

TITLE

[0001] COMPOSITIONS AND METHODS FOR MEASURING AND CALIBRATING AMPLIFICATION BIAS IN MULTIPLEXED PCR REACTIONS

CROSS REFERENCE TO RELATED APPLICATIONS

[0002] This application claims the benefit of U.S. Provisional Application No. 61/726,489, filed November 14, 2012 and U.S. Provisional Application No. 61/644,294, filed on May 8, 2012, the entire disclosures of which are hereby incorporated by reference in their entireties for all purposes.

BACKGROUND OF THE INVENTION

Field of the invention

[0003] The present disclosure relates generally to quantitative high-throughput sequencing of adaptive immune receptor encoding DNA (e.g., DNA encoding T cell receptors (TCR) and immunoglobulins (IG) in multiplexed nucleic acid amplification reactions. In particular, the compositions and methods described herein overcome undesirable distortions in the quantification of adaptive immune receptor encoding sequences that can result from biased over-utilization and/or under-utilization of specific oligonucleotide primers in multiplexed DNA amplification.

Description of the Related Art

[0004] The adaptive immune system employs several strategies to generate a repertoire of T- and B-cell antigen receptors, *i.e.*, adaptive immune receptors, with sufficient diversity to recognize the universe of potential pathogens. The ability of T cells to recognize the universe of antigens associated with various cancers or infectious organisms is conferred by its T cell antigen receptor (TCR), which is a heterodimer of an α (alpha) chain from the TCRA locus and a β (beta) chain from the TCRB locus, or a heterodimer of a γ (gamma) chain from the TCRG locus and a δ (delta) chain from the TCRD locus. The proteins which make up these chains are encoded by DNA, which in lymphoid cells employs a unique rearrangement mechanism for generating the tremendous diversity of the TCR. This multi-subunit immune recognition receptor associates with the CD3 complex and binds to peptides presented by either the major histocompatibility complex (MHC) class I or MHC class II proteins on the surface of antigen-presenting cells (APCs). Binding of TCR to the antigenic peptide on the APC is the central event in T cell activation, which occurs at an immunological synapse at the point of contact between the T cell and the APC.

[0005] Each TCR peptide contains variable complementarity determining regions (CDRs), as well as framework regions (FRs) and a constant region. The sequence diversity of $\alpha\beta$ T cells is largely determined by the amino acid sequence of the third complementarity-determining region (CDR3) loops of the α and β chain variable domains, which diversity is a result of recombination between variable (V_β), diversity (D_β), and joining (J_β) gene segments in the β chain locus, and between analogous V_α and J_α gene segments in the α chain locus, respectively. The existence of multiple such gene segments in the TCR α and β chain loci allows for a large number of distinct CDR3 sequences to be encoded. CDR3 sequence diversity is further increased by independent addition and deletion of nucleotides at the V_β - D_β , D_β - J_β , and V_α - J_α junctions during the process of TCR gene rearrangement. In this respect, immunocompetence is derived from the diversity of TCRs.

[0006] The $\gamma\delta$ TCR heterodimer is distinctive from the $\alpha\beta$ TCR in that it encodes a receptor that interacts closely with the innate immune system, and recognizes antigen in a non-HLA-dependent manner. TCR $\gamma\delta$ is expressed early in development, and has specialized anatomical distribution, unique pathogen and small-molecule specificities, and a broad spectrum of innate and adaptive cellular interactions. A biased pattern of TCR γ V and J segment expression is established early in ontogeny. Consequently, the diverse TCR γ repertoire in adult tissues is the result of extensive peripheral expansion following stimulation by environmental exposure to pathogens and toxic molecules.

[0007] Immunoglobulins (Igs or IG), also referred to herein as B cell receptors (BCR), are proteins expressed by B cells consisting of four polypeptide chains, two heavy chains (H chains) from the IGH locus and two light chains (L chains) from either the IGK or the IGL locus, forming an H_2L_2 structure. H and L chains each contain three complementarity determining regions (CDR) involved in antigen recognition, as well as framework regions and a constant domain, analogous to TCR. The H chains of Igs are initially expressed as membrane-bound isoforms using either the IGM or IGD constant region exons, but after antigen recognition the constant region can class-switch to several additional isotypes, including IGG, IGE and IGA. As with TCR, the diversity of naïve Igs within an individual is mainly determined by the hypervariable complementarity determining regions (CDR). Similar to TCRB, the CDR3 domain of H chains is created by the combinatorial joining of the V_H , D_H , and J_H gene segments. Hypervariable domain sequence diversity is further increased by independent addition and deletion of nucleotides at the V_H - D_H , D_H - J_H , and V_H - J_H junctions during the process of Ig gene rearrangement. Distinct from TCR, Ig sequence

diversity is further augmented by somatic hypermutation (SHM) throughout the rearranged IG gene after a naïve B cell initially recognizes an antigen. The process of SHM is not restricted to CDR3, and therefore can introduce changes to the germline sequence in framework regions, CDR1 and CDR2, as well as in the somatically rearranged CDR3.

[0008] As the adaptive immune system functions in part by clonal expansion of cells expressing unique TCRs or BCRs, accurately measuring the changes in total abundance of each T cell or B cell clone is important to understanding the dynamics of an adaptive immune response. For instance, a healthy human has a few million unique rearranged TCR β chains, each carried in hundreds to thousands of clonal T-cells, out of the roughly trillion T cells in a healthy individual. Utilizing advances in high-throughput sequencing, a new field of molecular immunology has recently emerged to profile the vast TCR and BCR repertoires. Compositions and methods for the sequencing of rearranged adaptive immune receptor gene sequences and for adaptive immune receptor clonotype determination are described in U.S.A.N. 13/217,126; U.S.A.N. 12/794,507; PCT/US2011/026373; and PCT/US2011/049012, all herein incorporated by reference.

[0009] To date, several different strategies have been employed to sequence nucleic acids encoding adaptive immune receptors quantitatively at high throughput, and these strategies may be distinguished, for example, by the approach that is used to amplify the CDR3-encoding regions, and by the choice of sequencing genomic DNA (gDNA) or messenger RNA (mRNA).

[0010] Sequencing mRNA is a potentially easier method than sequencing gDNA, because mRNA splicing events remove the intron between J and C segments. This allows for the amplification of adaptive immune receptors (*e.g.*, TCRs or Igs) having different V regions and J regions using a common 3' PCR primer in the C region. For each TCR β , for example, the thirteen J segments are all less than 60 base pairs (bp) long. Therefore, splicing events bring identical polynucleotide sequences encoding TCR β constant regions (regardless of which V and J sequences are used) within less than 100 bp of the rearranged VDJ junction. The spliced mRNA can then be reverse transcribed into complementary DNA (cDNA) using poly-dT primers complementary to the poly-A tail of the mRNA, random small primers (usually hexamers or nonamers) or C-segment-specific oligonucleotides. This should produce an unbiased library of TCR cDNA (because all cDNAs are primed with the same oligonucleotide, whether poly-dT, random hexamer, or C segment-specific oligo) that may then be sequenced to obtain information on the V and J segment used in each rearrangement,

as well as the specific sequence of the CDR3. Such sequencing could use single, long reads spanning CDR3 (“long read”) technology, or could instead involve shotgun assembly of the longer sequences using fragmented libraries and higher throughput shorter sequence reads.

[0011] Efforts to quantify the number of cells in a sample that express a particular rearranged TCR (or Ig) based on mRNA sequencing are difficult to interpret, however, because each cell potentially expresses different quantities of TCR mRNA. For example, T cells activated in vitro have 10-100 times as much mRNA per cell than quiescent T cells. To date, there is very limited information on the relative amount of TCR mRNA in T cells of different functional states, and therefore quantitation of mRNA in bulk does not necessarily accurately measure the number of cells carrying each clonal TCR rearrangement.

[0012] Most T cells, on the other hand, have one productively rearranged TCR α and one productively rearranged TCR β gene (or two rearranged TCR γ and TCR δ), and most B cells have one productively rearranged Ig heavy-chain gene and one productively rearranged Ig light-chain gene (either IGK or IGL) so quantification in a sample of genomic DNA encoding TCRs or BCRs should directly correlate with, respectively, the number of T or B cells in the sample. Genomic sequencing of polynucleotides encoding any one or more of the adaptive immune receptor chains desirably entails amplifying with equal efficiency all of the many possible rearranged CDR3 sequences that are present in a sample containing DNA from lymphoid cells of a subject, followed by quantitative sequencing, such that a quantitative measure of the relative abundance of each rearranged CDR3 clonotype can be obtained.

[0013] Difficulties are encountered with such approaches, however, in that equal amplification and sequencing efficiencies may not be achieved readily for each rearranged clone using multiplex PCR. For example, at TCRB each clone employs one of 54 possible germline V region-encoding genes and one of 13 possible J region-encoding genes. The DNA sequence of the V and J segments is necessarily diverse, in order to generate a diverse adaptive immune repertoire. This sequence diversity makes it impossible to design a single, universal primer sequence that will anneal to all V segments (or J segments) with equal affinity, and yields complex DNA samples in which accurate determination of the multiple distinct sequences contained therein is hindered by technical limitations on the ability to quantify a plurality of molecular species simultaneously using multiplexed amplification and high throughput sequencing.

[0014] One or more factors can give rise to artifacts that skew the correlation between sequencing data outputs and the number of copies of an input clonotype, compromising the

ability to obtain reliable quantitative data from sequencing strategies that are based on multiplexed amplification of a highly diverse collection of TCR β gene templates. These artifacts often result from unequal use of diverse primers during the multiplexed amplification step. Such biased utilization of one or more oligonucleotide primers in a multiplexed reaction that uses diverse amplification templates may arise as a function of differential annealing kinetics due to one or more of differences in the nucleotide base composition of templates and/or oligonucleotide primers, differences in template and/or primer length, the particular polymerase that is used, the amplification reaction temperatures (*e.g.*, annealing, elongation and/or denaturation temperatures), and/or other factors (*e.g.*, Kanagawa, 2003 *J. Biosci. Bioeng.* 96:317; Day et al., 1996 *Hum. Mol. Genet.* 5:2039; Ogino et al., 2002 *J. Mol. Diagnost.* 4:185; Barnard et al., 1998 *Biotechniques* 25:684; Aird et al., 2011 *Genome Biol.* 12:R18).

[0015] Clearly there remains a need for improved compositions and methods that will permit accurate quantification of adaptive immune receptor-encoding DNA sequence diversity in complex samples, in a manner that avoids skewed results such as misleading over- or underrepresentation of individual sequences due to biases in the amplification of specific templates in an oligonucleotide primer set used for multiplexed amplification of a complex template DNA population. The presently described embodiments address this need and provide other related advantages.

SUMMARY OF THE INVENTION

[0016] A composition for standardizing the amplification efficiency of an oligonucleotide primer set that is capable of amplifying rearranged nucleic acid molecules encoding one or more adaptive immune receptors in a biological sample that comprises rearranged nucleic acid molecules from lymphoid cells of a mammalian subject, each adaptive immune receptor comprising a variable region and a joining region, the composition comprising a plurality of template oligonucleotides having a plurality of oligonucleotide sequences of general formula: 5'-U1-B1-V-B2-R-B3-J-B4-U2-3' [I] wherein: (a) V is a polynucleotide comprising at least 20 and not more than 1000 contiguous nucleotides of an adaptive immune receptor variable (V) region encoding gene sequence, or the complement thereof, and each V polynucleotide comprising a unique oligonucleotide sequence; (b) J is a polynucleotide comprising at least 15 and not more than 600 contiguous nucleotides of an adaptive immune receptor joining (J) region encoding gene sequence, or the complement thereof, and each J polynucleotide comprising a unique oligonucleotide sequence; (c) U1 is either nothing or comprises an

oligonucleotide sequence that is selected from (i) a first universal adaptor oligonucleotide sequence and (ii) a first sequencing platform-specific oligonucleotide sequence that is linked to and positioned 5' to a first universal adaptor oligonucleotide sequence; (d) U2 is either nothing or comprises an oligonucleotide sequence that is selected from (i) a second universal adaptor oligonucleotide sequence, and (ii) a second sequencing platform-specific oligonucleotide sequence that is linked to and positioned 5' to a second universal adaptor oligonucleotide sequence; (e) B1, B2, B3, and B4 are each independently either nothing or each comprises an oligonucleotide B that comprises a barcode sequence of 3-25 contiguous nucleotides, wherein each B1, B2, B3 and B4 comprises an oligonucleotide sequence that uniquely identifies, as a paired combination, (i) the unique V oligonucleotide sequence of (a) and (ii) the unique J oligonucleotide sequence of (b); (f) R is either nothing or comprises a restriction enzyme recognition site that comprises an oligonucleotide sequence that is absent from (a)-(e), and wherein: (g) the plurality of template oligonucleotides comprises at least a or at least b unique oligonucleotide sequences, whichever is larger, wherein a is the number of unique adaptive immune receptor V region-encoding gene segments in the subject and b is the number of unique adaptive immune receptor J region-encoding gene segments in the subject, and the composition comprises at least one template oligonucleotide for each unique V polynucleotide and at least one template oligonucleotide for each unique J polynucleotide.

