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(71) Applicant *(for all designated States except US)*: **SEQUENTA, INC.** [US/US]; 400 East Jamie Court, Suite 301, South San Francisco, CA 94080 (US).

(72) Inventors; and

(71) Applicants *(for US only)*: **FAHAM, Malek** [US/US]; 400 East Jamie Court, Suite 301, South San Francisco, CA 94080 (US). **KLINGER, Mark** [CA/US]; 400 East Jamie Court, Suite 301, South San Francisco, CA 94080 (US).

(74) Agents: **EASTERDAY, Mathew, C.** et al.; WILSON SONSINI GOODRICH & ROSATI, 650 Page Mill Road, Palo Alto, CA 94304-1050 (US).

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(54) Title: MONITORING IMMUNE RESPONSIVENESS TO CANCER VACCINATION

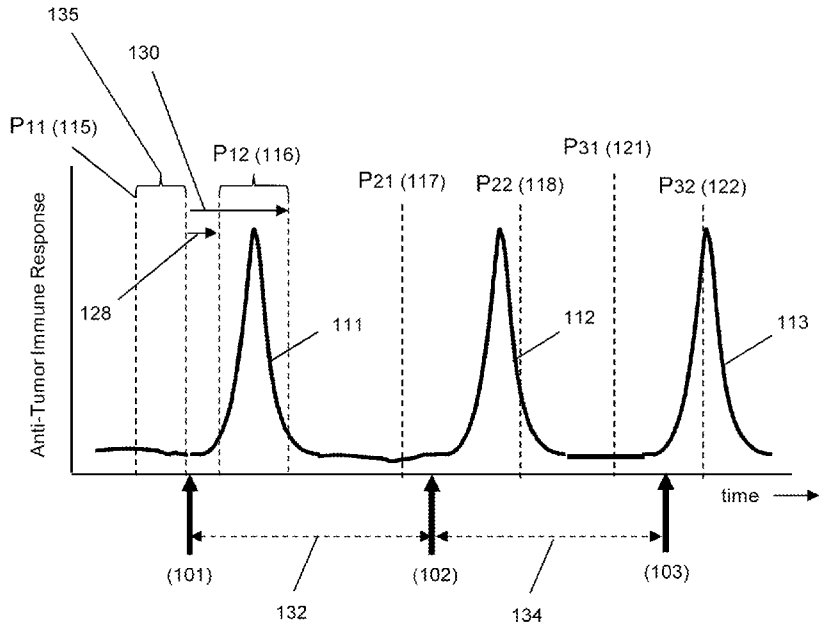

Fig. 1

(57) Abstract: The invention is direct to a method for determining a cancer patient's immune responsiveness to anti-cancer vaccination. In one aspect, for each of a plurality of vaccinations, pairs of clonotype profiles are obtained, one immediately prior to vaccination and one during the period of peak immune response, usually within two to twenty days after the vaccination. Responsiveness is correlated to successive increases in identical clonotypes within each pair of clonotype profiles in at least two successive vaccinations.

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MONITORING IMMUNE RESPONSIVENESS TO CANCER VACCINATION

BACKGROUND OF THE INVENTION

[0001] This application calims priority under U.S. provisional patent application Ser. No. 61/606,653 filed 05 March 2012, which application is incorporated herein by reference in its entirety.

[0002] Cancer immunotherapy has been an attractive and difficult field. Evidence of immunosurveillance and immunoediting of cancerous cells suggests that efficient and effective cancer therapies may be attainable by informed manipulation of the immune system , e.g. Schreiber et al, Science, 331: 1565-1570 (2011); Brody et al, J. Clin. Oncol., 29: 1864-1875 (2011); Klebanoff et al, Immunological Reviews, 239: 27-44 (2011). Results of such approaches to date have been inconclusive, but tantalizing, which is due in part to the complexity and still limited understanding of many features of cancer and the immune system, including such features as exhaustion of tumor-reactive T cell populations, immunosuppression by regulatory T cells in tumors, mutability of tumor antigens, and the like, e.g. Turcotte et al, Adv. Surg. 45: 341-360 (2011). Such challenges are compounded by a dearth of techniques for conveniently detecting and monitoring immune responses, particularly T cell responses, that are correlated with traditional measures of treatment success, such as overall survival, tumor shrinkage, or the like, e.g. Hoos et al, J. Natl. Cancer Inst., 102: 1388-1397 (2010). Current methods for monitoring T cell response to cancer vaccination include enumeration of antitumor T cells by fluorochrome-labeled tetramer conjugates of MHC molecules with tumor antigen peptides, measurement of T cell proliferation in response to antigen exposure in vitro, measurement of T cell production of cytokines, measurement of T-cell activation markers in response to antigen re-exposure in vitro, and the like, Brody et al (cited above).

[0003] Recently, more and more diagnostic and prognostic applications are being developed that use large-scale DNA sequencing as the per-base cost of DNA sequencing has dropped and sequencing techniques have become more convenient, e.g. Faham and Willis, U.S. patent publication 2010/0151471; Freeman et al, Genome Research, 19: 1817-1824 (2009); Boyd et al, Sci. Transl. Med., 1(12): 12ra23 (2009); He et al, Oncotarget (March 8, 2011); Palomaki et al, Genetics in Medicine (online publication 2 February 2012).

[0004] In view of the potential impact of effective cancer vaccines, it would be highly desirable if there was available a new method for determining anti-tumor immune responses.

SUMMARY OF THE INVENTION

[0005] The present invention is drawn to methods for determining responsiveness of a patient's immune system to cancer vaccination. The invention is exemplified in a number of implementations and applications, some of which are summarized below and throughout the specification.

[0006] In one aspect, the invention includes a method of measuring immune responsiveness of a patient to a cancer vaccine, the method comprising the steps of (a) generating a pair of clonotype profiles at each of a plurality of successive vaccinations of a patient with a cancer vaccine, wherein a first clonotype profile of each pair is from a sample from the patient prior to vaccination and a second clonotype profile of each pair is from a sample from the patient after vaccination at a time within a peak immune response to vaccination, each clonotype profile comprising at least 1000 sequence reads of at least 30 nucleotides; and (b) correlating immune responsiveness of the patient to the cancer vaccine with an increase of identical clonotypes within each pair of clonotype profiles of at least two successive vaccinations. In this and other embodiments, the size and type of clonotype profiles used with the method may vary widely. In some embodiments, clonotype profiles comprise at least 10^3 clonotypes; in other embodiments, clonotype profiles comprise at least 10^4 clonotypes; in still other embodiments, clonotype profiles comprise at least 10^5 clonotypes. In some embodiments, rearranged nucleic acids of clonotypes may be 25-200 nucleotide segments of a VDJ rearrangement of IgH, a DJ rearrangement of IgH, a VJ rearrangement of IgK, a VJ rearrangement of IgL, a VDJ rearrangement of TCR β, a DJ rearrangement of TCR β, a VJ rearrangement of TCR α, a VJ rearrangement of TCR γ, a VDJ rearrangement of TCR δ, a VD rearrangement of TCR δ, a Kde-V rearrangement, or the like. In another embodiment, rearranged nucleic acids of clonotypes may be 25-200 nucleotide segments of a VDJ rearrangement of TCR β, a DJ rearrangement of TCR β, a VJ rearrangement of TCR α, a VJ rearrangement of TCR γ, a VDJ rearrangement of TCR δ, or a VD rearrangement of TCR δ. In still other embodiments, rearranged nucleic acids of clonotypes may be 25-200 nucleotide segments of a VDJ rearrangement of TCR β.

[0007] These above-characterized aspects, as well as other aspects, of the present invention are exemplified in a number of illustrated implementations and applications, some of which are shown in the figures and characterized in the claims section that follows. However, the above

summary is not intended to describe each illustrated embodiment or every implementation of the invention.

BRIEF DESCRIPTION OF THE DRAWINGS

[0008] The novel 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 is 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 of which:

[0009] Fig. 1 illustrates a vaccination regimen of a cancer vaccine and a positive immune response.

[0010] Figs. 2A-2C show a two-staged PCR scheme for amplifying TCRβ genes.

[0011] Fig. 3A illustrates details of determining a nucleotide sequence of the PCR product of Fig. 2C. Fig. 3B illustrates details of another embodiment of determining a nucleotide sequence of the PCR product of Fig. 2C.

[0012] Fig. 4A illustrates a PCR scheme for generating three sequencing templates from an IgH chain in a single reaction. Figs. 4B-4C illustrates a PCR scheme for generating three sequencing templates from an IgH chain in three separate reactions after which the resulting amplicons are combined for a secondary PCR to add P5 and P7 primer binding sites. Fig. 4D illustrates the locations of sequence reads generated for an IgH chain. Fig. 4E illustrates the use of the codon structure of V and J regions to improve base calls in the NDN region.

DETAILED DESCRIPTION OF THE INVENTION

[0013] The practice of the present invention may employ, unless otherwise indicated, conventional techniques and descriptions of molecular biology (including recombinant techniques), bioinformatics, cell biology, and biochemistry, which are within the skill of the art. Such conventional techniques include, but are not limited to, sampling and analysis of blood cells, nucleic acid sequencing and analysis, and the like. Specific illustrations of suitable techniques can be had by reference to the example herein below. However, other equivalent conventional procedures can, of course, also be used. Such conventional techniques and descriptions can be found in standard laboratory manuals such as *Genome Analysis: A Laboratory Manual Series* (Vols. I-IV); *PCR Primer: A Laboratory Manual; and Molecular Cloning: A Laboratory Manual* (all from Cold Spring Harbor Laboratory Press); and the like.

[0014] The invention is directed to a method of determining the responsiveness of a patient to repeated vaccinations with a cancer vaccine. One aspect of the invention is illustrated in Fig. 1, where results of three vaccinations are illustrated. Heavy arrows (101), (102) and (103) indicate the times of three consecutive vaccinations, which result in three successive peaks (111, 112 and 113, respectively) of immune response to the vaccinations. Such peaks would be expected in a patient whose tumor-specific T cells were induced to proliferate and differentiate in response to the cancer vaccine. The vertical axis of the figure may be, for example, the magnitude of a conventional measure of T cell activation, e.g. T cell proliferation in response to tumor antigen stimulation, ELISPOT assay, enumeration T cells label by tetramer-antigenic peptide conjugate, or the like. As with conventional vaccinations, there is a delay of a few days before the immune response to the vaccine peaks. Such peak response may be within a period in the range of from 2 to 20 days after vaccination, which for peak (111) is illustrated by arrows (128) and (130). The interval between vaccinations, e.g. (132) and (134), may vary widely. Such intervals may be the same or different in the course of several vaccinations. In one aspect, the intervals are in the range of 2-3 weeks to 6-9 months. In accordance with the invention, samples for generating clonotype profiles are taken before each vaccination and within the peak response period following each vaccination. That is, for each vaccination a pair of clonotype profiles is generated from samples, a first profile of a pair being immediately before a vaccination and a second member of the pair being within the peak response period. Typically the sample for the first clonotype profile is taken from a few hours to a few days before a vaccination, as illustrated by interval (135) in Fig. 1 for vaccination (101). In one embodiment, the first sample of a first clonotype profile of a pair is taken from 1 to 20 days before the vaccination, or from 1 to 10 days before the vaccination; or in another embodiment, from 1 to 5 days before the vaccination. In one aspect, the invention is implemented by taking a plurality of pairs of samples from which clonotype profiles are generated. Such plurality may be 2 or more; in some embodiments, such plurality is in the range of from 2 to 6; in some embodiments, such plurality is in the range of from 2 to 4. In Fig. 1, these are illustrated as P_{11} (115) and P_{12} (116) for the first pair, P_{21} (117) and P_{22} (118) for the second pair, and P_{31} (121) and P_{32} (122) for the third pair. In one aspect of the invention, the clonotype profiles comprise sequences of recombined nucleic acids (i.e. clonotypes) that encode a T cell receptor chain or a portion thereof. In one embodiment, such chains are T cell receptor chain beta (TCRβ). In another embodiment, T cell receptor chains are from CD8+ T cells. Once at least two successive pairs of clonotype profiles are generated, they are analyzed to determine the identities of clonotypes that are up-regulated, i.e. that are increased fractionally or in absolute numbers, in the second profiles of each pair. If the same

clonotypes are up-regulated in each of two successive pairs then a patient has an immune response to the cancer vaccine. The magnitude of such a response, which is correlated to patient responsiveness, is measured by number of different clonotypes up-regulated and the level of up-regulation for each such clonotype for the successive pairs. In one embodiment, the levels of a set of clonotypes increase between pairs of clonotype profiles from samples taken before and after a plurality, or series, of successive vaccinations. In a further embodiment, such increases in levels are each monotonically increasing levels over a plurality, or series, of successive vaccinations. In still another embodiment, such series is in the range of from 2 to 4 vaccinations.

Guidance for generating clonotype profiles for those of ordinary skill in the art is provided in Faham and Willis, U.S. patent publications 2010/015471 and 2011/0207134; and Warren et al, International patent publication WO 2011/106738; which are incorporated herein by reference. Additionally, in the sections below, in one aspect, steps for generating clonotype profiles for use in the present invention are disclosed.

[0015] In one aspect, methods of the invention may be used with treatment of solid tumors. In another aspect, methods of the invention may be used with treatment of lymphoid and myeloid proliferative disorders. In another aspect, methods of the invention are applicable to lymphomas and leukemias. In another aspect, methods of the invention are applicable lymphomas or leukemias, such as follicular lymphoma, chronic lymphocytic leukemia (CLL), acute lymphocytic leukemia (ALL), chronic myelogenous leukemia (CML), acute myelogenous leukemia (AML), Hodgkins's and non-Hodgkin's lymphomas, multiple myeloma (MM), monoclonal gammopathy of undetermined significance (MGUS), mantle cell lymphoma (MCL), diffuse large B cell lymphoma (DLBCL), myelodysplastic syndromes (MDS), T cell lymphoma, or the like.

