT	740

IGHM_chr14:106324290-106324390	CAACCCAGCCCAGCCCAACCCAGCTCGGCTTAACCCAGCTCGGCTCAGCCCAGATCAGCCTGGCTCAACT CAGCCCAGCCCAGCTCAACCCAGCCCAGTT	741
IGHM_chr14:106324490-106324590	CAGCTCAGCTGAGCCCAGCCCAGTCCGGCTCAGCTCAGCCCCGCCCCACTCAGCCCAGCTCAGCT CAGCCCAGCTCAGCCCAGCTCAGCTTAGCC	742
IGHM_chr14:106324750-106324850	CAGCCCAGATCATCCCAGCTCAGCTCAGCTCGGCTTAGCCCAGCTCAACCTGGCCCAGCCTGGTCC AGGTCAGCCCAGCCTGGACCACCCAGCCC	743
IGHM_chr14:106324850-106324950	AGCTCAGCTCAGCCCAGCTCATCCTGGTTCAGCTCAGCTCAACCCGGCTCAGCCCAGGTCTGCTCAACCCA GCCCAAATCAGCTCAGCCCAGCCCAGGTC	744
IGHM_chr14:106324950-106325050	ATCCCAGCTCAGCCCAGCACAGCCTACTTCAGCTCAGCTCAGCCTAGGTCAGCTCAGTTGAGGTC AGCTCAACTCAGCCCAATCCAGCCTGGCTC	745
IGHM_chr14:106325050-106325150	AGCCCAGCTCACCCTAGCTCAGCTTAGCTCAGCCCAACTCAACCCAGCCCAGCCTTGCCCAACCCAGCTCA GCTCAGCCCAGCCCAGGTTAGCCCAGCCC	746
IGHM_chr14:106325150-106325250	AGCCTCGGCTTAGCTCTGCTCAGCTCGGCCCTGCTCGCCTCAGCCCAGTTCAGCTCAGCTCA GCTCAGCCCAGCTCAGCCCAGCCCTGGTT	747
IGHM_chr14:106325250-106325350	AGCTCAGCCCAGCTAAGCTCAGCTCGGCTTGGCTCTGCTGAGCTTGGCCTAGCCTGATACA ACCTGCTCAGCCCAGTTCAGCTCGGCTCA	748
IGHM_chr14:106325360-106325460	GCCCAGCGTAGCTCAGCTCAGCTGAGCCCAGCCCAGGTTAGCTCAGGTCAGCTCAACTC AGCCCAAACCAGCCTGGCTCGGCCCAGCTC	749
IGHM_chr14:106325460-106325560	ACCCTAGTTCAGCTTAGCTCAGCCCAGCCCAGCCCTGCCCAACCCAGCTCAGCTCAGCCCAGCCCAGGTTA GCCCAGCCCAGCCTCGGCTTAGCTCTGCT	750
IGHM_chr14:106325515-106326615	AGCCCAGCCCAGGTTAGCCCAGCCCAGCCTCGGCTTAGCTCTGCTCAGCTCGGCCCAGCCCAGGTTAGCC CAGCCCAGCCTCGGCTTAGCTCTGCTCAGC	751
IGHM_chr14:106325615-106325715	TCGGCCCTGCTCGCCTCAGCCCGTTCAGCCCAGTTCAGCTCAGCTCAGCCCAGCTCAGCCCAGCCC TGGTTAGCTCAGCCCAGCTAAGCTCAGCT	752
IGHM_chr14:106325715-106325815	CGGCTCAGCTCTGCTGAGCTCGGCCCAGCTTGGCTCAGCCCCGACACAGCCTGCTCAGCCCAGTTCAGCTC GGCTCAGCCCAGCCCAGCCCAGCGTAGCTC	753
IGHJ6_chr14:106325820-106325920	AGCTGAGCCCAGCCCAGGTTAGCTCAGCCCCAGCCCCAGGTTAGCTCAGCTCTGCCCAGGT TAGCTCAGCCCCCAGTCCAGGTTAGCTCAGC	754
IGHJ6_chr14:106325920-106326020	CCAGCTCAGCTCTGCCCCAGGTTAGCTCAGCCCCCAGTCCAGGTTAGCTCAGCCCAGCTCAGGCCTTGCCCAGG TTAGCTCAGCCCAGCTAAGCTCAACTTGG	755
IGHJ6_chr14:106326020-106326120	CTCAGCTCAGCCTAGCTTGGCTCAGCCCAGCACAGCACGCTCAACCCGGTTCAGCTTGGCTCAGCCCAGC CCAGCCCAGCCTAGCTCAGCTCAGCCCCGC	756
IGHJ6_chr14:106326245-106326345	CCAGCTCAGCGCAGCCCAGCTCAGCTCAGCTCAGCCTAGCCTTGCTCGGCCCAGCTCAGCTCAGCCCAGCT CAGCCTAGCCTTGCTCAGCCCAGCTCAGC	757
IGHJ6_chr14:106326450-106326550	TCAGCCCAGCCCTGCCCAGCTCAGCCCAGCTTAGTGCAGCCAAGCCCAGCTCAGCTCAGCTCACCTGGTG CAACTTAGCCCAGCTCAGCTCAGCTCAGCT	758
IGHJ6_chr14:106326550-106326650	CAACCCAGTTCAACTCAGCCCAGTTCAGCTCAGCTCAGCCCAGTTCAGCCTTGTTTAGTCTAGGTCAGCTT AGGTCAGTTTTGCCCATCTGAGTCCATTT	759

IGHJ6_chr14:106326650-106326750	CTGAAAGCTGGATGGAGTTGTCATGGCCAGAAATGGTCAGCCCACCAGACCTGCTTGTCTCAGCTAAAGC CATCTCATTGCCAGGTTCCTGCACAGCCAG	760
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IGHJ6_chr14:106326850-106326950	TACCACCCTCCACTACCTGGGTGGAATATTTCTTTGCTGCTTTAAAGTCATTAAAACATCTTGAGAATGAG ACCAAGAATTTAGGAGCCTGTGCTGTGAT	762
IGHJ6_chr14:106326950-106327050	AAAAATGAGCAGGTCCCCTTGCTCTAGAAGTGGCAGCATATCTTCTGCACCAAGAGGAGGGTATTGAGAT GCTCAGAGCCTCCACCTTCCCGGAGCATCC	763
IGHJ6_chr14:106327050-106327150	CCTCCCTTCTGAGTCTGCAGTAAACCCCTGCCTTTAAATTCCCTCTAGATAACAGTCATCATTGGAAACAA CCAAGAAATGCATTTTATCTGAATTTGCC	764
IGHJ6_chr14:106327150-106327250	ACTTAAAATTCTGCCATTTACCATAAATCGCTTTGGAAGGCATGGGCTACTTTCAAGGGTGCGATGATGA CCTACAGTCAATGACTTAGACAAGGGCGAT	765
IGHJ6_chr14:106327250-106327350	GCCAGTGGGCTTGGTATGTTCTCAAGCATCATTACCCATGCCATCCCCATTCAGAGGTTGTGGAGCAGCT CGTGCGACCTCTCCTTCAAATGGGCTTTA	766
IGHJ6_chr14:106327350-106327450	GGGAAAGTTAAATGGGAGTGACCCAGACAATGGTCACTCAAAAGACTCACATAAATGAGTCTCCTGCTCT TCATCAAGCAATTAAGACCAGTTCCCCTTC	767
IGHJ6_chr14:106327450-106327550	TAGTGGAAATAAGACGTCAAATACAAAGTTTTAAGAGAAGCAAATGCAGCAGCGGCGGCTGCCTGTCTCT TACCATGTCCGGCGCCTGGTCACTGCGAGC	768
IGHJ6_chr14:106327550-106327650	CTTGCAAAGCTTTGGCATGGAATCATTCCTCCAAGTCCATTAACAAGGGCTGGGGCCTGAGCAGCCAGTC GGCCCGGCAGCAGAAGCCACGCATCCCAGC	769
IGHJ6_chr14:106327650-106327750	TCTGGGTAGTCCGGGGAGACCCAAAGCCCAGGCCGGGCCTGGCAGCCACCCTCCCAGAGCCTCCGCTAGG CCAGTCCTGCTGACGCCGCATCGGTGATTC	770
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IGHJ6_chr14:106327850-106327950	TAATTCAGGATAAATGATGCACATTTTACCTAAAACTTATCCTAAAGTGAGTAGTTGAAAAGTGGTCTTGA AAAATACTAAAATGAAGGCCACTCTATCAG	772
IGHJ6_chr14:106327950-106328050	AATATCAAAGTGTTTCTCCTTAATCACACAAAGAGAAAACGAGTTAACCTAAAAAAGATTGTGAACACAGTCA TTATGAAAATAATGCTCTGAGGTATCGAAA	773
IGHJ6_chr14:106328050-106328150	AAGTATTTGAGATTAGTTATCACATGAAGGGATAACAAGCTAATTTAAAAAACTTTTTGAATACAGTCAT AAACTCTCCCTAAGACTGTTTAATTTCTTA	774
IGHJ6_chr14:106328150-106328250	AACATCTTACTTTAAAAATGAATGCAGTTTAGAAGTTGATATGCTGTTTGCACAAACTAGCAGTTGATAA GCTAAGATTGGAAATGAAATTCAGATAGTT	775
IGHJ6_chr14:106328250-106328350	AAAAAAAGCCTTTTCAGTTTCGGTCAGCCTCGCCTTATTTTAGAAACGCAAATTGTCCAGGTGTTGTTTTG CTCAGTAGAGCACTTTCAGATCTGGCCT	776
IGHJ6_chr14:106328350-106328450	GGGCAAAACCACCTCTTCACAACCAGAAGTGATAAATTTACCAATTGTGTTTTTTTGCTTCCTAAAATAGA CTCTCGCGGTGACCTGCTTCCTGCCACCT	777
IGHJ6_chr14:106328450-106328550	GCTGTGGGTGCCGGAGACCCCCATGCAGCCATCTTGACTCTAATTCATCATCTGCTTCCAGCTTCGCTCAA TTAATTAAAAAAATAAACTTGATTTATGA	778

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IGHJ6_chr14:106328650-106328750	TGTTAATCAAATGATAAGAATTTCAAATACTTGGACAGTTAAAAAAAATTAATATACTTGAAAATCTCTCAC ATTTTTAAGTCATAATTTTCTTAACCATT	780
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IGHJ6_chr14:106328850-106328950	AGGTCCTGGAGCCTCCCTAAGCCCCTGTCAGGACGGCAGCCACCGTTTCTGGGCTACCCCTGCCCCCAACC CTGCTCTCATCAAGACCGGGGCTACGCGT	782
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IGHJ6_chr14:106329050-106329150	AATATTTCACGATTCGCTGCTGTGCAGCGATCTTGCAGTCCTACAGACACCGCTCCTGAGACACATTCCTC AGCCATCACTAAGACCCCTGGTTTGTTCA	784
IGHJ6_chr14:106329150-106329250	GGCATCTCGTCCAAATGTGGCTCCCCAAGCCCCCAGGCTCAGTTACTCCATCAGACGCACCCAACCTGAGT CCCATTTTCCAAAGGCATCGGAAAATCCA	785
IGHJ6_chr14:106329250-106329350	CAGAGGCTCCCAGATCCTCAAGGCACCCCAGTGCCCGTCCCCTCCTGGCCAGTCCGCCCAGGTCCCCTCGG AACATGCCCCGAGGACCAACCTGCAATGC	786
IGHJ6_chr14:106329350-106329450	TCAGGAAACCCCCACAGGCAGTAGCAGAAAACAAAGGCCCTAGAGTGGCCATTCTTACCTGAGGAGACGG TGACCGTGGTCCCTTTGCCCCCAGACGTCCAT	787
IGHJ6_chr14:106329450-106329550	GTAGTAGTAGTAGTAATCACAATGGCAGAATTGTCCATCCTCACCCCACACAAAAACCCAGCCACCCAGA GACCTTCTGTCTCCGGGCGTCACATGGAAG	788
IGHJ6_chr14:106329550-106329650	CTGACTGTCCGTGGCCCTGTCCTGCCCTTCTCATGGAACCCTCTGCTGGCCTCCCACGTACCCCACACATTCT GGCCTGACCCCCTCAGAAGCCAGACCACTG	789
IGHJ6_chr14:106329650-106329750	TCGGCCTGGGAAGTCCAACTGCAAGCAGACGGCTGCTAAGTCACCCCCAGGAGTCCAAAAAACCCCGGGG GGCACCCGTCCCAGAGAGCGGTGCCTTGGA	790
IGHJ5_chr14:106329750-106329850	GCGGGACAGAGTCCCACCACGCAATCATCACGACAGCCCCTGAGAATGCTCCAGGTGAAGCGGAGAGAG GTCACCCCAGACCAGCCGAAGGAGCCCCCCA	791
IGHJ5_chr14:106329850-106329950	GCTGCCGACATCTGTGGCCGGACTTGGGGAGGACAGGCTGGGTTCCCATTCGAAGGGTCCCTCTCCCCGG CTTTCTTTCCTGACCTCCAAAATGCCTCCA	792
IGHJ5_chr14:106329950-106330050	AGACTCTGACCCTGAGACCCTGGCAAGCTGAGTCTCCCTAAGTGGACTCAGAGAGGGGGGTGGTGAGGACT CACCTGAGGAGACGGTGACCAGGGTTCCCT	793
IGHJ5_chr14:106330050-106330150	GGCCCCAGGGGTCGAACCAGTTGTCACATTGTGACAACAATGCCAGGACCCCAGGCAAGAACTGGCGCCC CGCTACGTCCCTGGGACCCTCTCAGACTGA	794
IGHJ5_chr14:106330150-106330250	GCCCGGGGAGGGCCCGGGGGTTGTTGGGCATTGGACCCCAGAGGGCCTAGGGTGGCCCTGGCCACAGAGA GACCCGTGCTGCTGGGCTCAGGAGGAAGGAG	795
IGHJ4_chr14:106330250-106330350	CATCTGGAGCCCCTTGCCCCTCGTCTGTGTGGCCGCTGTTGCCTCAGGGCATCCTCCTCCTGAGCCCCCCAGGAT GCTCCGGGGGCTCTCTTGGCAGGAGACCCA	796
IGHJ4_chr14:106330350-106330450	GCACCCTTATTTCCCCCCAGAAATGCAGCAAAAACCCTTCAGAGTTAAAGCAGGAGAGAGGTTGTGAGGAC TCACCTGAGGAGACGGTGACCAGGGTTCCC	797

IGHJ4_chr14:106330450-106330550	TGGCCCCAGTAGTCAAAGTAGTCACATTGTGGAGGCCCCATTAAGGGGTGCACAAAAACCTGACTCTCC GACTGTCCCGGGCCGGCCGTGGCAGCCAGC	798
IGHJ4_chr14:106330550-106330650	CCCGTGTCCCCAAGGTCATTTTGTCCCCAGCACAAGCATGACTCTGCCCACCCTTTGCCCCAGCAGCAGAGT CCCAGTTCCCAAAGAAAGGCCTTCTGCTG	799
IGHJ3_chr14:106330650-106330750	AACGTGGTCCCAAACAGCCGGAGAAGGAGCCCCGGAGGGCCCCACATGGCCCAGCGCAGACCAAGGAGC CCCCGGACATTATCTCCCAGCTCCAGGACAG	800
IGHJ3_chr14:106330750-106330850	AGGACGCTGGGCCCAGAGAAAGGAGGCAGAAGGAAAGCCATCTTACCTGAAGAGACGGTGACCATTGTC CCTTGGCCCCCAGATATCAAAAGCATCACACA	801
IGHJ3_chr14:106330850-106330950	GGGACACAGTCCCTGTTCCTGCCCAGACACAAACCTGTGCCCGTGCAGGACACTCGAATGGGTCACATGG CCCAAGCACAGAGCAGAGGCAGCCGGCGTC	802
IGHJ3_chr14:106330950-106331050	CCTGTCCCCAGCCACACAGACCCCCGGGCTGAGACCCAGGGCAGGGAGGGGTGACGTTCCCAGGGAGACG GTGGCCGGCTGCCCCTGGCCCCAGTGCTCCA	803
IGHJ3_chr14:106331050-106331150	AGCACTTGTAGCCACACTAAAGCGCAGGCCTGGTCCCCCGGCACATGAACAGCCAGCGCCCAGCCCCAGCC CAGGCTCTGCCCACAACTTCTCCTTCCCGT	804
IGHJ2_chr14:106331150-106331250	CCCTGCCCCTCGGCCTGCTTGCTACCTGTGGAGGGGTCCCTGACGGGGCTGAAGCCCAGCGGGGTCCCCTGCC TGTCCTTGGGGGCTCCAGCTGGCCCCAGGG	805
IGHJ2_chr14:106331250-106331350	CTAAGTGACAGCAGGGCTCTGGCATGCAGCCCATGGCGGAGACCCCAGGGATGGCAGCTGGTGTGGCCTC AGGCCAGACCCAGGCCGGCTGCAGACCCCA	806
IGHJ2_chr14:106331350-106331450	GATACCTGGCCTGGTGCCTGGACAGAGAAGACTGGGAGGGGGCTGCAGTGGGACTCACCTGAGGAGACA GTGACCAGGGTGCCACGGCCCCAGAGATCGA	807
IGHJ2_chr14:106331450-106331550	AGTACCAGTAGCACAGCCTCTGCCCTCCTGCTTCTCCCATACAAAAACACACCCTCCGCCCTCCTGCCGAC CTCCTTTGCTGAGCACCTGTCCCCAAGTC	808
IGHJ1_chr14:106331550-106331650	TGAAGCCAAAGCCCTTGCCTGGCCCAGTACACCTGGCTCCCCGCTATCCCCAGACAGCAGACTCACCTGA GGAGACGGTGACCAGGGTGCCCTGGCCCCA	809
IGHJ1_chr14:106331650-106331750	GTGCTGGAAGTATTCAGCCACGGTGAGTCAGCCCTGAGCCAGGGGCTACAGAAACCCACAGCCCGGGGTC CCGGGGGAGCATGGTTTTTGTAGAGCTGCC	810
IGHD7-27_chr14:106331750-106331850	AATCACTGTGTCCCCAGTTAGCACACAGTGGTTCTCAGCTCAGCCAAAACCCTGCCGGCTGGTAGGGGGCCTG TGGGGCTGGGGGCTGATGTGGCTGCGGTCT	811
IGHD6-19_chr14:106357890-106357990	TGCTGGGTCTGTCCTCTGTGGGAGGGGGCTGCTACCCAGGCCCAGGACTGCAGTGGAGGGGCTCACTGAGGG GCTTTTGGGTCTGGCCTGAGCCGCTGTGGG	812
IGHD3-3_chr14:106380360-106380460	GCTCTCAGGTCTACTGCGGGGACACTCGGGTCTGCCCCTGGCTTAGGTGGACAGTGTCCGTGCCCACCTG TGCCCTGAGGCTCCATTTCAGGCTGATATC	813
IGHD3-3_chr14:106380460-106380560	TGTCTGTATTGTCCCTACCCGCTGCATGGCCATGTCCTTTTGGGTTTATAAATTGCCCCCAAATCACGCAG GCATCATTCAGGCTTTTTATATTCCCTGG	814
IGHD3-3_chr14:106380550-106380650	TATTCCCTGGGCCACCAGGTGCCTCCACCCAGAAAGCTGAGATGTGGGAGGTTCTAGAGTCATTCTGCAA CCCTGGATGAGCCCCTGCAGCCTCAGTGCT	815
IGHD3-3_chr14:106380650-106380750	ACTGAGGTTCCAGCAAGACCTGGAGCAGGTGCAGATGAGGCCTGAGGCCAGGTGAAGCCCAGGCCAGGT GAGGTCCAGGCCAGTGAGGCCCAGGTCAGAT	816