[0017] In one embodiment, a is 1 to a number of maximum V gene segments in the mammalian genome of the subject. In another embodiment, b is 1 to a number of maximum J gene segments in the mammalian genome of the subject. In other embodiments, a is 1 or b is 1.

[0018] In some embodiments, the plurality of template oligonucleotides comprises at least ($a \times b$) unique oligonucleotide sequences, where a is the number of unique adaptive immune receptor V region-encoding gene segments in the mammalian subject and b is the number of unique adaptive immune receptor J region-encoding gene segments in the mammalian subject, and the composition comprises at least one template oligonucleotide for every possible combination of a V region-encoding gene segment and a J region-encoding gene segment. In one embodiment, J comprises a constant region of the adaptive immune receptor J region encoding gene sequence.

[0019] In another embodiment, the adaptive immune receptor is selected from the group consisting of TCRB, TCRG, TCRA, TCRD, IGH, IGK, and IGL. In some embodiments, the V polynucleotide of (a) encodes a TCRB, TCRG, TCRA, TCRD, IGH, IGK, or IGL receptor

V-region polypeptide. In other embodiments, the J polynucleotide of (b) encodes a TCRB, TCRG, TCRA, TCRD, IGH, IGK, or IGL receptor J-region polypeptide.

[0020] In some embodiments, a stop codon is between V and B2.

[0021] In one embodiment, each template oligonucleotide in the plurality of template oligonucleotides is present in a substantially equimolar amount. In another embodiment, the plurality of template oligonucleotides have a plurality of sequences of general formula (I) that is selected from: (1) the plurality of oligonucleotide sequences of general formula (I) in which the V and J polynucleotides have the TCRB V and J sequences set forth in at least one set of 68 TCRB V and J SEQ ID NOS. in Figures 5a-5l as TCRB V/J set 1, TCRB V/J set 2, TCRB V/J set 3, TCRB V/J set 4, TCRB V/J set 5, TCRB V/J set 6, TCRB V/J set 7, TCRB V/J set 8, TCRB V/J set 9, TCRB V/J set 10, TCRB V/J set 11, TCRB V/J set 12 and TCRB V/J set 13; (2) the plurality of oligonucleotide sequences of general formula (I) in which the V and J polynucleotides have the TCRG V and J sequences set forth in at least one set of 14 TCRG V and J SEQ ID NOS. in Figures 6a and 6b as TCRG V/J set 1, TCRG V/J set 2, TCRG V/J set 3, TCRG V/J set 4 and TCRG V/J set 5; (3) the plurality of oligonucleotide sequences of general formula (I) in which the V and J polynucleotides have the IGH V and J sequences set forth in at least one set of 127 IGH V and J SEQ ID NOS. in Figures 7a-7m as IGH V/J set 1, IGH V/J set 2, IGH V/J set 3, IGH V/J set 4, IGH V/J set 5, IGH V/J set 6, IGH V/J set 7, IGH V/J set 8 and IGH V/J set 9; (4) the plurality of oligonucleotide sequences of general formula (I) as set forth in SEQ ID NOS:3157-4014;(5)the plurality of oligonucleotide sequences of general formula (I) as set forth in SEQ ID NOS:4015-4084; (6)the plurality of oligonucleotide sequences of general formula (I) as set forth in SEQ ID NOS:4085-5200; (7) the plurality of oligonucleotide sequences of general formula (I) as set forth in SEQ ID NOS:5579-5821;(8) the plurality of oligonucleotide sequences of general formula (I) as set forth in SEQ ID NOS: 5822-6066; and (9) the plurality of oligonucleotide sequences of general formula (I) as set forth in SEQ ID NOS: 6067-6191.

[0022] In some embodiments, V is a polynucleotide comprising at least 30, 60, 90, 120, 150, 180, or 210 contiguous nucleotides of the adaptive immune receptor V region encoding gene sequence, or the complement thereof. In another embodiment, V is a polynucleotide comprising not more than 900, 800, 700, 600 or 500 contiguous nucleotides of an adaptive immune receptor V region encoding gene sequence, or the complement thereof.

[0023] In other embodiments, J is a polynucleotide comprising at least 16-30, 31-60, 61-90, 91-120, or 120-150 contiguous nucleotides of an adaptive immune receptor J region encoding gene sequence, or the complement thereof. In another embodiment, J is a polynucleotide comprising not more than 500, 400, 300 or 200 contiguous nucleotides of an adaptive immune receptor J region encoding gene sequence, or the complement thereof.

[0024] In some embodiments, each template oligonucleotide is less than 1000, 900, 800, 700, 600, 500, 400, 300 or 200 nucleotides in length.

[0025] In other embodiments, the composition includes a set of oligonucleotide primers that is capable of amplifying rearranged nucleic acid molecules encoding one or more adaptive immune receptors comprising a plurality *a'* of unique V-segment oligonucleotide primers and a plurality *b'* of unique J-segment oligonucleotide primers. In some embodiments, *a'* is 1 to a number of maximum V gene segments in the mammalian genome, and *b'* is 1 to a number of maximum number of J gene segments in the mammalian genome. In one embodiment, *a'* is *a*. In another embodiment, *b'* is *b*.

[0026] In yet another embodiment, each V-segment oligonucleotide primer and each J-segment oligonucleotide primer in the oligonucleotide primer set is capable of specifically hybridizing to at least one template oligonucleotide in the plurality of template oligonucleotides. In other embodiments, each V-segment oligonucleotide primer comprises a nucleotide sequence of at least 15 contiguous nucleotides that is complementary to at least one adaptive immune receptor V region-encoding gene segment. In another embodiment, each J-segment oligonucleotide primer comprises a nucleotide sequence of at least 15 contiguous nucleotides that is complementary to at least one adaptive immune receptor J region-encoding gene segment.

[0027] In other embodiments, the composition comprises at least one template oligonucleotide having an oligonucleotide sequence of general formula (I) to which each V-segment oligonucleotide primer can specifically hybridize, and at least one template oligonucleotide having an oligonucleotide sequence of general formula (I) to which each J-segment oligonucleotide primer can specifically hybridize.

[0028] The invention comprises a method for determining non-uniform nucleic acid amplification potential among members of a set of oligonucleotide primers that is capable of amplifying rearranged nucleic acid molecules encoding one or more adaptive immune receptors in a biological sample that comprises rearranged nucleic acid molecules from lymphoid cells of a mammalian subject. The method includes steps for: (a) amplifying the

composition as described herein in a multiplex PCR reaction to obtain a plurality of amplified template oligonucleotides; (b) sequencing said plurality of amplified template oligonucleotides to determine, for each unique template oligonucleotide comprising said plurality, (i) a template oligonucleotide sequence and (ii) a frequency of occurrence of said template oligonucleotide sequence; and (c) comparing a frequency of occurrence of each of said template oligonucleotide sequences to an expected distribution, wherein said expected distribution is based on predetermined molar ratios of said plurality of template oligonucleotides comprising said composition, and wherein a deviation between said frequency of occurrence of said template oligonucleotide sequences and said expected distribution indicates a non-uniform nucleic acid amplification potential among members of the set of oligonucleotide amplification primers.

[0029] In one embodiment, the predetermined molar ratios are equimolar. In another embodiment, the expected distribution comprises a uniform amplification level for said set of template oligonucleotides amplified by said set of oligonucleotide primers. In yet another embodiment, each amplified template nucleic acid molecule is less than 1000, 900, 800, 700, 600, 500, 400, 300, 200, 100, 90, 80 or 70 nucleotides in length.

[0030] The method includes steps comprising for each member of the set of oligonucleotide primers that exhibits non-uniform amplification potential relative to the expected distribution, adjusting the relative representation of the oligonucleotide primer member in the set of oligonucleotide amplification primers. In one embodiment, adjusting comprises increasing the relative representation of the member in the set of oligonucleotide primers, thereby correcting non-uniform nucleic acid amplification potential among members of the set of oligonucleotide primers. In another embodiment, adjusting comprises decreasing the relative representation of the member in the set of oligonucleotide primers, thereby correcting non-uniform nucleic acid amplification potential among members of the set of oligonucleotide primers.

[0031] In other embodiments, the set of oligonucleotide primers does not include oligonucleotide primers that specifically hybridize to a V-region pseudogene or orphon or to a J-region pseudogene or orphon.

[0032] The method also includes steps comprising: for each member of the set of oligonucleotide amplification primers that exhibits non-uniform amplification potential relative to the expected distribution, calculating a proportionately increased or decreased frequency of occurrence of the amplified template nucleic acid molecules, the amplification

of which is promoted by said member, thereby correcting for non-uniform nucleic acid amplification potential among members of the set of oligonucleotide primers.

[0033] The invention includes a method for quantifying a plurality of rearranged nucleic acid molecules encoding one or a plurality of adaptive immune receptors in a biological sample that comprises rearranged nucleic acid molecules from lymphoid cells of a mammalian subject, each adaptive immune receptor comprising a variable (V) region and a joining (J) region, the method comprising: (A) amplifying rearranged nucleic acid molecules in a multiplex polymerase chain reaction (PCR) that comprises: (1) rearranged nucleic acid molecules from the biological sample that comprises lymphoid cells of the mammalian subject; (2) the composition as described herein wherein a known number of each of the plurality of template oligonucleotides having a unique oligonucleotide sequence is present; (3) an oligonucleotide amplification primer set that is capable of amplifying rearranged nucleic acid molecules encoding one or a plurality of adaptive immune receptors from the biological sample.

[0034] In some embodiments, the primer set comprises: (a) in substantially equimolar amounts, a plurality of V-segment oligonucleotide primers that are each independently capable of specifically hybridizing to at least one polynucleotide encoding an adaptive immune receptor V-region polypeptide or to the complement thereof, wherein each V-segment primer comprises a nucleotide sequence of at least 15 contiguous nucleotides that is complementary to at least one functional adaptive immune receptor V region-encoding gene segment and wherein the plurality of V-segment primers specifically hybridize to substantially all functional adaptive immune receptor V region-encoding gene segments that are present in the composition, and (b) in substantially equimolar amounts, a plurality of J-segment oligonucleotide primers that are each independently capable of specifically hybridizing to at least one polynucleotide encoding an adaptive immune receptor J-region polypeptide or to the complement thereof, wherein each J-segment primer comprises a nucleotide sequence of at least 15 contiguous nucleotides that is complementary to at least one functional adaptive immune receptor J region-encoding gene segment and wherein the plurality of J-segment primers specifically hybridize to substantially all functional adaptive immune receptor J region-encoding gene segments that are present in the composition.

[0035] In another embodiment, the V-segment and J-segment oligonucleotide primers are capable of promoting amplification in said multiplex polymerase chain reaction (PCR) of (i) substantially all template oligonucleotides in the composition to produce a multiplicity of

amplified template oligonucleotides, said multiplicity of amplified template nucleic acid molecules being sufficient to quantify diversity of the template oligonucleotides in the composition, and (ii) substantially all rearranged nucleic acid molecules encoding adaptive immune receptors in the biological sample to produce a multiplicity of amplified rearranged DNA molecules, said multiplicity of amplified rearranged nucleic acid molecules being sufficient to quantify diversity of the rearranged nucleic acid molecules in the DNA from the biological sample.