Samples

[0016] Clonotype profiles may be obtained from samples of immune cells. For example, immune cells can include T-cells and/or B-cells. T-cells (T lymphocytes) include, for example, cells that express T cell receptors. T-cells include helper T cells (effector T cells or Th cells), cytotoxic T cells (CTLs), memory T cells, and regulatory T cells. In one aspect a sample of T cells includes at least 1,000T cells; but more typically, a sample includes at least 10,000 T cells, and more typically, at least 100,000 T cells. In another aspect, a sample includes a number of T cells in the range of from 1000 to 1,000,000 cells. A sample of immune cells may also comprise B cells. B-cells include, for example, plasma B cells, memory B cells, B1 cells, B2 cells, marginal-zone B cells, and follicular B cells. B-cells can express immunoglobulins (antibodies,

B cell receptor). As above, in one aspect a sample of B cells includes at least 1,000 B cells; but more typically, a sample includes at least 10,000 B cells, and more typically, at least 100,000 B cells. In another aspect, a sample includes a number of B cells in the range of from 1000 to 1,000,000 B cells.

[0017] Samples used in the methods of the invention can come from a variety of tissues, including, for example, tumor tissue, blood and blood plasma, lymph fluid, cerebrospinal fluid surrounding the brain and the spinal cord, synovial fluid surrounding bone joints, and the like. In one embodiment, the sample is a blood sample. The blood sample can be about 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.5, 2.0, 2.5, 3.0, 3.5, 4.0, 4.5, or 5.0 mL. The sample can be a tumor biopsy. The biopsy can be from, for example, from a tumor of the brain, liver, lung, heart, colon, kidney, or bone marrow. Any biopsy technique used by those skilled in the art can be used for isolating a sample from a subject. For example, a biopsy can be an open biopsy, in which general anesthesia is used. The biopsy can be a closed biopsy, in which a smaller cut is made than in an open biopsy. The biopsy can be a core or incisional biopsy, in which part of the tissue is removed. The biopsy can be an excisional biopsy, in which attempts to remove an entire lesion are made. The biopsy can be a fine needle aspiration biopsy, in which a sample of tissue or fluid is removed with a needle.

[0018] The sample can include nucleic acid, for example, DNA (e.g., genomic DNA) or RNA (e.g., messenger RNA). The nucleic acid can be cell-free DNA or RNA, e.g. extracted from the circulatory system, Vlassov et al, Curr. Mol. Med., 10: 142-165 (2010); Swarup et al, FEBS Lett., 581: 795-799 (2007). In the methods of the invention, the amount of RNA or DNA from a subject that can be analyzed includes, for example, as low as a single cell in some applications (e.g., a calibration test) and as many as 10 million of cells or more translating to a range of DNA of 6pg-60ug, and RNA of approximately 1pg-10ug.

[0019] As discussed more fully below (Definitions), a sample containing lymphocytes is sufficiently large so that substantially every T cell or B cell with a distinct clonotype is represented therein, thereby forming a repertoire (as the term is used herein). In one embodiment, a sample is taken that contains with a probability of ninety-nine percent every clonotype of a population present at a frequency of .001 percent or greater. In another embodiment, a sample is taken that contains with a probability of ninety-nine percent every clonotype of a population present at a frequency of .0001 percent or greater. In one embodiment, a sample of B cells or T cells includes at least a half million cells, and in another embodiment such sample includes at least one million cells.

[0020] Whenever a source of material from which a sample is taken is scarce, such as, clinical study samples, or the like, DNA from the material may be amplified by a non-biasing technique, such as whole genome amplification (WGA), multiple displacement amplification (MDA); or like technique, e.g. Hawkins et al, Curr. Opin. Biotech., 13: 65-67 (2002); Dean et al, Genome Research, 11: 1095-1099 (2001); Wang et al, Nucleic Acids Research, 32: e76 (2004); Hosono et al, Genome Research, 13: 954-964 (2003); and the like.

[0021] Blood samples are of particular interest and may be obtained using conventional techniques, e.g. Innis et al, editors, PCR Protocols (Academic Press, 1990); or the like. For example, white blood cells may be separated from blood samples using convention techniques, e.g. RosetteSep kit (Stem Cell Technologies, Vancouver, Canada). Blood samples may range in volume from 100 μL to 10 mL; in one aspect, blood sample volumes are in the range of from 200 100 μL to 2 mL. DNA and/or RNA may then be extracted from such blood sample using conventional techniques for use in methods of the invention, e.g. DNeasy Blood & Tissue Kit (Qiagen, Valencia, CA). Optionally, subsets of white blood cells, e.g. lymphocytes, may be further isolated using conventional techniques, e.g. fluorescently activated cell sorting (FACS)(Becton Dickinson, San Jose, CA), magnetically activated cell sorting (MACS)(Miltenyi Biotec, Auburn, CA), or the like.

[0022] Since the identifying recombinations are present in the DNA of each individual's adaptive immunity cells as well as their associated RNA transcripts, either RNA or DNA can be sequenced in the methods of the provided invention. A recombined sequence from a T-cell or B-cell encoding a T cell receptor or immunoglobulin molecule, or a portion thereof, is referred to as a clonotype. The DNA or RNA can correspond to sequences from T-cell receptor (TCR) genes or immunoglobulin (Ig) genes that encode antibodies. For example, the DNA and RNA can correspond to sequences encoding α, β, γ, or δ chains of a TCR. In a majority of T-cells, the TCR is a heterodimer consisting of an α-chain and β-chain. The TCRα chain is generated by VJ recombination, and the β chain receptor is generated by V(D)J recombination. For the TCRβ chain, in humans there are 48 V segments, 2 D segments, and 13 J segments. Several bases may be deleted and others added (called N and P nucleotides) at each of the two junctions. In a minority of T-cells, the TCRs consist of γ and δ delta chains. The TCR γ chain is generated by VJ recombination, and the TCR δ chain is generated by V(D)J recombination (Kenneth Murphy, Paul Travers, and Mark Walport, *Janeway's Immunology* 7th edition, Garland Science, 2007, which is herein incorporated by reference in its entirety).

[0023] The DNA and RNA analyzed in the methods of the invention can correspond to sequences encoding heavy chain immunoglobulins (IgH) with constant regions (α, δ, ε, γ, or μ) or light chain immunoglobulins (IgK or IgL) with constant regions λ or κ. Each antibody has two identical light chains and two identical heavy chains. Each chain is composed of a constant (C) and a variable region. For the heavy chain, the variable region is composed of a variable (V), diversity (D), and joining (J) segments. Several distinct sequences coding for each type of these segments are present in the genome. A specific VDJ recombination event occurs during the development of a B-cell, marking that cell to generate a specific heavy chain. Diversity in the light chain is generated in a similar fashion except that there is no D region so there is only VJ recombination. Somatic mutation often occurs close to the site of the recombination, causing the addition or deletion of several nucleotides, further increasing the diversity of heavy and light chains generated by B-cells. The possible diversity of the antibodies generated by a B-cell is then the product of the different heavy and light chains. The variable regions of the heavy and light chains contribute to form the antigen recognition (or binding) region or site. Added to this diversity is a process of somatic hypermutation which can occur after a specific response is mounted against some epitope.

[0024] As mentioned above, in accordance with the invention, primers may be selected to generate amplicons of subsets of recombined nucleic acids extracted from lymphocytes. Such subsets may be referred to herein as "somatically rearranged regions." Somatically rearranged regions may comprise nucleic acids from developing or from fully developed lymphocytes, where developing lymphocytes are cells in which rearrangement of immune genes has not been completed to form molecules having full V(D)J regions. Exemplary incomplete somatically rearranged regions include incomplete IgH molecules (such as, molecules containing only D-J regions), incomplete TCRδ molecules (such as, molecules containing only D-J regions), and inactive IgK (for example, comprising Kde-V regions).

[0025] Adequate sampling of the cells is an important aspect of interpreting the repertoire data, as described further below in the definitions of "clonotype" and "repertoire." For example, starting with 1,000 cells creates a minimum frequency that the assay is sensitive to regardless of how many sequencing reads are obtained. Therefore one aspect of this invention is the development of methods to quantitate the number of input immune receptor molecules. This has been implemented this for TCRβ and IgH sequences. In either case the same set of primers are used that are capable of amplifying all the different sequences. In order to obtain an absolute number of copies, a real time PCR with the multiplex of primers is performed along with a standard with a known number of immune receptor copies. This real time PCR measurement

can be made from the amplification reaction that will subsequently be sequenced or can be done on a separate aliquot of the same sample. In the case of DNA, the absolute number of rearranged immune receptor molecules can be readily converted to number of cells (within 2 fold as some cells will have 2 rearranged copies of the specific immune receptor assessed and others will have one). In the case of cDNA the measured total number of rearranged molecules in the real time sample can be extrapolated to define the total number of these molecules used in another amplification reaction of the same sample. In addition, this method can be combined with a method to determine the total amount of RNA to define the number of rearranged immune receptor molecules in a unit amount (say 1 μg) of RNA assuming a specific efficiency of cDNA synthesis. If the total amount of cDNA is measured then the efficiency of cDNA synthesis need not be considered. If the number of cells is also known then the rearranged immune receptor copies per cell can be computed. If the number of cells is not known, one can estimate it from the total RNA as cells of specific type usually generate comparable amount of RNA. Therefore from the copies of rearranged immune receptor molecules per 1 μg one can estimate the number of these molecules per cell.

[0026] One disadvantage of doing a separate real time PCR from the reaction that would be processed for sequencing is that there might be inhibitory effects that are different in the real time PCR from the other reaction as different enzymes, input DNA, and other conditions may be utilized. Processing the products of the real time PCR for sequencing would ameliorate this problem. However low copy number using real time PCR can be due to either low number of copies or to inhibitory effects, or other suboptimal conditions in the reaction.

[0027] Another approach that can be utilized is to add a known amount of unique immune receptor rearranged molecules with a known sequence, i.e. known amounts of one or more internal standards, to the cDNA or genomic DNA from a sample of unknown quantity. By counting the relative number of molecules that are obtained for the known added sequence compared to the rest of the sequences of the same sample, one can estimate the number of rearranged immune receptor molecules in the initial cDNA sample. (Such techniques for molecular counting are well-known, e.g. Brenner et al, U.S. patent 7,537,897, which is incorporated herein by reference). Data from sequencing the added unique sequence can be used to distinguish the different possibilities if a real time PCR calibration is being used as well. Low copy number of rearranged immune receptor in the DNA (or cDNA) would create a high ratio between the number of molecules for the spiked sequence compared to the rest of the sample sequences. On the other hand, if the measured low copy number by real time PCR is due to inefficiency in the reaction, the ratio would not be high.

Amplification of Nucleic Acid Populations

[0028] Amplicons of target populations of nucleic acids may be generated by a variety of amplification techniques. In one aspect of the invention, multiplex PCR is used to amplify members of a mixture of nucleic acids, particularly mixtures comprising recombined immune molecules such as T cell receptors, or portions thereof. Guidance for carrying out multiplex PCRs of such immune molecules is found in the following references, which are incorporated by reference: Morley, U.S. patent 5,296,351; Gorski, U.S. patent 5,837,447; Dau, U.S. patent 6,087,096; Von Dongen et al, U.S. patent publication 2006/0234234; European patent publication EP 1544308B1; and the like.

[0029] After amplification of DNA from the genome (or amplification of nucleic acid in the form of cDNA by reverse transcribing RNA), the individual nucleic acid molecules can be isolated, optionally re-amplified, and then sequenced individually. Exemplary amplification protocols may be found in van Dongen et al, Leukemia, 17: 2257-2317 (2003) or van Dongen et al, U.S. patent publication 2006/0234234, which is incorporated by reference. Briefly, an exemplary protocol is as follows: Reaction buffer: ABI Buffer II or ABI Gold Buffer (Life Technologies, San Diego, CA); 50 μL final reaction volume; 100 ng sample DNA; 10 pmol of each primer (subject to adjustments to balance amplification as described below); dNTPs at 200 μM final concentration; $MgCl_2$ at 1.5 mM final concentration (subject to optimization depending on target sequences and polymerase); Taq polymerase (1-2 U/tube); cycling conditions: preactivation 7 min at 95°C; annealing at 60°C; cycling times: 30s denaturation; 30s annealing; 30s extension. Polymerases that can be used for amplification in the methods of the invention are commercially available and include, for example, Taq polymerase, AccuPrime polymerase, or Pfu. The choice of polymerase to use can be based on whether fidelity or efficiency is preferred.

[0030] Real time PCR, picogreen staining, nanofluidic electrophoresis (e.g. LabChip) or UV absorption measurements can be used in an initial step to judge the functional amount of amplifiable material.

[0031] In one aspect, multiplex amplifications are carried out so that relative amounts of sequences in a starting population are substantially the same as those in the amplified population, or amplicon. That is, multiplex amplifications are carried out with minimal amplification bias among member sequences of a sample population. In one embodiment, such relative amounts are substantially the same if each relative amount in an amplicon is within five

fold of its value in the starting sample. In another embodiment, such relative amounts are substantially the same if each relative amount in an amplicon is within two fold of its value in the starting sample. As discussed more fully below, amplification bias in PCR may be detected and corrected using conventional techniques so that a set of PCR primers may be selected for a predetermined repertoire that provide unbiased amplification of any sample.