IGHD3-3_chr14:106380750-106380850	GAGGCCCAGGTCAGGTGAAGCCCAGGTCAGGTGAAACCCAGGTCAGGTGAGGCCCAGATCATGTGAGCT CAGGACAGGCAAGGTCCAAGTCAGGTGAGGC	817
IGHD3-3_chr14:106380850-106380950	CGAGCTCAGGTGAAGCCCAGAGGTGAGGTCTAGGCCAGGTGAGGTCCAGGCCAGGTCA GGTGAGGCCCAGGTCAGGCAAGGCTGAGGTA	818
IGHD3-3_chr14:106380910-106381010	TCCAGGTCAGGTGAGGCCCAGGTCAGGCAAGGCTGAGGTAGATGTATGAGACTTCTGTAATTTTCAGTTG GTGCCAACCCTGCCTGGTGTCCCTGCCCCT	819
IGHD3-3_chr14:106381010-106381110	CCTCCCAGCCCATGCTCTGTGCCTGCCAGATGGCCGGCCCCTGCACAGGTGCTGCTGGCTGTGGAGGAGCT GGGCTCTGCCTCCCTGTGCATGGGCGTCCC	820
IGHD3-3_chr14:106381275-106381375	GCCTGCAGCCTGTCCGGGGATGCCCAGGGAGGTGAGTGCCACCACATATCAGGCCTTTTCTCTTTAAAGT CATTTCTTTGGGGATACATCATCAATGTCT	821
IGHD2-2_chr14:106381485-106381585	TCTAAACACAGCTGTGTGCATTTTCCTCTTCTTGCAATTTAGAATTTTAACTGCTGTTTTCAAGGTACTGTA ATGTATTTGTTCTCTTCTTGTTAGGAGA	822
IGHD2-2_chr14:106381585-106381685	CTTGCCAACCCTGTGTGTCTCAGTTCATACCCTCTTCCTTCCCCAGTAGAAGTAACGACCACTGTGTTTAT GTGATCATCCTTTTCTTGATTTTCCTTAT	823
IGHD2-2_chr14:106381655-106381755	TGTGATCATCCTTTTCTTGATTTTCCTTATAGTTTTCCTAGTGGAAAGTTTATCCCTTAAGAAGATAGTTCA TTTTGCCGGCTGTAAATTTTATTTAGAA	824
IGHD2-2_chr14:106381890-106381990	CTGCCATCGTTTATTTGCCTGTTTTCCTTCAGATGGCTGTTTGCTTCATTCTCAGTTTGGGGCTATGACAAA CATATGTTCTGCACATCTTTGCCCATGA	825
IGHD2-2_chr14:106381990-106382090	GGCTCTCAGGGAGGGCTCTGGAGCTGGCATTGCCTGCAGGGCTCTGCTTTGTTGCAGGGAGTTCCTGCCA AGGCTTTTCAGAGTGTCTGTGCCCAGCCTG	826
IGHD2-2_chr14:106382090-106382190	AAGGTACACACTGTACTTTGCCCTTGCATCAGGCACTTTCCTTGTGCTTGCTTCTGTGTGGCTCCACATTCT GGAGAATTTATTCAGATCTGTGCTGCAA	827
IGHD2-2_chr14:106382325-106382425	CTTCCCACACTGTCCTCCTGGGCTCACTCCCAGCCATCGATCTTGAACACCAGTTTATGGAACTATCTGCA CAGGAAAGCAGAAACAGCAAAAGGCCCTG	828
IGHD2-2_chr14:106382905-106383005	TTGCGTGGACCCTGTTTTTGGTCAAGGAAGTACTTGCTGGTGAAGGAGACCTCCCCCTCCTTTCTTTCTCA GGAGCCCCCTCTGATGCCGTTGCCTGGTG	829
IGHD2-2_chr14:106383005-106383105	TTTCTCAGGGCTGGTGCTGGGGGCTCAGCAGTGTCTGCCCTGTTCCAGGTGGGAATGTGGGTCTGTTCTGT TTCCACGCGGTGTTCTGGGGCCGCCAGTG	830
IGHD2-2_chr14:106383030-106383130	CAGCAGTGTCTGCCCTGTTCCAGGTGGGAATGTGGGGTCTGTTCTGTTTCTGTTTCCACGCGGTGTTCTGGGGCCGCC AGTGAGGGGGCTCGGGATGTCAGCGGCTGG	831
IGHD2-2_chr14:106383130-106383230	TCTCTGTCCCTATGGTCTGGGCTCCGGTTCACTGCTCCCCTGCCCTCCAGGTCGGTCACTGACTCAGTTAC TATCCAGCGGGCTCCGTGGCTGTTCAGTG	832
IGHD2-2_chr14:106383980-106384080	GGGAGCAAATGGAGAGGGAAGTGGCAGCGGCCCGAGTGCCAGGCGGTCCCGGTTTGGGGTTGATCTTTG TGGAACAGCTCCCTGGCCCGTGTGTAAGTGG	833
IGHD1-1_chr14:106384080-106384180	TCGGGGGAGGCACGGAGGTCTGGAGCTACAAGCGGTGGCAGGAAGGCAGGTCCCAGTCTTGGGGGTCTG GAGCTTATCTTCTTCCTGTGAACTGAGTGTG	834
IGHD1-1_chr14:106384630-106384730	ATGGAGGACCTGCCTCGGATGACACCCCTATCTTAAGAAGGTCATGGTGGGTTCCAGCTGGGAGGAAGGG AAGTGGGCCACCTCCTGGGGGTCTTCCACC	835

IGHD1-1_chr14:106384720-106384820	GTCTTCCACCCCCACCACCTCAGCCTGGGGCCTCTGTGATTCCTCTCTGCACAGACCCCAAAGTCTGTGCT GCCGCAGGGCAGGAAGGAAGGGCCTGTGG	836
IGHD1-1_chr14:106384825-106384925	TCGAGGTTGGGGCCACAGTGGTGTTCCCTAAGCCCGAGTCTGGTCTCATGGCCCCGCCCCGGCAGCAGGTCC TGAGTGAGGGACAGAGACCGGGGCGGGGTC	837
IGHD1-1_chr14:106384925-106385025	TTTGGTCCTGGTGGACTCTGGGGTGGATTCCAGTGGGGAGTCATCAGGGTCGGTGTCCCCCAGGGTACTG GGGTGTCTCTGCTCCTGGAGTCGGCTCTGG	838
IGHV2-5_chr14:106494090-106494190	CCTGGGTTTTTGTACAGGAGGTGCCCTGGGCTGTGTCTTTGTGGTCTGTGTGCACAGTAATATGTGGCTGT GTCCACAGGGTCCATGTTGGTCATTGTAA	839
IGHV2-5_chr14:106494210-106494310	GTGTCCTTGGTGATGGTGAGCCTGCTCTTCAGAGATGGGCTGTAGCGCTTATCATTCCAATAAATGAG TGCAAGCCACTCCAGGGCCTTTCCTGGGG	840
IGHV2-5_chr14:106494310-106494410	GCTGACGGATCCAGCCCACACCCACTCCACTAGTGCTGAGTGAGAACCCAGAGAAGGTGCAGGTCAGCGT GAGGGTCTGTGTGGGTTTCACCAGCGTAGG	841
IGHV2-5_chr14:106494445-106494545	CTGTGGAGAAAGCATAAGAAGATGAAGCCCACAAACAAGAAAACTGATGTTTCACCCGTGAAGGAGTCC CTGACCACAGCACTCACATGAAGGGATGGTC	842
IGHV2-5_chr14:106494545-106494645	AGCAGCAGGAGCGTGGAGCAAAGTGTGTCCATGGTGGGGCACAGGAGTCACTGAGCTGGGACCTGTGCT CGGCTTTTTCAACCCAGAGGAGGGTGGAGCT	843
IGHV2-5_chr14:106494565-106494665	AAGTGTGTCCATGGTGGGGCACAGGAGTCACTGAGCTGGGACCTGTGCTCGGCTTTTTCAACCCAGAGGA GGGTGGAGCTGGTGGAGATTTGCATTCCCC	844
IGHV2-5_chr14:106494650-106494750	AGATTTGCATTCCCCTCATCTGTGCCCTACTCTATGGGATGGAGTCAGGTTTCAGGACTCAGGAGGGTGTT GCATCTGTGGTGAGGACCAGTGATAGTAA	845
IGHV2-5_chr14:106494750-106494850	CATGATCAGTGTAATTCAGATGGCATTAATCTAAGGCTGGGCAAGTAGATTCTGAGTAGAAGTCTTTGCA GAAGTCATGATTATGAGGTCATGTTGGTCT	846
IGHV3-7_chr14:106518495-106518595	GCCCTTCACAGAGTCCACATAGTATTTCTCACTTCCATCTTGCTTTATGTTGGCCACCCACTCCAGCCCCTT CCCTGGAGCCTGGCGGACCCAGCTCATC	847
IGHV3-7_chr14:106518855-106518955	TGAGTCCTCTGTGCTCAGTGCTGATCACCAAGTGGAAAGGCCTTGGAGTCCAGGGCTAAGGCTCCTCTCT GAGACCTGCAGGGTCAGGGTTGGGTTGGTT	848
IGHV3-7_chr14:106518955-106519055	TTCATCAGTAGAGGGAGGGCCCTATTTGCATGTCTCCTACTATATAAGAAGCTCTAGTGGGATGCTGGAG GAATAGGCTGTACCCATATAAGAAGACGGT	849
IGHV3-7_chr14:106518970-106519070	AGGGCCCTATTTGCATGTCTCCTACTATATAAGAAGCTCTAGTGGGATGCTGGAGGAATAGGCTGTACCC ATATAAGAAGACGGTGCTCTCTGCAGAAGTTT	850
IGHV3-7_chr14:106519070-106519170	GCTGACAATGATGGTATTTGGAAAATATGCTGTCTTATGAAATTGTGCTGTGATAAACACTTTGCCCTGAT CACCCTATTACATTTTTTTAAAAAATGTGT	851
IGHV3-11_chr14:106573540-106573640	CAAACACAGAGACAACCTAGTCAGAAACTGCCACATATATTCACTGCTTATCTCACTCACGTCCACTCAAT GTCTCTAGTTCTCCATAAATCACCTTTTA	852
IGHV3-11_chr14:106573640-106573740	TAATAGCAACAAGGAAAACCCAGCTCAGCCCAAACTCCATGGTGAGTCCTCTGTGTTCAGTGCTGATCAC CGAATGGAAACTCCTGGGAATTCTGGGGCT	853
IGHV3-11_chr14:106573685-106573785	GTCCTCTGTGTTCAGTGCTGATCACCGAATGGAAACTCCTGGGAATTCTGGGGCTCTTCTCCCCAG AGCTGCAGGGTCTGGGCTCGGCTGGTTTT	854

IGHV3-11_chr14:106573785-106573885	TATCAGCAGAGGGAGGGCCCTATTTGCATGTCTCCTACTATATAGCAAGCTCTAGTGGGACGCTGGAGGA GAGGGCAGTGCCCAGAGCAGATGAGAGGGT	855
IGHV3-11_chr14:106573885-106573985	CCCGGAAAACACTGGAGGTAATCCTATCTCTCAGGAAAATATAACTTCAGATTATGTGATTGTGACTTGA TGATCAATTAGCAGTCATCATCTTATTTAA	856
IGHV3-11_chr14:106573985-106574085	TGTTTACATATTTGCAGAATATATTCAGTGCAAGTGTCAATGTTACATTTTTAGAGAAGATGAATTACATA CATAACAGAGCAGTTGTGCAATGTGTCCA	857
IGHV3-15_chr14:106610690-106610790	ACTCACACTTAATCTCTCTAGTTCTCCATAAATCACCTTTTAAAATAGCAGCAAGGAAAATCCAGCTCAGC CCAAACTCCATGGTGAGTCCTCTGTGTTC	858
IGHV1-18_chr14:106642110-106642210	GATGCTATTTAATAGCCCAATTCCTGACCCAGGATGAGAAAGAGCAAATACATGACACATGGACGACACA ATTGTAGAAGCTGAGGGTTCAAGCCGTAAT	859
IGHV1-18_chr14:106642210-106642310	CCTGTTAGAGGCCACGCATCCCCTACCCATCCCTGAACTCTGTGTTGACAGAGCTTCCCCCACTGGAGAAC AAGCTCCCCCAGGACACGCACCTCACTTA	860
IGHV3-23_chr14:106725295-106725395	GGCCCTTCACGGAGTCTGCGTAGTATGTGCTACCACCACTACCACTAATAGCTGAGACCCACTCCAGCCCC TTCCCTGGAGCCTGGCGGACCCAGCTCAT	861
IGHV3-23_chr14:106725395-106725495	GGCATAGCTGCTAAAGGTGAATCCAGAGGCTGCACAGGAGAGTCTCAGGGACCCCCCCAGGCTGTACCAA GCCTCCCCCAGACTCCCAACAGCTGCACCTCA	862
IGHV3-23_chr14:106725550-106725650	ACTGTTTCTCTCACTCTTTATCCATTCACACTCAATTTTTCTATTTCTCCATGAATTACCTTTTTAAAATAGCC ACAAGAAAAAGCCAGCTCAGCCCAAACT	863
IGHV3-23_chr14:106725650-106725750	CCATGGTGAGTTCTCTCTGTTCAGTCCTGATCACCAAATGAAAACACCTGAAAATCCCAGGGCTGGGCTC CTCTCTCAGAGCTGCAGGGTCAGGGCTGGG	864
IGHV3-23_chr14:106725780-106725880	TTTGCATATCTCCTACTATATAGTAAGCTCTGGGGTGAGAGGCCTTTGGAGATAGTGGGGCTCAGAGCAT GTCAGAATGTCCTCGGGAGATCTGTGATA	865
IGHV3-23_chr14:106725880-106725980	TTGAAAGCATTGGGAAATTGTGCTTTCCTATTGTCAGTTTGTTTTGTGATAAACTTAAACCTTAAAACCTA AAAATCTTATAATTTTGTAATTTTTATTT	866
IGHV3-23_chr14:106725995-106726095	GAGGTACCATAGATCTACATAAAACTGCATATTTTTAAAGTTAGCACCAATCATCTTTTATTTTTACATACG CAGAGAAACCATGGTATATAGTATCAATA	867
IGHV3-23_chr14:106726095-106726195	TTATTTCCATGTTAAAGATGAAAAATTATCAGCAAAAGCACAGGTGGGTTTTACAATGTCCCCAGTGCTC ACTTTTGGTCAGAGTGAGCCTGGGCATCTG	868
IGHV1-24_chr14:106732970-106733070	TCCTACATAAATGACAGTGTACACATCTTTCCATTGCTGTTTTACTCAATTACTCAACCCATTTTCTAAACAG ATTTAAACTTCATAAATCCTGTCATCTC	869
IGHV1-24_chr14:106733070-106733170	CTCAGCCTCAGCACAGCTGCCTCATTCCTCAGGGTTTCTGACGCTCTCAGGATGTGGGTTTTCACACTGTG TCTGTTGCACAGTAATACACGGCCGTGTC	870
IGHV1-24_chr14:106733185-106733285	GCTCAGCTCCATGTAGGCTGTGTCTGTAGATGTGTCCTCGGTCATGGTGACTCTGCCCTGGAACTTCTGTG CGTAGATTGTTTCACCATCTTCAGGATCA	871
IGHV1-24_chr14:106733275-106733375	TTCAGGATCAAAACCTCCCATCCACTCAAGCCCTTTTCCAGGAGCCTGTCGCACCCAGTGCATGGATAAATT CAGTGAGGGTGTATCCGGAAACCTTGCAG	872
IGHV1-24_chr14:106733375-106733475	GAGACCTTCACTGAGGCCCCAGGCTTCTTCACCTCAGCCCCAGACTGTACCAGCTGGACCTGGGCGTGGG TGCCTGTGGAGAGGACAGAGGAGTGGATGA	873

IGHV1-24_chr14:106733475-106733575	GACACCACTTAACTGGACCCAGTCCCCTCATCAGCCCTGGAACTCAGGATTCTCTTGCCTGTAGCTGCTGC CACCAAGAAGAGGATCCTCCAGGTGCAGT	874
IGHV2-26_chr14:106758470-106758570	GAGGGTGGGAATCTGGGAGAGCAAGGGGCTTCCCATAAGTGTTCTGATAAAAATCCTCTTTGTTTAGGGG GAAAGTGATGATTTTTTTTGAATGATAGAGA	875
IGHV2-26_chr14:106758570-106758670	ATACATCACCCAAACATTTAAAAATGTATTGTGTAAAGAAGTGTAAATGGCATCTCAGCCATTTACACAC TGCAAGACACACAGCTTATTAGTGTGCCTG	876
IGHV3-30_chr14:106791090-106791190	TGGTGAATCGGCCCTTCACGGAGTCTGCATAGTATTTATTACTTCCATCATATGATATAACTGCCACCCAC TCCAGCCCCTTGCCTGGAGCCTGGCGGAC	877
IGHV4-31_chr14:106805945-106806045	ACAATCACTTGAGTTCAGACACACCAGGATTCACTTAATGTTATTTTTAGTTCAGAACCTCTATCAGGTTT AGAGGGAATCGCTCTGTCCCAGGGAGTGG	878
IGHV4-31_chr14:106806045-106806145	ATCTTACAATAGCAAAAACGGTCTTAGAAAACCCAACATAATCTACAGCGAGACCTCAGCATGGCAAGCAA GGAATCACTAAAGCCACCAGGGAGATCCGG	879
IGHV4-31_chr14:106806120-106806220	CACTAAAGCCACCAGGGAGATCCGGATGCACTGATACGATCCAGAAACATAGCGAGTCCGGGAACTGAT GCGGACTTTGAGGCAGCCTCTTTTTTTTTTT	880
IGHV3-33_chr14:106815805-106815905	GATGGTGAATCGGCCCTTCACGGAGTCTGCATAGTATTTATTACTTCCATCATACCATATAACTGCCACCC ACTCCAGCCCCTTGCCTGGAGCCTGGCGG	881
IGHV3-33_chr14:106815905-106816005	ACCCAGTGCATGCCATAGCCATACTGAAGGTGAATCCAGACGCTGCACAGGAGAGTCTCAGGGACCTCCCAG GCTGGACCACGCCTCCCCCAGACTCCACCA	882
IGHV4-34_chr14:106829685-106829785	CTCGACTCTTGAGGGACGGGTTGTAGTTGGTGCTTCCACTATGATTGATTTCCCCAATCCACTCCAGCCCC TTCCCTGGGGGCTGGCGGATCCAGCTCCA	883
IGHV4-34_chr14:106829765-106829865	GGCTGGCGGATCCAGCTCCAGTAGTAACCACTGAAGGACCCACCATAGACAGCGCAGGTGAGGGACAGG GTCTCCGAAGGCTTCAACAGTCCTGCGCCCC	884
IGHV4-34_chr14:106829865-106829965	ACTGCTGTAGCTGCACCTGGGACAGGACCCCTGTGGAACAGAGAAACCCACAGTGAGGCCCTGGGATCAGA GGCAGCATCTCATATCTTCATATCCGCATTC	885
IGHV4-34_chr14:106829965-106830065	CTGAGACACTCACATCTGGGAGCTGCCACCAGGAGGAAGAACCACAGGTGTTTCATGTTCTTGTGCA GGAGGTCCATGACTCTCAGAAAGCACTTCC	886
IGHV4-34_chr14:106830125-106830225	GAGGATTTGCATGTGGTGGTGCCTTTGTATGGATAGGTAAAAAGGGATGAGGGAGGCCCCAGTCTTTTG GGCTCACCCTGGGAGGTGTATGCTGGCTGT	887
IGHV4-34_chr14:106830240-106830340	AGTTCTCTTCCTGTGGCCTCCCCTCACCAAACCCAGAGTCCTCTTCTTCCAGGTAGGAAATGTGCTGAAGG AGCTGGTCTGGGAGACAAGTGTGATCATG	888
IGHV4-34_chr14:106830315-106830415	GGTCTGGGAGACAAGTGTGATCATGGATCAAAGACAGATTTTGGAATACAGTTAATACTGTTCTACATTT AAAGATTCATATAACACCAACCATACACCC	889
IGHV4-34_chr14:106830415-106830515	AGGTCACCTAAATTGTCATTTACCCCTTCAGACATATTGAAACAGCTGCTGAGTGTAATAAATCACAGTGA ATTGAGACAAACCTGGATCCATGCAATGTG	890
IGHV4-34_chr14:106830515-106830615	TACTGTAGTTCAGAACATCCATCATGGTTAGAAGGATGCTACCTGTCCCAGGAAGTGGGTTATTTTTAAAT AGTACCTGAGAGCTGCCCTTCTGAGACCT	891
IGHV4-34_chr14:106830615-106830715	TTTGAAATTTGAGATTGTGTGAGATCTCAGGAGAAGGTAGTAGAATATATCTCCATCCTTCTCAATGTG TAACCCTGAGAATATGGCCTGACCTCTAA	892