[0036] In one embodiment, each amplified nucleic acid molecule in the plurality of amplified template oligonucleotides and in the plurality of amplified rearranged nucleic acid molecules is less than 1000 nucleotides in length; (B) quantitatively sequencing said amplified template oligonucleotides and said amplified rearranged nucleic acid molecules to quantify (i) a template product number of amplified template oligonucleotides which contain at least one oligonucleotide barcode sequence, and (ii) a rearranged product number of amplified rearranged nucleic acid molecules which lack an oligonucleotide barcode sequence; (C) calculating an amplification factor by dividing the template product number of (B)(i) by the known number of each of the plurality of template oligonucleotides having a unique oligonucleotide sequence of (A)(2); and (D) dividing the rearranged product number of (B)(ii) by the amplification factor calculated in (C) to quantify the number of unique adaptive immune receptor encoding rearranged nucleic acid molecules in the sample.

[0037] In other embodiments, the quantified number of unique adaptive immune receptor encoding rearranged nucleic acid molecules in the sample is the number of unique B cell or unique T cell genome templates in the sample.

[0038] The invention includes a method for calculating an average amplification factor in a multiplex PCR assay, comprising: obtaining a biological sample that comprises rearranged nucleic acid molecules from lymphoid cells of a mammalian subject; contacting said sample with a known quantity of template oligonucleotides comprising a composition as described herein; amplifying the template oligonucleotides and the rearranged nucleic acid molecules from lymphoid cells of the mammalian subject in a multiplex PCR reaction to obtain a plurality of amplified template oligonucleotides and a plurality of amplified rearranged nucleic acid molecules; sequencing said plurality of amplified template oligonucleotides to determine, for each unique template oligonucleotide comprising said plurality, (i) a template oligonucleotide sequence and (ii) a frequency of occurrence of said template oligonucleotide sequence; and determining an average amplification factor for said multiplex PCR reaction

based on an average number of copies of said plurality of amplified template oligonucleotides and said known quantity of said template oligonucleotides.

[0039] The method also includes sequencing said plurality of amplified rearranged nucleic acid molecules from lymphoid cells of the mammalian subject to determine for each unique rearranged nucleic acid molecule comprising said plurality, i) a rearranged nucleic acid molecule sequence and (ii) a number of occurrences of said rearranged nucleic acid molecule sequence; and determining the number of lymphoid cells in said sample, based on the average amplification factor for said multiplex PCR reaction and said number of occurrences of said rearranged nucleic acid molecules.

[0040] In other embodiments, the method comprises determining the number of lymphoid cells in said sample comprises generating a sum of the number of occurrences of each of said amplified rearranged nucleic acid sequences and dividing said sum by said average amplification factor. In some embodiments, the known quantity is one copy each of said template oligonucleotides. In one embodiment, $100 \leq a \leq 500$. In another embodiment, $100 \leq b \leq 500$.

[0041] A method is provided for correcting for amplification bias in an multiplex PCR amplification reaction to quantify rearranged nucleic acid molecules encoding one or a plurality of adaptive immune receptors in a biological sample that comprises rearranged nucleic acid molecules from lymphoid cells of a mammalian subject, comprising: (a) contacting said sample with a composition described herein to generate a template-spiked sample, wherein said templates and said rearranged nucleic acid molecules comprise corresponding V and J region sequences; (b) amplifying said template-spiked sample in a multiplex PCR reaction to obtain a plurality of amplified template oligonucleotides and a plurality of amplified rearranged nucleic acid molecules encoding a plurality of adaptive immune receptors; (c) sequencing said plurality of amplified template oligonucleotides to determine, for each unique template oligonucleotide comprising said plurality, (i) a template oligonucleotide sequence and (ii) a frequency of occurrence of said template oligonucleotide sequence; (d) sequencing said plurality of amplified rearranged nucleic acid molecules encoding one or a plurality of adaptive immune receptors, for each unique rearranged nucleic acid molecules encoding said plurality of adaptive immune receptors comprising said plurality, (i) a rearranged nucleic acid molecule sequence and (ii) a frequency of occurrence of said rearranged nucleic acid molecule sequence; (e) comparing frequency of occurrence of said template oligonucleotide sequences to an expected distribution, wherein said expected

distribution is based on predetermined molar ratios of said plurality of template oligonucleotides comprising said composition, and wherein a deviation between said frequency of occurrence of said template oligonucleotide sequences and said expected distribution indicates non-uniform nucleic acid amplification potential among members of the set of oligonucleotide amplification primers; (f) generating a set of correction values for a set of template molecules and rearranged nucleic acid molecule sequences amplified by said members of the set of oligonucleotide amplification primers having said indicated non-uniform nucleic acid amplification potential, wherein said set of correction values corrects for amplification bias in said multiplex PCR reaction; and (g) optionally applying said set of correction values to said frequency of occurrence of said rearranged nucleic acid molecule sequences to correct for amplification bias in said multiplex PCR reaction.

[0042] The invention comprises a kit, comprising: reagents comprising: a composition comprising a plurality of template oligonucleotides and a set of oligonucleotide primers as described herein; instructions for determining a non-uniform nucleic acid amplification potential among members of the set of oligonucleotide primers that are capable of amplifying rearranged nucleic acid molecules encoding one or more adaptive immune receptors in a biological sample that comprises rearranged nucleic acid molecules from lymphoid cells of a mammalian subject.

[0043] In another embodiment, the kit comprises instructions for correcting for one or more members of the set of oligonucleotide primers having a non-uniform nucleic acid amplification potential.

[0044] In other embodiments, the kit comprises instructions for quantifying the number of unique adaptive immune receptor encoding rearranged nucleic acid molecules in the sample

[0045] These and other aspects of the herein described invention embodiments will be evident upon reference to the following detailed description and attached drawings. All of the U.S. patents, U.S. patent application publications, U.S. patent applications, foreign patents, foreign patent applications and non-patent publications referred to in this specification and/or listed in the Application Data Sheet are incorporated herein by reference in their entirety, as if each was incorporated individually. Aspects and embodiments of the invention can be modified, if necessary, to employ concepts of the various patents, applications and publications to provide yet further embodiments.

BRIEF DESCRIPTION OF THE SEVERAL VIEWS OF THE DRAWINGS

[0046] These and other features, aspects, and advantages of the present invention will become better understood with regard to the following description, and accompanying drawings, where:

[0047] Figure (Fig.) 1 shows a schematic diagram of an exemplary template oligonucleotide for use in standardizing the amplification efficiency of an oligonucleotide primer set that is capable of amplifying rearranged DNA encoding an adaptive immune receptor (TCR or BCR). U1, U2, universal adaptor oligonucleotides; B1-4, barcode oligonucleotides; V, variable region oligonucleotide; J, joining region oligonucleotide; R, restriction enzyme recognition site; S, optional stop codon.

[0048] Fig. 2 shows post-amplification frequencies of individual TCRB V gene segment sequences amplified from a standardizing oligonucleotide template composition (an equimolar pool of the templates set forth in SEQ ID NOS:872-1560) using an equimolar (unadjusted) pool of 52 PCR primers (SEQ ID NOS:1753-1804) and quantitatively sequenced on the Illumina HiSeq™ DNA sequencer. Frequency in the absence of bias was calculated as 0.0188.

[0049] Fig. 3 shows the results of quantitative sequencing following cross-amplification of template oligonucleotides using TCRB V region-specific primers. Y-axis indicates individual amplification primers (SEQ ID NOS:1753-1804) that were present in each separate amplification reaction at twice the molar concentration (2X) of the other primers from the same primer set, for amplification of a standardizing oligonucleotide template composition (an equimolar pool of the templates set forth in SEQ ID NOS:872-1560); X-axis is not labeled but data points are presented in the same order as for Y-axis, with X-axis representing corresponding amplified V gene templates as identified by quantitative sequencing. Black squares indicate no change in degree of amplification with the respective primer present at 2X relative to equimolar concentrations of all other primers; white squares indicate 10-fold increase in amplification; grey squares indicate intermediate degrees (on a greyscale gradient) of amplification between zero and 10-fold. Diagonal line of white squares indicates that 2X concentration for a given primer resulted in about 10-fold increase in amplification of the respective template for most primers. Off-diagonal white squares indicate non-corresponding templates to which certain primers were able to anneal and amplify.

[0050] Fig. 4 shows post-amplification frequencies of individual TCRB V gene segment sequences amplified from a standardizing oligonucleotide template composition (an equimolar pool of the templates set forth in SEQ ID NOS:872-1560), using equimolar concentrations of all members of a TCRB amplification primer set (SEQ ID NOS:1753-1804) prior to adjusting for primer utilization bias (black bars, all V-region primers present in equimolar concentrations), and using the same primer set (SEQ ID NOS:1753-1804) after adjusting multiple individual primer concentrations to compensate for bias (grey bars, concentrations of highly efficient primers were reduced and concentrations of poorly efficient primers were increased, see Table 6). Post-amplification frequencies were determined by quantitative sequencing on the Illumina HiSeq™ DNA sequencer.

[0051] Figs. 5a-5l show TCRB V/J sets (68 V + 13 J) for use in template compositions that comprise a plurality of oligonucleotide sequences of general formula 5'-U1-B1-V-B2-R-B3-J-B4-U2-3' [I], for use in standardizing the amplification efficiency of an oligonucleotide primer set that is capable of amplifying rearranged DNA encoding one or a plurality of human T cell receptor β (TCRB) chain polypeptides.

[0052] Figs. 6a and 6b show TCRG V/J sets (14 V + 5 J) for use in template compositions that comprise a plurality of oligonucleotide sequences of general formula 5'-U1-B1-V-B2-R-B3-J-B4-U2-3' [I], for use in standardizing the amplification efficiency of an oligonucleotide primer set that is capable of amplifying rearranged DNA encoding one or a plurality of human T cell receptor γ (TCRG) chain polypeptides.

[0053] Figs. 7a-7m show IGH V/J sets (127 V + 9 J) for use in template compositions that comprise a plurality of oligonucleotide sequences of general formula 5'-U1-B1-V-B2-R-B3-J-B4-U2-3' [I], for use in standardizing the amplification efficiency of an oligonucleotide primer set that is capable of amplifying rearranged DNA encoding one or a plurality of human immunoglobulin heavy (IGH) chain polypeptides.

[0054] Fig. 8 shows the results of calculating an amplification factor for each VJ pair in a template composition that was added to a multiplexed PCR amplification of IGH sequences, and then averaging the amplification factor across all synthetic templates to estimate fold sequence coverage across all synthetic template molecules.

[0055] Fig. 9 shows a plot of the numbers of B cells that were estimated using a synthetic template composition and amplification factor as described herein, versus the known numbers of B cells used as a source of natural DNA templates.

[0056] Fig. 10 shows a pre-PCR amplification sequencing count for each of 1116 IGH VJ bias control molecules and 243 IGH DJ bias control molecules.

[0057] Fig. 11 shows TCRB-primer iterations for synthetic TCRB VJ templates graphed against relative amplification bias.

[0058] Fig. 12 shows IGH primer iterations for synthetic IGH VJ templates graphed against relative amplification bias.

[0059] Fig. 13 shows the relative amplification bias for 27 synthetic IGH DJ templates of the V gene.

[0060] Figs. 14a-d show TCRG-primer iterations for 55 synthetic TCRG VJ templates. Relative amplification bias was determined for the TCRG VJ primers prior to chemical bias control correction (Fig. 14a), 1st iteration of chemical correction (Fig. 14b), 2nd iteration of chemical correction (Fig. 14c), and final iteration of chemical correction (Fig. 14d).

The present invention also provides any one of the embodiments disclosed below and indicated with the numbers 1 to 46.