[0032] In regard to many repertoires based on TCR or BCR sequences, a multiplex amplification optionally uses all the V segments. The reaction is optimized to attempt to get amplification that maintains the relative abundance of the sequences amplified by different V segment primers. Some of the primers are related, and hence many of the primers may "cross talk," amplifying templates that are not perfectly matched with it. The conditions are optimized so that each template can be amplified in a similar fashion irrespective of which primer amplified it. In other words if there are two templates, then after 1,000 fold amplification both templates can be amplified approximately 1,000 fold, and it does not matter that for one of the templates half of the amplified products carried a different primer because of the cross talk. In subsequent analysis of the sequencing data the primer sequence is eliminated from the analysis, and hence it does not matter what primer is used in the amplification as long as the templates are amplified equally.

[0033] In one embodiment, amplification bias may be avoided by carrying out a two-stage amplification (as described in Faham and Willis, cited above) wherein a small number of amplification cycles are implemented in a first, or primary, stage using primers having tails non-complementary with the target sequences. The tails include primer binding sites that are added to the ends of the sequences of the primary amplicon so that such sites are used in a second stage amplification using only a single forward primer and a single reverse primer, thereby eliminating a primary cause of amplification bias. Preferably, the primary PCR will have a small enough number of cycles (e.g. 5-10) to minimize the differential amplification by the different primers. The secondary amplification is done with one pair of primers and hence the issue of differential amplification is minimal. One percent of the primary PCR is taken directly to the secondary PCR. Thirty-five cycles (equivalent to ~28 cycles without the 100 fold dilution step) used between the two amplifications were sufficient to show a robust amplification irrespective of whether the breakdown of cycles were: one cycle primary and 34 secondary or 25 primary and 10 secondary. Even though ideally doing only 1 cycle in the primary PCR may decrease the amplification bias, there are other considerations. One aspect of this is representation. This plays a role when the starting input amount is not in excess to the number of reads ultimately obtained. For example, if 1,000,000 reads are obtained and starting with 1,000,000 input

molecules then taking only representation from 100,000 molecules to the secondary amplification would degrade the precision of estimating the relative abundance of the different species in the original sample. The 100 fold dilution between the 2 steps means that the representation is reduced unless the primary PCR amplification generated significantly more than 100 molecules. This indicates that a minimum 8 cycles (256 fold), but more comfortably 10 cycle (~1,000 fold), may be used. The alternative to that is to take more than 1% of the primary PCR into the secondary but because of the high concentration of primer used in the primary PCR, a big dilution factor is can be used to ensure these primers do not interfere in the amplification and worsen the amplification bias between sequences. Another alternative is to add a purification or enzymatic step to eliminate the primers from the primary PCR to allow a smaller dilution of it. In this example, the primary PCR was 10 cycles and the second 25 cycles.

Generating Sequence Reads for Clonotypes

[0034] Any high-throughput technique for sequencing nucleic acids can be used in the method of the invention. Preferably, such technique has a capability of generating in a cost-effective manner a volume of sequence data from which at least 1000 clonotypes can be determined, and preferably, from which at least 10,000 to 1,000,000 clonotypes can be determined. DNA sequencing techniques include classic dideoxy sequencing reactions (Sanger method) using labeled terminators or primers and gel separation in slab or capillary, sequencing by synthesis using reversibly terminated labeled nucleotides, pyrosequencing, 454 sequencing, allele specific hybridization to a library of labeled oligonucleotide probes, sequencing by synthesis using allele specific hybridization to a library of labeled clones that is followed by ligation, real time monitoring of the incorporation of labeled nucleotides during a polymerization step, polony sequencing, and SOLiD sequencing. Sequencing of the separated molecules has more recently been demonstrated by sequential or single extension reactions using polymerases or ligases as well as by single or sequential differential hybridizations with libraries of probes. These reactions have been performed on many clonal sequences in parallel including demonstrations in current commercial applications of over 100 million sequences in parallel. These sequencing approaches can thus be used to study the repertoire of T-cell receptor (TCR) and/or B-cell receptor (BCR). In one aspect of the invention, high-throughput methods of sequencing are employed that comprise a step of spatially isolating individual molecules on a solid surface where they are sequenced in parallel. Such solid surfaces may include nonporous surfaces (such as in Solexa sequencing, e.g. Bentley et al, Nature,456: 53-59 (2008) or Complete Genomics sequencing, e.g. Drmanac et al, Science, 327: 78-81 (2010)), arrays of wells, which may include

bead- or particle-bound templates (such as with 454, e.g. Margulies et al, Nature, 437: 376-380 (2005) or Ion Torrent sequencing, U.S. patent publication 2010/0137143 or 2010/0304982), micromachined membranes (such as with SMRT sequencing, e.g. Eid et al, Science, 323: 133-138 (2009)), or bead arrays (as with SOLiD sequencing or polony sequencing, e.g. Kim et al, Science, 316: 1481-1414 (2007)). In another aspect, such methods comprise amplifying the isolated molecules either before or after they are spatially isolated on a solid surface. Prior amplification may comprise emulsion-based amplification, such as emulsion PCR, or rolling circle amplification. Of particular interest is Solexa-based sequencing where individual template molecules are spatially isolated on a solid surface, after which they are amplified in parallel by bridge PCR to form separate clonal populations, or clusters, and then sequenced, as described in Bentley et al (cited above) and in manufacturer's instructions (e.g. TruSeq™ Sample Preparation Kit and Data Sheet, Illumina, Inc., San Diego, CA, 2010); and further in the following references: U.S. patents 6,090,592; 6,300,070; 7,115,400; and EP0972081B1; which are incorporated by reference. In one embodiment, individual molecules disposed and amplified on a solid surface form clusters in a density of at least 10^5 clusters per cm^2; or in a density of at least $5x10^5$ per cm^2; or in a density of at least 10^6 clusters per cm^2. In one embodiment, sequencing chemistries are employed having relatively high error rates. In such embodiments, the average quality scores produced by such chemistries are monotonically declining functions of sequence read lengths. In one embodiment, such decline corresponds to 0.5 percent of sequence reads have at least one error in positions 1-75; 1 percent of sequence reads have at least one error in positions 76-100; and 2 percent of sequence reads have at least one error in positions 101-125.

[0035] In one aspect, a sequence-based clonotype profile of an individual is obtained using the following steps: (a) obtaining a nucleic acid sample from T-cells and/or B-cells of the individual; (b) spatially isolating individual molecules derived from such nucleic acid sample, the individual molecules comprising at least one template generated from a nucleic acid in the sample, which template comprises a somatically rearranged region or a portion thereof, each individual molecule being capable of producing at least one sequence read; (c) sequencing said spatially isolated individual molecules; and (d) determining abundances of different sequences of the nucleic acid molecules from the nucleic acid sample to generate the clonotype profile. In one embodiment, each of the somatically rearranged regions comprise a V region and a J region. In another embodiment, the step of sequencing comprises bidirectionally sequencing each of the spatially isolated individual molecules to produce at least one forward sequence read and at least one reverse sequence read. Further to the latter embodiment, at least one of the forward sequence reads and at least one of the reverse sequence reads have an overlap region such that

bases of such overlap region are determined by a reverse complementary relationship between such sequence reads. In still another embodiment, each of the somatically rearranged regions comprise a V region and a J region and the step of sequencing further includes determining a sequence of each of the individual nucleic acid molecules from one or more of its forward sequence reads and at least one reverse sequence read starting from a position in a J region and extending in the direction of its associated V region. In another embodiment, individual molecules comprise nucleic acids selected from the group consisting of complete IgH molecules, incomplete IgH molecules, complete IgK complete, IgK inactive molecules, TCRβ molecules, TCRγ molecules, complete TCRδ molecules, and incomplete TCRδ molecules. In another embodiment, the step of sequencing comprises generating the sequence reads having monotonically decreasing quality scores. Further to the latter embodiment, monotonically decreasing quality scores are such that the sequence reads have error rates no better than the following: 0.2 percent of sequence reads contain at least one error in base positions 1 to 50, 0.2 to 1.0 percent of sequence reads contain at least one error in positions 51-75, 0.5 to 1.5 percent of sequence reads contain at least one error in positions 76-100. In another embodiment, the above method comprises the following steps: (a) obtaining a nucleic acid sample from T-cells and/or B-cells of the individual; (b) spatially isolating individual molecules derived from such nucleic acid sample, the individual molecules comprising nested sets of templates each generated from a nucleic acid in the sample and each containing a somatically rearranged region or a portion thereof, each nested set being capable of producing a plurality of sequence reads each extending in the same direction and each starting from a different position on the nucleic acid from which the nested set was generated; (c) sequencing said spatially isolated individual molecules; and (d) determining abundances of different sequences of the nucleic acid molecules from the nucleic acid sample to generate the clonotype profile. In one embodiment, the step of sequencing includes producing a plurality of sequence reads for each of the nested sets. In another embodiment, each of the somatically rearranged regions comprise a V region and a J region, and each of the plurality of sequence reads starts from a different position in the V region and extends in the direction of its associated J region.

[0036] In one aspect, for each sample from an individual, the sequencing technique used in the methods of the invention generates sequences of least 1000 clonotypes per run; in another aspect, such technique generates sequences of at least 10,000 clonotypes per run; in another aspect, such technique generates sequences of at least 100,000 clonotypes per run; in another aspect, such technique generates sequences of at least 500,000 clonotypes per run; and in another aspect, such technique generates sequences of at least 1,000,000 clonotypes per run. In still another

aspect, such technique generates sequences of between 100,000 to 1,000,000 clonotypes per run per individual sample.

[0037] The sequencing technique used in the methods of the provided invention can generate about 30 bp, about 40 bp, about 50 bp, about 60 bp, about 70 bp, about 80 bp, about 90 bp, about 100 bp, about 110, about 120 bp per read, about 150 bp, about 200 bp, about 250 bp, about 300 bp, about 350 bp, about 400 bp, about 450 bp, about 500 bp, about 550 bp, or about 600 bp per read.

Clonotype Determination from Sequence Data

[0038] Constructing clonotypes from sequence read data depends in part on the sequencing method used to generate such data, as the different methods have different expected read lengths and data quality. In one approach, a Solexa sequencer is employed to generate sequence read data for analysis as described in Faham and Willis, cited above). In one embodiment, a sample is obtained that provides at least 0.5-1.0x10^6 lymphocytes to produce at least 1 million template molecules, which after optional amplification may produce a corresponding one million or more clonal populations of template molecules (or clusters). For most high throughput sequencing approaches, including the Solexa approach, such over sampling at the cluster level is desirable so that each template sequence is determined with a large degree of redundancy to increase the accuracy of sequence determination. For Solexa-based implementations, preferably the sequence of each independent template is determined 10 times or more. For other sequencing approaches with different expected read lengths and data quality, different levels of redundancy may be used for comparable accuracy of sequence determination. Those of ordinary skill in the art recognize that the above parameters, e.g. sample size, redundancy, and the like, are design choices related to particular applications.

[0039] In one aspect of the invention, sequences of clonotypes (including but not limited to those derived from IgH, TCRα, TCRβ, TCRγ, TCRδ, and/or IgLκ (IgK)) may be determined by combining information from one or more sequence reads, for example, along the V(D)J regions of the selected chains. In another aspect, sequences of clonotypes are determined by combining information from a plurality of sequence reads. Such pluralities of sequence reads may include one or more sequence reads along a sense strand (i.e. "forward" sequence reads) and one or more sequence reads along its complementary strand (i.e. "reverse" sequence reads). When multiple sequence reads are generated along the same strand, separate templates are first generated by amplifying sample molecules with primers selected for the different positions of the sequence

reads. This concept is illustrated in Fig. 4A where primers (404, 406 and 408) are employed to generate amplicons (410, 412, and 414, respectively) in a single reaction. Such amplifications may be carried out in the same reaction or in separate reactions. In one aspect, whenever PCR is employed, separate amplification reactions are used for generating the separate templates which, in turn, are combined and used to generate multiple sequence reads along the same strand. This latter approach is preferable for avoiding the need to balance primer concentrations (and/or other reaction parameters) to ensure equal amplification of the multiple templates (sometimes referred to herein as "balanced amplification" or "unbias amplification"). The generation of templates in separate reactions is illustrated in Figs. 4B-4C. There a sample containing IgH (400) is divided into three portions (472, 474, and 476) which are added to separate PCRs using J region primers (401) and V region primers (404, 406, and 408, respectively) to produce amplicons (420, 422 and 424, respectively). The latter amplicons are then combined (478) in secondary PCR (480) using P5 and P7 primers to prepare the templates (482) for bridge PCR and sequencing on an Illumina GA sequencer, or like instrument.

[0040] Sequence reads of the invention may have a wide variety of lengths, depending in part on the sequencing technique being employed. For example, for some techniques, several trade-offs may arise in its implementation, for example, (i) the number and lengths of sequence reads per template and (ii) the cost and duration of a sequencing operation. In one embodiment, sequence reads are in the range of from 20 to 400 nucleotides; in another embodiment, sequence reads are in a range of from 30 to 200 nucleotides; in still another embodiment, sequence reads are in the range of from 30 to 120 nucleotides. In one embodiment, 1 to 4 sequence reads are generated for determining the sequence of each clonotype; in another embodiment, 2 to 4 sequence reads are generated for determining the sequence of each clonotype; and in another embodiment, 2 to 3 sequence reads are generated for determining the sequence of each clonotype. In the foregoing embodiments, the numbers given are exclusive of sequence reads used to identify samples from different individuals. The lengths of the various sequence reads used in the embodiments described below may also vary based on the information that is sought to be captured by the read; for example, the starting location and length of a sequence read may be designed to provide the length of an NDN region as well as its nucleotide sequence; thus, sequence reads spanning the entire NDN region are selected. In other aspects, one or more sequence reads that in combination (but not separately) encompass a D and /or NDN region are sufficient.