IGHV4-34_chr14:106830715-106830815	ACATTTCTGTGTGAAAAGATGTACATTGGGGATAGCAGTGACAGCTTCAGATGAAAACTCTATAGTACAT CAGCACTGGAGGATAGTCTCATCACCAAGA	893
IGHV4-34_chr14:106830815-106830915	TTAGTGAAATTACCTTTCCTGGGAACCAGAGAGGACCTCTGTGAGCTCTACCCTCTGAGAGAACAAGGAA CTCTGGTTCTTCCCTGACAGGTCACACCTG	894
IGHV4-34_chr14:106831185-106831285	AACAAGTGGGCTGGCCTTCTATGAGACGACAGAGGGAAAGAGACAGACTCAATATCCAGAGCGAGGTGA GCTCCTTACCTACCTACCAGGTGGTCTCTGG	895
IGHV4-34_chr14:106831285-106831385	GCCATTTGTTTGAGCAGACCCAGAAGTACCTTCCTCACCCTCAGGAGAATTATGAACATTGAGAGAAACT GAGATACTTTTTTTATTTTACAGGGAATATT	896
IGHV4-34_chr14:106831385-106831485	TCATCGGCGTGTTTACATCTACCTGGGTGTGTACAGGGATGCTAGGATGTGCTCATACACAGAAGAGCAA GAATTATATTTCGTGGAAAGAAAACCAAAG	897
IGHV4-34_chr14:106831485-106831585	AGCTTCTGAATTTGTAGGTATTGTTTGCTGCAAATGTGTCAGGTCACTAGATCATGTTATGCTGCTAGAAG AAAAACTTCCCAACATTGTCATGGAGACA	898
IGHV4-34_chr14:106831585-106831685	AAATGCAAAACAGTAAAGATTCAACTGAGATTCCCTTGAAAATCACCAGTAATGAACAGGCCAAAAGAA ATCAACCATTGTGGAAAGAGTGGTCATTAAG	899
IGHV3-35_chr14:106846385-106846485	CCCAGTGTCACCTTACACATCCTGCAGGTCACCTCACACATCCACCAGGTCACCGCACATATACCCCACAT CACCTCAGACACACCCTGGTCACCTCATA	900
IGHV3-35_chr14:106846485-106846585	CATACGTCAGGTCACCTCACGCTCACCCAAGGTCACCTCACACATCCCGCAGGTCACCTCGTAAATCCCCC AGGTCACCACATACATGCACCAGTTCACC	901
IGHV4-39_chr14:106877715-106877815	CTCTTGAGGGACGGGTTGTAGTAGGTGCTCCCACTATAATAGATACTCCCAATCCACTCCAGCCCCTTCCC TGGGGGCTGGCGGATCCAGCCCCAGTAGT	902
IGHV4-39_chr14:106877815-106877915	AACTACTACTGCTGATGGAGCCACCAGAGACAGTGCAGGTGAGGGACAGGGTCTCCGAAGGCTTCACCA GTCCTGGGCCCGACTCCTGCAGCTGCAGCTG	903
IGHV4-39_chr14:106877930-106878030	GAACAGAAAAACCCACAGTGAGCCCTGGGATCAGAGGCAGCCTCCCATATCTCCATGTCTGCATCCTAGA AACACTCACATCTGGGAGCCGCCACCAGCA	904
IGHV4-39_chr14:106878030-106878130	GGAGGAAGAACCACAGGTGCTTCATTTTCTTGCACATGAGATCCATGACTCTCAGAAAGCATTTCCCTTAT GAGTTGGACCTGAATTTAAGGAAATGTGT	905
IGHV4-39_chr14:106878130-106878230	GGTGGCTTCCTGTGGGCGCCTAAGTGAGGATTTGCATGGGGGTGGTGCGTTTGTACGGAGCAGTGAAAAG GGATGAGAGGCGCCAGTCTTTTGAGCTC	906
IGHV4-39_chr14:106878230-106878330	ACCCTGGGAGGAGAATGCTGGCTGTGCCCTTTGAGAACTCAGTTCTCTTCTTGGGCCTCCCCTCTCCAAGC CCAGAGTCCTCTTCTTCCAGGTAAAGAGA	907
IGHV4-39_chr14:106878330-106878430	TGTGCTGAAGGAGCTGGTCTGAGAGATGAGTGTGATCCTGGATCAAGGACAGATTTTGGAATAGGGTCAG TACTGTTCAACCCTTAAAGATTCATATAAA	908
IGHV4-39_chr14:106878430-106878530	ACCCACCACACACCCAGGCCATCTAAATAGTCATTTACCCTTTCAGACACATTGAAACAACAGCTGAATGT AATAATGACAGTGACTTCAAACAATACTG	909
IGHV4-39_chr14:106878540-106878640	ATGTTTATTGTAGTTCAGAACATCCACCATGGTTACAGGGAAGCTCACTGTCCCTGGAAGTGGGTCATTTT TTAAAAGCACCTGAGAGCTGTCCTTCTGT	910
IGHV4-39_chr14:106878680-106878780	AAGGTAGTGGGACATATCTCCATACTTCTCAATGTGTGACCTTGAAGATGTGTCCTGCCCTCTAAACACTT CTGATTGAAAATATGTAGATTGGGGATTA	911

IGHV3-48_chr14:106994300-106994400	GTGGAAATGCCTTGGAATCCAGGGCTAAGGCACCTCTCTGAGAGCTGCAGGGTCAGGGTTGGGTTGGTTT TCATCAGTAGAGGGAGGGCCCTATTTGCAT	912
IGHV3-48_chr14:106994430-106994530	GGACCCTTGAGGAGTAGGCTGTACCCAGATAAGACGACGGTGCCCTGTAGAAGTTTGCTGGCAATGATTG CATTTGGAAAATATGCTGTCTTATTATGAA	913
IGHV3-48_chr14:106994530-106994630	ATTGTGCTGTGATAAACACTTTGCACTAATCACCCTATTTCATTTTAAATATTCATGTAAACTATGTTCTGT AGGAGACAATATTTTTCTCCATTTACAGA	914
IGHV3-48_chr14:106994545-106994645	ACACTTTGCACTAATCACCCTATTTCATTTTAAATATTCATGTAAACTATGTTCTGTAGGAGACAATATTTTT CTCCATTTACAGAAGTGGAAGTAAACCC	915
IGHV3-48_chr14:106994660-106994760	CTGTATGCATCTAGGAGCTCATGTCTGGGATGAGTGAAACCCCGGTATCTGGCCCTGTGCTCTTCATCACTG TCTCTGACATCCCCCCTAAACCAACTCCAG	916
IGHV3-48_chr14:106994760-106994860	GACAAAGCTGGATGTGTCTAGTGTTTTTATCAGAACCCACTTTCCGTAATAAGAGCATGTGTGGTTTTGCT GCCCTCCAGCACTCTCTTCTGAAAATATGGA	917
IGHV3-48_chr14:106994860-106994960	GAGAACTAGGATCCAGGCACATTAATTTTCAGGTACTTCTGACATTGAACTTATTTTTTCTATCTTTCTATT ACTCTTTCCTTGTCTAAGTTTCCATTTG	918
IGHV4-59_chr14:107083565-107083665	AGAGAGACCCACAGTGAGCCCTGGGATCAGAGGCACCTCCCATATCCCCATGTCTGGATCCCCTGAGATAC TCACATCTGGGAGCTGCCACCAGGAGAAGG	919
IGHV4-59_chr14:107083665-107083765	AAGAACCACAGATGTTTCATGTTCTTGCACAGGAGGTCCAGGACTCTCAGAAAAGTATTTCCCATGTGAGC TGGAACCTGAATTTAAGGAAATGTGTGGTG	920
IGHV4-59_chr14:107083790-107083890	ATTTGCATGTGGGTGGTGCCTTTGTATGGAGAGGTGAAAAAAGGAGGAGGGCCCCAGTCTTTTGGGCT CGCCCTGGGAGTAGGATGCTGGCTGTGTGCCC	921
IGHV4-59_chr14:107083890-107083990	TTTGAGAACTCAGTTGTCTTCTTGGGGTCTCCCCTCTCCAAGCCCAGAGTCCTCTTCTTTCAGGTAAAGAG ACGTGCTGAAGGACCTGGTCTGGGAGATG	922
IGHV3-64_chr14:107113405-107113505	CTGACAGTGGTGACCATGGTTGAGAACTTTTCATCTCCTCTGTGAGGATCAATCTGCATTTTCTGCATAGG AGAATAGGTTTTTCATATTAAAACAATCAT	923
IGHV3-64_chr14:107113505-107113605	TTTAAAAATATGTAGAAATGACCCTAGTAATCACAGAATTCCGAACTTAGGTTCAGTAGAGAAACTTTAA GAAGATGAAGTCCCACATCGTGACAGGAAA	924
IGHV3-64_chr14:107113820-107113920	TGGAGATGGTGAATCTGCCCTTCACAGAGTCTGCATAATATGTGCTACCCCCATTACTACTAATAGCTGAA ACATATTCCAGTCCCTTCCCTGGAGCCTG	925
IGHV3-64_chr14:107113920-107114020	GCGGACCCAGTGCATAGCATAGCTACTGAAGGTGAATCCAGAGGCTGCACAGGAGAGTCTCAGGGACCC CCCAGGCTGGACCAAGCCTTCCCCAGACTCC	926
IGHV3-64_chr14:107114095-107114195	TTCTCTCACTCATGTCCACTCACACTCAATATCTCTATTTCCTCATGAATCACCTTTAAAATAGCAACAA GGAAAACCCAGCTCAGCCCAAACTCCATC	927
IGHV3-64_chr14:107114195-107114295	ATGACTCTTCTGTGTTCAGTGCTGATCACCAAATGAAAACACCTGGGAATCCCAGGGCGGGGGCTCCTCT CCCAGAGCTGCGGAGTCAGGGCTGGGCTGG	928
IGHV3-66_chr14:107136755-107136855	TAGGGCACATCCTTCCCATCCACTCAAGCCCTTGTGCATGGGCCTGGCGCACCTAGTGCATAGAGTAACT GGTGAAGGTAGGTGTATCCACAAGTCTTGC	929
IGHV3-66_chr14:107136855-107136955	AGGAGACTTTCACTGATGCCCCAGCCTTCTTCATCTCATCCCCAGACTGCACCAGCTGCACCTGGGACTGG GCACCTGTGGAGAGGACACGGGAGTGGAT	930

IGHV1-69_chr14:107169645-107169745	GAAAACTTGTTCACAGTAGCACCTTCATGGAATGTTTGTATCAACGTTATAGAGTGTGGCCTTTTCCACTC TGTGAATTTGGCTTATATTACGACTCTTG	931
IGHV1-69_chr14:107169745-107169845	AATGGAATATTTATCTTAAAATTAGAGTATGTACTTGTTTCTACTGTTCTTTTTTTCTCAAATATATAACCC ATTTTGTAAACAGCCTTAAACCTAATAA	932
IGHV1-69_chr14:107169970-107170070	CTGCTCAGCTCCATGTAGGCTGTGCTCGTGGATTTGTCCGCGGTAATCGTGACTCTGCCCTGGAACTTCTG TGCGTAGTTTGCTGTACCAAAGATAGGGA	933
IGHV1-69_chr14:107170070-107170170	TGATCCCTCCCATCCACTCAAGCCCTTGTCCAGGGGCCTGTCGCACCCAGCTGATAGCATAGCTGCTGAAG GTGCCTCCAGAAGCCTTGCAGGAGACCTT	934
IGHV1-69_chr14:107170170-107170270	CACCGAGGACCCAGGCTTCTTTCACCTCAGCCCCAGACTGCACCAGCTGCACCTGGGACTGGACACCTGTG GAGAGGACACAGGGGTGAATAAAATCCTCT	935
IGHV1-69_chr14:107170220-107170320	CCTGGGACTGGACACCTGTGGAGAGGACACAGGGGTGAATAAAATCCTCTTTAACTAAACCAGGATCCCT TCCTCAGCCTTAGGACTAGGAAGCCCCTTA	936
IGHV1-69_chr14:107170320-107170420	CCTGTAGCTGCTGCCACCACAAAGAGGAACCTCCAGGTCCAGTCCATGGTGATGAGCTGTGTGCTCCCAGGG GCTTCTTCAGAGGAGGAATGTGGTTGTTAT	937
IGHV1-69_chr14:107170420-107170520	GTGATGCTCTCAGGGCACCAATATATCTATTTATCTCAGAAGACCTCAGGTTATTTGCATATGCATGAG GCAGGGTATTTCACAGCTCAAAGCCTGAT	938
IGHV1-69_chr14:107170475-107170575	TTTGCATATGCATGAGGCAGGGTATTTCACAGCTCAAAGCCTGATCTAGGATGAGAAAGAAAAACACAGAT GCCACATCAGCTGTACAAGTGTGGGATGCT	939
IGHV1-69_chr14:107170660-107170760	CAGAACAAACCCCAACCCCAGGATGCACTCCTCACTGTGAACCCACATTTTATTGGCCTAAAGATTACCTG GGTTTTTTGTGGGACCATTGCTGTCTCTG	940
IGHV1-69_chr14:107170760-107170860	ACATTGAGCAGGCACCTAGACCCATCCTGGTCCCATTAGGAACACTCAGAGCTCACTGGTAACACTGAAA AGGTGGCCACTCGTTACCCTACATGAGTGT	941
IGHV1-69_chr14:107170860-107170960	CCAGCAGGACCCATGGAGAGTTCTGAGATCTGCTGGGCACTCCCAAGACAGGGTCCCCAGCACTTTCCTG AGGGTCCTGACCTCCCAGGTCCTTCAGTGG	942
IGHV2-70_chr14:107178305-107178405	TTATCCATTTCTATGTGTTCTTTTGAAAATGTCTACTCATGTCCTTTGCTCATTTTAACGGAGTTATTTGGT TCTTGTTGCTGTTGTTGTGTAGAGTTG	943
IGHV2-70_chr14:107178415-107178515	TTGCAAATTCTTCATATTAGTTCCCTGTCACAGGCAAAGTGTGCAAAAGTTTTCTGTCATTCTGTAAATTG CGTATTCACTCTGTTGTTGTGAAAAAAAT	944
IGHV2-70_chr14:107178515-107178615	TATTTAGGTTAATTAAATCTCATCTGTCTATTTTTTTTTAGGTAGCAGGACCTTTCATGCTGAATCTTTGTC AAACAGGATACAGCTTTCTGCTTGCATGA	945
IGHV2-70_chr14:107178615-107178715	ACCACTAACAGGGGACATGCCATTTATTAGTAAGAAAAAGGAGGAAAACAAGGCTCTGAGTCAGATGG GGATGGGAAACGCACGCCCTGGGCAGGAAAT	946
IGHV2-70_chr14:107178715-107178815	GGCATCTCAGCCACACTATCCTGTTCTGCAGAAGTGGGGAGGGAGCACCACTGAAAAACACCTGGGTTCT TGTACAGGAAGCGCCCTGGGCTGTGTCTCT	947
IGHV2-70_chr14:107178815-107178915	GTGGTATCCGTGCACAATAATACGTGGCTGTGTCCACAGGGTCCATGTTGGTCATTGTAAGGACCACCTG GTTTTTGGAGGTGTCCTTGGAGATGGTGAG	948
IGHV2-70_chr14:107178880-107178980	ACCTGGTTTTTGGAGGTGTCCTTGGAGATGGTGAGCCTGGTCTTCAGAGATGTGCTGTAGTATTTATCATC ATCCCAATCAATGAGTGCAAGCCACTCCA	949

IGHV2-70_chr14:107178980-107179080	GGGCCTTCCCTGGGGGCTGACGGATCCAGCTCACACACATTCCACTAGTGCTGAGTGAGAAACCCAGAGAA GGTGCAGGTCAGTGTGAGGGTCTGTGTGGG	950
IGHV2-70_chr14:107179080-107179180	TTTCACCAGCGCAGGACCAGACTCCCTCAAGGTGACCTGGGATAAGACCCCTGTGGAGAAGACATAAGAA GATGAAGCCCACACAAAGGAGAGAATAGATTT	951
IGHV2-70_chr14:107179130-107179230	CTGTGGAGAAGACATAAGAAGATGAAGCCCACACAAAGGAGAGAATAGATTTTTTGCTTCTGAAGTACTACC TGACCACAGCACTCACAGGACGGGACAGTC	952
IGHV2-70_chr14:107179230-107179330	AGTAGCAGGAGCGTGGAACAAAGTATGTCCATGGTGGAGAGCAGGATTCACTGAGCGAGGCCCTGTCCT CGTCTTTTGAACCCAGGGGAGGGGTGGAGCTG	953
IGHV2-70_chr14:107179330-107179430	GTGGAGATTTGCATCCCCTCATCTGAGCCCTACTCTATGGGGTGCACTCAGGTCTCAGGACTCAGTAGGG GAGTGCATCTGTGGTGAGGAGCAGTGAGCC	954
IGHV2-70_chr14:107179360-107179460	TACTCTATGGGGTGCACTCAGGTCTCAGGACTCAGTAGGGGAGTGCATCTGTGGTGAGGAGCAGTGAGCC CTCAGGTGTGGGGGTCCACGTGTGCTCTCC	955
IGHV2-70_chr14:107179460-107179560	ATCAGGGAATCTATCTCATTTCAGCACCATGGCTCTCAGTCAAGTCTTGACGCTCCTGCTTCTACAGACAG GATCTTCTTCGATGCTCCCCGCACCGGACA	956
IGHV2-70_chr14:107179560-107179660	TGCAACCTTCTGGTTTTAGTCCTAGAGGATTAGAGTAGAAATCAAGAGAGCTGCCGTTCCTCCTCCCTTCA AGAATAATGATGGTGGGCATCTGGGGGGC	957
IGHV2-70_chr14:107179660-107179760	AAGGGGCTCCCCACAAGCATTCTGATCAAAATCCTCTTTGATTATGGGGAAAAGTGATGAATTTGTGTAA AAAAATTGGAGAGAATAAATAAGAAAATAC	958
IGHV2-70_chr14:107179760-107179860	AGTTACAAGTAATTATGTAAAGAAGTGTGTGCTTAGCAGTGTGTGTGCACACAGCTGCATTCCTAGAGGC ATGTTCCATGAAAAATCGATGTTGTCCTTG	959
IGHV2-70_chr14:107179860-107179960	TGCCCCGTCAGTTCTGTGGAGAGAGTAGACTGCATGAATGACTTCCCTTTTCTCAGCCCATGAATGAGCG GATGCTTTGGACAAGGGAATTGGAAGACTC	960
IGHV2-70_chr14:107179960-107180060	CTGAGGGAGCAGCAGGCTGACTGTTGCAGCCTTGCTCTGCACCTGCACTGGATGTGGTCTCTGTGCTCAT AAGGCCGTGGAAACTCATCAATCCAGGTTC	961
IGHV7-81_chr14:107258910-107259010	CAAAAAGGGGTTAAATGATTTTGGAAAAGTAAGTAGAAAATAAAAGAAGGAGGGAGTAAGAGCGGACA GAAGGGAGGGAAGGCAAGCAATGATGAAC	962
IGHV7-81_chr14:107259010-107259110	TGTGTAAAATTTTCACTAATTAAAAGACTATTATATTGAAGAGGTGCCTATTAGGCAGCCTTTTGATGTTA ACCATGTAATATACACCATGAACAACCTT	963
IGHV7-81_chr14:107259100-107259200	GAACAACCTTGTAGAACACACAAGAGCCCCCTCAGAGAACTGGATGGGTCAGGTCTCCCATCCAGTTGCC TTAGGGGTTAGGAACGCTCCCATGTTGTTC	964
IGHV7-81_chr14:107259200-107259300	TCTGGTTTTTGCTCCTGAGGACACAAACAGCCAGTGTTTCCTCCCCGGATGAATAGAGAGGCCCCTGGGG AGGGTGTGTCTGGCAGCTCACTCTGCACCT	965
IGHV7-81_chr14:107259235-107259335	GTTTCCTCCCCGGATGAATAGAGAGGCCCCTGGGGAGGGTGTGTCTGGCAGCTCACTCTGCACCTGCACC GCGGAAGGTTTTAGATGGTCCCTCTCACAC	966
IGHV7-81_chr14:107259335-107259435	AATAATACATGGCGGCGTCCGAGGCCTTCAGGCTGCTCCACTGCAGGTAGGCGGTGCTGCTGGAGCTGTC GGCTGAGATGGTGACGTGGCCTTGGAAGGA	967
IGHV7-81_chr14:107259435-107259535	TGGGCTGTATCTGGTATCAGAGTTCCCAGGATAGATGCTCCCCATCCACTCCAGTTCTTTCCCGGGCATCT GGCGCACCCAGTGGATCCAGTAGCTGGTA	968