1. A composition for standardizing the amplification efficiency of an oligonucleotide primer set that is capable of amplifying rearranged nucleic acid molecules encoding one or more adaptive immune receptors in a biological sample that comprises rearranged nucleic acid molecules from lymphoid cells of a mammalian subject, each adaptive immune receptor comprising a variable region and a joining region, the composition comprising:

a plurality of template oligonucleotides having a plurality of oligonucleotide sequences of general formula:

5'-U1-B1-V-B2-R-B3-J-B4-U2-3' [I]

wherein:

- (a) V is a polynucleotide comprising at least 20 and not more than 1000 contiguous nucleotides of an adaptive immune receptor variable (V) region encoding gene sequence, or the complement thereof, and each V polynucleotide comprising a unique oligonucleotide sequence;
- (b) J is a polynucleotide comprising at least 15 and not more than 600 contiguous nucleotides of an adaptive immune receptor joining (J) region encoding gene sequence, or the complement thereof, and each J polynucleotide comprising a unique oligonucleotide sequence;
- (c) U1 is either nothing or comprises an oligonucleotide sequence that is selected from (i) a first universal adaptor oligonucleotide sequence and (ii) a first sequencing platform-specific oligonucleotide sequence that is linked to and positioned 5' to a first universal adaptor oligonucleotide sequence;
- (d) U2 is either nothing or comprises an oligonucleotide sequence that is selected from (i) a second universal adaptor oligonucleotide sequence, and (ii) a second sequencing platform-specific oligonucleotide sequence that is linked to and positioned 5' to a second universal adaptor oligonucleotide sequence;
- (e) B1, B2, B3, and B4 are each independently either nothing or each comprises an oligonucleotide B that comprises a barcode sequence of 3-25 contiguous nucleotides, wherein each B1, B2, B3 and B4 comprises an oligonucleotide sequence that uniquely identifies, as a paired combination, (i) the unique V oligonucleotide sequence of (a) and (ii) the unique J oligonucleotide sequence of (b);

(f) R is either nothing or comprises a restriction enzyme recognition site that comprises an oligonucleotide sequence that is absent from (a)-(e),

and wherein:

(g) the plurality of template oligonucleotides comprises at least a or at least b unique oligonucleotide sequences, whichever is larger, wherein a is the number of unique adaptive immune receptor V region-encoding gene segments in the subject and b is the number of unique adaptive immune receptor J region-encoding gene segments in the subject, and the composition comprises at least one template oligonucleotide for each unique V polynucleotide and at least one template oligonucleotide for each unique J polynucleotide.

2. The composition of claim 1, wherein a ranges from 1 to a number of maximum V gene segments in the mammalian genome of the subject.

3. The composition as in any one of claims 1 or 2, wherein b ranges from 1 to a number of maximum J gene segments in the mammalian genome of the subject.

4. The composition as in any one of claims 1-3, wherein a is 1 or b is 1.

5. The composition of claim 1, wherein the plurality of template oligonucleotides comprises at least $(a \times b)$ unique oligonucleotide sequences, where a is the number of unique adaptive immune receptor V region-encoding gene segments in the mammalian subject and b is the number of unique adaptive immune receptor J region-encoding gene segments in the mammalian subject, and the composition comprises at least one template oligonucleotide for every possible combination of a V region-encoding gene segment and a J region-encoding gene segment.

6. The composition as in any one of claims 1-5, wherein J comprises a constant region of the adaptive immune receptor J region encoding gene sequence.

7. The composition as in any one of claims 1-6, wherein the adaptive immune receptor is selected from the group consisting of TCRB, TCRG, TCRA, TCRD, IGH, IGK, and IGL.

8. The composition as in any one of claims 1-7, wherein the V polynucleotide of (a) encodes a TCRB, TCRG, TCRA, TCRD, IGH, IGK, or IGL receptor V-region polypeptide.

9. The composition as in any one of claims 1-8, wherein the J polynucleotide of (b) encodes a TCRB, TCRG, TCRA, TCRD, IGH, IGK, or IGL receptor J-region polypeptide.

10. The composition as in any one of claims 1-9, further comprising a stop codon between V and B2.

11. The composition as in any one of claims 1-10, wherein each template oligonucleotide in the plurality of template oligonucleotides is present in a substantially equimolar amount.

12. The composition as in any one of claims 1-11, wherein the plurality of template oligonucleotides have a plurality of sequences of general formula (I) that is selected from:

(1) the plurality of oligonucleotide sequences of general formula (I) in which the V and J polynucleotides have the TCRB V and J sequences set forth in at least one set of 68 TCRB V and J SEQ ID NOS. in Figures 5a-5l as TCRB V/J set 1, TCRB V/J set 2, TCRB V/J set 3, TCRB V/J set 4, TCRB V/J set 5, TCRB V/J set 6, TCRB V/J set 7, TCRB V/J set 8, TCRB V/J set 9, TCRB V/J set 10, TCRB V/J set 11, TCRB V/J set 12 and TCRB V/J set 13;

(2) the plurality of oligonucleotide sequences of general formula (I) in which the V and J polynucleotides have the TCRG V and J sequences set forth in at least one set of 14 TCRG V and J SEQ ID NOS. in Figures 6a and 6b as TCRG V/J set 1, TCRG V/J set 2, TCRG V/J set 3, TCRG V/J set 4 and TCRG V/J set 5;

(3) the plurality of oligonucleotide sequences of general formula (I) in which the V and J polynucleotides have the IGH V and J sequences set forth in at least one set of 127 IGH V and J SEQ ID NOS. in Figures 7a-7m as IGH V/J set 1, IGH V/J set 2, IGH V/J set 3, IGH V/J set 4, IGH V/J set 5, IGH V/J set 6, IGH V/J set 7, IGH V/J set 8 and IGH V/J set 9;

(4) the plurality of oligonucleotide sequences of general formula (I) as set forth in SEQ ID NOS:3157-4014;

(5) the plurality of oligonucleotide sequences of general formula (I) as set forth in SEQ ID NOS:4015-4084;

(6) the plurality of oligonucleotide sequences of general formula (I) as set forth in SEQ ID NOS:4085-5200;

(7) the plurality of oligonucleotide sequences of general formula (I) as set forth in SEQ ID NOS:5579-5821;

(8) the plurality of oligonucleotide sequences of general formula (I) as set forth in SEQ ID NOS: 5822-6066; and

(9) the plurality of oligonucleotide sequences of general formula (I) as set forth in SEQ ID NOS: 6067-6191.

13. The composition as in any one of claims 1-12, wherein V is a polynucleotide comprising at least 30, 60, 90, 120, 150, 180, or 210 contiguous nucleotides of the adaptive immune receptor V region encoding gene sequence, or the complement thereof.

14. The composition as in any one of claims 1-13, wherein V is a polynucleotide comprising not more than 900, 800, 700, 600 or 500 contiguous nucleotides of an adaptive immune receptor V region encoding gene sequence, or the complement thereof.

15. The composition as in any one of claims 1-14, wherein J is a polynucleotide comprising at least 16-30, 31-60, 61-90, 91-120, or 120-150 contiguous nucleotides of an adaptive immune receptor J region encoding gene sequence, or the complement thereof.

16. The composition as in any one of claims 1-15, wherein J is a polynucleotide comprising not more than 500, 400, 300 or 200 contiguous nucleotides of an adaptive immune receptor J region encoding gene sequence, or the complement thereof.

17. The composition as in any one of claims 1-16, wherein each template oligonucleotide is less than 1000, 900, 800, 700, 600, 500, 400, 300 or 200 nucleotides in length.

18. The composition as in any one of claims 1-17, further comprising: a set of oligonucleotide primers that is capable of amplifying rearranged nucleic acid molecules encoding one or more adaptive immune receptors comprising a plurality a' of unique V-segment oligonucleotide primers and a plurality b' of unique J-segment oligonucleotide primers.

19. The composition of claim 18, wherein a' ranges from 1 to a number of maximum V gene segments in the mammalian genome, and b' ranges from 1 to a number of maximum number of J gene segments in the mammalian genome.

20. The composition of claim 19, wherein a' is a .

21. The composition of claim 19, wherein b' is b .

22. The composition as in any one of claims 18-21, wherein each V-segment oligonucleotide primer and each J-segment oligonucleotide primer in the oligonucleotide primer set is capable of specifically hybridizing to at least one template oligonucleotide in the plurality of template oligonucleotides.

23. The composition as in any one of claims 18-22, wherein each V-segment oligonucleotide primer comprises a nucleotide sequence of at least 15 contiguous nucleotides

that is complementary to at least one adaptive immune receptor V region-encoding gene segment.

24. The composition as in any one of claims 18-23, wherein each J-segment oligonucleotide primer comprises a nucleotide sequence of at least 15 contiguous nucleotides that is complementary to at least one adaptive immune receptor J region-encoding gene segment.

25. The composition as in any one of claims 18-24, wherein the composition comprises at least one template oligonucleotide having an oligonucleotide sequence of general formula (I) to which each V-segment oligonucleotide primer can specifically hybridize, and at least one template oligonucleotide having an oligonucleotide sequence of general formula (I) to which each J-segment oligonucleotide primer can specifically hybridize.

26. A method for determining non-uniform nucleic acid amplification potential among members of a set of oligonucleotide primers that is capable of amplifying rearranged nucleic acid molecules encoding one or more adaptive immune receptors in a biological sample that comprises rearranged nucleic acid molecules from lymphoid cells of a mammalian subject, the method comprising:

- (a) amplifying the composition as in any one of claims 18-25 in a multiplex PCR reaction to obtain a plurality of amplified template oligonucleotides;
- (b) sequencing said plurality of amplified template oligonucleotides to determine, for each unique template oligonucleotide comprising said plurality, (i) a template oligonucleotide sequence and (ii) a frequency of occurrence of said template oligonucleotide sequence; and
- (c) comparing a frequency of occurrence of each of said template oligonucleotide sequences to an expected distribution, wherein said expected distribution is based on predetermined molar ratios of said plurality of template oligonucleotides comprising said composition, and wherein a deviation between said frequency of occurrence of said template oligonucleotide sequences and said expected distribution indicates a non-uniform nucleic acid amplification potential among members of the set of oligonucleotide amplification primers.

27. The method of claim 26, wherein said predetermined molar ratios are equimolar.

28. The method of claim 27, wherein said expected distribution comprises a uniform amplification level for said set of template oligonucleotides amplified by said set of oligonucleotide primers.

29. The method of claim 26, wherein each amplified template nucleic acid molecule is less than 1000, 900, 800, 700, 600, 500, 400, 300, 200, 100, 90, 80 or 70 nucleotides in length.

30. The method as in any one of claims 26-29, further comprising: for each member of the set of oligonucleotide primers that exhibits non-uniform amplification potential relative to the expected distribution, adjusting the relative representation of the oligonucleotide primer member in the set of oligonucleotide amplification primers.

31. The method of claim 30, wherein adjusting comprises increasing the relative representation of the member in the set of oligonucleotide primers, thereby correcting non-uniform nucleic acid amplification potential among members of the set of oligonucleotide primers.

32. The method of claim 30, wherein adjusting comprises decreasing the relative representation of the member in the set of oligonucleotide primers, thereby correcting non-uniform nucleic acid amplification potential among members of the set of oligonucleotide primers.

33. The method as in any one of claims 26-32, wherein said set of oligonucleotide primers does not include oligonucleotide primers that specifically hybridize to a V-region pseudogene or orphon or to a J-region pseudogene or orphon.

34. The method as in any one of claims 26-33, further comprising: for each member of the set of oligonucleotide amplification primers that exhibits non-uniform amplification potential relative to the expected distribution, calculating a proportionately increased or decreased frequency of occurrence of the amplified template nucleic acid molecules, the amplification of which is promoted by said member, thereby correcting for non-uniform nucleic acid amplification potential among members of the set of oligonucleotide primers.