[0041] In another aspect of the invention, sequences of clonotypes are determined in part by aligning sequence reads to one or more V region reference sequences and one or more J region reference sequences, and in part by base determination without alignment to reference

sequences, such as in the highly variable NDN region. A variety of alignment algorithms may be applied to the sequence reads and reference sequences. For example, guidance for selecting alignment methods is available in Batzoglou, Briefings in Bioinformatics, 6: 6-22 (2005), which is incorporated by reference. In one aspect, whenever V reads or C reads (as mentioned above) are aligned to V and J region reference sequences, a tree search algorithm is employed, e.g. as described generally in Gusfield (cited above) and Cormen et al, Introduction to Algorithms, Third Edition (The MIT Press, 2009).

[0042] In another aspect, an end of at least one forward read and an end of at least one reverse read overlap in an overlap region (e.g. 308 in Fig. 3A), so that the bases of the reads are in a reverse complementary relationship with one another. Thus, for example, if a forward read in the overlap region is "5'-acgttgc", then a reverse read in a reverse complementary relationship is "5'-gcaacgt" within the same overlap region. In one aspect, bases within such an overlap region are determined, at least in part, from such a reverse complementary relationship. That is, a likelihood of a base call (or a related quality score) in a prospective overlap region is increased if it preserves, or is consistent with, a reverse complementary relationship between the two sequence reads. In one aspect, clonotypes of TCR β and IgH chains (illustrated in Fig. 3A) are determined by at least one sequence read starting in its J region and extending in the direction of its associated V region (referred to herein as a "C read" (304)) and at least one sequence read starting in its V region and extending in the direction of its associated J region (referred to herein as a "V read" (306)). Overlap region (308) may or may not encompass the NDN region (315) as shown in Fig. 3A. Overlap region (308) may be entirely in the J region, entirely in the NDN region, entirely in the V region, or it may encompass a J region-NDN region boundary or a V region-NDN region boundary, or both such boundaries (as illustrated in Fig. 3A). Typically, such sequence reads are generated by extending sequencing primers, e.g. (302) and (310) in Fig. 3A, with a polymerase in a sequencing-by-synthesis reaction, e.g. Metzger, Nature Reviews Genetics, 11: 31-46 (2010); Fuller et al, Nature Biotechnology, 27: 1013-1023 (2009). The binding sites for primers (302) and (310) are predetermined, so that they can provide a starting point or anchoring point for initial alignment and analysis of the sequence reads. In one embodiment, a C read is positioned so that it encompasses the D and/or NDN region of the TCR β or IgH chain and includes a portion of the adjacent V region, e.g. as illustrated in Figs. 3A and 3B. In one aspect, the overlap of the V read and the C read in the V region is used to align the reads with one another. In other embodiments, such alignment of sequence reads is not necessary, e.g. with TCRβ chains, so that a V read may only be long enough to identify the particular V region of a clonotype. This latter aspect is illustrated in Fig. 3B. Sequence read

(330) is used to identify a V region, with or without overlapping another sequence read, and another sequence read (332) traverses the NDN region and is used to determine the sequence thereof. Portion (334) of sequence read (332) that extends into the V region is used to associate the sequence information of sequence read (332) with that of sequence read (330) to determine a clonotype. For some sequencing methods, such as base-by-base approaches like the Solexa sequencing method, sequencing run time and reagent costs are reduced by minimizing the number of sequencing cycles in an analysis. Optionally, as illustrated in Fig. 3A, amplicon (300) is produced with sample tag (312) to distinguish between clonotypes originating from different biological samples, e.g. different patients. Sample tag (312) may be identified by annealing a primer to primer binding region (316) and extending it (314) to produce a sequence read across tag (312), from which sample tag (312) is decoded.

[0043] The IgH chain is more challenging to analyze than TCRβ chain because of at least two factors: i) the presence of somatic mutations makes the mapping or alignment more difficult, and ii) the NDN region is larger so that it is often not possible to map a portion of the V segment to the C read. In one aspect of the invention, this problem is overcome by using a plurality of primer sets for generating V reads, which are located at different locations along the V region, preferably so that the primer binding sites are nonoverlapping and spaced apart, and with at least one primer binding site adjacent to the NDN region, e.g. in one embodiment from 5 to 50 bases from the V-NDN junction, or in another embodiment from 10 to 50 bases from the V-NDN junction. The redundancy of a plurality of primer sets minimizes the risk of failing to detect a clonotype due to a failure of one or two primers having binding sites affected by somatic mutations. In addition, the presence of at least one primer binding site adjacent to the NDN region makes it more likely that a V read will overlap with the C read and hence effectively extend the length of the C read. This allows for the generation of a continuous sequence that spans all sizes of NDN regions and that can also map substantially the entire V and J regions on both sides of the NDN region. Embodiments for carrying out such a scheme are illustrated in Figs. 4A and 4D. In Fig. 4A, a sample comprising IgH chains (400) are sequenced by generating a plurality amplicons for each chain by amplifying the chains with a single set of J region primers (401) and a plurality (three shown) of sets of V region (402) primers (404, 406, 408) to produce a plurality of nested amplicons (e.g., 410, 412, 416) all comprising the same NDN region and having different lengths encompassing successively larger portions (411, 413, 415) of V region (402). Members of a nested set may be grouped together after sequencing by noting the identify (or substantial identity) of their respective NDN, J and/or C regions, thereby allowing reconstruction of a longer V(D)J segment than would be the case otherwise for a

sequencing platform with limited read length and/or sequence quality. In one embodiment, the plurality of primer sets may be a number in the range of from 2 to 5. In another embodiment the plurality is 2-3; and still another embodiment the plurality is 3. The concentrations and positions of the primers in a plurality may vary widely. Concentrations of the V region primers may or may not be the same. In one embodiment, the primer closest to the NDN region has a higher concentration than the other primers of the plurality, e.g. to insure that amplicons containing the NDN region are represented in the resulting amplicon. In a particular embodiment where a plurality of three primers is employed, a concentration ratio of 60:20:20 is used. One or more primers (e.g. 435 and 437 in Fig. 4D) adjacent to the NDN region (444) may be used to generate one or more sequence reads (e.g. 434 and 436) that overlap the sequence read (442) generated by J region primer (432), thereby improving the quality of base calls in overlap region (440). Sequence reads from the plurality of primers may or may not overlap the adjacent downstream primer binding site and/or adjacent downstream sequence read. In one embodiment, sequence reads proximal to the NDN region (e.g. 436 and 438) may be used to identify the particular V region associated with the clonotype. Such a plurality of primers reduces the likelihood of incomplete or failed amplification in case one of the primer binding sites is hypermutated during immunoglobulin development. It also increases the likelihood that diversity introduced by hypermutation of the V region will be capture in a clonotype sequence. A secondary PCR may be performed to prepare the nested amplicons for sequencing, e.g. by amplifying with the P5 (401) and P7 (404, 406, 408) primers as illustrated to produce amplicons (420, 422, and 424), which may be distributed as single molecules on a solid surface, where they are further amplified by bridge PCR, or like technique.

[0044] Base calling in NDN regions (particularly of IgH chains) can be improved by using the codon structure of the flanking J and V regions, as illustrated in Fig. 4E. (As used herein, "codon structure" means the codons of the natural reading frame of segments of TCR or BCR transcripts or genes outside of the NDN regions, e.g. the V region, J region, or the like.) There amplicon (450), which is an enlarged view of the amplicon of Fig. 4B, is shown along with the relative positions of C read (442) and adjacent V read (434) above and the codon structures (452 and 454) of V region (430) and J region (446), respectively, below. In accordance with this aspect of the invention, after the codon structures (452 and 454) are identified by conventional alignment to the V and J reference sequences, bases in NDN region (456) are called (or identified) one base at a time moving from J region (446) toward V region (430) and in the opposite direction from V region (430) toward J region (446) using sequence reads (434) and (442). Under normal biological conditions, only the recombined TCR or IgH sequences that

have in frame codons from the V region through the NDN region and to the J region are expressed as proteins. That is, of the variants generated somatically only ones expressed are those whose J region and V region codon frames are in-frame with one another and remain in-frame through the NDN region. (Here the correct frames of the V and J regions are determined from reference sequences). If an out-of-frame sequence is identified based one or more low quality base calls, the corresponding clonotype is flagged for re-evaluation or as a potential disease-related anomaly. If the sequence identified is in-frame and based on high quality base calls, then there is greater confidence that the corresponding clonotype has been correctly called. Accordingly, in one aspect, the invention includes a method of determining V(D)J-based clonotypes from bidirectional sequence reads comprising the steps of: (a) generating at least one J region sequence read that begins in a J region and extends into an NDN region and at least one V region sequence read that begins in the V regions and extends toward the NDN region such that the J region sequence read and the V region sequence read are overlapping in an overlap region, and the J region and the V region each have a codon structure; (b) determining whether the codon structure of the J region extended into the NDN region is in frame with the codon structure of the V region extended toward the NDN region. In a further embodiment, the step of generating includes generating at least one V region sequence read that begins in the V region and extends through the NDN region to the J region, such that the J region sequence read and the V region sequence read are overlapping in an overlap region.

[0045] Somatic Hypermutations. In one embodiment, IgH-based clonotypes that have undergone somatic hypermutation are determined as follows. A somatic mutation is defined as a sequenced base that is different from the corresponding base of a reference sequence (of the relevant segment, usually V, J or C) and that is present in a statistically significant number of reads. In one embodiment, C reads may be used to find somatic mutations with respect to the mapped J segment and likewise V reads for the V segment. Only pieces of the C and V reads are used that are either directly mapped to J or V segments or that are inside the clonotype extension up to the NDN boundary. In this way, the NDN region is avoided and the same 'sequence information' is not used for mutation finding that was previously used for clonotype determination (to avoid erroneously classifying as mutations nucleotides that are really just different recombined NDN regions). For each segment type, the mapped segment (major allele) is used as a scaffold and all reads are considered which have mapped to this allele during the read mapping phase. Each position of the reference sequences where at least one read has mapped is analyzed for somatic mutations. In one embodiment, the criteria for accepting a non-reference base as a valid mutation include the following: 1) at least N reads with the given

mutation base, 2) at least a given fraction N/M reads (where M is the total number of mapped reads at this base position) and 3) a statistical cut based on the binomial distribution, the average Q score of the N reads at the mutation base as well as the number (M-N) of reads with a non-mutation base. Preferably, the above parameters are selected so that the false discovery rate of mutations per clonotype is less than 1 in 1000, and more preferably, less than 1 in 10000.

TCRβ Repertoire Analysis

[0046] In this example, TCRβ chains are analyzed. The analysis includes amplification, sequencing, and analyzing the TCRβ sequences. One primer is complementary to a common sequence in Cβ1 and Cβ2, and there are 34 V primers capable of amplifying all 48 V segments. Cβ1 or Cβ2 differ from each other at position 10 and 14 from the J/C junction. The primer for Cβ1 and Cβ2 ends at position 16 bp and has no preference for Cβ1 or Cβ2. The 34 V primers are modified from an original set of primers disclosed in Van Dongen et al, U.S. patent publication 2006/0234234, which is incorporated herein by reference. The modified primers are disclosed in Faham et al, U.S. patent publication 2010/0151471, which is also incorporated herein by reference.

[0047] The Illumina Genome Analyzer is used to sequence the amplicon produced by the above primers. A two-stage amplification is performed on messenger RNA transcripts (200), as illustrated in Figs. 2A-2B, the first stage employing the above primers and a second stage to add common primers for bridge amplification and sequencing. As shown in FIG. 2A, a primary PCR is performed using on one side a 20 bp primer (202) whose 3' end is 16 bases from the J/C junction (204) and which is perfectly complementary to Cβ1(203) and the two alleles of Cβ2. In the V region (206) of RNA transcripts (200), primer set (212) is provided which contains primer sequences complementary to the different V region sequences (34 in one embodiment). Primers of set (212) also contain a non-complementary tail (214) that produces amplicon (216) having primer binding site (218) specific for P7 primers (220). After a conventional multiplex PCR, amplicon (216) is formed that contains the highly diverse portion of the J(D)V region (206, 208, and 210) of the mRNA transcripts and common primer binding sites (203 and 218) for a secondary amplification to add a sample tag (221) and primers (220 and 222) for cluster formation by bridge PCR. In the secondary PCR, on the same side of the template, a primer (222 in Fig. 2B and referred to herein as "C10-17-P5") is used that has at its 3'end the sequence of the 10 bases closest to the J/C junction, followed by 17 bp with the sequence of positions 15-31 from the J/C junction, followed by the P5 sequence (224), which plays a role in cluster formation

by bridge PCR in Solexa sequencing. (When the C10-17-P5 primer (222) anneals to the template generated from the first PCR, a 4 bp loop (position 11-14) is created in the template, as the primer hybridizes to the sequence of the 10 bases closest to the J/C junction and bases at positions 15-31 from the J/C junction. The looping of positions 11-14 eliminates differential amplification of templates carrying Cβ1 or Cβ2. Sequencing is then done with a primer complementary to the sequence of the 10 bases closest to the J/C junction and bases at positions 15-31 from the J/C junction (this primer is called C'). C10-17-P5 primer can be HPLC purified in order to ensure that all the amplified material has intact ends that can be efficiently utilized in the cluster formation.)

[0048] In FIG. 2A, the length of the overhang on the V primers (212) is preferably 14 bp. The primary PCR is helped with a shorter overhang (214). Alternatively, for the sake of the secondary PCR, the overhang in the V primer is used in the primary PCR as long as possible because the secondary PCR is priming from this sequence. A minimum size of overhang (214) that supports an efficient secondary PCR was investigated. Two series of V primers (for two different V segments) with overhang sizes from 10 to 30 with 2 bp steps were made. Using the appropriate synthetic sequences, the first PCR was performed with each of the primers in the series and gel electrophoresis was performed to show that all amplified.