IGHV7-81_chr14:107259555-107259655	ACAGGAGATCCTCAGAGACTCCCCGGGTCTTTTCACCTCTGCTGCAGACTGCAACAGCTGCACCTCGGCA AAGACACCTGTGTGGGAGACACAAAATTTG	969
CHTA_chr16:10971440-10971540	GTGTCTGGAGTATGAACCATGTATCAGCACCGAAAGGTTCTAGAAGTCAGACTTTCGGGCAGTGTGTCAC TAACTCTCAGCATGCTGGCCTGGCTCGGCC	970
CHTA_chr16:10971540-10971640	CACAGCAAGGTCTTCTCGCCTCCCTTTGGGTAAATACTGAGGGGTGCCTCTGCAGGACGGGACCTCTGCC AGACTCCACTCCATACCCAGAGAAGCAGGG	971
CHTA_chr16:10971640-10971740	AAACCAAAATTGGAGTCAGCCTTGAGGTGTAGCTGTTGAGCCCTCAGCAGCTGGGGAGAGCTGGCGGAT GCTGCCCTCCCCCCCAGTTTCCTAATGGTGTT	972
CHTA_chr16:10971740-10971840	GTTTAAAAAGGGTCAGGGGACGGGGAACAGATGGTGGGAAGAGCACAGTGCAGACACCTGGCACCGGC TCTGAAGGCAGCATGGCAGCTACACCGTTGG	973
CHTA_chr16:10971840-10971940	CTGGGAAGGGTGTGCCCCTGAAGAAGTCGTTTACATTCTCGAGTCAATTTTCCTGGAGTGTACAATGGAC CTGTGGGAAAGCCTGTATGAAAGGGTAATG	974
CHTA_chr16:10971940-10972040	ATGAGGGACCTAGCACAGTGTCCAATATTTTATAGGAACTGGAATTGAGCTCATAGGAGCTCAATTTTAT TGGCATTGCTGTTGTTGGATGGTTAAAGGG	975
CHTA_chr16:10972040-10972140	GTGGTATCCCTTTTCTCAGACTCCCCTGAAATGTATGGTTTTGCTTTGAACCCAGAGACTGATGACAGGTCT GCCGGTGTGGTTGGGTGCAGCCTTAAGTT	976
CHTA_chr16:10972140-10972240	GCTACGGGAAAGTGTTGGAGGGGGAGAAGTCAGAGGTAACCTTGCCCCCTCCCTCAATTCCAGATGAGGA AATTCAGGCCTGAAAAGGGAAAGTGACCAC	977
CHTA_chr16:10972240-10972340	CTCAAAGTCTCATGCCTTGGAGGACCCAGCAGGAATCCAAGACCTCTGAAAAGGACCGGCAGGGCTCTTG CCACGGCTGGGGGTGTGGTCATGGTAACAC	978
CHTA_chr16:10972340-10972440	AGGTTTTCCATCCATGGAAGGTACCTGAGGGATTTTCTCTTCCTCCCTAGGGCCAGCATCAGAGGAGTGA ATAGCTCAGTTAGCTCATCTCAGGGGCCAT	979
CHTA_chr16:10972440-10972540	GTGCCCTCGGAGGTGGTTTGCCACTTTCACGGTTGGACTGAGTTGGAGAGAAACAGAGACCCACCCAGGG GTGGGGACAAGCTCCCTGCAACTCAGGACT	980
CHTA_chr16:10972540-10972640	TGCAGATCACTTGCCCAAGTGGCTCCCTAGCTCCTGGCTCCGGGGCCTGGGACTCTCCCCGAAGT GGGGCTGGCCACTGTGAGGAACCGACTGG	981
CHTA_chr16:10972640-10972740	AGGCAGGGACCTCTTGGATGCCCCAGGCAGTTGGGATGCCACTTCTGATAAAGCACCGTGGTGGCCACAGT AGGTGCTTGGTTGCTCCACAGCCTGGCCCG	982
CHTA_chr16:10972740-10972840	AGCTCAGCGCTGCAGAAAGAAAGTGAAAGGGAAAAAGAACTGCGGGGAGGCGGGGAGGTAGGATGACC AGCGGACGAGCTGCCACAGACTTGCCGCGGCC	983
CHTA_chr16:10972840-10972940	CCAGAGCTGGCGGGAGGAGGCCACCAGCAGCGCGCGGCGGGAGCCCGGGGAACAGCGGTAGGTGAC CAAAGTCTCCTCTGTAACCCCTAAGGTCGGGC	984
CHTA_chr16:10972940-10973040	TGAGAATCGAGGCTCCGAGACTGTCAGCTACTTGCTCAAGGTCACACAGCAAGTCTGGGAGGATGGGGG GATGGAATATGCAAAATGTAGGGCCGGGAAA	985
CHTA_chr16:10973040-10973140	CACCTCGTTTCCAGCATCCCCCGCAACGACTCTGCGCGGGGAACCAGGAGCCGGGAACCCGGAGCTTGGCTT GCTGTGCCCAGAGCTCCGGGGCCGTGGGCG	986
CHTA_chr16:10973140-10973240	GGTGGCAGGAAAGCCTGGCGGCAGCTTCTGCAGAGAAGCCGGAGCGCAGACTGGGAGCGCGGAGGCAGAC ACACTCCCCCGGCCACCCTTGGCCGACTCCG	987

CIITA_chr16:10973240-10973340	CGCGCCCGGGATCCTGCAGAGGTGCGCGCCCTTCTTGTACGCCAGACTTTGGACCAGGGCCGCCGTTCCC	988
	TGAGCTTCACTTTCCCTGTTGGGTCATATT	
CIITA_chr16:10973340-10973440	CCATCTCTAACTCTGGAATCTTGGGTATTGGGCTCTCCAGGCGGGGGGCCCTGCTCAGGGAGGCAGTAGG	989
	GAGCCAAACCTTTAACCAGAGGATGGGATA	
CIITA_chr16:10973440-10973540	AGTCCTCAACTCTCGTTGAACATCTTGGCGAAGGTGTGTGTTGTTGGGAGGGGTGGGGGAGGGATCCCCC	990
	CGGACTGAACCGATCTCTCTTGATCTCTCACT	
CIITA_chr16:10973540-10973640	TCTCTACCTCGCTTTGGGGCCCTGAGTCACACCCTCTAAGGAGAGAGGCTAAAGCGCCCCGGAAAGCCAG	991
	CGTGCGAATGCCGGGGTGGGAGTGGGAGAT	
CIITA_chr16:10973640-10973740	TGGATCTCCCTGGGGTCCAGGAAAGCCGGAATCGGAGCCACCATGCTTAGTCTGGAACTCTTAAA	992
	AGCCGCGGTCCTCCTGAGTCCCACAGCCCC	
CIITA_chr16:10973740-10973840	TCTCCACCCTAGGTGGCACAGGAGAGGTGGCAAAAAGCCTAGAAGTTCAAGGCATGGCTCCCTCCCCAGCC	993
	GCAGCCTGGAGTGTCTAACTTTGGCAGGAA	
CIITA_chr16:10973840-10973940	GTCTTCCGTTTCTGCTCCCCACTCCAGAGAAAAAATAAATAAATACTTCTCCGGAGTGAGATTAAGGAAA	994
	CAGGTACTTCTTCCTCTTTGGAGAAAGAGGA	
CIITA_chr16:10973885-10973985	CTTCTTCCGGAGTGAGATTAAGGAAACAGGTACTTCTTCCTCTTGGAGAAAGAGGAGGCCAAAGGAACTTGA	995
	CTCCAACAAATGATCCACCTTGCAAACCCCC	
CIITA_chr16:10973985-10974085	GGCTCCCTTAGGGGATGACCTGGTCTCCAACAATCTCAGAGCGTTTGGAGGCAGGGTCTTTGGAGATGAC	996
	TGAGTGGGCGAATCCCAGGCTCCCCACACAT	
CIITA_chr16:10974085-10974185	GAACATCACCTGGGATGATCAACCTGTTCAGGATGTAGGTTCCCGGGCTCACCCCCAGGCCCGGTTGGCT	997
	AGGCCTGGGGTGAGGCTGAGATCCCTGCAGG	
CIITA_chr16:10974185-10974285	TTAAACCATCTATCCCAGGTGACTCCAATGTTCGTTTGTGGGGCAAAAGTCCCTCAAGTCAGAGAGACACTG	998
	GGAGGCGCTGATGTGGTCTCATCTCTTTAC	
SOCS1_chr16:11348520-11348620	CAAGAGGTGAGAAGGGGTCTGCGGCCTCGTCTCCAGCCGAGGGCGGGAGGCGCCTCGCCCCTACACCCAT	999
	CCGCTCCCTCCAACCCAGGCCGGGGAGGGT	
SOCS1_chr16:11348620-11348720	ACCCACATGGTTCCAGGCAAGTAATAACAAAATAACACGGCATCCCAGTTAATGCTGCGTGCACGGCGGG	1000
	CGCTGCCGGTCAAATCTGGAAGGGGAAGGA	
SOCS1_chr16:11348720-11348820	GCTCAGGTAGTCGCGGAGGACGGGGGTTGAGGGGGATGCGAGCCAGGTTCTCGGCGGCCCACGGTGGCCAC	1001
	GATGCGCTGGCGGCACAGCTCCTGCAGCGGC	
SOCS1_chr16:11348820-11348920	CGCACGCGGCGCTGGCGCAGCGGGGCCCCCAGCATGCGGCGCGGCCGCCACGTAGTGCTCCAGCAGCT	1002
	CGAAGAGGCAGTCGAAGCTCTCTGCGGCTGC	
SOCS1_chr16:11348920-11349020	CATCCAGGTGAAAGCGGCCGGCCTGAAAGTGCACGCGGATGCTCGTGGGTCCCGAGGCCATCTTCACGCT	1003
	AAGGGCGAAAAAGCAGTTCCGCTGGCGGCT	
SOCS1_chr16:11349020-11349120	GTCGCGCACCAGGAAGGTGCCCACGGGCTCGGCGCGCAGCCGCTCGTGCGCCCCGTGCACGCTCAGGGGC	1004
	CCCCAGTAGAATCCGCAGGCGTCCAGGAGC	
SOCS1_chr16:11349120-11349220	GCGCTGGCGCGCGTGATGCGCCGGTAATCGGCGTGCGAACGGAATGTGCGGAAGTGCGTGTCGCCGGGG	1005
	GCCGGGGCCGGGACCGCGGGGCACCGGCCGCG	
SOCS1_chr16:11349220-11349320	GGCGCGCGGGGCCGGCGGAGGAGGAAGGAAGGTTCTGGCCGCCGTCGGGGCTCTGCTG	1006
	CTGTGGAGACTGCATTGTCGGCTGCCACCTG	

IGHV3OR16-12_chr16:33523607-33523707	TTTAAAATCACCCAAATCAAAATAATTTTATCTTCATTAATAAATAATCATCAGAAGTTTAACTAATTTTT ACTTTATAATACTAGGTTTAAAAATTCTT	1007
IRF8_chr16:85933003-85933103	AATCTGAATGCCCAAGTCGTTGATTGTCGTTTGCCTGTTTCCAAAGATTGGTAGATAGATGCCTTTTTAAA AATCTCATTTTTCTTTAAATCTGGTTTAC	1008
IRF8_chr16:85933103-85933203	ATGGAAAACGTTAGGAGAGCTCATATAATGAACGGCAATAGCAACCCCTATCTTGAAACGCGCTCTATC ATCCCACTGAAATTCTACCACGTGGAATAA	1009
IRF8_chr16:85933203-85933303	TGCTTGGAGGGTCAGAGTTGTGGAACTGCCCAATAACCAGTCGTTACTGAGGGTTAGTTTGTGAAGGAGG GGACAGACTGCTTCTAAAATTCTGTTTAAT	1010
IRF8_chr16:85933303-85933403	GACAGTCAATTAAGATTTCTGAGTCTGGCTTGAGGGCCTTTGCTTCCATCACAGCCCAGTCGTCCTTGGCA AGAGAGTCTGTATATGGGCCACAGCTCAC	1011
IRF8_chr16:85933403-85933503	AAAAGCATTGTTTGAAAAAATTTATTGAAAGAACATTGTTTGTAAAATGAGTCCCAATACATAGGACAGA CTTTCCTAAGGTGAGATGTGTTACTTACCC	1012
IRF8_chr16:85933503-85933603	AGAGCTGTGAAAGGCTTTACGGATGGAAACTAGAGACTGAATTTTTCCAGAATTTTAAGAAGTCTCCCCAA CCAATGGCCCCCCACTTTCTTTTTTTAAAC	1013
BZRAP1_chr17:56408574-56408674	GGCGTGATCTCCGAAGCCCACAGTACACTCATCCATAAAGTAGGAAACACTACACCCTCCAGTGCTGTTA GTAGTGCTTTCTACTTTATGGGTGACTGCA	1014
BZRAP1_chr17:56408674-56408774	CTGTCTGTCTGTCCGTCGGCGTGTACTCTTCAGGCTGCCCAGGCCTCCTGACTCCTGCTCCAAGAGCCCCC CAGCCCTCCTTGTGGCTTCCTAAGATCCC	1015
BZRAP1_chr17:56408884-56408984	CCCTCTTCCCTTCCCCCTAAAGGCTCCACACCCATCCCCCCAGTTTCAGAGACACTCAGGTAGAGACTAGGG CCTCTGGAGGCCTCACCTTCAGTTCTGTG	1016
BZRAP1_chr17:56408984-56409084	AACCCCTGGCTGGCCGCTTCCAGCCACGCTAGCCACCCTCCAGCGTCCAAATGAGGCAGCCACACAGCTCCC CTGCCAAGGTCTTGGTCTCCAGTCCACCCC	1017
BZRAP1_chr17:56409084-56409184	AACCGTGAGGTCCTGACTGCCCAGAGCCTCAGTCCCCACCCTTCAGCCTCCCCACCAGCCCAAGATCCTGA CCCCCAGGGCCTAAGTCCCCAGCCTCCC	1018
BZRAP1_chr17:56409184-56409284	CAACAGCCCAGGGTCCTGACCCCCCAGGGCCTCAGGCCCTGGCCTCCCCACCAGCCCAAGGTCTTGAACA CACCAGGGCCTCAATTCCCAGCCTCCCCAC	1019
BZRAP1_chr17:56409284-56409384	CAGCTCAAGGTCCTGACTCCCCCAGAGCCTCAGTCCCAGCCTCCATAGCAGCCCAAGGTCCTGACCCCCCA GGGCCTCAGTCCCCAGCCACTCCACCAGC	1020
BZRAP1_chr17:56409384-56409484	CCCAAAGTCCTGACTCCCCAGAGCCTTGATTCTCGGCCTCCCCACCAGCCCAAAGTCCTGACTCCCTCACT GCCCTGCTGTTCCCCTGGCAGGAGCCCAA	1021
BZRAP1_chr17:56409484-56409584	GGCTATCCCAACAAAAATGGTGGCCATGTTGGGCGGAGGAAGAGGCTGGCGCCCCTTGAGACACTGGTCC CACTTCTCAGCCTCTCGCGTACCCTCTGCCA	1022
BZRAP1_chr17:56409584-56409684	TCCCCGCCTTACTCTCCAGCCCTCCTCCTTGGACACCTCTTTCCCCGCCTGGGGTCCCGGAGCCATTTTACC TTCCTTCACTAGAGAGGGTTTCAAGGCG	1023
GNA13_chr17:63010240-63010340	CTAAGATTTTCAAGAAGTTAAACGTAGAATTAAGATTGTTCTAATTCTGGTTGTAAACTGCTATTTTAAAA AACAAAACAAACAGAAAAACATCAAAAAACA	1024
GNA13_chr17:63010315-63010415	AAACAAACAGAAAACATCAAAAACACAAAAAAGATATTAAAACAGCAAGTCTTTTGTACATCACTGTAGCA TAAGCTGCTTGAGGTTGTCATGCAGAATAG	1025

GNA13_chr17:63010415-63010515	TATCCTTCACGTCACGGAAAACAAGGCGGATGTTCTCCGTGTTGATAGCAGTGGTGAAGTGGTGGTATAA GGGCTTCTGTTGCTGGTCCCGGCGTTTGTT	1026
GNA13_chr17:63010515-63010615	CCGGAAACATTCCACCAGGAATTTTTGGACGTCTCTTAAGCAGTGGGGGATCCCCCTTCAAATTCTAGGAAA TAGTCTTTGATGCTCACAAATTTGCACCTTC	1027
GNA13_chr17:63010615-63010715	TCCTCAAGCAAGTCTGTCTTGTTTAAGAACAGAATTATGGAGACATTGCTGAAAAACCCGGTTATTGACGA TTGTTTCAAAAATGTTCAGAGACTCTGTAA	1028
GNA13_chr17:63010715-63010815	GGCGATTGGTCAGTCGATCTTCCATAAGCACCTGGTCAAATTCACTTGAGGAAACAAGGAAAAGTATTGA TGTCACACTGTCGAAACATTCAAACCAACG	1029
GNA13_chr17:63010815-63010915	TTTCCTTTCTGATCTCTGACCACCTACATCAACCATTTTGAAAGGAACATTTTTTATTTCAAAGTCGTATTC ATGGATGCCTTTGGTGGGTCTTCTGGCA	1030
GNA13_chr17:63010915-63011015	AGCAGAATATCTTGTTGTGATGGAATATAATCCTGGAAAAGAAAAAACTTGTTTTATACCTATTAATCCCG AAGTAATGCGAATTTTTAATGGACTACTA	1031
43717_chr17:75447868-75447968	TGTAAATATTTGGCCAACTAAGCTGAGTGGCTAAGTTCTCCTGCTGCCCGGAGCTTCTTGGAACATGTTTC CTTTTCGCAAGGGGTTTCCCTGGCTTCCA	1032
43717_chr17:75447968-75448068	GGAGGGCCAGGAAGAAATTCGAATTGGCCACCGCTTTCTCTAAAATCACTCCGCTCAAGTTATCACCCCT CTGGGCTCCCGAAGACCGGCTGGCTGGAGG	1033
43717_chr17:75448068-75448168	CTGGAGATAGTCTCAATGCTCGAAATGCCGTAACCGAAGCTCCCCGCGGCGCCGGCACTGGGATCCAGGG AGCTGCTGCTACAGCCGCAGCTCTGGATTCC	1034
43717_chr17:75448168-75448268	TGGATGTGTTGATATGTGCAGGGCGTTCCTGGGAGGAGGGAGCGGGGAGGGTGCTGCTGGCGGGGCTG GTCTGCGTGTGCTTTGCTTCTCTACAATGGC	1035
43717_chr17:75448268-75448368	ATGCTGCGTGTCGGCCATGCAGAGGCATGTCAGTGAGCAGGGGCTGAGGGATCTCCCTAACGGACCTGCT TTCAGAGGGTCTTTTCATGCTGGGAGAACC	1036
43717_chr17:75448368-75448468	CCAGAGACTAAATCATGCAGCCAACGGGGTGGTCCCCGGCCTCAAAGCAGGGAGGGGCGAGGAGCTTTG TAGGCAATGCCATCTGCTCCTGAAACGCCGT	1037
ADCYAP1_chr18:1477565-1477665	CAGCCTCCTTAGTAGCTACCGCCTTAGTAAGTACCACTTAGTAAGTACCGCCTTAGTAAGTACCACTTAGT AGCTACCTCCTTAGTAAGTACCACTTAGT	1038
ADCYAP1_chr18:1477665-1477765	AAGTACCTCCTTAGTAAGTACCACTTAGTACTACCACCACGCCTGGCTAATTTCGTATTTTTTTTTTTTAG TAGAGACGGGGTTTCTCCATATTGGTCA	1039
AC012123.1_chr18:30349775-30349875	AGGTCAGGCGCGCATACTGCATGCGGGTCTCGCGGTCGTGCTCCAGCCACACGGACATCTGGAAGAGCG CCAGCTCCGACTCCACGGGGGGCGGCAGCG	1040
AC012123.1_chr18:30349875-30349975	AGTCCAGCAGGGCGCGCATCTCCTCGAAGTTGAGCAGCAGCACATCCTCCACCAGGTACTTGTTGGCCAG CTTCTTGGTCTCCTCCAGGCCGTGCAGCGC	1041
KLHL14_chr18:30349975-30350075	GGCGATCTTGCACACCTGCTTGTAGTTCTGCACCGAGATCTGGTCGTTGAGGAACTGCACGCAGAGCTTG GTGACCTGGGGGATGTGCAGGATCTTGCTG	1042
KLHL14_chr18:30350075-30350175	ACCGACAGCACCTCCTCCACCGTGTCCAGGGACAGGGTCACGTTGGCCGTGTAGAGGTACTCGAGCACCA GGCGCAGCCCGATGGACGAGCAGCCCTGCA	1043
KLHL14_chr18:30350175-30350275	GCACCAGGTTGTTGATGGCCCGGGGGCTGGTCAGCAGCTTGTCGTCGGGGGAGGAAGGAAGGAGTCCCGG GCTCCTCCTGCCGGCGGCGGCTGCTGCTG	1044