35. A method for quantifying a plurality of rearranged nucleic acid molecules encoding one or a plurality of adaptive immune receptors in a biological sample that comprises rearranged nucleic acid molecules from lymphoid cells of a mammalian subject, each adaptive immune receptor comprising a variable (V) region and a joining (J) region, the method comprising:

(A) amplifying rearranged nucleic acid molecules in a multiplex polymerase chain reaction (PCR) that comprises:

- (1) rearranged nucleic acid molecules from the biological sample that comprises lymphoid cells of the mammalian subject,
- (2) the composition as in any one claims 1-17, wherein a known number of each of the plurality of template oligonucleotides having a unique oligonucleotide sequence is present,
- (3) an oligonucleotide amplification primer set that is capable of amplifying rearranged nucleic acid molecules encoding one or a plurality of adaptive immune receptors from the biological sample, the primer set comprising:
 - (a) in substantially equimolar amounts, a plurality of V-segment oligonucleotide primers that are each independently capable of specifically hybridizing to at least one polynucleotide encoding an adaptive immune receptor V-region polypeptide or to the complement thereof, wherein each V-segment primer comprises a nucleotide sequence of at least 15 contiguous nucleotides that is complementary to at least one functional adaptive immune receptor V region-encoding gene segment and wherein the plurality of V-segment primers specifically hybridize to substantially all functional adaptive immune receptor V region-encoding gene segments that are present in the composition, and
 - (b) in substantially equimolar amounts, a plurality of J-segment oligonucleotide primers that are each independently capable of specifically hybridizing to at least one polynucleotide encoding an adaptive immune receptor J-region polypeptide or to the complement thereof, wherein each J-segment primer comprises a nucleotide sequence of at least 15 contiguous nucleotides that is complementary to at least one functional adaptive immune receptor J region-encoding gene segment and wherein the plurality of J-segment primers specifically hybridize to substantially all functional adaptive immune receptor J region-encoding gene segments that are present in the composition,
 wherein the V-segment and J-segment oligonucleotide primers are capable of promoting amplification in said multiplex polymerase chain reaction (PCR) of (i) substantially all template oligonucleotides in the composition to produce a multiplicity of amplified template oligonucleotides, said multiplicity of amplified template nucleic acid molecules being sufficient to quantify diversity of the template oligonucleotides in the composition, and (ii) substantially all rearranged nucleic acid molecules encoding adaptive immune receptors in the biological sample to produce a multiplicity of amplified rearranged

DNA molecules, said multiplicity of amplified rearranged nucleic acid molecules being sufficient to quantify diversity of the rearranged nucleic acid molecules in the DNA from the biological sample,

and wherein each amplified nucleic acid molecule in the plurality of amplified template oligonucleotides and in the plurality of amplified rearranged nucleic acid molecules is less than 1000 nucleotides in length;

(B) quantitatively sequencing said amplified template oligonucleotides and said amplified rearranged nucleic acid molecules to quantify (i) a template product number of amplified template oligonucleotides which contain at least one oligonucleotide barcode sequence, and (ii) a rearranged product number of amplified rearranged nucleic acid molecules which lack an oligonucleotide barcode sequence;

(C) calculating an amplification factor by dividing the template product number of (B)(i) by the known number of each of the plurality of template oligonucleotides having a unique oligonucleotide sequence of (A)(2); and

(D) dividing the rearranged product number of (B)(ii) by the amplification factor calculated in (C) to quantify the number of unique adaptive immune receptor encoding rearranged nucleic acid molecules in the sample.

36. The method of claim 35, wherein said the quantified number of unique adaptive immune receptor encoding rearranged nucleic acid molecules in the sample is the number of unique B cell or unique T cell genome templates in the sample.

37. A method for calculating an average amplification factor in a multiplex PCR assay, comprising:

obtaining a biological sample that comprises rearranged nucleic acid molecules from lymphoid cells of a mammalian subject;

contacting said sample with a known quantity of template oligonucleotides comprising a composition as in any one of claim 18-25;

amplifying the template oligonucleotides and the rearranged nucleic acid molecules from lymphoid cells of the mammalian subject in a multiplex PCR reaction to obtain a plurality of amplified template oligonucleotides and a plurality of amplified rearranged nucleic acid molecules;

sequencing said plurality of amplified template oligonucleotides to determine, for each unique template oligonucleotide comprising said plurality, (i) a template

oligonucleotide sequence and (ii) a frequency of occurrence of said template oligonucleotide sequence; and

determining said average amplification factor for said multiplex PCR reaction based on an average number of copies of said plurality of amplified template oligonucleotides and said known quantity of said template oligonucleotides.

38. The method of claim 37, further comprising:

sequencing said plurality of amplified rearranged nucleic acid molecules from lymphoid cells of the mammalian subject to determine for each unique rearranged nucleic acid molecule comprising said plurality, i) a rearranged nucleic acid molecule sequence and (ii) a number of occurrences of said rearranged nucleic acid molecule sequence; and

determining the number of lymphoid cells in said sample, based on the average amplification factor for said multiplex PCR reaction and said number of occurrences of said rearranged nucleic acid molecules.

39. The method of claim 38, wherein determining the number of lymphoid cells in said sample comprises generating a sum of the number of occurrences of each of said amplified rearranged nucleic acid sequences and dividing said sum by said average amplification factor.

40. The method of claim 37, wherein said known quantity is one copy each of said template oligonucleotides.

41. The method of claim 40, wherein $100 \leq a \leq 500$.

42. The method of claim 40, wherein $100 \leq b \leq 500$.

43. A method for correcting for amplification bias in an multiplex PCR amplification reaction to quantify rearranged nucleic acid molecules encoding one or a plurality of adaptive immune receptors in a biological sample that comprises rearranged nucleic acid molecules from lymphoid cells of a mammalian subject, comprising:

(a) contacting said sample with a composition of any one of claims 18-25 to generate a template-spiked sample, wherein said templates and said rearranged nucleic acid molecules comprise corresponding V and J region sequences;

(b) amplifying said template-spiked sample in a multiplex PCR reaction to obtain a plurality of amplified template oligonucleotides and a plurality of amplified rearranged nucleic acid molecules encoding a plurality of adaptive immune receptors;

(c) sequencing said plurality of amplified template oligonucleotides to determine, for each unique template oligonucleotide comprising said plurality, (i) a template

oligonucleotide sequence and (ii) a frequency of occurrence of said template oligonucleotide sequence;

(d) sequencing said plurality of amplified rearranged nucleic acid molecules encoding one or a plurality of adaptive immune receptors, for each unique rearranged nucleic acid molecules encoding said plurality of adaptive immune receptors comprising said plurality, (i) a rearranged nucleic acid molecule sequence and (ii) a frequency of occurrence of said rearranged nucleic acid molecule sequence;

(e) comparing said frequency of occurrence of said template oligonucleotide sequences to an expected distribution, wherein said expected distribution is based on predetermined molar ratios of said plurality of template oligonucleotides comprising said composition, and wherein a deviation between said frequency of occurrence of said template oligonucleotide sequences and said expected distribution indicates non-uniform nucleic acid amplification potential among members of the set of oligonucleotide amplification primers;

(f) generating a set of correction values for a set of template molecules and rearranged nucleic acid molecule sequences amplified by said members of the set of oligonucleotide amplification primers having said indicated non-uniform nucleic acid amplification potential, wherein said set of correction values corrects for amplification bias in said multiplex PCR reaction; and

(g) optionally applying said set of correction values to said frequency of occurrence of said rearranged nucleic acid molecule sequences to correct for amplification bias in said multiplex PCR reaction.

44. A kit, comprising:

reagents comprising: a composition comprising a plurality of template oligonucleotides and a set of oligonucleotide primers as in any one of claims 18-25;

instructions for determining a non-uniform nucleic acid amplification potential among members of the set of oligonucleotide primers that are capable of amplifying rearranged nucleic acid molecules encoding one or more adaptive immune receptors in a biological sample that comprises rearranged nucleic acid molecules from lymphoid cells of a mammalian subject.

45. The kit of claim 44, further comprising instructions for correcting for one or more members of the set of oligonucleotide primers having a non-uniform nucleic acid amplification potential.

46. The kit of claim 44, further comprising instructions for quantifying the number of unique adaptive immune receptor encoding rearranged nucleic acid molecules in the sample

DETAILED DESCRIPTION OF THE INVENTION

[0061] The present invention provides, in certain embodiments and as described herein, compositions and methods that are useful for reliably quantifying large and structurally diverse populations of rearranged genes encoding adaptive immune receptors, such as immunoglobulins (Ig) and/or T cell receptors (TCR). These rearranged genes may be present in a biological sample containing DNA from lymphoid cells of a subject or biological source, including a human subject.

[0062] A “rearranged nucleic acid molecule,” as used herein, can include any genomic DNA, cDNA, or mRNA obtained directly or indirectly from a lymphoid cell line that includes sequences that encode a rearranged adaptive immune receptor.

[0063] Disclosed herein are unexpectedly advantageous approaches for the standardization and calibration of complex oligonucleotide primer sets that are used in multiplexed nucleic acid amplification reactions to generate a population of amplified rearranged DNA molecules from a biological sample containing rearranged genes encoding adaptive immune receptors, prior to quantitative high throughput sequencing of such amplified products. Multiplexed amplification and high throughput sequencing of rearranged TCR and BCR (IG) encoding DNA sequences are described, for example, in Robins et al., 2009 *Blood* 114, 4099; Robins et al., 2010 *Sci. Translat. Med.* 2:47ra64; Robins et al., 2011 *J. Immunol. Meth.* doi:10.1016/j.jim.2011.09. 001; Sherwood et al. 2011 *Sci. Translat. Med.* 3:90ra61; U.S.A.N. 13/217,126 (US Pub. No. 2012/0058902), U.S.A.N. 12/794,507 (US Pub. No. 2010/0330571), WO/2010/151416, WO/2011/106738 (PCT/US2011/026373),

WO2012/027503 (PCT/US2011/049012), U.S.A.N. 61/550,311, and U.S.A.N. 61/569,118; accordingly these disclosures are incorporated by reference and may be adapted for use according to the embodiments described herein.

[0064] Briefly and according to non-limiting theory, the present compositions and methods overcome inaccuracies that may arise in current methods which quantify TCR and BCR gene diversity by sequencing the products of multiplexed nucleic acid amplification. To accommodate the vast diversity of TCR and BCR gene template sequences that may be present in a biological sample, oligonucleotide primer sets used in multiplexed amplification reactions typically comprise a wide variety of sequence lengths and nucleotide compositions (*e.g.*, GC content). Consequently, under a given set of amplification reaction conditions, the efficiencies at which different primers anneal to and support amplification of their cognate template sequences may differ markedly, resulting in non-uniform utilization of different primers, which leads to artifactual biases in the relative quantitative representation of distinct amplification products.

[0065] For instance, relative overutilization of some highly efficient primers results in overrepresentation of certain amplification products, and relative underutilization of some other low-efficiency primers results in underrepresentation of certain other amplification products. Quantitative determination of the relative amount of each template species that is present in the lymphoid cell DNA-containing sample, which is achieved by sequencing the amplification products, may then yield misleading information with respect to the actual relative representation of distinct template species in the sample prior to amplification. In pilot studies, for example, it was observed that multiplexed PCR, using a set of oligonucleotide primers designed to be capable of amplifying a sequence of every possible human TCRB variable (V) region gene from human lymphoid cell DNA templates, did not uniformly amplify TCRB V gene segments. Instead, some V gene segments were relatively overamplified (representing ~10% of total sequences) and other V gene segments were relatively underamplified (representing about $4 \times 10^{-3}\%$ of total sequences); see also, *e.g.*, Fig. 2.

[0066] To overcome the problem of such biased utilization of subpopulations of amplification primers, the present disclosure provides for the first time a template composition and method for standardizing the amplification efficiencies of the members of an oligonucleotide primer set, where the primer set is capable of amplifying rearranged DNA encoding a plurality of adaptive immune receptors (TCR or Ig) in a biological sample that

comprises DNA from lymphoid cells. The template composition comprises a plurality of diverse template oligonucleotides of general formula (I) as described in greater detail herein:

[0067] 5'-U1-B1-V-B2-R-B3-J-B4-U2-3' (I)

[0068] The constituent template oligonucleotides, of which the template composition is comprised, are diverse with respect to the nucleotide sequences of the individual template oligonucleotides. The individual template oligonucleotides thus may vary in nucleotide sequence considerably from one another as a function of significant sequence variability amongst the large number of possible TCR or BCR variable (V) and joining (J) region polynucleotides. Sequences of individual template oligonucleotide species may also vary from one another as a function of sequence differences in U1, U2, B (B1, B2, B3, and B4) and R oligonucleotides that are included in a particular template within the diverse plurality of templates.

[0069] In certain embodiments barcode oligonucleotides B (B1, B2, B3, and B4) may independently and optionally comprise an oligonucleotide barcode sequence, wherein the barcode sequence is selected to identify uniquely a particular paired combination of a particular unique V oligonucleotide sequence and a particular unique J oligonucleotide sequence. The relative positioning of the barcode oligonucleotides B1 and B4 and universal adaptors advantageously permits rapid identification and quantification of the amplification products of a given unique template oligonucleotide by short sequence reads and paired-end sequencing on automated DNA sequencers (*e.g.*, Illumina HiSeq™ or Illumina MiSEQ®, or GeneAnalyzer™-2, Illumina Corp., San Diego, CA). In particular, these and related embodiments permit rapid high-throughput determination of specific combinations of a V and a J sequence that are present in an amplification product, thereby to characterize the relative amplification efficiency of each V-specific primer and each J-specific primer that may be present in a primer set which is capable of amplifying rearranged TCR or BCR encoding DNA in a sample. Verification of the identities and/or quantities of the amplification products may be accomplished by longer sequence reads, optionally including sequence reads that extend to B2.