[0049] As illustrated in FIG. 2A, the primary PCR uses 34 different V primers (212) that anneal to V region (206) of RNA templates (200) and contain a common 14 bp overhang on the 5' tail. The 14 bp is the partial sequence of one of the Illumina sequencing primers (termed the Read 2 primer). The secondary amplification primer (220) on the same side includes P7 sequence, a tag (221), and Read 2 primer sequence (223) (this primer is called Read2_tagX_P7). The P7 sequence is used for cluster formation. Read 2 primer and its complement are used for sequencing the V segment and the tag respectively. A set of 96 of these primers with tags numbered 1 through 96 are created (see below). These primers are HPLC purified in order to ensure that all the amplified material has intact ends that can be efficiently utilized in the cluster formation.

[0050] As mentioned above, the second stage primer, C-10-17-P5 (222, FIG. 2B) has interrupted homology to the template generated in the first stage PCR. The efficiency of amplification using this primer has been validated. An alternative primer to C-10-17-P5, termed CsegP5, has perfect homology to the first stage C primer and a 5' tail carrying P5. The efficiency of using C-10-17-P5 and CsegP5 in amplifying first stage PCR templates was compared by performing real time

PCR. In several replicates, it was found that PCR using the C-10-17-P5 primer had little or no difference in efficiency compared with PCR using the CsegP5 primer.

[0051] Amplicon (230) resulting from the 2-stage amplification illustrated in Figs. 2A-2C has the structure typically used with the Illumina sequencer as shown in FIG. 2C. Two primers that anneal to the outmost part of the molecule, Illumina primers P5 and P7 are used for solid phase amplification of the molecule (cluster formation). Three sequence reads are done per molecule. The first read of 100 bp is done with the C' primer, which has a melting temperature that is appropriate for the Illumina sequencing process. The second read is 6 bp long only and is solely for the purpose of identifying the sample tag. It is generated using a tag primer provided by the manufacturer (Illumina). The final read is the Read 2 primer, also provided by the manufacturer (Illumina). Using this primer, a 100 bp read in the V segment is generated starting with the 1st PCR V primer sequence.

[0052] While the present invention has been described with reference to several particular example embodiments, those skilled in the art will recognize that many changes may be made thereto without departing from the spirit and scope of the present invention. The present invention is applicable to a variety of sensor implementations and other subject matter, in addition to those discussed above.

Definitions

[0053] Unless otherwise specifically defined herein, terms and symbols of nucleic acid chemistry, biochemistry, genetics, and molecular biology used herein follow those of standard treatises and texts in the field, e.g. Kornberg and Baker, DNA Replication, Second Edition (W.H. Freeman, New York, 1992); Lehninger, Biochemistry, Second Edition (Worth Publishers, New York, 1975); Strachan and Read, Human Molecular Genetics, Second Edition (Wiley-Liss, New York, 1999); Abbas et al, Cellular and Molecular Immunology, 6th edition (Saunders, 2007).

[0054] "Aligning" means a method of comparing a test sequence, such as a sequence read, to one or more reference sequences to determine which reference sequence or which portion of a reference sequence is closest based on some sequence distance measure. An exemplary method of aligning nucleotide sequences is the Smith Waterman algorithm. Distance measures may include Hamming distance, Levenshtein distance, or the like. Distance measures may include a component related to the quality values of nucleotides of the sequences being compared.

[0055] "Amplicon" means the product of a polynucleotide amplification reaction; that is, a clonal population of polynucleotides, which may be single stranded or double stranded, which

are replicated from one or more starting sequences. The one or more starting sequences may be one or more copies of the same sequence, or they may be a mixture of different sequences. Preferably, amplicons are formed by the amplification of a single starting sequence. Amplicons may be produced by a variety of amplification reactions whose products comprise replicates of the one or more starting, or target, nucleic acids. In one aspect, amplification reactions producing amplicons are "template-driven" in that base pairing of reactants, either nucleotides or oligonucleotides, have complements in a template polynucleotide that are required for the creation of reaction products. In one aspect, template-driven reactions are primer extensions with a nucleic acid polymerase or oligonucleotide ligations with a nucleic acid ligase. Such reactions include, but are not limited to, polymerase chain reactions (PCRs), linear polymerase reactions, nucleic acid sequence-based amplification (NASBAs), rolling circle amplifications, and the like, disclosed in the following references that are incorporated herein by reference: Mullis et al, U.S. patents 4,683,195; 4,965,188; 4,683,202; 4,800,159 (PCR); Gelfand et al, U.S. patent 5,210,015 (real-time PCR with "taqman" probes); Wittwer et al, U.S. patent 6,174,670; Kacian et al, U.S. patent 5,399,491 ("NASBA"); Lizardi, U.S. patent 5,854,033; Aono et al, Japanese patent publ. JP 4-262799 (rolling circle amplification); and the like. In one aspect, amplicons of the invention are produced by PCRs. An amplification reaction may be a "real-time" amplification if a detection chemistry is available that permits a reaction product to be measured as the amplification reaction progresses, e.g. "real-time PCR" described below, or "real-time NASBA" as described in Leone et al, Nucleic Acids Research, 26: 2150-2155 (1998), and like references. As used herein, the term "amplifying" means performing an amplification reaction. A "reaction mixture" means a solution containing all the necessary reactants for performing a reaction, which may include, but not be limited to, buffering agents to maintain pH at a selected level during a reaction, salts, co-factors, scavengers, and the like.

[0056] "Cancer vaccine" means a composition comprising one or more tumor antigens. A cancer vaccine may also comprise components found in vaccines for infectious agents, such as, solvents, stabilizers, adjuvants, buffers, surfactants, preservatives, salts, and the like. Tumor antigens may be incorporated into a cancer vaccine in a variety of formats, including but not limited to, whole tumor cells, lysates of tumor cells, gene-modified tumor cells, DNA encoding one or more tumor antigens, peptides, plasmids, viral gene transfer vectors, RNA encoding one or more tumor antigens, dendritic cells loaded with tumor antigen (e.g. tumor antigen peptides, tumor lysates, whole protein tumor antigen, transfection solutions containing RNA that encodes one or more tumor antigen, and so on), see Berzofsky et al, J. Clin. Investigation, 113: 1515-1525 (2004). In one embodiment, a cancer vaccine comprises one or more tumor antigens and

an adjuvant. In another embodiment, one or more tumor antigens are included in a cancer vaccine as whole tumor cells, lysates of tumor cells, or one or more tumor proteins expressed from genes derived from tumor cells. In another embodiment, one or more tumor antigens comprise one or more tumor antigen peptides operationally associated with an antigen presenting cell. In another embodiment, an antigen presenting cell is a dendritic cell. In one aspect, cancer vaccines are designed to directly or indirectly stimulate a recipient's cytotoxic T cells to react to and destroy tumor cells.

[0057] "Clonality" as used herein means a measure of the degree to which the distribution of clonotype abundances among clonotypes of a repertoire is skewed to a single or a few clonotypes. Roughly, clonality is an inverse measure of clonotype diversity. Many measures or statistics are available from ecology describing species-abundance relationships that may be used for clonality measures in accordance with the invention, e.g. Chapters 17 & 18, in Pielou, An Introduction to Mathematical Ecology, (Wiley-Interscience, 1969). In one aspect, a clonality measure used with the invention is a function of a clonotype profile (that is, the number of distinct clonotypes detected and their abundances), so that after a clonotype profile is measured, clonality may be computed from it to give a single number. One clonality measure is Simpson's measure, which is simply the probability that two randomly drawn clonotypes will be the same. Other clonality measures include information-based measures and McIntosh's diversity index, disclosed in Pielou (cited above).

[0058] "Clonotype" means a recombined nucleotide sequence of a lymphocyte which encodes an immune receptor or a portion thereof. More particularly, clonotype means a recombined nucleotide sequence of a T cell or B cell which encodes a T cell receptor (TCR) or B cell receptor (BCR), or a portion thereof. In various embodiments, clonotypes may encode all or a portion of a VDJ rearrangement of IgH, a DJ rearrangement of IgH, a VJ rearrangement of IgK, a VJ rearrangement of IgL, a VDJ rearrangement of TCR β, a DJ rearrangement of TCR β, a VJ rearrangement of TCR α, a VJ rearrangement of TCR γ, a VDJ rearrangement of TCR δ, a VD rearrangement of TCR δ, a Kde-V rearrangement, or the like. Clonotypes may also encode translocation breakpoint regions involving immune receptor genes, such as Bcl1-IgH or Bcl1-IgH. In one aspect, clonotypes have sequences that are sufficiently long to represent or reflect the diversity of the immune molecules that they are derived from; consequently, clonotypes may vary widely in length. In some embodiments, clonotypes have lengths in the range of from 25 to 400 nucleotides; in other embodiments, clonotypes have lengths in the range of from 25 to 200 nucleotides.

[0059] "Clonotype profile" means a listing of distinct clonotypes and their relative abundances that are derived from a population of lymphocytes. Typically, the population of lymphocytes are obtained from a tissue sample. The term "clonotype profile" is related to, but more general than, the immunology concept of immune "repertoire" as described in references, such as the following: Arstila et al, Science, 286: 958-961 (1999); Yassai et al, Immunogenetics, 61: 493-502 (2009); Kedzierska et al, Mol. Immunol., 45(3): 607-618 (2008); and the like. The term "clonotype profile" includes a wide variety of lists and abundances of rearranged immune receptor-encoding nucleic acids, which may be derived from selected subsets of lymphocytes (e.g. tissue-infiltrating lymphocytes, immunophenotypic subsets, or the like), or which may encode portions of immune receptors that have reduced diversity as compared to full immune receptors. In some embodiments, clonotype profiles may comprise at least 10^3 distinct clonotypes; in other embodiments, clonotype profiles may comprise at least 10^4 distinct clonotypes; in other embodiments, clonotype profiles may comprise at least 10^5 distinct clonotypes; in other embodiments, clonotype profiles may comprise at least 10^6 distinct clonotypes. In such embodiments, such clonotype profiles may further comprise abundances or relative frequencies of each of the distinct clonotypes. In one aspect, a clonotype profile is a set of distinct recombined nucleotide sequences (with their abundances) that encode T cell receptors (TCRs) or B cell receptors (BCRs), or fragments thereof, respectively, in a population of lymphocytes of an individual, wherein the nucleotide sequences of the set have a one-to-one correspondence with distinct lymphocytes or their clonal subpopulations for substantially all of the lymphocytes of the population. In one aspect, nucleic acid segments defining clonotypes are selected so that their diversity (i.e. the number of distinct nucleic acid sequences in the set) is large enough so that substantially every T cell or B cell or clone thereof in an individual carries a unique nucleic acid sequence of such repertoire. That is, preferably each different clone of a sample has different clonotype. In other aspects of the invention, the population of lymphocytes corresponding to a repertoire may be circulating B cells, or may be circulating T cells, or may be subpopulations of either of the foregoing populations, including but not limited to, CD4+ T cells, or CD8+ T cells, or other subpopulations defined by cell surface markers, or the like. Such subpopulations may be acquired by taking samples from particular tissues, e.g. bone marrow, or lymph nodes, or the like, or by sorting or enriching cells from a sample (such as peripheral blood) based on one or more cell surface markers, size, morphology, or the like. In still other aspects, the population of lymphocytes corresponding to a repertoire may be derived from disease tissues, such as a tumor tissue, an infected tissue, or the like. In one embodiment, a clonotype profile comprising human TCR β chains or fragments thereof comprises a number of

distinct nucleotide sequences in the range of from 0.1 x 10^6 to 1.8 x 10^6, or in the range of from 0.5 x 10^6 to 1.5 x 10^6, or in the range of from 0.8 x 10^6 to 1.2 x 10^6. In another embodiment, a clonotype profile comprising human IgH chains or fragments thereof comprises a number of distinct nucleotide sequences in the range of from 0.1 x 10^6 to 1.8 x 10^6, or in the range of from 0.5 x 10^6 to 1.5 x 10^6, or in the range of from 0.8 x 10^6 to 1.2 x 10^6. In a particular embodiment, a clonotype profile of the invention comprises a set of nucleotide sequences encoding substantially all segments of the V(D)J region of an IgH chain. In one aspect, "substantially all" as used herein means every segment having a relative abundance of .001 percent or higher; or in another aspect, "substantially all" as used herein means every segment having a relative abundance of .0001 percent or higher. In another particular embodiment, a clonotype profile of the invention comprises a set of nucleotide sequences that encodes substantially all segments of the V(D)J region of a TCR β chain. In another embodiment, a clonotype profile of the invention comprises a set of nucleotide sequences having lengths in the range of from 25-200 nucleotides and including segments of the V, D, and J regions of a TCR β chain. In another embodiment, a clonotype profile of the invention comprises a set of nucleotide sequences having lengths in the range of from 25-200 nucleotides and including segments of the V, D, and J regions of an IgH chain. In another embodiment, a clonotype profile of the invention comprises a number of distinct nucleotide sequences that is substantially equivalent to the number of lymphocytes expressing a distinct IgH chain. In another embodiment, a clonotype profile of the invention comprises a number of distinct nucleotide sequences that is substantially equivalent to the number of lymphocytes expressing a distinct TCR β chain. In still another embodiment, "substantially equivalent" means that with ninety-nine percent probability a clonotype profile will include a nucleotide sequence encoding an IgH or TCR β or portion thereof carried or expressed by every lymphocyte of a population of an individual at a frequency of .001 percent or greater. In still another embodiment, "substantially equivalent" means that with ninety-nine percent probability a repertoire of nucleotide sequences will include a nucleotide sequence encoding an IgH or TCR β or portion thereof carried or expressed by every lymphocyte present at a frequency of .0001 percent or greater. In some embodiments, clonotype profiles are derived from samples comprising from 10^5 to 10^7 lymphocytes. Such numbers of lymphocytes may be obtained from peripheral blood samples of from 1-10 mL.