KLHL14_chr18:30350275-30350375	TGACGGCTGCTGCTGCGGCGGCTGCTGCTGGTCCTTGGGGGCCCCCAGGCCGTCCTGGCCGCCGACCCCT CCCCCGAGAGGGGGGTGGCTGGAGAAGAGC	1045
BCL2_chr18:60806264-60806364	GAGACTTCAGCCGGAGCTGGCTATTCCAGAGATGGACCTCAGAGGATTCCTTAGTCTAATTACCTTCTGG GCTGGGGTAGAAGATGGTGTCTGGAGGGAA	1046
BCL2_chr18:60806364-60806464	GCACAGAACCAAGTTCCCTACTGCCGCACTAGCTATGCAAATACTGCAGGGCACCTGTGGGCTCATGTCC CTCCTGCAAGAAGGTGTGGTCAGTCCAGTA	1047
BCL2_chr18:60806464-60806564	ATTCAAAAGACGTACTTCTGAAATAGGTGGAGAAATGCATTTATAGCAAAAAAGTGCTAAAAATATGTTAA TAGTTATGCTATTTGGTTCACCAGGTTAGT	1048
BCL2_chr18:60806564-60806664	GTAATAAACCATAACAAGAGAGACTAAAGGCCGTATCTATATGACCTTGAAATCTCATCTTCAGCGGGCT TATTCATTCAGTAACCAAACTATTTTTGTA	1049
BCL2_chr18:60806664-60806764	AGGTGCTGAGTATTTAGCTTAAAGCTAAATAAGACACATGCCCTGCCCTATAGTAACTGCTTGGTAATATT CCCAGTGGCTTCCATGGGCCTGATAATTT	1050
BCL2_chr18:60806764-60806864	TCTTAGTACTGAATTCAAAGCACTTTGTGTCTTGTCTGCAGGCCCATTTGCCCAGCAGTGGCCTTGCCAGG AGAGAACAGGCCCATGCTCCTGTCCTCAT	1051
BCL2_chr18:60983784-60983884	CAAACAAACAATTCAAGAAGAGGATTTAAATTTTAGAAATTTAAATTGGGGCATTTTAGTTAATCTTACTT TTAAACACCAAACAGTGGCATCAATATTT	1052
BCL2_chr18:60983884-60983984	TGTCAACTTTGGTCAAATAAGATCAGATGTTCACATCAATCATCTACTTTTCTTGGCCTTTTCTCTATTTGG CCTCCTAGTATGAGCACACTTTGTAAAA	1053
BCL2_chr18:60983984-60984084	TGTAATAAAAACATGTGGTGTGCTTCTTGACATCTAATCCACTTGCAGTAATTTCTAGGCTTTTTGCTCCT GTTAGGTCCTATAAAATAATGACATTAGT	1054
BCL2_chr18:60984454-60984554	ATAGATACCTAGATGCAAATTTTTTTTCAGCCGACCACACAAAATTAGGTCCACTCTGAGTGGTGAAAAACAA AAGATTCTAACATTCTAGCAAACTGGTAAA	1055
BCL2_chr18:60984554-60984654	CCATACACAAATTATAGAATACAAAGAATGCAGCCGATGCAAATTCTGTCACTGACAAGGTAGCAAAGCC ATAGCCTGATACTCCTCAGGACACCTCATC	1056
BCL2_chr18:60984654-60984754	ACGCCCACTGGGAACATGGCACACACTGGAGATTCCAGTCCAAGGACTTTGGAATGTCAACTTAGCTCTT TACAAACACAACTAAGTTTTTTCAGGGAAAA	1057
BCL2_chr18:60984754-60984854	AGACTTACATTGGTTTTCCTCTTTTGGAAAATTTTTACCGATTGATGATGCCCTTGGTCTTCTGTGGAGTCT ATTCTTCTAATCGGGTTGTTCTCCAATTT	1058
BCL2_chr18:60984854-60984954	TAGTGTACAACGGGGCTTGTTTTCAGGGGAGCTTGTTTGGGATGCAGACTGTCAAGACCCAACCTGGTATCT GGTTCATAAGCAGTCCCTGAAACCTCCCTC	1059
BCL2_chr18:60984954-60985054	CGGTTCCAACAAGCTGCTCAAGCCAGGAAACGGTGGTCCTGGGGACTCCTGGACCTTCAGCTTGAGAAAC ACTGAAGGGGTACCATTTACCACCACATCC	1060
BCL2_chr18:60985054-60985154	TACTGGATTACAAACGCTAGATCTTTGGATCTCCACGACTAGCAAGCAAGTTAAAGACTTTTAGATGGCA GGCGTTATCGGTCAGGTTGGGAGTGAACGC	1061
BCL2_chr18:60985154-60985254	TTTGTCCAGAGGAGGAGGTAGGGACGCCGGGAAGCAACAACTCTGATTTTATTTCGCCGGCTCCACAGCC TCCCATTGCCCCAGGAGCCCACCCGCACTC	1062
BCL2_chr18:60985254-60985354	CAACCCCCGCATCTCGGACCTGTGGCCTCAGCCCAGACTCACATCACCAAGTGCACCTACCCAGCCTCCGT TATCCTGGATCCAGGTGTGCAGGTGCCGG	1063

BCL2_chr18:60985354-60985454	TTCAGGTACTCAGTCATCCACACAGGGCGATGTTGTCCACCAGGGCCGACATCTCCCGGTTGACGCTCTCCAC ACACATGACCCCCACCGAACTCAAAGAAGG	1064
BCL2_chr18:60985454-60985554	CCACAATCCTCCCCCAGTTCACCCCGTCCCTGAAGAGCTCCTCCACCACCGTGGCAAAGCGTCCCCGCGCG GTGAAGGGCGTCAGGTGCAGCTGGCTGGA	1065
BCL2_chr18:60985554-60985654	CATCTCGGCGAAGTCGCGGCGGTAGCGGCGGGAGAAGTCGTCGCCGGCCTGGCGGAGGGTCAGGTGGAC CACAGGTGGCACCGGGCTGAGCGCAGGCCCC	1066
BCL2_chr18:60985654-60985754	GCGGCGGCGCCGGGGGCAGCCGGGGTCTGCAGCGGCGAGGTCCTGGCGACCGGGTCCCGGGATGCGGCT GGATGGGGCGTGTGCCCGGGCTGGGAGGAGA	1067
BCL2_chr18:60985754-60985854	AGATGCCCGGTGCGGGGGCGGCCCCCGGGGGCGCGGCGCCCACATCTCCCGCATCCCACTCGTAGCCCCT CTGCGACAGCTTATAATGGATGTACTTCAT	1068
BCL2_chr18:60985854-60985954	CACTATCTCCCGGTTATCGTACCCTGTTCTCCCAGCGTGCGCCATCCTTCCCAGAGGAAAAGCAACGGGG GCCAACGGCACCTCTCGCCCCAGCTCCCAC	1069
BCL2_chr18:60985954-60986054	CCCACGGCCCCCAGAGAAAGAAGAGGAGTTATAATCCAGCTATTTTATTGGATGTGCTTTGCATTCTTGG ACGAGGGGGTGTCTTCAATCACGCGGAACA	1070
BCL2_chr18:60986054-60986154	CTTGATTCTGGTGTTTCCCCCTTGGCATGAGATGCAGGAAATTTTTATTCCAATTCCTTTCGGATCTTTATT TCATGAGGCACGTTATTATTAGTAAGTA	1071
BCL2_chr18:60986154-60986254	TTGTTAATATCAGTCTACTTCCTCTGTGATGCTGAAAGGTTAAAGAAAAAAACAAACTAATAAGTAAAAAA TCAGGTGCGTTTCCCTGTACACACTGAGTG	1072
BCL2_chr18:60986254-60986354	AAAGCAGGGCATACACACTACAAGTAACACGGCTAAAAAGAATGTATTAAGCTGCCTGGAAATTAAATTT ACTCGAATGCACTTTAAGTAAAAAAATCTCA	1073
BCL2_chr18:60986354-60986454	AAGGTTTCCATTGAAAGTTACATTAAACCAATTTCCTGTGCAGAGAACTTACTTGTATTTTTTAAGTACAG CATGATCCTCTGTCAAGTTTCCTTTTTGT	1074
BCL2_chr18:60986454-60986554	AAAACCAAAACAAATGCATAAGGCAACGATCCCATCAATCTTCAGCACTCTCCAGTTATAGCTGATTTGA AACTTCCCAATGAATCAGGAGTCGCGGGGA	1075
BCL2_chr18:60986554-60986654	GAGGGAGTAAAAATTAGGAGGATTTCCAGATCGATTCCCAGACTTCTGCTTCACAGAAATGTCAATCCGC AGGAATCCCAACCGGAGATCTCAAGAGCTC	1076
BCL2_chr18:60986654-60986754	GAGAAAAAAAAAAGGCAGCGGCGGCAGATGAATTACAATTTTCAGTCCGGTATTCGCAGAAGTCCT GTGATGTTTTCCCCTTCTCGGCAATTTACAC	1077
BCL2_chr18:60986844-60986944	TGAAGGAGCCGGGGGACGGAGGCAGGAATCCTCTTCTGATTAAACTCCGAACAGCAAATGCATTTTCCGAAA AAGCTGCTGGATAAATGAAGGCAGGACGCG	1078
BCL2_chr18:60986944-60987044	CCTGGCCCGCCGGTGCCGAGCGCTAGAAGCCCGCGCTGTGTGTGGTGCGGCGAGGGGGTGGGGAGAAGGA GGTGGTGGGGGAGGGTTTTATTTTTTCCCTC	1079
BCL2_chr18:60987044-60987144	TTTTCCTAAAAAGGATGACTGCTACGAAGTTCTCCCCCCTGGACCCCCTCTTCCGCTGCACCCCACCGGCG CACCCCGCCTCCGGGCTGCGCACCCTTTC	1080
BCL2_chr18:60987964-60988064	GTGTGTGTCTCGCCTGGACCTTTTCTAGCCGTGTATGTGGGAGTGTGTGTCGCCTGGACCCTTTCTAGC CGTGTATGAGAGTGTGTACACGCGCCTAC	1081
BCL2_chr18:60988064-60988164	ACACACACACGTTGTGTTACCGGCGCTCGGCCGCGGGGGAAGACCCAGGCCAATGCCGCCCCCCACCGC CCCCAGCAGTGGGACCTCAGCGCTGCCCTG	1082

BCL2_chr18:60988164-60988264	CTGTGAAGACAGGTGACTCTGCACGTTTTAAGCAATGTCTAGGGACGCCCCGAGCGTGGTGTTTACTTTC AAGTAGCTTCCTAGGTGTCCGCGCACTACA	1083
BCL2_chr18:60988264-60988364	CACGCACCGCGCATCCCCCGCCCGTGTCCACCTGAACACCTAGTCCGTGGTGGCCCAGGCCATGCAGAACTCAGC GCTCCAGGGAAGGGGTTTATCAAGGGCTTT	1084
BCL2_chr18:60988364-60988464	ACGACAGTTTAAGTCAATGTTTTCCCTCTGTCCCTAACACCTTTTACACTGGTTTAGTGCTACACGATGAG GACTTCCATATAGTAACTTTCAGGCCCAC	1085
BCL2_chr18:60988464-60988564	CGTCCTAACGCTGGGGTGGGTGGCTCCTAAAGGTCTCCACCTTTGCCTCGTAGCCAATCCTAGTTGGCCG CACTTTCTCAAATGAGGTACATAGATACA	1086
S1PR2_chr19:10340823-10340923	GTGTCTCCATGGAGATGGCAGCAGGACCCGACCCCGTGCTGGCCCGCACTCTCGGCCTCCTTATCTGGTTT AGGAATGCGCGGTATCCACGCTCGCTCGC	1087
S1PR2_chr19:10340923-10341023	GCGGGAGCCACGCCTCCTCTCCCCCCCGCCCCCGAGACCGCCACACGCGCGCGGGGCCCCCACGTCTCCAAG CGGCACTGGAAGGATTCCTCCTCTCCGTCCCGC	1088
S1PR2_chr19:10341023-10341123	CAGGGGTCCCGCCTCGAGATTCTGGGAAGACTGGGGGTGGGGGACCAGATCGCAGCAGCTGCACCG CGAGTTCCGCGCCTGGCCGTGTCGCCCCACG	1089
S1PR2_chr19:10341123-10341223	AGGGGGACTGTGGGCTCAGCGCGTGGGGCCCGGAGCATCTGACAAGGACAGAGACAGAGGAGGGGGTG GAAATCCCCGGGTGAGTCAACCCGTGCCTGAG	1090
S1PR2_chr19:10341223-10341323	AAGGGGGCGAGTTCCGACGCTCCGCCCGGCTCGGGGGCCACGCGAGGTCCGCGCCACGCGCCTTCACCC ACGACCCATCCCTGAGCCGGAGTTGAAAGA	1091
S1PR2_chr19:10341323-10341423	GGAGGCGTCTGAGCCACGCAGTCACTTTCTCTTTCCTTACAAAACAAAGCCACGCCCCCCGCCGGGGGAC CGGAGGAGGCAAACAACTTGGGGAAACCGA	1092
NCOA3_chr20:46131072-46131172	CCCACTTTCCCCTTCTGTCCCTAAAGTTTTTTTCTTCCTCTTGCCTCCCCCAGCCCTTTTGAAAGCTCCCCGC GTCGTCCTCCTGCTGCCCCCGGCTCCTTA	1093
NCOA3_chr20:46131172-46131272	GCAGCTTCTGGGACGCACGGGAGAGGGAAAAGCCGCGGGGACCCCCCCCACCCCCAGCCTCCCAGCCGGGTG AGATTTGGTTGCTGTGTTTCCTCCTCACTTG	1094
NCOA3_chr20:46131217-46131317	CCACCCCAGCCTCCCAGCCGGGTGAGATTTGGTTGCTGTGTTTCCTCCTCACTTGGGCATTTAAAAAATAT TTTAACACGAATTGTCCGCGGAATTTTTCA	1095
IGLV4-69_chr22:22380472-22380572	CATGGCCTGGACCCCTCTCCTCCTCCAGCTTCTCTCACCCTCTGCTCAGGTGACTGCCTGTGGAATGCCAAAG TGATTATTGGGGACACATGGGATGACTTT	1096
IGLV4-69_chr22:22380572-22380672	TCTCTTATATTTTAACATTGTGGGGTGGGTAGTGAACCCAGACTCACCTCTCTGTGCCTGCCTCCTCTGTT CCAGGGTCCTGGGCACAGTCTGCGCTGAC	1097
IGLV4-69_chr22:22380672-22380772	CCAGGAAGCCTCGGTGTCAGGGACCGTGGGACAGAAGGTCACCCTCTCCTGTACTGGAAACAGCAACAAC GTTGGAAGTTATGCTGTGGGCTGGTACCAA	1098
IGLV4-69_chr22:22380772-22380872	CAGATTTCTCACGGTGCTCCCAAAACTGTGATGTTTGGAAATTCTCTGCCCTCAGGGATCCCTGACCGCTT CTCTGGCTCAAAGTCTGGGACCACAGCCT	1099
IGLV4-69_chr22:22380872-22380972	CCCTGACTATCTCGGGCCTCTAGCCTGAGGACGAGGCTGATTATTACTGTTCAACATGGGACTACAGCCTC AGTGCTCACACAGTGCTGCAGGCACATGG	1100
IGLV4-69_chr22:22380972-22381072	GGAACCGAGACAAAAAACCTGCCCTTGGCCTGTCCCGAGGCTGATCACTCCATACTTGCCTATGACAAACA AAGAGGGTGCCTGTGGCTGATCGTACAGTT	1101

IGLV4-60_chr22:22516707-22516807	GAAATGTTGTTTGCTCTTGTCCTTCCTTCAGGCCATAATGAGCGTCTCTGTTTTCAGGGTCTCTCCCAGC CTGTGCTGACTCAATCATCCTCTGCCTC	1102
IGLV4-60_chr22:22516827-22516927	TCAAGCTCACCTGCACTCTGAGCAGTGGGCACAGTAGCTACATCATCGCATGGCATCAGCAGCCAGGG GAAGGCCCCTCGGTACTTGATGAAGCTTGA	1103
IGLV4-60_chr22:22516927-22517027	AGGTAGTGGAAGCTACAACAAGGGGAGCGGAGTTCCTGATCGCTTCTCAGGCTCCAGCTCTGGGGCTGAC CGCTACCTCACCATCTCCAACCTCCAGTTT	1104
IGLV4-60_chr22:22517027-22517127	GAGGATGAGGCTGATTATTACTGTGAGACCTGGGACAGTAACACTCACACAGTGATACAGGCAGATGAG GAAGTGGGACAAAATCCTCAACCTGCTGAGG	1105
IGLV1-51_chr22:22677077-22677177	AAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAATTATGTATCCTGGTACCAGCAGC TCCCAGGAACAGCCCCCAAACTCCTCATTT	1106
IGLV1-51_chr22:22677177-22677277	ATGACAATAATAAGCGACCCTCAGGGATTCCTGACCGATTCTCTGGCTCCAAGTCTGGCACGTCAGCCAC CCTGGGCATCACCGGACTCCAGACTGGGGA	1107
IGLV5-48_chr22:22707517-22707617	TCAGCCAGACTCACCTGCACCTTGCGCAGTGGCATCAATCTTGGTAGCTACAGGATATTCTGGTACCAGC AGAAGCCAGAGAGCCCTCCCCGGTATCTCC	1108
IGLV5-48_chr22:22707617-22707717	TGAGCTACTACTCAGACTCAAGTAAGCATCAGGGCTCTGGAGTCCCCAGCCGCTTCTCTGGATCCAAAGA TGCTTCGAGCAATGCAGGGATTTTAGTCAT	1109
IGLV1-47_chr22:22712077-22712177	AGAGATCTGGGGGAAGCTCAGCTTCAGCTGTGGTAGAGAAGACAGGATTCAGGACAATCTCCAGCATGG CCGGCTTCCCTCTCCTCCTCACCCTCCTCAC	1110
IGLV1-47_chr22:22712177-22712277	TCACTGTGCAGGTGACAGGATGGGGACCAAGAGAGGGGCCCTGGGAAGCCCATGGGGCCCTGCTTTCTCC TCTTGTCTCCTTTCGTCTCTTGTCAATCAC	1111
IGLV1-47_chr22:22712277-22712377	CATGTCTGTGTCTCTCTCACTTCCAGGGTCCTGGGCCCAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCT	1112
IGLV1-47_chr22:22712377-22712477	TGTTCTGGAAGCAGCTCCAACATCGGAAGTAATTATGTATACTGGTACCAGCAGCTCCCAGGAACGGCCC CCAAACTCCTCATCTATAGTAATAATCAGC	1113
IGLV1-47_chr22:22712477-22712577	GGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTCCTGGCCATCAGTGGG CTCCGGTCCGAGGATGAGGCTGATTATTA	1114
IGLV7-46_chr22:22723897-22723997	ATTTGCATAAAGCAGCACACAGCACACCCCCTCCGTGCGGAGAGCTCAATAGGAGATAAAGAGCCATCAG AATCCAGCCCCCAGCTCTGGCACCAGGGGTC	1115
IGLV7-46_chr22:22723997-22724097	CCTTCCAATATCAGCACCATGGCCTGGACTCCTCTCTTTCTGTTCCTCCTCACTTGCTGCCCAGGTTAAGA GAGATTTCAAATACCAGCCTTTGGAGGGA	1116
IGLV7-46_chr22:22724097-22724197	TCCCTTTTTCTCCCTTTCTAATTCCTAATATATGTCTGTTTTTTTTGTTTCAGGGTCCAATTCCCAGGCTGTG GTGACTCAGGAGCCCTCACTGACTGTG	1117
IGLV7-46_chr22:22724207-22724307	GGACAGTCACTCTCACCTGTGGCTCCAGCACTGGAGCTGTCACCAGTGGTCATTATCCCTACTGGTTCCAG CAGAAGCCTGGCCAAGCCCCCAGGACACT	1118
IGLV7-46_chr22:22724307-22724407	GATTTATGATACAAGCAACAAACACTCCTGGACACCTGCCCGGTTCTCAGGCTCCCTCCTTGGGGGCAAA GCTGCCCTGACCCTTTTGGGTGCGCAGCCT	1119
IGLV7-46_chr22:22724407-22724507	GAGGATGAGGCTGAGTATTACTGCTTGTCTCCTATAGTGGTGGCTCGGCACAGTGACAGACACCCATGAGAG GAACCAAGACATAAACCTCCCTCGGCCCTT	1120