[0070] In use, each template oligonucleotide in the plurality of template oligonucleotides is present in a substantially equimolar amount, which in certain preferred embodiments includes preparations in which the molar concentrations of all oligonucleotides are within 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25 percent of each other. In certain other preferred embodiments as provided herein, template oligonucleotides are

regarded as being present in a substantially equimolar amount when the molar concentrations of all oligonucleotides are within one order of magnitude of each other, including preparations in which the greatest molar concentration that any given unique template oligonucleotide species may have is no more than 1000, 900, 800, 700, 600, 500, 440, 400, 350, 300, 250, 200, 150, 100, 90, 80, 70, 60, 50, 40 or 30 percent greater than the molar concentration at which is present the unique template oligonucleotide species having the lowest concentration in the composition.

[0071] In a similar manner, certain embodiments disclosed herein contemplate oligonucleotide primer sets for amplification, in which sets the component primers may be provided in substantially equimolar amounts. As also described herein, according to certain other embodiments, the concentration of one or more primers in a primer set may be adjusted deliberately so that certain primers are not present in equimolar amounts or in substantially equimolar amounts.

[0072] The template composition described herein may, in preferred embodiments, be employed as a nucleic acid amplification (*e.g.*, PCR) template to characterize an oligonucleotide primer set, such as the complex sets of V-segment and J-segment oligonucleotide primers that may be used in multiplexed amplification of rearranged TCR or Ig genes, for example, a primer set as provided herein or any of the primer sets described in Robins et al., 2009 *Blood* 114, 4099; Robins et al., 2010 *Sci. Translat. Med.* 2:47ra64; Robins et al., 2011 *J. Immunol. Meth.* doi:10.1016/j.jim.2011.09. 001; Sherwood et al. 2011 *Sci. Translat. Med.* 3:90ra61; U.S.A.N. 13/217,126 (US Pub. No. 2012/0058902), U.S.A.N. 12/794,507 (US Pub. No. 2010/0330571), WO/2010/151416, WO/2011/106738 (PCT/US2011/026373), WO2012/027503 (PCT/US2011/049012), U.S.A.N. 61/550,311, and U.S.A.N. 61/569,118,; or the like.

[0073] Preferably all templates in the template composition for standardizing amplification efficiency, which is described herein and which comprises a plurality of template oligonucleotides having diverse sequences and the general structure of general formula (I), are oligonucleotides of substantially identical length. Without wishing to be bound by theory, it is generally believed that in a nucleic acid amplification reaction such as a polymerase chain reaction (PCR), template DNA length can influence the amplification efficiency of oligonucleotide primers by affecting the kinetics of interactions between primers and template DNA molecules to which the primers anneal by specific, nucleotide sequence-directed hybridization through nucleotide base complementarity. Longer templates

are generally regarded as operating less efficiently than relatively shorter templates. In certain embodiments, the presently disclosed template composition for standardizing the amplification efficiency of an oligonucleotide primer set that is capable of amplifying rearranged DNA encoding a plurality of TCR or BCR comprises a plurality of template oligonucleotides of general formula (I) as provided herein, wherein the template oligonucleotides are of an identical length or a substantially identical length that is not more than 1000, 950, 900, 850, 800, 750, 700, 650, 600, 550, 500, 450, 400, 350, 300, 250, 200, 150 or 100 nucleotides in length, including all integer values therebetween.

[0074] Accordingly, in order to reduce, remove or minimize the potential contribution to undesirable biases in oligonucleotide primer utilization during multiplexed amplification, preferred embodiments disclosed herein may employ a plurality of template oligonucleotides wherein all template oligonucleotides in the sequence-diverse plurality of template oligonucleotides are of substantially identical length. A plurality of template oligonucleotides may be of substantially identical length when all (*e.g.*, 100%) or most (*e.g.*, greater than 50%) such oligonucleotides in a template composition are oligonucleotides that each have the exact same number of nucleotides, or where one or more template oligonucleotides in the template composition may vary in length from one another by no more than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 60, 70, 80, 90 or 100 nucleotides in length. It will be appreciated from the present disclosure that even in situations where not all template oligonucleotides have exactly the same length, the herein described compositions and methods may still be employed to determine and optionally correct non-uniform nucleic acid amplification potential among members of a set of oligonucleotide amplification primers.

[0075] According to certain presently disclosed embodiments, (i) each template oligonucleotide of the presently described template composition is provided in a substantially equimolar amount, (ii) the oligonucleotide primer set that is capable of amplifying rearranged DNA encoding a plurality of adaptive immune receptor comprises a plurality of V-segment oligonucleotide primers that are provided in substantially equimolar amounts, (iii) the oligonucleotide primer set that is capable of amplifying rearranged DNA encoding a plurality of adaptive immune receptor comprises a plurality of J-segment oligonucleotide primers that are provided in substantially equimolar amounts, and (iv) amplification scales linearly with the number of starting templates of a given sequence.

[0076] Hence, an expected yield for the amplification product of each template can be calculated and arbitrarily assigned a theoretical uniform amplification level value of 100%. After permitting the primer sets to amplify the sequences of the template oligonucleotides in an amplification reaction, any statistically significant deviation from substantial equivalence that is observed among the relative proportions of distinct amplification products indicates that there has been bias (*i.e.*, unequal efficiency) in primer utilization during amplification. In other words, quantitative differences in the relative amounts of different amplification products that are obtained indicate that not all primers in the primer set have amplified their respective templates with comparable efficiencies. Certain embodiments contemplate assigning a range of tolerances above and below a theoretical 100% yield, such that any amplification level value within the range of tolerances may be regarded as substantial equivalence.

[0077] In certain such embodiments, the range of amplification product yields may be regarded as substantially equivalent when the product yields are all within the same order of magnitude (*e.g.*, differ by less than a factor of ten). In certain other such embodiments, the range of amplification product yields may be regarded as substantially equivalent when the product yields differ from one another by no more than nine-fold, eight-fold, seven-fold, six-fold, five-fold, four-fold or three-fold. In certain other embodiments, product yields that may be regarded as being within an acceptable tolerance range may be more or less than a calculated 100% yield by as much as 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 30, 40, 50, 60, 100, or 200%.

[0078] Because the method involves determining the nucleotide sequence of each amplification product using known techniques as part of the quantification process, the primer(s) responsible for amplification of each unique (as defined by sequence) product can be identified and their relative amount(s) in the primer set can be adjusted (*e.g.*, increased or decreased in a statistically significant manner) accordingly. The concentrations of excessively efficient primers in the primer set can be reduced relative to the concentrations of other primers, so that the level of specific amplification by such primers of templates in the herein described template composition is substantially equivalent to the level of amplification delivered by the majority of primers which deliver the theoretical uniform amplification level, or which deliver a level that is within the acceptable tolerance range. The concentrations of poorly efficient primers in the primer set can be increased relative to the concentrations of other primers, so that the level of specific amplification by such primers of

templates in the herein described template composition is substantially equivalent to the level of amplification delivered by the majority of primers which deliver the theoretical uniform amplification level, or which deliver a level within the acceptable tolerance range.

[0079] Accordingly and as described herein, there are thus presently provided a template composition for standardizing the amplification efficiency of an oligonucleotide primer set that is designed to amplify coding sequences for a complete repertoire of a given TCR or Ig chain, a method for determining non-uniform amplification efficiency (“non-uniform amplification potential”) among members of such a primer set, and a method for correcting such non-uniform amplification potential. By providing the herein described template composition as a standard with which oligonucleotide primer sets can be calibrated, and in particular embodiments, where each template oligonucleotide is present in a substantially equimolar amount so that individual primer concentrations can be adjusted to yield substantially uniform amplification of a structurally diverse array of amplification products, the present disclosure thus advantageously overcomes the above described problems associated with biases in individual primer efficiency.

[0080] Using the compositions and methods provided herein, individual primers may be identified as having a non-uniform amplification potential by virtue of their promotion of non-uniform amplification as evidenced by increased (*e.g.*, greater in a statistically significant manner) or decreased (*e.g.*, lower in a statistically significant manner) amplification of specific template oligonucleotides relative to the uniform amplification level, despite the presence in an amplification reaction (i) of all template oligonucleotides in substantially equimolar amounts to one another, (ii) of all V-segment primers in substantially equimolar amounts to one another, and (iii) of all J-segment primers in substantially equimolar amounts to one another.

[0081] The relative concentrations of such primers may then be decreased or increased to obtain a modified complete set of primers in which all primers are not present in substantially equimolar amounts relative to one another, to compensate, respectively, for the increased or decreased level of amplification relative to the uniform amplification level. The primer set may then be retested for its ability to amplify all sequences in the herein disclosed template composition at the uniform amplification level, or within an acceptable tolerance range.

[0082] The process of testing modified primer sets for their ability to amplify the herein disclosed template composition, in which all template oligonucleotides are provided in substantially equimolar amounts to one another, may be repeated iteratively until all products

are amplified at the uniform amplification level, or within an acceptable tolerance range. By such a process using the herein disclosed template composition, the amplification efficiency of an oligonucleotide primer set may be standardized, where the primer set is capable of amplifying productively rearranged DNA encoding one or a plurality of adaptive immune receptors in a biological sample that comprises DNA from lymphoid cells of a subject.

[0083] Additionally or alternatively, according to the present disclosure it may be determined whether any particular pair of oligonucleotide amplification primers exhibits non-uniform amplification potential, such as increased or decreased amplification of the template composition relative to a uniform amplification level exhibited by a majority of the oligonucleotide amplification primers, and a normalizing adjustment factor can then be used to calculate, respectively, a proportionately decreased or increased frequency of occurrence of the amplification products that are promoted by each such amplification primer pair. The present template compositions thus, in certain embodiments, provide a method of correcting for non-uniform nucleic acid amplification potential among members of a set of oligonucleotide amplification primers.

[0084] Certain such embodiments may advantageously permit correction, calibration, standardization, normalization, or the like, of data that are obtained as a consequence of non-uniform amplification events. Thus, the present embodiments permit correction of data inaccuracies, such as may result from biased oligonucleotide primer utilization, without the need for iteratively adjusting the concentrations of one or more amplification primers and repeating the steps of amplifying the herein described template compositions. Advantageous efficiencies may thus be obtained where repetition of the steps of quantitatively sequencing the amplification products can be avoided. Certain other contemplated embodiments may, however, employ such an iterative approach.

[0085] Accordingly, and as described herein, there is presently provided a template composition for standardizing the amplification efficiency of an oligonucleotide primer set, along with methods for using such a template composition to determine non-uniform nucleic acid amplification potential (*e.g.*, bias) among individual members of the oligonucleotide primer set. Also described herein are methods for correcting such non-uniform nucleic acid amplification potentials (*e.g.*, biases) among members of the oligonucleotide primer set. These and related embodiments exploit previously unrecognized benefits that are obtained by calibrating complex oligonucleotide primer sets to compensate for undesirable amplification biases using the template composition for standardizing amplification efficiency having the

features described herein, and will find uses in improving the accuracy with which specific clonotypic TCR and/or Ig encoding DNA sequences can be quantified, relative to previously described methodologies.

[0086] As also noted above and described elsewhere herein, prior to the present disclosure there existed unsatisfactory and difficult-to-discern discrepancies between (i) the actual quantitative distribution of rearranged adaptive immune receptor-encoding DNA templates having unique sequences in a biological sample comprising lymphoid cell DNA from a subject, and (ii) the relative representation of nucleic acid amplification products of such templates, following multiplexed amplification using a complex set of oligonucleotide amplification primers designed to amplify substantially all productively rearranged adaptive immune receptor genes in the sample. Due to, *e.g.*, the heterogeneity of both the template population and the amplification primer set, and as shown herein, significant disparities in the amplification efficiencies of different amplification primers may be common, leading to substantial skewing in the relative proportions of amplification products that are obtained and quantitatively sequenced following an amplification reaction.