[0060] "Complementarity determining regions" (CDRs) mean regions of an immunoglobulin (i.e., antibody) or T cell receptor where the molecule complements an antigen's conformation, thereby determining the molecule's specificity and contact with a specific antigen. T cell

receptors and immunoglobulins each have three CDRs: CDR1 and CDR2 are found in the variable (V) domain, and CDR3 includes some of V, all of diverse (D) (heavy chains only) and joint (J), and some of the constant (C) domains.

[0061] "Immune response" means the tumor-antigen induced proliferation and differentiation of lymphocytes into effector cells. An aspect of an immune response of particular interest is a tumor-antigen induced proliferation of T cells. In one aspect, immune response means the proliferation of cytotoxic T cells capable of specifically recognizing tumor cells. As used herein, the term proliferation means an increase in absolute number or an increase in proportion within a population, e.g. as determined by clonotype profiles. "Immune responsiveness" means the magnitude or level of an immune response.

[0062] "Lymphoid or myeloid proliferative disorder" means any abnormal proliferative disorder in which one or more nucleotide sequences encoding one or more rearranged immune receptors can be used as a marker for monitoring such disorder. "Lymphoid or myeloid neoplasm" means an abnormal proliferation of lymphocytes or myeloid cells that may be malignant or non-malignant. A lymphoid cancer is a malignant lymphoid neoplasm. A myeloid cancer is a malignant myeloid neoplasm. Lymphoid and myeloid neoplasms are the result of, or are associated with, lymphoproliferative or myeloproliferative disorders, and include, but are not limited to, follicular lymphoma, chronic lymphocytic leukemia (CLL), acute lymphocytic leukemia (ALL), chronic myelogenous leukemia (CML), acute myelogenous leukemia (AML), Hodgkins's and non-Hodgkin's lymphomas, multiple myeloma (MM), monoclonal gammopathy of undetermined significance (MGUS), mantle cell lymphoma (MCL), diffuse large B cell lymphoma (DLBCL), myelodysplastic syndromes (MDS), T cell lymphoma, or the like, e.g. Jaffe et al, Blood, 112: 4384-4399 (2008); Swerdlow et al, WHO Classification of Tumours of Haematopoietic and Lymphoid Tissues (e. 4^{th}) (IARC Press, 2008).

[0063] "Pecent homologous," "percent identical," or like terms used in reference to the comparison of a reference sequence and another sequence ("comparison sequence") mean that in an optimal alignment between the two sequences, the comparison sequence is identical to the reference sequence in a number of subunit positions equivalent to the indicated percentage, the subunits being nucleotides for polynucleotide comparisons or amino acids for polypeptide comparisons. As used herein, an "optimal alignment" of sequences being compared is one that maximizes matches between subunits and minimizes the number of gaps employed in constructing an alignment. Percent identities may be determined with commercially available

implementations of algorithms, such as that described by Needleman and Wunsch, J. Mol. Biol., 48: 443-453 (1970)("GAP" program of Wisconsin Sequence Analysis Package, Genetics Computer Group, Madison, WI), or the like. Other software packages in the art for constructing alignments and calculating percentage identity or other measures of similarity include the "BestFit" program, based on the algorithm of Smith and Waterman, Advances in Applied Mathematics, 2: 482-489 (1981) (Wisconsin Sequence Analysis Package, Genetics Computer Group, Madison, WI). In other words, for example, to obtain a polynucleotide having a nucleotide sequence at least 95 percent identical to a reference nucleotide sequence, up to five percent of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to five percent of the total number of nucleotides in the reference sequence may be inserted into the reference sequence.

[0064] "Polymerase chain reaction," or "PCR," means a reaction for the in vitro amplification of specific DNA sequences by the simultaneous primer extension of complementary strands of DNA. In other words, PCR is a reaction for making multiple copies or replicates of a target nucleic acid flanked by primer binding sites, such reaction comprising one or more repetitions of the following steps: (i) denaturing the target nucleic acid, (ii) annealing primers to the primer binding sites, and (iii) extending the primers by a nucleic acid polymerase in the presence of nucleoside triphosphates. Usually, the reaction is cycled through different temperatures optimized for each step in a thermal cycler instrument. Particular temperatures, durations at each step, and rates of change between steps depend on many factors well-known to those of ordinary skill in the art, e.g. exemplified by the references: McPherson et al, editors, PCR: A Practical Approach and PCR2: A Practical Approach (IRL Press, Oxford, 1991 and 1995, respectively). For example, in a conventional PCR using Taq DNA polymerase, a double stranded target nucleic acid may be denatured at a temperature >90°C, primers annealed at a temperature in the range 50-75°C, and primers extended at a temperature in the range 72-78°C. The term "PCR" encompasses derivative forms of the reaction, including but not limited to, RT-PCR, real-time PCR, nested PCR, quantitative PCR, multiplexed PCR, and the like. Reaction volumes range from a few hundred nanoliters, e.g. 200 nL, to a few hundred μL, e.g. 200 μL. "Reverse transcription PCR," or "RT-PCR," means a PCR that is preceded by a reverse transcription reaction that converts a target RNA to a complementary single stranded DNA, which is then amplified, e.g. Tecott et al, U.S. patent 5,168,038, which patent is incorporated herein by reference. "Real-time PCR" means a PCR for which the amount of reaction product, i.e. amplicon, is monitored as the reaction proceeds. There are many forms of real-time PCR that differ mainly in the detection chemistries used for monitoring the reaction product, e.g. Gelfand

et al, U.S. patent 5,210,015 ("taqman"); Wittwer et al, U.S. patents 6,174,670 and 6,569,627 (intercalating dyes); Tyagi et al, U.S. patent 5,925,517 (molecular beacons); which patents are incorporated herein by reference. Detection chemistries for real-time PCR are reviewed in Mackay et al, Nucleic Acids Research, 30: 1292-1305 (2002), which is also incorporated herein by reference. "Nested PCR" means a two-stage PCR wherein the amplicon of a first PCR becomes the sample for a second PCR using a new set of primers, at least one of which binds to an interior location of the first amplicon. As used herein, "initial primers" in reference to a nested amplification reaction mean the primers used to generate a first amplicon, and "secondary primers" mean the one or more primers used to generate a second, or nested, amplicon. "Multiplexed PCR" means a PCR wherein multiple target sequences (or a single target sequence and one or more reference sequences) are simultaneously carried out in the same reaction mixture, e.g. Bernard et al, Anal. Biochem., 273: 221-228 (1999)(two-color real-time PCR). Usually, distinct sets of primers are employed for each sequence being amplified. Typically, the number of target sequences in a multiplex PCR is in the range of from 2 to 50, or from 2 to 40, or from 2 to 30. "Quantitative PCR" means a PCR designed to measure the abundance of one or more specific target sequences in a sample or specimen. Quantitative PCR includes both absolute quantitation and relative quantitation of such target sequences. Quantitative measurements are made using one or more reference sequences or internal standards that may be assayed separately or together with a target sequence. The reference sequence may be endogenous or exogenous to a sample or specimen, and in the latter case, may comprise one or more competitor templates. Typical endogenous reference sequences include segments of transcripts of the following genes: β-actin, GAPDH, β_2-microglobulin, ribosomal RNA, and the like. Techniques for quantitative PCR are well-known to those of ordinary skill in the art, as exemplified in the following references that are incorporated by reference: Freeman et al, Biotechniques, 26: 112-126 (1999); Becker-Andre et al, Nucleic Acids Research, 17: 9437-9447 (1989); Zimmerman et al, Biotechniques, 21: 268-279 (1996); Diviacco et al, Gene, 122: 3013-3020 (1992); Becker-Andre et al, Nucleic Acids Research, 17: 9437-9446 (1989); and the like.

[0065] "Primer" means an oligonucleotide, either natural or synthetic that is capable, upon forming a duplex with a polynucleotide template, of acting as a point of initiation of nucleic acid synthesis and being extended from its 3' end along the template so that an extended duplex is formed. Extension of a primer is usually carried out with a nucleic acid polymerase, such as a DNA or RNA polymerase. The sequence of nucleotides added in the extension process is determined by the sequence of the template polynucleotide. Usually primers are extended by a DNA polymerase. Primers usually have a length in the range of from 14 to 40 nucleotides, or in

the range of from 18 to 36 nucleotides. Primers are employed in a variety of nucleic amplification reactions, for example, linear amplification reactions using a single primer, or polymerase chain reactions, employing two or more primers. Guidance for selecting the lengths and sequences of primers for particular applications is well known to those of ordinary skill in the art, as evidenced by the following references that are incorporated by reference: Dieffenbach, editor, PCR Primer: A Laboratory Manual, 2nd Edition (Cold Spring Harbor Press, New York, 2003).

[0066] "Quality score" means a measure of the probability that a base assignment at a particular sequence location is correct. A variety methods are well known to those of ordinary skill for calculating quality scores for particular circumstances, such as, for bases called as a result of different sequencing chemistries, detection systems, base-calling algorithms, and so on. Generally, quality score values are monotonically related to probabilities of correct base calling. For example, a quality score, or Q, of 10 may mean that there is a 90 percent chance that a base is called correctly, a Q of 20 may mean that there is a 99 percent chance that a base is called correctly, and so on. For some sequencing platforms, particularly those using sequencing-by-synthesis chemistries, average quality scores decrease as a function of sequence read length, so that quality scores at the beginning of a sequence read are higher than those at the end of a sequence read, such declines being due to phenomena such as incomplete extensions, carry forward extensions, loss of template, loss of polymerase, capping failures, deprotection failures, and the like.

[0067] "Sequence read" means a sequence of nucleotides determined from a sequence or stream of data generated by a sequencing technique, which determination is made, for example, by means of base-calling software associated with the technique, e.g. base-calling software from a commercial provider of a DNA sequencing platform. A sequence read usually includes quality scores for each nucleotide in the sequence. Typically, sequence reads are made by extending a primer along a template nucleic acid, e.g. with a DNA polymerase or a DNA ligase. Data is generated by recording signals, such as optical, chemical (e.g. pH change), or electrical signals, associated with such extension. Such initial data is converted into a sequence read.

What is claimed is:

1. A method of measuring immune responsiveness of a patient to a cancer vaccine, the method comprising the steps of:

generating a pair of clonotype profiles at each of a plurality of successive vaccinations of a patient with a cancer vaccine, wherein a first clonotype profile of each pair is from a sample from the patient prior to vaccination and a second clonotype profile of each pair is from a sample from the patient after vaccination at a time within a peak immune response to vaccination, each clonotype profile comprising at least 1000 sequence reads of at least 30 nucleotides; and

correlating immune responsiveness of the patient to the cancer vaccine with an increase of identical clonotypes within each pair of clonotype profiles of at least two successive vaccinations.

2. The method of claim 1 wherein said sample is a peripheral blood sample or a tumor sample.

3. The method of claim 1 wherein said peak immune response is in a period from two to twenty days, inclusive, after said vaccination.

4. The method of claim 1 wherein said step of correlating includes correlating said immune responsiveness with an increase of identical clonotypes within each pair of clonotype profiles of at least three successive vaccinations.

5. The method of claim 1 wherein said identical clonotypes encode immunoglobulins and/or T cell receptors specific for antigens of the cancer vaccine.

6. The method of claim 1 wherein a number and frequency of said identical clonotypes increase between said successive vaccinations.

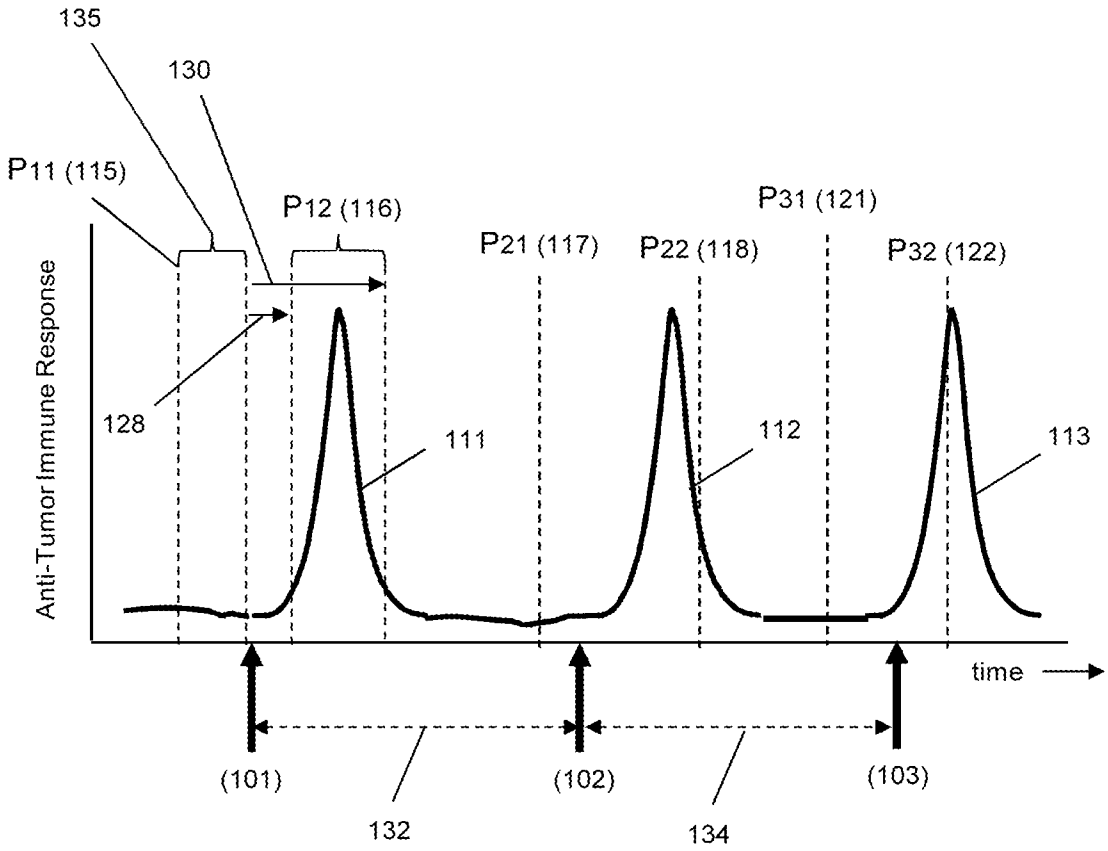
135
130
P11 (115)
P12 (116)
P21 (117)
P22 (118)
P31 (121)
P32 (122)
128
111
112
113
Anti-Tumor Immune Response
time
(101)
(102)
(103)
132
134