IGLV5-45_chr22:22730452-22730552	GGTCAGCCACCCAGCCTGATTCTGACTCTTCTGGCAAAGATCCCTGAAAAACTTTACCCTGGTTTCTGCCT TAGCACCCCATTAATGTCTGTGTTTCCAGG	1121
IGLV5-45_chr22:22730552-22730652	TTCCCTCTCGCAGGCTGTGCTGACTCAGCCGTCTTCCCTCTCTGCATCTCCTGGAGCATCAGCCAGTCTCA CCTGCACCTTGCGCAGTGGCATCAATGTT	1122
IGLV5-45_chr22:22730607-22730707	GCATCAGCCAGTCTCACCTGCACCTTGCGCAGTGGCATCAATGTTGGTACCTACAGGATATACTGGTACC AGCAGAAGCCAGGGAGTCCTCCCCAGTATC	1123
IGLV5-45_chr22:22730707-22730807	TCCTGAGGTACAAATCAGACTCAGATAAGCAGCAGGGCTCTGGAGTCCCCAGCCGCTTCTCTGGATCCAA AGATGCTTCGGCCAATGCAGGGATTTTACT	1124
IGLV5-45_chr22:22730887-22730987	ACAGATGGGGAAGTGGGACAAAAACCTCACCCTGCTCTGGGTCTTGCTCTGTACCAATTTTTAAATTTTAA AATAACTGGCCTAGGCACAAACTATATTT	1125
IGLV1-44_chr22:22735417-22735517	GCCCAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTTC TGGAAGCAGCTCCAACATCGGAAGTAATA	1126
IGLV1-44_chr22:22735517-22735617	CTGTAAACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAACTCCTCATCTATAGTAATAATCAGCGGCC CTCAGGGGTCCCTGACCGATTCTCTGGCTC	1127
IGLV1-44_chr22:22735792-22735892	TGCTGCTCAGGCCTGGCCTGTGGCTTCTGCTGCAGCTTCCTTCATGGGTCCAGGGGCATCCAGGGCCC TGCCTGAGAGTGGAGGCTCCTCCTCCCCT	1128
IGLV7-43_chr22:22749602-22749702	TCCAGCACTGGAGCAGTCACCAGTGGTTACTATCCAAACTGGTTCCAGCAGAAACCTGGACAAGCACCCA GGGCACTGATTTATAGTACAAGCAACAAAC	1129
IGLV7-43_chr22:22749732-22749832	CCCTCCTTGGGGCAAAGCTGCCCTGACACTGTCAGGTGTGCAGCCTGAGGACGAGGCTGAGTATTACTG CCTGCTCTACTATGGTGGTGCTCAGCACAG	1130
IGLV7-43_chr22:22749832-22749932	TGACAGACTCATAAGAGGAACCAAGACATAAACCTCCCTCGGCCCTTGTGATGTGGAGATTGTGTGATCA TACACACCAGCTCTCAAGACAGCCTACATG	1131
IGLV7-43_chr22:22749857-22749957	ACATAAACCTCCCTCGGCCCTTGTGATGTGGAGATTGTGTGATCATACACACCAGCTCTCAAGACAGCCTA CATGTGGACCAGCCATAGAAAGGGGAAGG	1132
IGLV7-43_chr22:22749942-22750042	ATAGAAAGGGGAAGGGAAAGGGTCTGAATTGATTTCTATCCCTCCTTGTGCCCTGAAGTGGAGGAAATGTG AGAGTGATTTGCAGTAATTGAATGAGACAA	1133
IGLV7-43_chr22:22750042-22750142	AGCAAAAGTTATTTGTTTTATATGAAAAAAAAAAACAGAAACAGCAGGATCAGATCTAAAGGCTGAGTCT AAATGCATTTCCTCCAGACAGAAGCTTCTT	1134
IGLV7-43_chr22:22750092-22750192	CAGATCTAAAGGCTGAGTCTAAATGCATTTCCTCCAGACAGAAGCTTCTTCAAACGATGGGCTTTCTGAG CTAAGAGCAAAGAAAATAAACTCTCCACGG	1135
IGLV7-43_chr22:22750192-22750292	GTATATTATTAAAGTTTATTTTATTGAGTTACTTTCAAAGCAATCCATGACTATTATATAAAGTCAGAAAG TATTAAAAATCACCAAGTTCTCTGCTAAG	1136
IGLV7-43_chr22:22750292-22750392	CTACCTTATCCCATGCAATCAAAATAAGTACTTTTCTTCATTTGGATGCATTTTTTATTTCTGTTTTTTAATA TTTCCACAATGGTGATTAAACCTGGTGC	1137
IGLV1-40_chr22:22758647-22758747	ACAGGGTCAGGGGAGGGGTCCAGGAAGCCCATGAGGCCCTGCTTTCTCCTTCTCTCTCTAGACCAAGAAT CACCGTGTCTGTGTCTCTCCTGCTTCCACG	1138
IGLV1-40_chr22:22758747-22758847	GTCCTGGGCCCAGTCTGTGTTGACGCAGCCGCCTTCAGTGTCTGCGGCCCCAGGACAGAAGGTCACCATC TCCTGCTCTGGAAGCAGCTCCGACATGGGG	1139

IGLV1-40_chr22:22738847-22758947	AATTATGCGGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCAAACTCCTCATCTATGAAAATAATA	1140
IGLV1-40_chr22:22758947-22759047	AGCGACCCTCAGGGATTCCTGACCGATTCT	
	CTGGCTCCAAGTCTGGCACCTCAGCCACCCTGGGCATCACTGGCCTCTGGCCTGAGGACTAGGCCGATTA	1141
	TTACTGCTTAGCATGGGATACCAGCCTGAG	
IGLV1-40_chr22:22759047-22759147	AGCTTGCACAGTGCTCCAGGCCAATGGGGAACTGAGACAAGAACCCTCTTCCTCCTCCGCCAGGAGGGTG	1142
	AGTGCCTGCAGCTGCTGCTCACACCTGACC	
IGLV1-40_chr22:22759147-22759247	TGTAGCTTCTGCTGCTGTAGCTTCCCCCATGGGCCTCGGGGCATCCAGGGCCTTGCCTAGGAGTGGAGGC	1143
	TCCACCACTTTTGTCCTCAGAGTCAGGAAC	
IGLV1-40_chr22:22759247-22759347	AGGGACCCCAGGAGACAGAATATCCTGCTCCTCAGCTTGGGACACAGGGTCTCTGCACTGAAATCGTGGG	1144
	CTGAGGTGGCAGGTCCAACTGTGTCTTCAC	
IGLV1-40_chr22:22759297-22759397	CTCTGCACTGAAATCGTGGGCTGAGGTGGCAGGTCCAACTGTGTCTTCACAGTCCTTCCTGTGCCTGCCCA	1145
	TGGTGTGGGGACGGAGTGAGGAAGTGTGG	
IGLV1-40_chr22:22764167-22764267	TCCTCACTCTCCTCGCTCACTGCACAGGTGACTGGATACAGGTCCAGGGGAGGGGCCCTGGGAAGCCTAT	1146
	GGATTCTTGCTTTCTCCTGTTGTCTCTAGA	
IGLV1-40_chr22:22764267-22764367	AGCCGAATAATGATGCCTGTGTGTCTCTCCCACTTCCAGGGTCCTGGGCCCAGTCTGTGCTGACGCAGCCGCC	1147
	CTCAGTGTCTGGGGCCCCAGGGCAGAGGG	
IGLV1-40_chr22:22764367-22764467	TCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGGGGCAGGTTATGATGTACACTGGTACCAGCAGCT	1148
	TCCAGGAACAGCCCCCAAACTCCTCATCTA	
IGLV1-40_chr22:22764552-22764652	CTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAGTGGTTCCACAGTGC	1149
	TCCAGGCCCCGGGGGGAACTGAGACAAGAAC	
IGLV2-23_chr22:23040452-23040552	GCTCCTCACTCTCCTCACTCAGGACACAGGTGACGCCTCCAGGGAAGGGGTCTTGGGGACCTCTGGGCTG	1150
	ATCCTTGGTCTCCTGCTCCTCAGGCTCACC	
IGLV2-23_chr22:23040592-23040692	TTCCAGGGTCCTGGGCCCAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATC	1151
	ACCATCTCCTGCACTGGAACCAGCAGTGA	
IGLV2-23_chr22:23040692-23040792	TGTTGGGAGTTATAACCTTGTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCCAAACTCATGATTTATG	1152
	AGGGCAGTAAGCGGCCCTCAGGGGTTTCT	
IGLV2-23_chr22:23040792-23040892	AATCGCTTCTCTGGCTCCAAGTCTGGCAACACCGGCCTCCCCTGACAATCTCTGGGCTCCAGGCTGAGGACG	1153
	AGGCTGATTATTACTGCTGCTCATATGCAG	
IGLV2-23_chr22:23040852-23040952	GCTGAGGACGAGGCTGATTATTACTGCTGCTCATATGCAGGTAGTAGCACTTTCCACAGTGGTCCAAGTT	1154
	CATGGGGAACTGAGACCAAAAACCTGCCCAG	
IGLV2-23_chr22:23041052-23041152	GGCCTTCAGACTTCCTCCTTGCTCTGAAGATGCTTCCTCACCCGGTGCAAGAGGCTTGCTGCAGCGGGCC	1155
	TTGAGAATTCTTTCTCTCCAGCTCCTTCC	
IGLV2-23_chr22:23041152-23041252	CTTTCCACCATGAATTCCAACAGGAAACCTGCCCTGTGGTTTCCCATCCAGGACAGGGACAGCTTCCTGAT	1156
	GCTTGTGTGCTGTGGTCCCTGAATGTGCA	
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	CAGGGATGTCTTCACCCTACATGTATCAT	
	CATCCCCTACACTGTGGGTAGAATTTTAGCAACTACATTCTAATGGTTATCGCCACAACTTTGATCTTAGA	1158
	AATAACAGTGCAGTGAACATCCCCTATGCA	

IGLV2-23_chr22:23041352-23041452	GGCTCCTTTGAGTTCCTGTGTGAATACGACCATAGGATTCATTTCTAAAAGTGAAATTGCGGGTCAGAAA GATGTGTGTTTGTGATTTTCACCCAATGTT	1159
IGLV3-21_chr22:23055497-23055597	ACCAGCAGAAGCCAGGCCCTGTGCTGGTCGTCTATGATGATAGCGACCGGCCCTCAGGGATCCC TGAGCGATTCTCTGGCTCCAACTCTGGGAA	1160
IGLV3-21_chr22:23055727-23055827	CCCAGCCTCGGTCACCCTCTTGCTCCAGCCCCGGGAAGCCTGTTGATAAAGCCATGAGTGAATCTGGCCC AGTTCACCTGGATCTGAGCCTTTCAGGTTG	1161
IGLV3-21_chr22:23055827-23055927	CCCTTCCCTCCAGCCCCCTCCAGGAGTCTCTACAGAAGATACATCAGGCATAAAATATGGCCTGGAAGGGC CAGAATCATCTGGTGACTTGGGGCTGTTGT	1162
IGLV2-14_chr22:23101392-23101492	GGTCCTGGGCCCAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATC TCCTGCACTGGAACCAGCAGTGACGTTGG	1163
IGLV2-14_chr22:23101532-23101632	AAAGCCCCCAAACTCATGATTTATAGGGTCAGTAATCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACCA	1164
IGLV3-10_chr22:23154347-23154447	AGGCTCAGTGCCCATAGACCCCAAGTTGGCCCTGCCCTGAACCCTGTGCAAAGCCCAGACACAGTCTTAG GGTAGGACCCCCTGGGAATGGGCTCTTGATC	1165
IGLV3-10_chr22:23154447-23154547	TTCAAGCCCCCCTCTCCTGTTTTCCTTGCAGTCTCTGAGGCCTCCTATGAGCTGACACAGCCACCCTCGGTG TCAGTGTCCCCCAGGACAAACGGCCAGGAT	1166
IGLV3-10_chr22:23154597-23154697	AGAAGTCAGGCCAGGCCCCTGTGCTGGTCATCTATGAGGACAGCAAACGACCCTCCGGGATCCCCTGAGAG ATTCTCTGGCTCCAGCTCAGGGACAATGGC	1167
IGLV3-10_chr22:23154697-23154797	CACCTTGACTATCAGTGGGGCCCAGGTGGAGGATGAAGCTGACTACTACTGTTACTCAACAGACAGCAGT GGTAATCATAGCACAGTGACACTGGCAGAT	1168
IGLV3-10_chr22:23154797-23154897	GGGGAAGTGAGACACAAAACCCCTTCTTCATCTATTTTACCCTCTCCCTCCAGCCCCAGGACCGCTGTGGAC CAACCCATAAGCAGGTCTGGCAGAATTCA	1169
IGLV2-8_chr22:23165422-23165522	AGGCTCACCTGGGCCCAGCACTGACTCACTAGACTGTGTTTCTCCCTTTCCAGGGTCCTGGGCCCAGTCTG CCCTGACTCAGCCTCCCTCCGCGTCCGGG	1170
IGLV2-8_chr22:23165542-23165642	CATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAGCACCCA GGCAAAGCCCCCAAACTCATGATTTATGAG	1171
IGLV2-8_chr22:23165642-23165742	GTCAGTAAGCGGCCCTCAGGGTCCCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGAC CGTCTCTGGGCTCCAGGCTGAGGATGAGG	1172
IGLV2-8_chr22:23165727-23165827	AGGCTGAGGATGAGGCTGATTATTACTGCAGCTCATATGCAGGCAGCAACAATTTCCACAGTGTTTTAAG TCAATGAGGAAGTAAGATCAAAACCTGCCC	1173
IGLV4-3_chr22:23192412-23192512	TCAGGCTCAGAACCCATAGGATCCTGAGCTGGGCCTGCCCAAACATGAGTTCATCCCAGGCACAACCTCA GGGTGGGACCCCCCTGGGAACAGATTCATCA	1174
IGLV4-3_chr22:23192512-23192612	TTTACAAGCCTCCTCTCCTGTCCTCTCTTGCAAGCTCCTATGAGCTTACACAGCCACCCTCAGTGTCAGTG TCACCAGGACAGGCAGCCATGATCACCTG	1175
IGLV4-3_chr22:23192612-23192712	CTCTTGAGATAACCTCAAAGATGAGTATGTTTACTGGTTCTGGCAGAAGCCAGACCAGGCCCATACTGGT GATATATGAAGGCAGCAAGCGGCCCTCAGG	1176
IGLV4-3_chr22:23192712-23192812	AATTTCTGATTTTCTGAGTCCAGCTCAGGGAACATGGCCACCCTGACCATCAGCAGGGCTCAGACTGAGG ACGAGGCTGACTATTACTGTCACAGGTACA	1177

IGLV4-3_chr22:23192812-23192912	ATAGAAACAGTGATGAGGCCCACAGTGACACAGGCAGATTAGGAAGTGAGACACAAACCCCTTCCCAATCT GTGTCACCCTCTTTCTCCAGCCCCAGGATG	1178
IGLV4-3_chr22:23197917-23198017	GGGATGAGAAGGGACCAGGGGCCTGGGATTGAGCTGTGAAGGGAACCAAAAGGCAGGAGGGACAGGGC AGGGGCTGTCAGCTATGACTCAGGGGAGGTTC	1179
IGLV4-3_chr22:23198017-23198117	CTGGGCCTCAGGATCCTCCCTCTGAGGCCACCAGGGGGCGGGGGTGGCACATGCCTGGACCTGGGAGGTC CCTGCTGGGCTTCACCCTGGGTGGGTCCTA	1180
IGLV4-3_chr22:23198067-23198167	ATGCCTGGACCTGGGAGGTCCCTGCTGGGCTTCACCCTGGGTGGGTCCTAGGAGCTCCTTCCTCCTAAGTC CCCCTAAAGAGACAGAGGCATTCTGGGGT	1181
IGLV4-3_chr22:23198167-23198267	CCTAAATCTGTCATGCCCCCATAAATGCATTTCTACGAGGGCCAATAAATGAACTCCAGGTTTATCCAAGC AGCAGCTTCAGGCGTCTGCAGACACAGAG	1182
IGLV4-3_chr22:23198267-23198367	CGGGGAGGAATTAGCCAACCTGAGGCACCCTAGAAGGGCTGAAGGGGGCTGAAGGGACTGAAGGGTCC CTGTGGGGCCTGTGGTCCTGGGGAGGGGAGA	1183
IGLV4-3_chr22:23198367-23198467	GCTGGGGTGTCTCCCAGCCACTCTGGGCCCTGTCCTGACACTTCTCCCACAAAGAAGGGAAGGGAAATCC TGGGACCCCACAGCCAGGACCAACCGTGAA	1184
IGLV4-3_chr22:23198467-23198567	CCACAGGACAGGAAGGACAGGGACCCCCAAGGCTGGCTCCATTTCCCAGGCACTGTCATGGGCTGAGTCT CAGGAAATCCAAGTCAAGGAGTTTCAATCC	1185
IGLV4-3_chr22:23198587-23198687	CCAAGGAAACAGAAGTCTACGGGCCCCAGGCCCAGGTGAGGGTGGGGTAAGAAGAGGAGCTTAGGATGCA GATTTGCATGGAGGCCCCGCCCTCCTCTGAG	1186
IGLV4-3_chr22:23198687-23198787	GCATCAGGGTAAGACAAGGCTGGGGGCAGGCCCAGTGCTGGGGTCTCAGGAGGCAGCGCTCTGGGGACG TCTCCACCATGGCCTGGGCTCTGCTCCTCCT	1187
IGLV4-3_chr22:23198797-23198897	CTCAGGGCACAGGTGACGCCTCCAGGGAAGGGGCCTCGGGGACCCTTGGGCTGATCCTTGGTCTCCTGCT CCTCAGGCTCACCTGGGCCCAGCACTGACT	1188
IGLV4-3_chr22:23199022-23199122	TTGGGAGTTATGACTATGTCTCCTGGTACCAACAGCACCCAGGCACAGTCCCCCAAACCCATGATCTACAA TGTCAATACTCAGCCCTCAGGGGTCCCTGA	1189
IGLV4-3_chr22:23199122-23199222	TCGTTTCTCTGGCTCCAAGTCTGGCAATACGGCCTCCATGACCATCTCTGGACTCCAGGCTGAGGACGAG GCTGATTATTAGTGCTGCTCATATACAAGC	1190
IGLV4-3_chr22:23199182-23199282	TGAGGACGAGGCTGATTATTAGTGCTGCTCATATACAAGCAGTGCCACTTAACCACAGTGGTCCAAGTTC TTGGGGAACTGAGACGAAAAACCTGCCCTGG	1191
IGLV4-3_chr22:23199277-23199377	CCTGGGCTCTCAGGCTCCCTTTTTGCTCTGAAGATGTTTCCTCACCCAGTGCAACGGGCTTCCTGAAGCAC AGCCTTGAGAATTCTTCTCCCTCAGCAAC	1192
IGLV4-3_chr22:23199377-23199477	TCTCTTTCCACCATGAAATCCAAAGGAAACCTGCTCTGTGGTTTCTCATCCAGGACAGGGACAGCTTCC TTTTGCTTGTGTGTTGTGGTCCCTGAGTG	1193
IGLV4-3_chr22:23199477-23199577	GGTGCAACTCTTCCTAGCTTTTTAAATTATGGGAGGGTGACAATGAGCTCCCTGACTGGTGCAGTCCCTGC TGTTTTCAGGAACATCCTCATCCTAAATG	1194
IGLV4-3_chr22:23199577-23199677	CATCTGAATCTCCCACTGTGTGCAGACCAATCTGGACAGATGTTATTAGGGGGAGTTTCCAGAAGCCACA TCTTACTCAACTCTGTATCCACCACACTCT	1195
IGLV3-1_chr22:23222927-23223027	TGCCTCAGCCATGGCATGGATCCCTCTCTTCCTCGGCGTCCTTGCTTACTGCACAGGTGCTGCCCCTAGGG TCCTAGCCACTGGTCCAGTCCCAGGGCTC	1196