Templates And Primers

[0087] According to certain preferred embodiments there is thus provided a template composition for standardizing the amplification efficiency of an oligonucleotide primer set that is capable of amplifying rearranged DNA (which in certain embodiments may refer to productively rearranged DNA but which in certain other embodiments need not be so limited) encoding one or a plurality of adaptive immune receptors in a biological sample that comprises DNA from lymphoid cells of a subject, the template composition comprising a plurality of template oligonucleotides of general formula (I):

[0088] 5'-U1-B1-V-B2-R-B3-J-B4-U2-3' (I)

[0089] as provided herein. In certain preferred embodiments each template oligonucleotide in the plurality of template oligonucleotides is present in a substantially equimolar amount, which in certain embodiments and as noted above may refer to a composition in which each of the template oligonucleotides is present at an equimolar concentration or at a molar concentration that deviates from equimolar by no more than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 50, 60, 70, 80, 90, 100 or 200% on a molar basis, and which in certain other embodiments may refer to a composition in which all of the template oligonucleotides are present at molar concentrations that are within an order of magnitude of one another. The plurality of templates may comprise at least 100, 200, 300,

400, 500, 600, 700, 800, 900, 1000, 1100 or more discrete oligonucleotide species each having a distinct nucleotide sequence, including every intermediate integer value therebetween.

[0090] The herein disclosed template composition thus comprises a plurality of template oligonucleotides of general formula:

[0091] 5'-U1-B1-V-B2-R-B3-J-B4-U2-3' [I]

[0092] wherein, briefly and as elaborated in greater detail elsewhere herein, according to certain preferred embodiments:

[0093] V is a polynucleotide comprising at least 20, 30, 60, 90, 120, 150, 180, or 210, and not more than 1000, 900, 800, 700, 600 or 500 contiguous nucleotides of an adaptive immune receptor variable (V) region encoding gene sequence, or the complement thereof, and in each of the plurality of template oligonucleotide sequences V comprises a unique oligonucleotide sequence;

[0094] J is a polynucleotide comprising at least 15-30, 31-60, 61-90, 91-120, or 120-150, and not more than 600, 500, 400, 300 or 200 contiguous nucleotides of an adaptive immune receptor joining (J) region encoding gene sequence, or the complement thereof, and in each of the plurality of template oligonucleotide sequences J comprises a unique oligonucleotide sequence;

[0095] U1 and U2 are each either nothing or each comprise an oligonucleotide having, independently, a sequence that is selected from (i) a universal adaptor oligonucleotide sequence, and (ii) a sequencing platform-specific oligonucleotide sequence that is linked to and positioned 5' to the universal adaptor oligonucleotide sequence;

[0096] B1, B2, B3, and B4 are each independently either nothing or each comprise an oligonucleotide B that comprises an oligonucleotide barcode sequence of 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500, 600, 700, 800, 900 or 1000 contiguous nucleotides (including all integer values therebetween), wherein in each of the plurality of template oligonucleotide sequences B comprises a unique oligonucleotide sequence that uniquely identifies, or identifies as a paired combination, (i) the unique V oligonucleotide sequence of the template oligonucleotide and (ii) the unique J oligonucleotide sequence of the template oligonucleotide; and

[0097] R is either nothing or comprises a restriction enzyme recognition site that comprises an oligonucleotide sequence that is absent from V, J, U1, U2, B1, B2, B3, and B4.

[0098] In some embodiments, the template oligonucleotide composition comprises additional non-coding or random oligonucleotides. These oligonucleotides may be inserted in various sections between or within the components in the general formula I (5'-U1-B1-V-B2-R-B3-J-B4-U2-3') and be of various lengths in size.

[0099] In one embodiment, *a* is 1 to a number of maximum V gene segments in the mammalian genome of the subject. In another embodiment, *b* is 1 to a number of maximum J gene segments in the mammalian genome of the subject. In other embodiments, *a* is 1 or *b* is 1. In some embodiments, *a* can range from 1 V gene segment to 54 V gene segments for TCRA, 1-76 V gene segments for TCRB, 1-15 V gene segments for TCRG, 1-7 V gene segments for TCRD, 1-165 V gene segments for IGH, 1-111 for IGK, or 1-79 V gene segments for IGL. In other embodiments, *b* can range from 1 J gene segment to 61 J gene segments for TCRA, 1-14 J gene segments for TCRB, 1-5 J gene segments for TCRG, 1-4 gene segments for TCRD, 1-9 J gene segments for IGH, 1-5 J gene segments for IGK, or 1-11 J gene segments for IGL.

[00100] The table below lists the number of V gene segments (*a*) and J gene segments (*b*) for each human adaptive immune receptor loci, including functional V and J segments.

	V segments *	functional V segments **	J segments *	Functional J segments **
TCRA	54	45	61	50
TCRB	76	48	14	13
TCRG	15	6	5	5
TCRD	7	7	4	4
IGH	165	51	9	6
IGK	111	44	5	5
IGL	79	33	11	7

[00101] * Total variable and joining segment genes

[00102] ** Variable and joining segment genes with at least one functional allele

[00103] In some embodiments, the J polynucleotide comprises at least 15-30, 31-60, 61-90, 91-120, or 120-150, and not more than 600, 500, 400, 300 or 200 contiguous nucleotides of an adaptive immune receptor J constant region, or the complement thereof.

[00104] In certain embodiments the plurality of template oligonucleotides comprises at least (*a* x *b*) unique oligonucleotide sequences, where *a* is the number of unique adaptive

immune receptor V region-encoding gene segments in a subject and b is the number of unique adaptive immune receptor J region-encoding gene segments in the subject, and the composition comprises at least one template oligonucleotide for every possible combination of a V region-encoding gene segment and a J region-encoding gene segment.

[00105] The presently contemplated invention is not intended to be so limited, however, such that in certain embodiments, a substantially fewer number of template oligonucleotides may advantageously be used. In these and related embodiments, where a is the number of unique adaptive immune receptor V region-encoding gene segments in a subject and b is the number of unique adaptive immune receptor J region-encoding gene segments in the subject, the minimum number of unique oligonucleotide sequences of which the plurality of template oligonucleotides is comprised may be determined by whichever is the larger of a and b , so long as each unique V polynucleotide sequence and each unique J polynucleotide sequence is present in at least one template oligonucleotide in the template composition. Thus, according to certain related embodiments the template composition may comprise at least one template oligonucleotide for each unique V polynucleotide, *e.g.*, that includes a single one of each unique V polynucleotide according to general formula (I), and at least one template oligonucleotide for each unique J polynucleotide, *e.g.*, that includes a single one of each unique J polynucleotide according to general formula (I).

[00106] In certain other embodiments, the template composition comprises at least one template oligonucleotide to which each oligonucleotide amplification primer in an amplification primer set can anneal.

[00107] That is, in certain embodiments, the template composition comprises at least one template oligonucleotide having an oligonucleotide sequence of general formula (I) to which each V-segment oligonucleotide primer can specifically hybridize, and at least one template oligonucleotide having an oligonucleotide sequence of general formula (I) to which each J-segment oligonucleotide primer can specifically hybridize.

[00108] According to such embodiments the oligonucleotide primer set that is capable of amplifying rearranged DNA encoding one or a plurality of adaptive immune receptors comprises a plurality a' of unique V-segment oligonucleotide primers and a plurality b' of unique J-segment oligonucleotide primers. The plurality of a' V-segment oligonucleotide primers are each independently capable of annealing or specifically hybridizing to at least one polynucleotide encoding an adaptive immune receptor V-region polypeptide or to the complement thereof, wherein each V-segment primer comprises a nucleotide sequence of at

least 15 contiguous nucleotides that is complementary to at least one adaptive immune receptor V region-encoding gene segment. The plurality of *b'* J-segment oligonucleotide primers are each independently capable of annealing or specifically hybridizing to at least one polynucleotide encoding an adaptive immune receptor J-region polypeptide or to the complement thereof, wherein each J-segment primer comprises a nucleotide sequence of at least 15 contiguous nucleotides that is complementary to at least one adaptive immune receptor J region-encoding gene segment.

[00109] In some embodiments, *a'* is the same as *a* (described above for template oligonucleotides). In other embodiments, *b'* is the same as *b* (described above for template oligonucleotides).

[00110] Thus, in certain embodiments and as also discussed elsewhere herein, the present template composition may be used in amplification reactions with amplification primers that are designed to amplify all rearranged adaptive immune receptor encoding gene sequences, including those that are not expressed, while in certain other embodiments the template composition and amplification primers may be designed so as not to yield amplification products of rearranged genes that are not expressed (*e.g.*, pseudogenes, orphans). It will therefore be appreciated that in certain embodiments only a subset of rearranged adaptive immune receptor encoding genes may desirably be amplified, such that suitable amplification primer subsets may be designed and employed to amplify only those rearranged V-J sequences that are of interest. In these and related embodiments, correspondingly, a herein described template composition comprising only a subset of interest of rearranged V-J rearranged sequences may be used, so long as the template composition comprises at least one template oligonucleotide to which each oligonucleotide amplification primer in an amplification primer set can anneal. The actual number of template oligonucleotides in the template composition may thus vary considerably among the contemplated embodiments, as a function of the amplification primer set that is to be used.

[00111] For example, in certain related embodiments, in the template composition the plurality of template oligonucleotides may have a plurality of sequences of general formula (I) that is selected from (1) the plurality of oligonucleotide sequences of general formula (I) in which polynucleotides V and J have the TCRB V and J sequences set forth in at least one set of 68 TCRB V and J SEQ ID NOS, respectively, as set forth in Figs. 5a-5l as TCRB V/J set 1, TCRB V/J set 2, TCRB V/J set 3, TCRB V/J set 4, TCRB V/J set 5, TCRB V/J set 6, TCRB V/J set 7, TCRB V/J set 8, TCRB V/J set 9, TCRB V/J set 10, TCRB V/J set 11,

TCRB V/J set 12 and TCRB V/J set 13; (2) the plurality of oligonucleotide sequences of general formula (I) in which polynucleotides V and J have the TCRG V and J sequences set forth in at least one set of 14 TCRG V and J SEQ ID NOS, respectively, as set forth in Fig. 6 as TCRG V/J set 1, TCRG V/J set 2, TCRG V/J set 3, TCRG V/J set 4 and TCRG V/J set 5; and (3) the plurality of oligonucleotide sequences of general formula (I) in which polynucleotides V and J have the IGH V and J sequences set forth in at least one set of 127 IGH V and J SEQ ID NOS, respectively, as set forth in Fig. 7 as IGH V/J set 1, IGH V/J set 2, IGH V/J set 3, IGH V/J set 4, IGH V/J set 5, IGH V/J set 6, IGH V/J set 7, IGH V/J set 8 and IGH V/J set 9.

[00112] In certain embodiments, V is a polynucleotide sequence that encodes at least 10-70 contiguous amino acids of an adaptive immune receptor V-region, or the complement thereof; J is a polynucleotide sequence that encodes at least 5-30 contiguous amino acids of an adaptive immune receptor J-region, or the complement thereof; U1 and U2 are each either nothing or comprise an oligonucleotide comprising a nucleotide sequence that is selected from (i) a universal adaptor oligonucleotide sequence, and (ii) a sequencing platform-specific oligonucleotide sequence that is linked to and positioned 5' to the universal adaptor oligonucleotide sequence; B1, B2, B3 and B4 are each independently either nothing or each comprise an oligonucleotide B that comprises an oligonucleotide barcode sequence of 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 contiguous nucleotides, wherein in each of the plurality of oligonucleotide sequences B comprises a unique oligonucleotide sequence that uniquely identifies, as a paired combination, (i) the unique V oligonucleotide sequence and (ii) the unique J oligonucleotide sequence; and R is either nothing or comprises a restriction enzyme recognition site that comprises an oligonucleotide sequence that is absent from V, J, U1, U2, B1, B2, B3, and B4. In certain preferred embodiments the plurality of template oligonucleotides comprises at least either *a* or *b* unique oligonucleotide sequences, where *a* is the number of unique adaptive immune receptor V region-encoding gene segments in the subject and *b* is the number of unique adaptive immune receptor J region-encoding gene segments in the subject, and the composition comprises a plurality of template oligonucleotides that comprise at least whichever is the greater of *a* or *b* unique template oligonucleotide sequences, provided that at least one V polynucleotide corresponding to each V region-encoding gene segment and at least one J polynucleotide corresponding to each J region-encoding gene segment is included.