Fig. 1

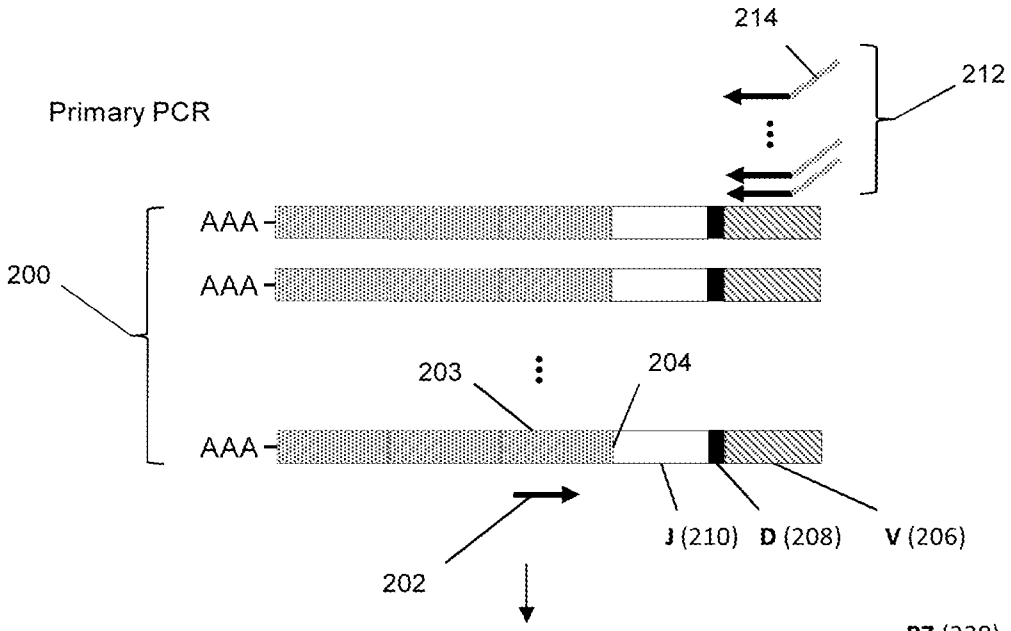

Fig. 2A

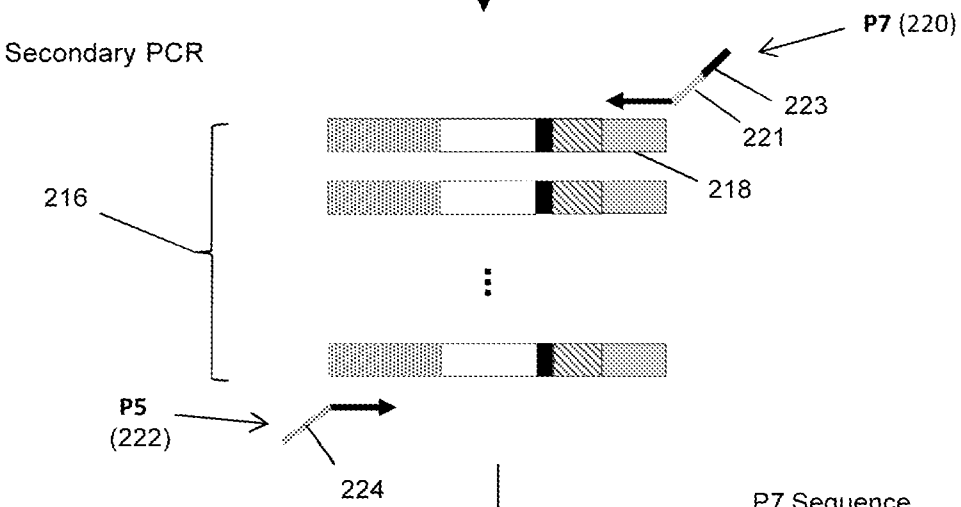

Fig. 2B

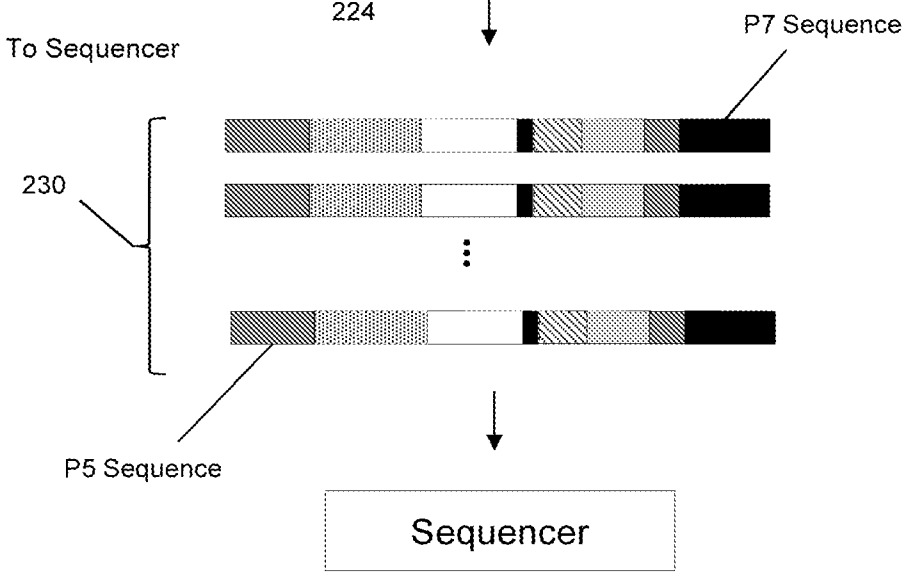

Fig. 2C

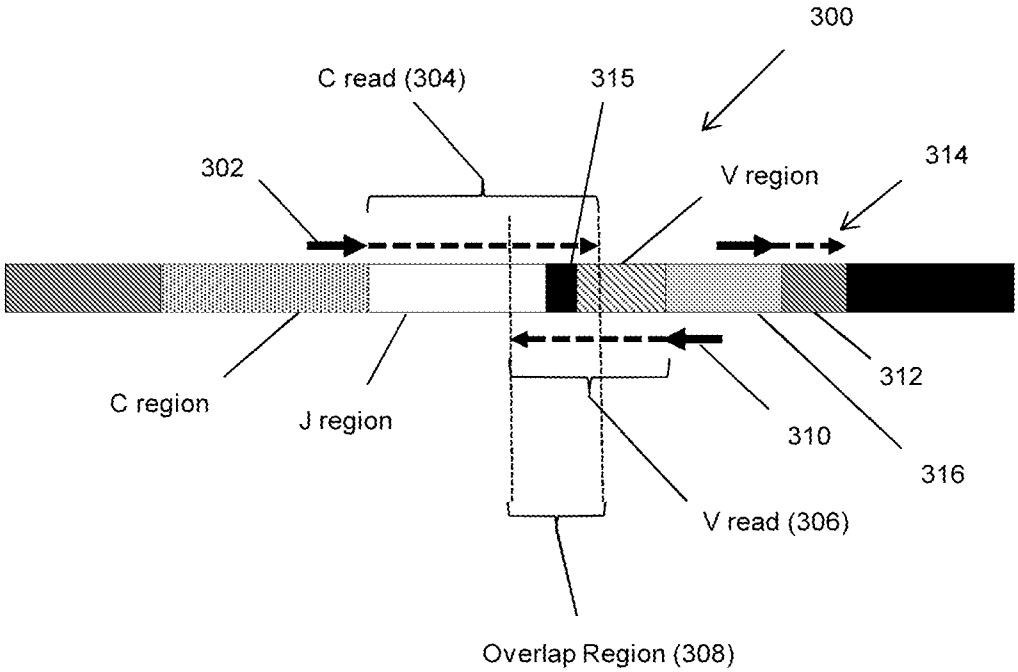
300
C read (304)
315
302
V region
314
C region
J region
312
310
316
V read (306)
Overlap Region (308)

Fig. 3A

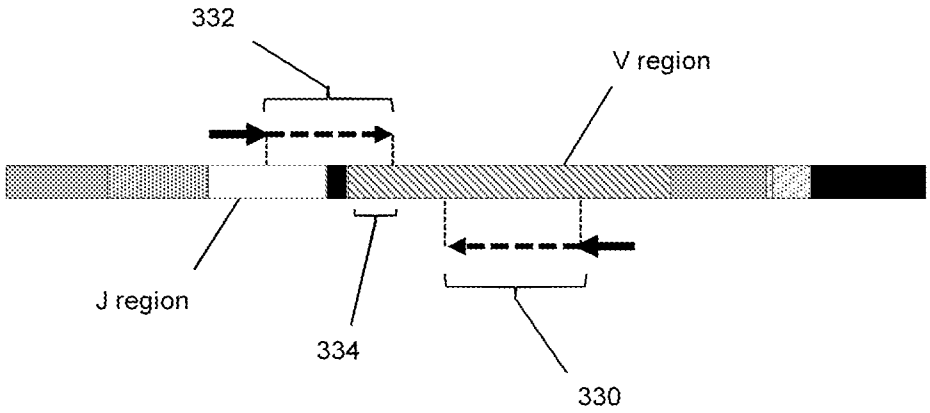
332
V region
J region
334
330

Fig. 3B

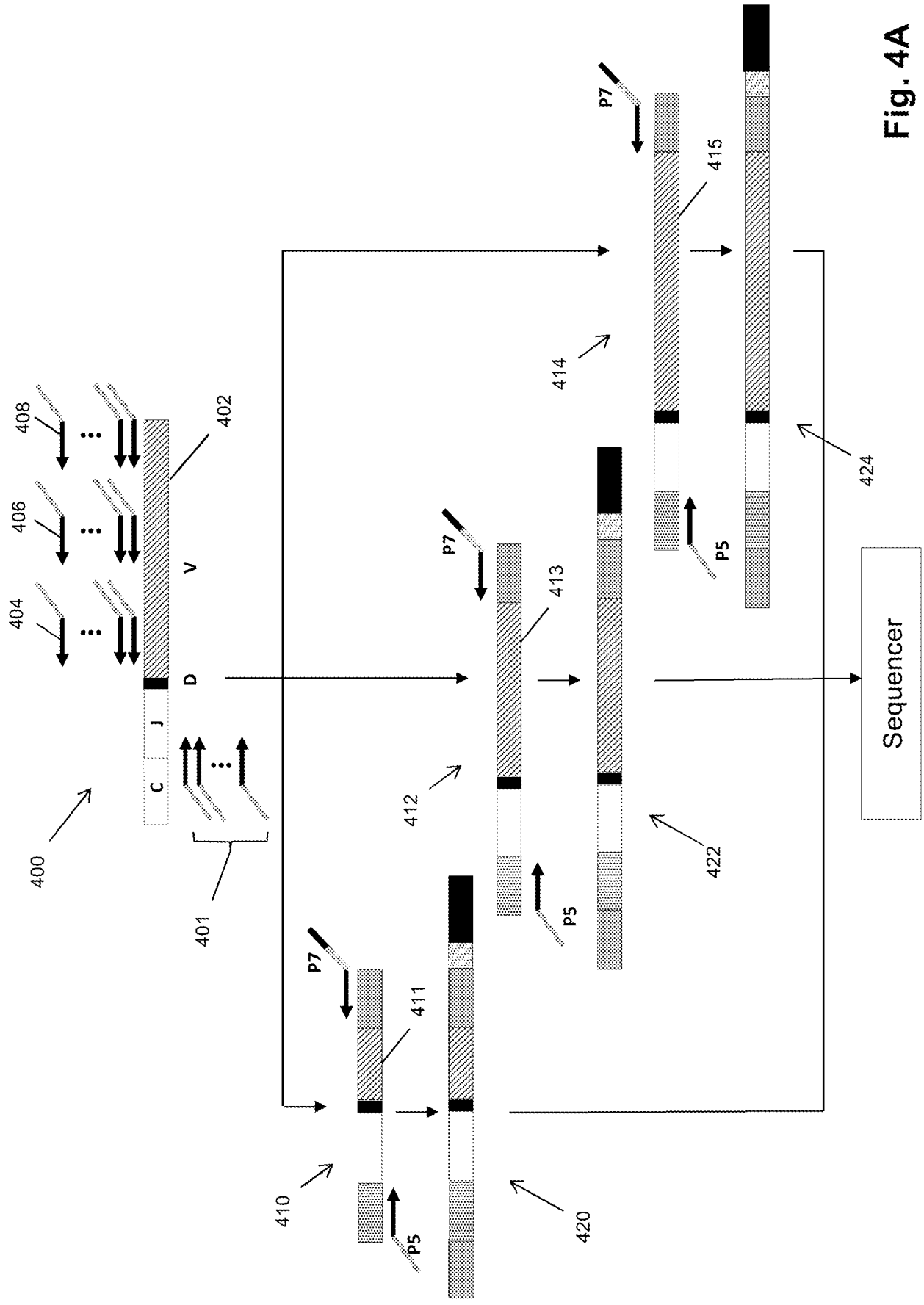
400
401
402
404
406
408
V
D
J
C
410
411
412
413
414
415
420
422
424
P5
P7
Sequencer