IGLV3-1_chr22:23223027-23223127	TGGGTCCAGCCTGGCCCTGACTCTGAGCTCAGCAGGGCCCCGCCTGTGGTGGCAGGATGCTCATGACC CTGCTGCAGGTGGATGGCTCGGCGGGGCT	1197
IGLV3-1_chr22:23223077-23223177	TGGGCAGGATGCTCATGACCCTGCTGCAGGTGGATGGGCTCGGCGGGGCTGAAATCCCCCCACACAGTGC TCATGTGCTCACACTGCCTTAGGGCTCTTT	1198
IGLV3-1_chr22:23223177-23223277	CATCCCTGGATCTGTGTCCAGGCCAGGCACGTGGGAAGATTTACTTGGAGTTCAGCTCCTCAGTTTCAAGC CTTTTCTCTCCCGTTTTCTCTCCTGTAGG	1199
IGLV3-1_chr22:23223277-23223377	ATCCGTGGCCTCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACACAGCCAGCATC ACCTGCTCTGGAGATAAATTGGGGGATAAA	1200
IGLV3-1_chr22:23223327-23223427	CAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAAATTGGGGGATAAATATGCTTGCTGGTATCAGCA GAAGCCAGGCCAGTCCCCTGTGCTGGTCAT	1201
IGLV3-1_chr22:23223427-23223527	CTATCAAGATAGCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGGAACACAGCC ACTCTGACCATCAGCGGGACCCAGGCTATG	1202
IGLV3-1_chr22:23223527-23223627	GATGAGGCTGACTATTACTGTCAGGCGTGGGACAGCAGCACTGCACACAGTGACACAGGCAGATGCGGA AGTGAGACAGAAACCAGCCACCTCGGCCTGG	1203
IGLV3-1_chr22:23223627-23223727	CTCACAAGACCCTTCCCTCTCTCCTGCCCTGTCACACTGAGCAGGAGGGAGCCTTCCATGTGGAATGGAA GTTTCCAGTCCTATCCCTGCCCTTATGTTC	1204
IGLV3-1_chr22:23223727-23223827	CTGAGAGACGGGAGCAAGTTCCTGCCCACCTCTAGGCTCAGCTTATCCCAGAATAAACTGAGCTAGTCAT TTTGATGATCAAATGCCAGCTCCCAAAAGA	1205
IGLV3-1_chr22:23223827-23223927	CCCCAGAAACCCTGATATCTAAGTAGCACCGACTCTATTAGTATCAAGGGAGACTAGCCCTAGGGTGGAA TCATTTTAGTGTCTCAGAAGGCACAGGGCA	1206
IGLV3-1_chr22:23223927-23224027	ATGGAAAGTGTTTATGAGGTTTCAGGATATGCACGTGAGCAGTTAAAGGCAGGTCTTACAAGGAAGGAA CCTACTAGAATTGGGGCCCATCTGTGACATC	1207
IGLL5_chr22:23227062-23227162	ACATCCCTCTGCTTTGGGAGAGAAGGGCCAGGGCGGGACCCAGAGAGCTCTGCAGAGGCACCACAGACC CTCAGCAGGGGGTCTGCCAAACAGGACAGCT	1208
IGLL5_chr22:23227162-23227262	GGACTTGGCTGCTTCTGCCCAGGCCTGGATCCAGCCCTTGCACATCTCAGGGCAGGGGATAGGCCTGGGT GGCCAGAGCTGCAGCTGCACCTGCTGGGGA	1209
IGLL5_chr22:23227262-23227362	GGCCTAGTCCAGTCCTCCAGGGTCCCCAGACAGACTCGGATTTCCGACTGCAGCCACCATGGAAGGATGT GGTCTGCGGTGACGATGTCTATCCAGAGGC	1210
IGLL5_chr22:23227567-23227667	CCGAATATCCAAGGAGCCCAAGATCAGAGGCAGGAATAGGCCAAGCTCCCCAGTGGAGAAGCTGTGCTG GACCAGGGGGTTTCCCAGGGCCCTCCCTTGTG	1211
IGLL5_chr22:23227667-23227767	CCCTGAATGATGTCTGTTAGGGCACCTACACCCTGTTACTGCTCAGTGCCTTGCCTATTTTGAAGGACAGG GATGTGTGGTGATTATTTGTATAATCCAG	1212
IGLL5_chr22:23227767-23227867	CCCCCAGCACCTGGTCCTCAAAAGTTACCCAAGCAATGTGTATAAAGATCCAGCCTGGAGATCTTTGAAA ACCGATTCGATGAGTCGAACCATTAAGTCA	1213
IGLL5_chr22:23227867-23227967	TGATCACCATCCTCAACTTCATCTCTTTCTTCCTCCTCCTCATTATCATCACCTTCAAGAACTGTTTAAG AGTCTGAGAACTTCATCCTATTTGCAGAC	1214
IGLL5_chr22:23227897-23227997	TCCTCCTCCTCCTCATTATCATCACCTTCAAGAACTGTTAAGAGTCTGAGACTTCATCCTATTTGCAGACTA AAAAGTAAGCCTGCCACAGTGCCATGGA	1215

IGLL5_chr22:23227997-23228097	TGCTGGCAGAAGATACAAGACTCCTGGGTCAGAGACAACGAATAATCTGTTTTTCACAGCAATAGCAGTT GCCAAGGTATCAGCATTGTCTTGCACCAGT	1216
IGLL5_chr22:23228097-23228197	TCCACAAGGTGATGCAAAGAGGGCCAGGTGACATCTGCATGCCAGAGGCTCAGGGATCCCAAATATTTCAT ACTTGACAGTAAGCATATATCTGTGTTTTG	1217
IGLL5_chr22:23228197-23228297	CTCCAAAGAGAGGCATTCTCTGTACCTTCCGAGGTTGTTCACTCCACAAACACTCTTGAAAAGATAATCCA CAATCAGTGCCTTTGCCCGAGAGACATGC	1218
IGLL5_chr22:23228297-23228397	AGAAATGCAGAGATCCATAGTAGACCACTGTCTCCCAACAACCATCAACTTTATCAATGAAATGAAGTCT CAGGCTATTTGTCTGTTACCATAGCCCACA	1219
IGLL5_chr22:23228397-23228497	AAAATGTCTGGCTTGATTGTCACCAAATGTATCAAGGAAGTTAAGGAGTATCTGACACAAAATGTGAACC AAGCAATTCTCAAAGGAGCCTCCCAGGAAA	1220
IGLL5_chr22:23228497-23228597	TTCACTTTAGGAAGTCCTAGGAGGCTCCTCTGAGAGTTGCTAAAACAAAACATTGAGAGTCCTAGAGGGC TGCAGATCTGAACTTGAGCAGATATTTTTA	1221
IGLL5_chr22:23228597-23228697	AAGATTTTGTGGCAGAAAAAGAAACTGGAAAGCAAGAGGGCAGACCCTCATTGCAGTTCTGTAATGTAA GGGGGCAGAGCAGGGGCCTTTCTCACCAGAG	1222
IGLL5_chr22:23229332-23229432	GATATTGGACCCTGCATTCATCTTCTCTGGATGGTAATTTTCTCACCTGTAAAACAGAGACACTGGCCCCA AGGACACCCCACAAGTAGTTGTGAATCCC	1223
IGLL5_chr22:23229432-23229532	AAAGTAAGAGAAGAACAAAAAAAGAACCAGAATTTATTCAACACCCACTGAGTGCTTAGCAAACACATG GTTTCTTTAACTCTCATAAGCTTCATGCTGC	1224
IGLL5_chr22:23229532-23229632	AGAGGAACTCTCCCCATTTTACAGATAAGGAAACTGAGGCCCAGAGGTAACCTAGGTCTAGATAGACTCC ACATTTATGACTTCACCACTCTTCCTTGCC	1225
IGLL5_chr22:23229562-23229662	AAACTGAGGCCCAGAGGTAACCTAGGTCTAGATAGACTCCACATTTATGACTTCACCACTCTTCCTTGCCT GAAGGATATAGAATCACTCCCTGCAGGGC	1226
IGLL5_chr22:23229662-23229762	TCTTGCCTGACTCAGGAAAGGGCCACAGGATAGCCAGGCTTAACCAACCCAGCCAAGAAAGGGCT GGTCCCAACTGGCTGGAGTGCAGTGTACAGG	1227
IGLL5_chr22:23230012-23230112	GTTGGTAGATGCCCCTCTGGGAGAGATCCCCAGGGGTGACAGCCATGGACCCTGGAAGGGGCCTGGGCTA GGGACAGGGACCAGAGCCAGTCCAGGGAGAG	1228
IGLL5_chr22:23230112-23230212	GACAGAGCCAATGGACTGGGGTGTACTGTAACAGCCCTGCTGGCGAGAGGGACCAGGGCACCGTCCTCC AGGGAGCCCATGCTGCAAGTCGGGCCAGAGG	1229
IGLL5_chr22:23230212-23230312	TGCCCCTGAACCTGAAGGCCAATGAGACCCAAGACAGGCCAAGTGGGTTGTGAGACCCCTGAGGAGCTG GGCCCTGGTCCCAGGCAGCGCTGGCCCCTGC	1230
IGLL5_chr22:23230312-23230412	TGCTGCTGGGTCTGGCCATGGTCGCCCATGGCCTGCTGCGCCCAATGGTTGCACCGCAAAGCGGGGGACCC AGACCCTGGAGCCCTCAGTTGGAAGCAGCCG	1231
IGLL5_chr22:23230412-23230512	ATCCAGCCTGCGGAGCCTGTGGGGCAGGTAAGGGGCAAGAGATTCCAGGGGATGTGGGGGTCCTGCAGC AGAGCTGGGAAAGGGTGACCAAGGGGAGACA	1232
IGLL5_chr22:23230512-23230612	AGCCAGAGGAGTGAGGAGGAAGGTTAACCCCTAAGAGGGGCCTGGGCTGACACTGGCTTTAGTAATGGG TTGATATTTTGTCCATCACAGATTTGTTTGA	1233
IGLL5_chr22:23230612-23230712	ATTACTGTTTTTTAATATCATATTACGATATTATTTTTCTTGATTTCTGAGTTTTCTGGCGCCACTTAAATTT TCACCAGGGTCAGTGCCTCAATCACCTA	1234

IGLL5_chr22:23230712-23230812	GTCCTAGTCCTCTGGGTAGGGAAGGAACAGAGGCAGGGACAGGACATCCACACAGGGGGTGGTGGCCACTG TCCCCACAGGGTGCCCAGGCCTGTTCCTCCC	1235
IGLL5_chr22:23230812-23230912	CCTCCTCCTCTCTGCCCATGTGCCTCCTGCCCAGTGAGGGCAGGGGCCACTCCCTGGAGAAGGCAGCAAG GGCTTGGTTTGGTCTCCCCCAAGGCTGTCT	1236
IGLL5_chr22:23231012-23231112	GTTCACCAACTTGCACATAAATGCTTACTGGGGCCAGGCTCAAGGACACAGGGAGGGTGGGATGAACCG AGGGGAGCTGTCCAGTCATTGGAACAGGCCC	1237
IGLL5_chr22:23231072-23231172	ACGGCCCATGTTTGGAGCAATAAAGGGAGAGGGATCTCCCTCTGGGATGATGCCCAGGCTGGTCTCACA GATCGAGGGGCACTGGCTGGTGATGGGTGC	1238
IGLL5_chr22:23231172-23231272	TGGTCTCACAGATCGAGGGGCACTGGCTGGTGATGGGTGCCCCCAAAAGACAGAGCAGCGTCAGAGGAG AGGAGAGCACAGGATGAGGCTGGGAGCTCCT	1239
IGLL5_chr22:23231272-23231372	GGGTGACTGGGAAGGGGAGGCAAGAAGACCATAGGGTCCGTGCACCATTCCCAGTCCAGGACGAGTCCT TGGATGGATTTAGGTAGATTGATTATCAGAG	1240
IGLL5_chr22:23231372-23231472	TCAGATTTGTGTTTTTGGAAAAATCAGCACCGGATTGGAGGCTGATGCGACGCCCGATTAGAGGAGGGAG GAGAGGGGGTGATGGCCAAGTCCAGGGTAG	1241
IGLL5_chr22:23231472-23231572	GTGGGGATCCTGGAGGAAGCCGTGCCTTGGGGAGGGACACTCAGATTCAGAGCACCCAGGGGCC CAGTTTCCTATGAAATGGGAGCATGAAGTTG	1242
IGLL5_chr22:23231572-23231672	AAGTGAGGGCTGAGCAGAGGGGAGCAGACACGCTCGGGGACTGTCTATGGGCATTAAAAATGTATAACC ATTTTAGCAACAGGCCGCGAGTCAAAAAACA	1243
IGLL5_chr22:23231672-23231772	AAGTGTGTTTATCTAAACTGGGCAATTCCACTTCTAGGAATTTATCCTAAGGGTTGGTTGGGGGAATAAATC AAAGCTGTAACCAAATCTTTATAACAAGG	1244
IGLL5_chr22:23231772-23231872	GTGGTTAGCTCAGCATTATTAGTGATGGGAGAAAACTGGAAAAAATCCAAATATCTACCAGAAAGGGTGT GAAAAAACACAATTGTATTTGGGGGACTGT	1245
IGLL5_chr22:23231927-23232027	TGGCTAATTTTGATTAGGATTATTATTAGTTTAGAGACAGAGCCTCGCTATATTGCTCAGGCCTGTCTCAA ATTCCTAAGCTCAAGCAATCTTTCTGCCT	1246
IGLL5_chr22:23232062-23232162	ACTGCACCTGACCCAACTGTGTTTTTAAAGTATATATGCATTTTCAAAAACCTGTCAGAAAATATAGAAAA ATGTCAATGGTGTGTCTGGCTGGCTGATG	1247
IGLL5_chr22:23232162-23232262	GGATTTCACCTAATTTTAATGTGGCTTTATAATTTTCTGGTTTTGTGAAGTTGTTCACAAAAAGAGACATT TCTTCTAATATAATTTTTAATACAACAGT	1248
IGLL5_chr22:23232262-23232362	AATGTACTCATGTGCATTACTCTTTTTGTAATGAGTATATTACAAAATGTAATGACTTTTGTACATTACTCT TTTTTCTTGCCAAAAAAAAAAAAAAGATTA	1249
IGLL5_chr22:23232362-23232462	AGCAGAGAAGTATATAAAGTAAAAGCAAGTGCTTCTGCTTACCATCTCTCACCTCTTCCCAGAGATAGCC ACTGTCAGGTTGGTCAATATACTTCCAGAA	1250
IGLL5_chr22:23232462-23232562	CTTTTCCTGTGTGTGTGTGTCCCTGAAAACACACACACACACACACACACACACACACAGTTGGTGC TGGGATTTTATTTTGCAAAAGTAAGAGCC	1251
IGLL5_chr22:23232517-23232617	CACACACAGTTGGTGCTGGGATTTTATTTTGCAAAAAGTAAGAGCCATATTCTGCATATTACCAACTTTTAA TCTATTATTGACACTTTCTGTATCAGTCC	1252
IGLL5_chr22:23232617-23232717	ATATGGATTAACCACATTCATTGCTTATAAACTTTGTTTTATAAGCAAAGTTTAGATGAGCCAGAAATTTAT TTCCACTAAAAAAATCTAAATGACAAATGA	1253

IGLL5_chr22:23232717-23232817	TGCTGCAGTGGAAATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTATGTGTAC AAAGTGCACTTATATATCTCCCCAGGATA	1254
IGLJ1_chr22:23234612-23234712	TGACCTGGGTGTTTTTCTTTTTCTCTGTAGGATGTTAATAGTATCTTGTGTCATGCTAGGATGTCTAGGAC AGAGGGCAATACAATGAGGGGAAGGCATT	1255
IGLJ1_chr22:23234712-23234812	CTGCGATGTCCCCAGGCCTCTGGCTTGAAGAGTAACTTGCTGAAGTGAGGACTCTGTGGAGGAGCAAGTT ATACAGAAAGAAGTTTAGTTGTGATCTGTT	1256
IGLJ1_chr22:23234812-23234912	GAGTTGGAGGTGTCTACAGGGCATCCAAGCAGACATAGGTTGAGGAGGCAGAATATATGTGAATCTGGA GCCAAGAAGAGAGGTAAGGGCTGGAAATAGG	1257
IGLJ1_chr22:23234912-23235012	GATCTAAGACCCCTGGACAGTTGTGAGTGTGCACAATGAGGGTCAGATGCAGAGAAAATTAGGAGACTA CAGAGAGCAGAACCCAGGGTGGGGATCTGGG	1258
IGLJ1_chr22:23235012-23235112	AGTCAGCAGTTGGGCATGGGCCTGGTAGAAAGGGAAGCCAAGGAGGAGGAGAGGGGGCAGTCTCAGAC ACCAAGGAGGGGAGAGTGACTAGAAAGAAAAC	1259
IGLJ1_chr22:23235112-23235212	CTTCTTGCAGAGACATAGGGGATGGGGAAGAACTGCAGACTGAACTGGGGCAAAGGACTGTTGGCCTTA ACCAGAGAGATTTGAGGGAGAGATGAGGCTG	1260
IGLJ1_chr22:23235212-23235312	AGAGCCAGGGGATCCTGCCATGTCCCAGCATAAAAACAGTACCTGACACAGATGGGTGCTTGGGAGCTGT TGTCGGATGAATGAGTGGACAGATGCATGG	1261
IGLJ1_chr22:23235312-23235412	ATGGACGGATGGATGGAAGGATGATAGATTGATGGACAAACAGATGAACAGATGAATAGCTGGATGGAC AACTGGATGGATGGGTAGACAGAATGATCTC	1262
IGLJ1_chr22:23235412-23235512	AGAGATCAGAAAAAGCTTCATGCACTAAGTGGGACTGAACCGCGTCTCCATGGGTAGAAAGCAGAGGAA TCTCCACTTGAGTCAGGAATGACCCAGTGCT	1263
IGLJ1_chr22:23235512-23235612	CTCAATCCAGGGAGAAAGCCAGCCTGGCTTCACTGGGGACACTTGTGTGGGGGACTCAGAGGCCCTTTAA ATGAGGCCAGACGAGGTTGGACAGGTCCAA	1264
IGLJ1_chr22:23235612-23235712	GCCAACTCAGCACTCCTCTGCCACACTGCACAGGAGGGGATGTGTCACTCAGGGAGTTGCTGGGACCTAT GGGTCCCAGTGTTGTCATCAGCACCGACAG	1265
IGLJ1_chr22:23235712-23235812	CCTCAGAGAGGAAAGACACACACTGGGGTAACTCCAAGGCTGTGTGTGGCACTTGCCTTGGACAGCAGAC AGGCACAGGGACACCTCTAGGGGGCTGGCC	1266
IGLJ1_chr22:23235812-23235912	ACCCCCCTGCCTCATGTCTAGGTCCCAGCCCCGCCCACTGCAACCCTGTGCCCGTCATGCCCAGCAGGCTC CTGCTCCAGCCCAGCCCCCAGAGAGCAGA	1267
IGLJ1_chr22:23235847-23235947	CACTGCAACCCTGTGCCCGTCATGCCCAGCAGGCTCCTGCTCCAGCCCAGCCCCCAGAGAGCAGACCCCA GGTGCTGGCCCCGGGGGTTTTGGTCTGAGC	1268
IGLJ1_chr22:23235947-23236047	CTCAGTCACTGTGTTATGTCTTCGGAACTGGGACCAAGGTCACCGTCCTAGGTAAGTGGCTCTCAACCTTT CCCAGCCTGTCTCACCCTCTGCTGTCCCT	1269
IGLJ1_chr22:23236047-23236147	GGAAAATCTGTTTTCTCTCTCTGGGGCTTCCTCCCCTCTGTCCTCCCAGCCTTAAGCACTGACCCTTACCTT TCTCCATGGGGCCTGGAGGAGGTGCATT	1270
IGLJ1_chr22:23236147-23236247	AGTCTCCGGGTAACCGGCAGGAAGGGCCTCCACAGTGGGAGCAGCCGGATGCAGCCTGGTCCCGGGGCC TGAGCTGGGATTGGGCAGGGTCAGGGCTCCT	1271
IGLJ1_chr22:23236247-23236347	CCTCTCTTCCAGGGCAGATGTCTGAGTGAGGGACAGAGGCTGGTTCTGATGAGGGGCCCTGCAGTGTCCT TAGGGACATTGCCCAGTGACTCCTGGGGTC	1272