Fig. 4A

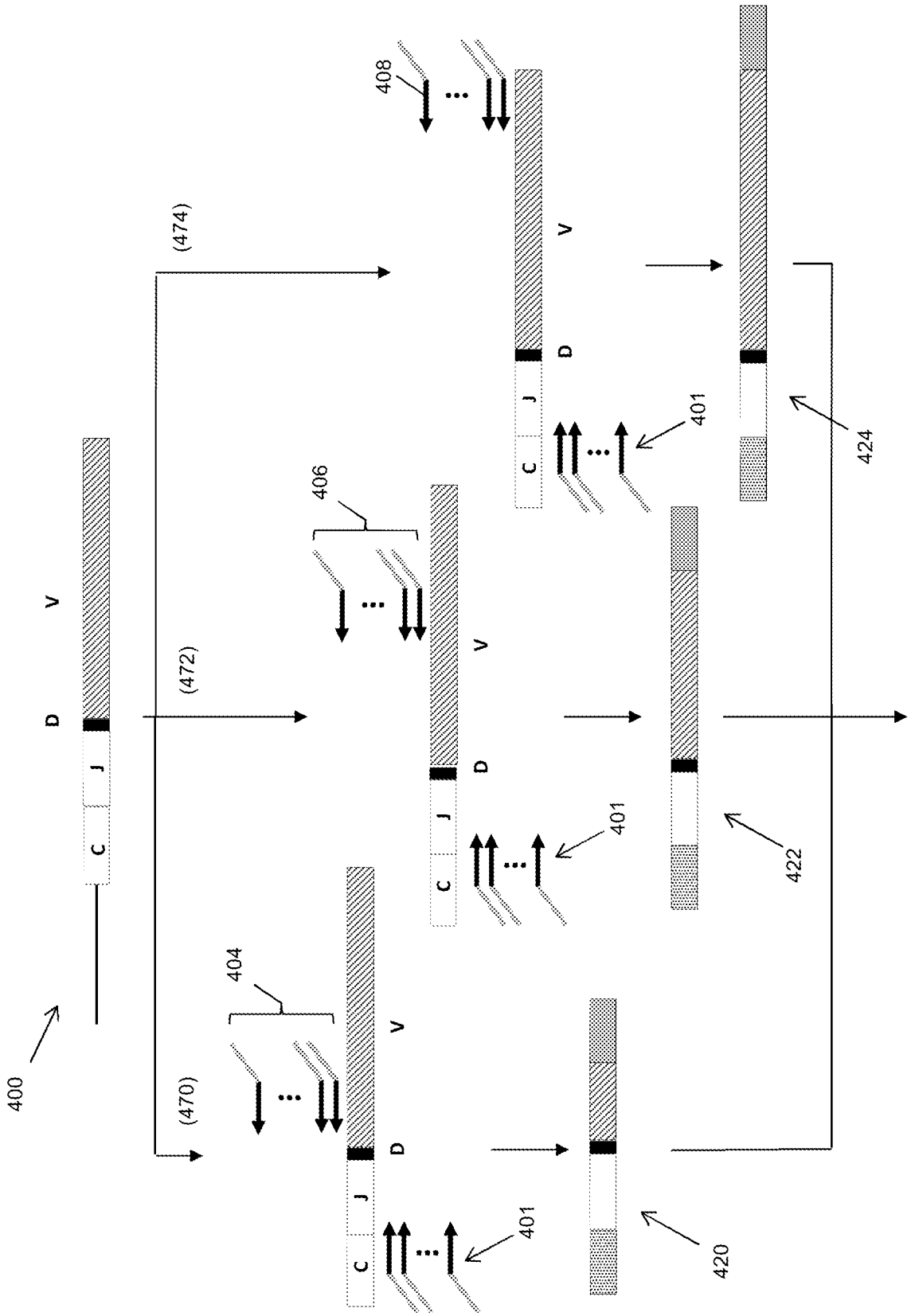

Fig. 4B

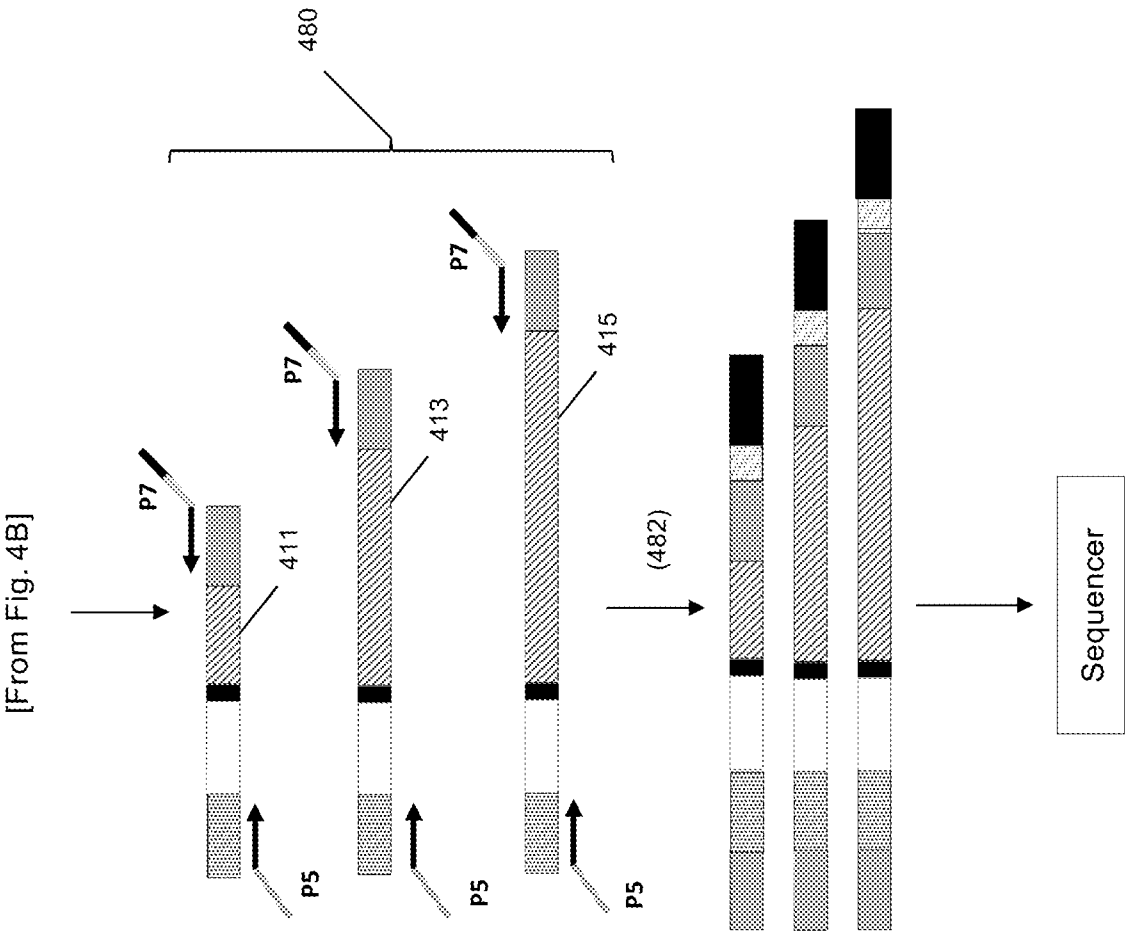

Fig. 4C

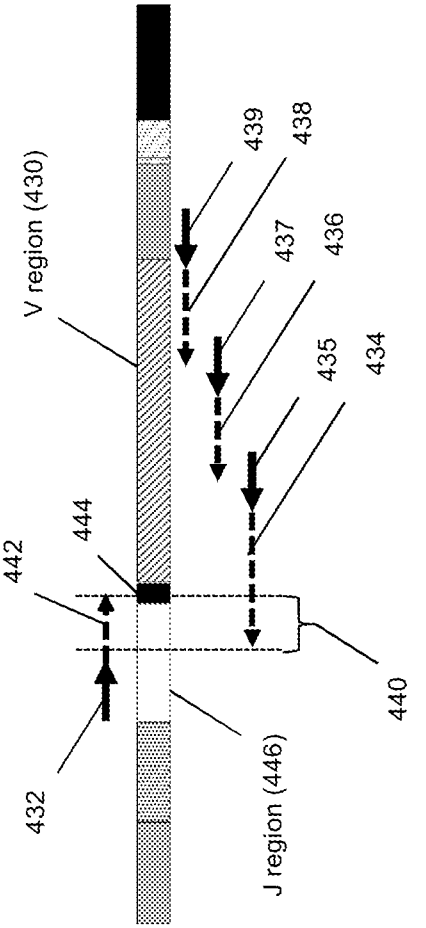
V region (430)
439
438
437
436
435
434
444
442
440
432
J region (446)

Fig. 4D

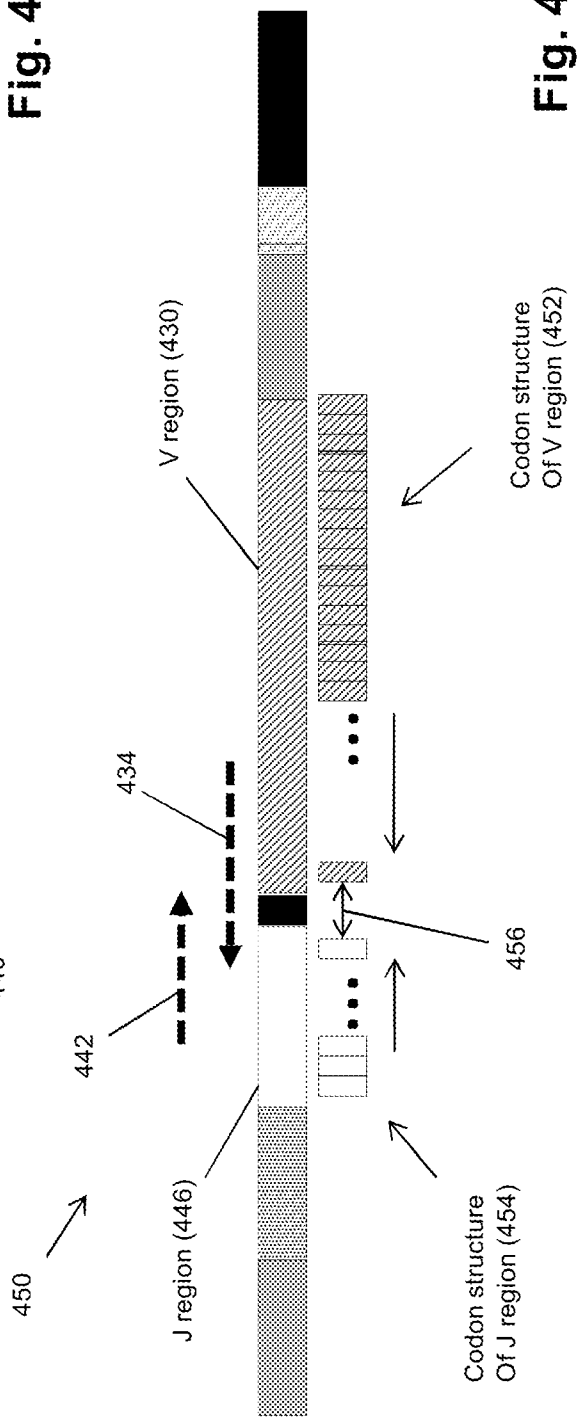
V region (430)
Codon structure
Of V region (452)
434
456
442
450
J region (446)
Codon structure
Of J region (454)

Fig. 4E

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US13/29181

A. CLASSIFICATION OF SUBJECT MATTER
IPC(8) - C12Q 1/68 (2013.01)
USPC - 435/6.11, 6.17, 7.24
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC(8): C12Q 1/68 (2013.01)
USPC: 435/6.11, 6.17, 7.24, 6.1, 4, 7.23, 6.12

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
MicroPatent (US-Granted, US-Applications, EP-A, EP-B, WO, JP, DE-G, DE-A, DE-T, DE-U, GB-A, FR-A); ScienceDirect; Pubmed; Google;Google Scholar; clonotype, 'immune repertoire,' 'cancer vaccine,' 'immune response,' 'vaccine schedule'

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 2010/053587 A2 (FAHAM, M et al.) May 14, 2010; paragraphs [0085]-[0087], [00192]	1-6
Y	GODELAINE, D et al. Polyclonal CTL Responses Observed In Melanoma Patients Vaccinated With Dendritic Cells Pulsed With A MAGE-3.A1 Peptide. The Journal of Immunology. 2003. Vol. 171, No. 9, pp 4893-4897.	1-6
L	IANCU, EM et al. Profile Of A Serial Killer: Cellular And Molecular Approaches To Study Individual Cytotoxic T-Cells Following Therapeutic Vaccination. Journal of Biomedicine and Biotechnology. 29 September 2010. Vol. 2011, Article ID 452606, pp 1-21. DOI:10.1155/2011/452606.	1-6
A	US 2004/0214779 A1 (MA, W et al.) October 28, 2004; entire document	1-6

☐ Further documents are listed in the continuation of Box C. ☐

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
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Date of the actual completion of the international search	Date of mailing of the international search report
29 April 2013 (29.04.2013)	31 MAY 2013
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