IGLJ1_chr22:23236277-23236377	GGACAGAGGCTGGTTCTGATGAGGGGCCCTGCAGTGTCCTTAGGGACATTGCCCAGTGACTCCTGGGGTC AAGGACAGAGGCTGCTGGGGTGGGCCTGGG	1273
IGLJ1_chr22:23236377-23236477	AGCTGCTGAGTCTCATAGTCTAGGGGAGCAGCCCCAAGAACAGCTGAGGGTCTAGGCTGAGGACTGGAT GCCAATCCAGCCTGGGAGGGCCACACGGCCT	1274
IGLJ1_chr22:23236387-23236487	TCTCATAGTCTAGGGGAGCAGCCCCAAGAACAGCTGAGGGTCTAGGCTGAGGACTGGATGCCAATCCAGC CTGGGAGGGCCACACGGCCTGGTGACACAG	1275
IGLJ1_chr22:23236487-23236587	AGGTCACCCCAAGGGGAGACCAATGGAGGGCACAGAGAGGGCTCTGGGTCTAGGCTGCAGCTCTGTGGGC CTGTGCTGGGTCATGAGGACATGGGGACACA	1276
IGLJ1_chr22:23236557-23236657	TGTGCTGGGTCATGAGGACATGGGGACACAGAGGGACGGGTGAGACTGGGTGAGGTGCCAGAATCCAAC CCTCCCAGGACAGTCACCAGAAAGGAGACAG	1277
IGLJ1_chr22:23236657-23236757	TCTCTTAGGGCAGAGATGTGTCTGTCCCTGGAGCCCCGTCACCTCTGGGGGCCCAGTGTCTCTCTGTTCACG GATCGGCCTCCTGCCTTCCTCAAAGGGCA	1278
IGLC1_chr22:23236757-23236857	TGTTAGACTCAGGAAATGACCAGAGGGGAGTGAATGAGGGGTGCAGAGAACTCCATGGCTACCAGGTGA AGTTTGGGGTCATCACAGGCTGCTGGGGTGG	1279
IGLC1_chr22:23236877-23236977	CATAGTCTGTGGGAGCAGCCCCCAGGAACAGCTGAGGTGAAGGGTTCTGTGGTCGGGCTTGTGGAGACAG GAAACATCTCAGAGCCTCAGAGGAGCCCTGA	1280
IGLC1_chr22:23237077-23237177	GGCTTGTCTAGGTGGAGCCCACTCCTTGCCAGGAGAGCCAAGTGGGCTGGGGCAGAGCCCGGTGC CTGTGAGGGATAGGAAGCTCCAGTTCAAAG	1281
IGLC1_chr22:23237177-23237277	CAGGCTTGGGTCTCCCCACACACTGCCTGCCAGGACAGTCCTACAGGATGAGCAGGGGACCCACAGTTCA CGGAGGAGGCTCTAGGTCCTGGAAGAATAA	1282
IGLC1_chr22:23237277-23237377	AGTGGGTGATGGAGGGGGGTATAGGGATGGAAATGAGGGATCCAGGGGTCAAGGCCAGATTCTAAACTC AGACTCCAGAGATCAGAGAAGAAGGAACACA	1283
IGLC2_chr22:23242602-23242702	GCCTGCCCTGGGTATATGGAGAAATTGAGGCTGTAGAGGAGAGGGGCTGGGCCAGGACACCTGTGAAAG GTGACTTGGGAGGGCTCCTAGGAAGGCACAG TGAAAGCCCCACTGCTATGACCAGGTAGCCGGGGACGTGGGGTGGATGCCAGAAAAGACTCCACGGAATA AGAGAGAGCCCCAGGACAGCAGGCAGGCTCTC	1284 1285
IGLC2_chr22:23242702-23242802	CGATCCCCCCCAGGCCCTTGCCCCATACACGGGCTCCAGAACACACACATTTGGCTGGAACAGCCTGAGGGAC CAAAAGGCCCCCAGTATCCCACAGAGCTGAG	1286
IGLC2_chr22:23242802-23242902	GAGCCAGGCCCAGAAAAGTAACCCCCAGAGTTCGCTGTGCCAGGGGAGACACAGAGCTCTCTTTATCTGTCAG GATGGCAGGAGGGGACAGGGTCAGGGCGCT	1287
IGLC2_chr22:23243002-23243102	GAGGGTCAGATGTCGGTGTTGGGGGCCAAGGCCCCGAGAGATCTCAGGACAGGTGGTCAGGTGTCTAAG GTAAAACAGCTCCCCGTGCAGATCAGGGCAT	1288
IGLC2_chr22:23244157-23244257	ATGCAGGACAGTCCGGAGAGGGAAATCAGGAGAAGTGAAGGGGTCTCTGGGGAGCCCAGATGTGGGCTA GAGGCAGAAGTAAGGGTGAAGAGCACCTATG	1289
IGLC2_chr22:23244257-23244357	AGTCAATGTCATGGTCTCAGCAGGAACACAGTTGAAAAATCCCCCATTCCACACAAGACCGTTTAGCAGGAA AGGAGTCCATACTTGTGCTGCCACCAGGAT	1290
IGLC2_chr22:23244357-23244457	GTCCTGAGAAGCCTTGGAGAATGAAACATACAGGTGCATTTCCTAGACTTGACAATGCACGTTAGCCAAG TAAAGGCAATGAAAAGTTCTCTACTAGGGA	1291

IGLJ3_chr22:23247257-23247357	TTTGTTTGTTTCTGTATCTTTGTCTCAACTTGTGGTCAGCCTTTCTCCCTGCATCCCAGGCCTGAGCAAGGAC CTCTGCCCTCCCTGTTCAGACCCTTGCT	1292
IGLJ3_chr22:23247357-23247457	TGCCTCAGCAGGTCACTACAACCACTTCACCTCTGACCGCAGGGGCAGGGGACTAGATAGAATGACCTAC TGAGCCTCGTCTGTCTGTCTCTGTCTGT	1293
IGLJ3_chr22:23247467-23247567	CTGTTTGTCTCTCTGTCTGTCTGACAGGCGCAGGCTGGGTCTCTAAGCCTTGTTCTGTTCTGGCCTCCTCA GTCTGGGTTCTTGTCGGAACAGCTTTGCC	1294
IGLJ3_chr22:23247567-23247667	CTTGGGTTACCTGGGTTCCATCTCCTGGGGAATTGGGAACAAGGGGTCTGAGGGAGGCACCTCCTGGGAG ACTTTAGAAGGACCCAGTGCCCTCGGGCT	1295
IGLC3_chr22:23248182-23248282	AGAGTTCGCTGTGCAGGGGAGACACAGAGCTCTCTTTATCTGTCAGGATGGCAGGAGGGGACAGGGTCA GGGCGCTGAGGGTCAGATGTCCGGTGTTGGGG	1296
IGLC3_chr22:23248282-23248382	GCCAAGGCCCCGAGAGATCTCAGGACAGGTGGTCAGGTGTCTAAGGTAAAACAGCTCCCCGTGCAGATCA GGACATAGTGGAAAACACCCTGACCCCTCT	1297
IGLC3_chr22:23248382-23248482	GCCTGGCATAGACCTTCAGACACAGAGCCCCTGAACAAGGGCACCCCAACACCTCATCATATACTGAGGT CAGGGGCTCCCCAGGTGGACACCAGGACTC	1298
IGLJ7_chr22:23263872-23263972	AGAATATTCCGTGAGAAGGTGGCCCCACAGCGCTGGGTCACACGCCATCCCCCAAGACAGGCAGGACACC ACAGACAGGGTGGTGGGTCTCAGAAAACTC	1299
IGLJ7_chr22:23263972-23264072	AGGCCCTAAACGTGGATGCTTACCAATTCCTCCACTGGAGGAAGACCTCAGAGCAGATGCCCAGGACAGG GACTTCTGGTAGGGACGGTGACTGGGACGG	1300
IGLJ7_chr22:23264072-23264172	GTGCCTGTTTGTCAGGGAAAACCCACTGGAGAGTCAGATCCCCCAGATAACTTCTCACGACATGGAGACT CTTTCGAACAGACAAAGCTCCACGTTCAGC	1301
IGLC7_chr22:23264172-23264272	TCAGGGAGTAAAAAAAAAAATGCCTCAAATGGAGGCCTTTGATCTACTGGAATCCAGCCCCCAGGACTGAC ACCCTGTCTCACCAGGCAGCCCAGAGGGT	1302
IGLC7_chr22:23278157-23278257	CAGGGTCCACCAGAAGGCATCTCAGAACCAGCCAGTGGCCCTGATTGTCAGCAGGACCCCAGGGAG GGGGGTGGCCAGGACAGGGCTCTGAAGCCCC	1303
IGLC7_chr22:23278257-23278357	CACCCCAGGACCTTCCCTGGGCAGAACGAGTTGGTGAGGGAGTGATGAGCAACCACAGGCCTCCTAACTT CCCAAGCTGGCGATTCTGAGAGGCCTCAAG	1304
IGLC7_chr22:23278357-23278457	GCTGAGACACGGTTCAGCCTTTTAGGCCCTCCTGAACGTGTCCCCTGTCTCCACAGCCTGGGAATGCACTC TCTTTTGACCCAGAAATCCTGCTCATAAG	1305
IGLC7_chr22:23282767-23282867	CTGTCATTGTACAACACATCATTTCACTTTGTTTTTCAAACATAGTGAATTCTTTCCTAATTAAAGAAGAA AAGAGTATAAAGAGAAAGTTTCCAGTGCA	1306
IGLC7_chr22:23282842-23282942	GTATAAAGAGAAAGTTTCCAGTGCAGCCTGGAGATCTGTACTGGTTGTATCTGGAATTCCAGACTCAGCC TTGCATTTCACATAGCAGATAGATGATGAT	1307
IGLC7_chr22:23282942-23283042	GATGGAGAAGGAGAAGAAGAAGGAGGAGGAAAGAAGGAAGAAGAAGAAGAGGAGGAGGAGG AAGAAGAAGACGAAGGGAAGAAGAAGAAGGATG	1308
TBC1D22A_chr22:47570209-47570309	TCCAGGTCTGCCAGGTGTAGGGGAGGTGTGACTGGTTCCATCATGGACCGGTTCCTCCATGGACCGGTTC CTCCGTGGACCGGTTCCGCCATGGACCGGT	1309
TBC1D22A_chr22:47570309-47570409	TCCGCCATGGACCACTCCTGCCCTGGACCACTCCTGCCCTGGACCGGTTCTGCCGTGGACTGGTTCCCGCC GTGGACCAGTTCCCGCTGTATACTGGTTC	1310

TBC1D22A_chr22:47570409-47570509	TGCCCTGGACTGGTTCCCGCTGTGGACTGGTTCCTTGGGGCTCTAAGTGCGGAAGGGCCCAGAGCTGGTC CCTGCCCAGCGCCCTGCTAGGGCTGTGTCC	1311
TMSB4X_chrX:12993264-12993364	TCGTACTCGTGCGCCTCGCTTCGGTGAGCCCCAGGGCCCCTGCCTCCTTCCTCCTGCCGTCCTCCGT CCCCGCCCTTTCATCATCCGCGTCCCTGT	1312
TMSB4X_chrX:12993364-12993464	GAAGGCATTCCCTAAATCCGAGCCCGAGTGGTTCTCCCCGGGAAGGCTACTTTGGGGAGCTGGGGGGATG CGAAACACCCTAGATACTGGATAATGGGGT	1313
TMSB4X_chrX:12993464-12993564	GGGGAAATCGATGATTTAAGAACAAAACCGAAAAACTGGCGTTTTGCCGTCCGCTCGGAGGGGACATT AAAAAATTTCTTAGTGTTTGCCCGCAAGGT	1314
TMSB4X_chrX:12993544-12993644	TAGTGTTTGCCCGCAAAGGTATTGTGCGTTGCCTTGGAGGCTGAGATATGGGGGAATAGACAAGTCCTTT GTTCTGAGGTTCATCTTCCGAGCCCCGAGC	1315
TMSB4X_chrX:12993644-12993744	CTCCTCCCAGCCTCGGACGGCTGCGCGGGCTGCATCTGTGCAGCCTGGCGGCGGGCGCTGTGCTATGA CATCTTTACAGTCCTTCTTGCAGAGACATG	1316
TMSB4X_chrX:12993744-12993844	TGTGCCAGGGATGCCGAATTGCCGGGAGAGCAGGCAAGACCGGCTTCGGGGCGCGCGGCCGGCTTTG TGTGCGGGGCTGCATTGTGACGCGGGCGATG	1317
TMSB4X_chrX:12993844-12993944	AAGCCGGTAGGGCGGTGGTCGGAAGCTCCAGCCGCGGCCGCCTTTGTGAGAGGACTAGAAAGCCGG ATCCGGCCCGCATCCTTGCGGAGAGGCCGCG	1318
TMSB4X_chrX:12993944-12994044	GCTAGGAAATGGAAACGCTTTTCCTACCTGGGCTCCATTTTAGGAATTCTTGCCGATTTTTCCCACTTGAA TTTGGAAGTGGCTTTCCTCTCTTCTTTCCTT	1319
TMSB4X_chrX:12994044-12994144	GTCCTAGCCAGCCTTTAATTTTAAACGCTGTAATTAACAATTCGCAGTGGTCAATTTCCTTTATTCTGCAA GATTCGGCTTTGAGAGGCATCCGCCCTCT	1320
TMSB4X_chrX:12994144-12994244	TTGGTCCACAGCGTTTTGAAATATGGGAGGAGGGCGCGGGGGGTGTCGCCTCTTTTTCTGTAGAAAGA GGAAGCTCGTGAGCGCGGAACGGCAGCAGT	1321
TMSB4X_chrX:12994289-12994389	AAGTGCAGTTCCCAGCCCAGAGACAGCGGGGCGGGTGGCTCTTCCTCACGCTCGCTCTTGGCTTGCTCCCT GCAGCTTTTCCTCCGCAACCATGTCTGAC	1322
TMSB4X_chrX:12994389-12994489	AAACCCGATATGGCTGAGATCGAGAAATTCGATAAGTCGAAACTGAAGAAGACAGAGACGCAAGAGAAA AATCCACTGCCTTCCAAAGAAAGTGAGCTCC	1323
TMSB4X_chrX:12994444-12994544	AGACGCAAGAGAAAAATCCACTGCCTTCCAAAGAAAGTGAGCTCCGACCCACCCCCATCTTTAGAAAGGC TGGGTGGGAGCCGGTGGAGGGCGGGA	1324
DMD_chrX:33146106-33146206	TTTATAGAAAGGCATATGGAACAGGAGTCATCCAAATATATCCCAGGGGTTGCAAATTGACCAAAAGAGT CACCTTTAGGGAAGCCTGCTTCTGAATGCT	1325
DMD_chrX:33146206-33146306	TGTGGAATTTATCATTCTTCTGAATGGCTGTTGCATTTATCTGCAGCTTTTACTCACCAGATGAGACCTCA GACATTTCAAATTCTGCGGAGGCTGGCTA	1326
DMD_chrX:33146306-33146406	CACACCTTCATAGGAAAGCTTTTTGCTGATTTCCCTGTTGGTACTTTTCTCTTACACATTCTATGGGGTATG GTAAACCTGGAGGTAGAGTCATAGCCAA	1327
DMD_chrX:33146406-33146506	GCACAGATAAAGCAGGCACAGAATCTCTGACCAGCCTCACAAAAGCAGACAAACACACAATCTTTTTGCA CCTGTTTCTTCCACTCCGGTTGCCGTGAAT	1328
PABPC5_chrX:90026453-90026553	TAGAAATGGTTCAACCAGTCCAATATCAATATAGCTGCTTATTACTCTATTCACTTACTTCAAAGTGGCAT TTGTTTTGAGTAAGACTTTATTTAATTCT	1329

PABPC5_chrX:90026553-90026653	TACCGTTAGCTTGAAACCATAGAGATCTTCTCTCTATTTGCCCTACTTCCTTCAAAAGTCAAAATGACCTCC TACAAATAAAAGACGTTCTTATTTTCATT	1330

CLAIMS

WHAT IS CLAIMED IS:

1. A method for identifying sets of validated phased variants from a tumor sample of a subject, the method comprising:

(a) obtaining, by a computer system, sequencing data from a tumor sample of a subject;

(b) obtaining, by the computer system, sequencing data from a matched non-tumor sample of the subject;

(c) analyzing, using the computer system, the sequencing data from the tumor sample and the sequencing data from the matched non-tumor sample to identify a plurality of regions of a genome of the subject that include a first putative phased variant and a second putative phased variant, wherein each of the plurality of regions is no more than 170 base pairs in length;

(d) after (c), performing targeted sequencing on nucleic acids from the tumor sample of the subject that are from the plurality of regions identified in (c) to a depth of at least 250×;

(e) identifying, using the computer system, sets of validated phased variants from the tumor sample of the subject based on sequencing data from the targeted sequencing in (d).

2. The method of claim 1, wherein the first putative phased variant and the second putative phased variant are separated by at least one nucleotide.

3. The method of any one of claims 1 to 2, wherein (c) further comprises:

determining a plurality of single nucleotide variants in the genome of the subject that are present in the tumor sample relative to the matched non-tumor sample; and

from the identified plurality of single nucleotide variants, identifying the plurality of regions of the genome that include the first phased variant and the second phased variant based at least in part on one or more of (1) a proximity of two or more of the identified plurality of single nucleotide variants within a genome, and (2) a presence of two or more of the identified plurality of the single nucleotide variants on a single read from the sequence data from the tumor sample of the subject.

4. The method of claim 3, wherein the sequencing data from the tumor sample of the subject in (a) and (b) each comprises data for at least 50% of the genome of the subject.

5. The method of claim 4, wherein (c) further comprises aligning the sequencing data from the tumor sample and the sequencing data from the matched non-tumor sample to a genome.

6. The method of claim 5, wherein the sequencing data from the tumor sample and the sequencing data from the matched non-tumor sample are obtained at a depth of between 10× and 100×.

7. The method of claim 6, wherein the identified plurality of regions of the genome in (c) has at least 400 regions and no more than 15,000 regions.

8. The method of any one of claims 1 to 7, wherein identifying the plurality of regions of the genome in (c) comprises determining one or more of (i) a presence of phased variants in individual reads from the tumor sample of the subject, (ii) a presence or an absence of read support in the matched non-tumor sample, (iii) a presence of other non-reference bases on supporting reads, (iv) base quality, (v) mapping quality, and (vi) uniqueness of genomic positions.

9. The method of any one of claims 1 to 8, wherein performing the targeted sequencing of (d) comprises (1) performing hybridization capture of nucleic acids from the tumor sample of the subject that correspond to the identified plurality of regions of the genome from (c) to obtain captured nucleic acids, and (2) sequencing the captured nucleic acids from the tumor sample of the subject.

10. The method of any one of claims 1 to 9, wherein the number of sets of validated phased variants is less than 1000 and greater than 10.

11. The method of any one of claims 1 to 10, wherein the plurality of regions identified in (c) are non-overlapping regions.

12. The method of any one of claims 1 to 11, wherein the nucleic acids of (d) are DNA molecules.

13. The method of any one of claims 1 to 12, wherein the first phased variant and the second phased variant are each single nucleotide variants.

14. The method of any one of claims 1 to 13, wherein the sets of validated phased variants are found to have an allele fraction of greater than 5% and no read support in the sequencing data from the matched non-tumor sample.

15. The method of any one of claims 1 to 14, wherein (d) further comprises: after (c), performing targeted sequencing on nucleic acids from the matched non-tumor sample of the subject that are from the plurality of regions identified in (c) to a depth of at least 500×.

16. The method of any one of claims 1 to 15, wherein (d) further comprises: after (c), performing targeted sequencing on nucleic acids from the matched non-tumor sample of the subject that are from the plurality of regions identified in (c) to a depth of at least 250×.

17. The method of any one of claims 1 to 16, wherein the sets of validated phased variants have a background signal of less than one in a million.

18. The method of any one of claims 1 to 17, wherein the tumor sample is a solid tumor sample.

19. The method of any one of claims 1 to 18, wherein:

the sequencing data from the tumor sample is obtained at a depth of between 10× and 100× and comprises at least 50% of the genome of the subject;

the sequencing data from the matched non-tumor sample is obtained at a depth of between 10× and 100× and comprises at least 50% of the genome of the subject;

(c) further comprises:

aligning the sequencing data from the tumor sample and the sequencing data from the matched non-tumor sample to a genome;

determining a plurality of single nucleotide variants in the genome of the subject

that are present in the tumor sample relative to the matched non-tumor sample; and

from the identified plurality of single nucleotide variants, identifying the plurality of regions of the genome that include the first phased variant and the second phased variant based at least in part on one or more of (1) a proximity of two or more of the identified plurality of single nucleotide variants within a genome, and (2) a presence of two or more of the identified plurality of the single nucleotide variants on a single read from the sequence data from the tumor sample of the subject;

wherein the plurality of regions identified in (c) are non-overlapping regions;

performing the targeted sequencing of (d) comprises (1) performing hybridization capture of nucleic acids from the tumor sample of the subject that correspond to the identified plurality of regions of the genome from (c) to obtain captured nucleic acids, and (2) sequencing the captured nucleic acids from the tumor sample of the subject; and

the first putative phased variant and the second putative phased variant are single nucleotide variants separated by at least one nucleotide.

20. The method of any one of claims 1 to 19, further comprising combining a set of nucleic acid probes with a plurality of cell-free nucleic acid molecules that are obtained or derived from a subject to form a mixture, wherein each nucleic acid probe of the set of nucleic acid probes is configured to hybridize to a cell-free nucleic acid molecule that comprises one or more of the identified sets of validated phased variants.

21. The method of claim 20, wherein each nucleic acid probe of the set of nucleic acid probes is configured to hybridize to a target nucleic acid molecule comprising a plurality of phased variants such that the nucleic acid probe is complementary to at least a region of the target nucleic acid molecule that extends from a first phased variant of the set of phased variants to a second phased variant of the set of phased variants.

22. The method of claim 20 or 21, wherein each nucleic acid probe of the set of nucleic acid probes comprises a biotin pull-down tag.

23. The method of any one of claims 20 to 22, further comprising:

separating target nucleic acid molecules that hybridize to at least one nucleic acid probe of the set of nucleic acid probes from nucleic acid molecules that do not hybridize to at least one nucleic acid probe of the set of nucleic acid probes, thereby capturing target nucleic acid molecules; and

sequencing the target nucleic acid molecules that hybridize to at least one of the set of nucleic acid probes.

24. The method of claim 23, further comprising identifying one or more cell-free nucleic acid molecules as being a cancer-derived molecule with a limit of detection of less than about 1 out of 50,000 observations from sequencing data obtained from the sequencing of the cell-free nucleic acid molecules.

25. The method of claim 24, wherein the limit of detection of is less than 1 out of 1,000,000 observations from the sequencing data.

26. The method of any one of claims 23 to 25, wherein the sequencing does not comprise use of molecular barcodes.

27. The method of any one of claims 23 to 26, further comprising determining a condition of the subject.

28. The method of claim 27, wherein the condition is a cancer.

29. The method of any one of claims 23 to 28, further comprising monitoring progression of a condition of the subject.

30. The method of claim 29, wherein the condition is a cancer.