[00113] A large number of adaptive immune receptor variable (V) region and joining (J) region gene sequences are known as nucleotide and/or amino acid sequences, including non-rearranged genomic DNA sequences of TCR and Ig loci, and productively rearranged DNA sequences at such loci and their encoded products, and also including pseudogenes at these loci, and also including related orphans. See, *e.g.*, U.S.A.N. 13/217,126; U.S.A.N. 12/794,507; PCT/US2011/026373; PCT/US2011/049012. These and other sequences known to the art may be used according to the present disclosure for the design and production of template oligonucleotides to be included in the presently provided template composition for standardizing amplification efficiency of an oligonucleotide primer set, and for the design and production of the oligonucleotide primer set that is capable of amplifying rearranged DNA encoding TCR or Ig polypeptide chains, which rearranged DNA may be present in a biological sample comprising lymphoid cell DNA.

[00114] In formula (I), V is a polynucleotide sequence of at least 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400 or 450 and not more than 1000, 900, 800, 700, 600 or 500 contiguous nucleotides of an adaptive immune receptor (*e.g.*, TCR or BCR) variable (V) region gene sequence, or the complement thereof, and in each of the plurality of oligonucleotide sequences V comprises a unique oligonucleotide sequence. Genomic sequences for TCR and BCR V region genes of humans and other species are known and available from public databases such as Genbank; V region gene sequences include polynucleotide sequences that encode the products of expressed, rearranged TCR and BCR genes and also include polynucleotide sequences of pseudogenes that have been identified in the V region loci. The diverse V polynucleotide sequences that may be incorporated into the presently disclosed templates of general formula (I) may vary widely in length, in nucleotide composition (*e.g.*, GC content), and in actual linear polynucleotide sequence, and are known, for example, to include “hot spots” or hypervariable regions that exhibit particular sequence diversity.

[00115] The polynucleotide V in general formula (I) (or its complement) includes sequences to which members of oligonucleotide primer sets specific for TCR or BCR genes can specifically anneal. Primer sets that are capable of amplifying rearranged DNA encoding a plurality of TCR or BCR are described, for example, in U.S.A.N. 13/217,126; U.S.A.N. 12/794,507; PCT/US2011/026373; or PCT/US2011/049012; or the like; or as described therein may be designed to include oligonucleotide sequences that can specifically hybridize

to each unique V gene and to each J gene in a particular TCR or BCR gene locus (*e.g.*, TCR α , β , γ or δ , or IgH μ , γ , δ , α or ϵ , or IgL κ or λ). For example by way of illustration and not limitation, an oligonucleotide primer of an oligonucleotide primer amplification set that is capable of amplifying rearranged DNA encoding one or a plurality of TCR or BCR may typically include a nucleotide sequence of 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39 or 40 contiguous nucleotides, or more, and may specifically anneal to a complementary sequence of 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39 or 40 contiguous nucleotides of a V or a J polynucleotide as provided herein. In certain embodiments the primers may comprise at least 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 30 nucleotides, and in certain embodiment the primers may comprise sequences of no more than 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39 or 40 contiguous nucleotides. Primers and primer annealing sites of other lengths are also expressly contemplated, as disclosed herein.

[00116] The entire polynucleotide sequence of each polynucleotide V in general formula (I) may, but need not, consist exclusively of contiguous nucleotides from each distinct V gene. For example and according to certain embodiments, in the template composition described herein, each polynucleotide V of formula (I) need only have at least a region comprising a unique V oligonucleotide sequence that is found in one V gene and to which a single V region primer in the primer set can specifically anneal. Thus, the V polynucleotide of formula (I) may comprise all or any prescribed portion (*e.g.*, at least 15, 20, 30, 60, 90, 120, 150, 180 or 210 contiguous nucleotides, or any integer value therebetween) of a naturally occurring V gene sequence (including a V pseudogene sequence) so long as at least one unique V oligonucleotide sequence region (the primer annealing site) is included that is not included in any other template V polynucleotide.

[00117] It may be preferred in certain embodiments that the plurality of V polynucleotides that are present in the herein described template composition have lengths that simulate the overall lengths of known, naturally occurring V gene nucleotide sequences, even where the specific nucleotide sequences differ between the template V region and any naturally occurring V gene. The V region lengths in the herein described templates may differ from the lengths of naturally occurring V gene sequences by no more than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 percent.

[00118] The V polynucleotide in formula (I) may thus, in certain embodiments, comprise a nucleotide sequence having a length that is the same or similar to that of the length of a typical V gene from its start codon to its CDR3 encoding region and may, but need not, include a nucleotide sequence that encodes the CDR3 region. CDR3 encoding nucleotide sequences and sequence lengths may vary considerably and have been characterized by several different numbering schemes (*e.g.*, Lefranc, 1999 *The Immunologist* 7:132; Kabat et al., 1991 *In: Sequences of Proteins of Immunological Interest*, NIH Publication 91-3242; Chothia et al., 1987 *J. Mol. Biol.* 196:901; Chothia et al., 1989 *Nature* 342:877; Al-Lazikani et al., 1997 *J. Mol. Biol.* 273:927; see also, *e.g.*, Rock et al., 1994 *J. Exp. Med.* 179:323; Saada et al., 2007 *Immunol. Cell Biol.* 85:323).

[00119] Briefly, the CDR3 region typically spans the polypeptide portion extending from a highly conserved cysteine residue (encoded by the trinucleotide codon TGY; Y = T or C) in the V segment to a highly conserved phenylalanine residue (encoded by TTY) in the J segment of TCRs, or to a highly conserved tryptophan (encoded by TGG) in IGH. More than 90% of natural, productive rearrangements in the TCRB locus have a CDR3 encoding length by this criterion of between 24 and 54 nucleotides, corresponding to between 9 and 17 encoded amino acids. The CDR3 lengths of the presently disclosed synthetic template oligonucleotides should, for any given TCR or BCR locus, fall within the same range as 95% of naturally occurring rearrangements. Thus, for example, in a herein described template composition for standardizing the amplification efficiency of an oligonucleotide primer set that is capable of amplifying rearranged DNA encoding a plurality of TCRB polypeptides, the CDR3 encoding portion of the V polynucleotide may have a length of from 24 to 54 nucleotides, including every integer therebetween. The numbering schemes for CDR3 encoding regions described above denote the positions of the conserved cysteine, phenylalanine and tryptophan codons, and these numbering schemes may also be applied to pseudogenes in which one or more codons encoding these conserved amino acids may have been replaced with a codon encoding a different amino acid. For pseudogenes which do not use these conserved amino acids, the CDR3 length may be defined relative to the corresponding position at which the conserved residue would have been observed absent the substitution, according to one of the established CDR3 sequence position numbering schemes referenced above.

[00120] It may also be preferred, in certain embodiments, that the plurality of V polynucleotides that are present in the herein described template composition have nucleotide

compositions (*e.g.*, percentage of GC content) that simulate the overall nucleotide compositions of known, naturally occurring V gene sequences, even where the specific nucleotide sequences differ. Such template V region nucleotide compositions may differ from the nucleotide compositions of naturally occurring V gene sequences by no more than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 percent. Optionally and according to certain embodiments, the V polynucleotide of the herein described template oligonucleotide includes a stop codon at or near the 3' end of V in general formula (I).

[00121] In formula (I) J is a polynucleotide comprising at least 15-30, 31-60, 61-90, 91-120, or 120-150, and not more than 600, 500, 400, 300 or 200 contiguous nucleotides of an adaptive immune receptor joining (J) region encoding gene sequence, or the complement thereof, and in each of the plurality of oligonucleotide sequences J comprises a unique oligonucleotide sequence.

[00122] The polynucleotide J in general formula (I) (or its complement) includes sequences to which members of oligonucleotide primer sets specific for TCR or BCR genes can specifically anneal. Primer sets that are capable of amplifying rearranged DNA encoding a plurality of TCR or BCR are described, for example, in U.S.A.N. 13/217,126; U.S.A.N. 12/794,507; PCT/US2011/026373; or PCT/US2011/049012; or the like; or as described therein may be designed to include oligonucleotide sequences that can specifically hybridize to each unique V gene and to each unique J gene in a particular TCR or BCR gene locus (*e.g.*, TCR α , β , γ or δ , or IgH μ , γ , δ , α or ϵ , or IgL κ or λ).

[00123] The entire polynucleotide sequence of each polynucleotide J in general formula (I) may, but need not, consist exclusively of contiguous nucleotides from each distinct J gene. For example and according to certain embodiments, in the template composition described herein, each polynucleotide J of formula (I) need only have at least a region comprising a unique J oligonucleotide sequence that is found in one J gene and to which a single V region primer in the primer set can specifically anneal. Thus, the V polynucleotide of formula (I) may comprise all or any prescribed portion (*e.g.*, at least 15, 20, 30, 60, 90, 120, 150, 180 or 210 contiguous nucleotides, or any integer value therebetween) of a naturally occurring V gene sequence (including a V pseudogene sequence) so long as at least one unique V oligonucleotide sequence region (the primer annealing site) is included that is not included in any other template J polynucleotide.

[00124] It may be preferred in certain embodiments that the plurality of J polynucleotides that are present in the herein described template composition have lengths that simulate the

overall lengths of known, naturally occurring J gene nucleotide sequences, even where the specific nucleotide sequences differ between the template J region and any naturally occurring J gene. The J region lengths in the herein described templates may differ from the lengths of naturally occurring J gene sequences by no more than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 percent.

[00125] The J polynucleotide in formula (I) may thus, in certain embodiments, comprise a nucleotide sequence having a length that is the same or similar to that of the length of a typical naturally occurring J gene and may, but need not, include a nucleotide sequence that encodes the CDR3 region, as discussed above.

[00126] Genomic sequences for TCR and BCR J region genes of humans and other species are known and available from public databases such as Genbank; J region gene sequences include polynucleotide sequences that encode the products of expressed and unexpressed rearranged TCR and BCR genes. The diverse J polynucleotide sequences that may be incorporated into the presently disclosed templates of general formula (I) may vary widely in length, in nucleotide composition (*e.g.*, GC content), and in actual linear polynucleotide sequence.

[00127] Alternatives to the V and J sequences described herein, for use in construction of the herein described template oligonucleotides and/or V-segment and J-segment oligonucleotide primers, may be selected by a skilled person based on the present disclosure using knowledge in the art regarding published gene sequences for the V- and J-encoding regions of the genes for each TCR and Ig subunit. Reference Genbank entries for human adaptive immune receptor sequences include: TCR α : (TCRA/D): NC_000014.8 (chr14:22090057..23021075); TCR β : (TCRB): NC_000007.13 (chr7:141998851..142510972); TCR γ : (TCRG): NC_000007.13 (chr7:38279625..38407656); immunoglobulin heavy chain, IgH (IGH): NC_000014.8 (chr14: 106032614..107288051); immunoglobulin light chain-kappa, IgL κ (IGK): NC_000002.11 (chr2: 89156874..90274235); and immunoglobulin light chain-lambda, IgL λ (IGL): NC_000022.10 (chr22: 22380474..23265085). Reference Genbank entries for mouse adaptive immune receptor loci sequences include: TCR β : (TCRB): NC_000072.5 (chr6: 40841295..41508370), and immunoglobulin heavy chain, IgH (IGH): NC_000078.5 (chr12:114496979..117248165).

[00128] Template and primer design analyses and target site selection considerations can be performed, for example, using the OLIGO primer analysis software and/or the BLASTN

2.0.5 algorithm software (Altschul et al., *Nucleic Acids Res.* 1997, 25(17):3389-402), or other similar programs available in the art.

[00129] Accordingly, based on the present disclosure and in view of these known adaptive immune receptor gene sequences and oligonucleotide design methodologies, for inclusion in the instant template oligonucleotides those skilled in the art can design a plurality of V region-specific and J region-specific polynucleotide sequences that each independently contain oligonucleotide sequences that are unique to a given V and J gene, respectively. Similarly, from the present disclosure and in view of known adaptive immune receptor sequences, those skilled in the art can also design a primer set comprising a plurality of V region-specific and J region-specific oligonucleotide primers that are each independently capable of annealing to a specific sequence that is unique to a given V and J gene, respectively, whereby the plurality of primers is capable of amplifying substantially all V genes and substantially all J genes in a given adaptive immune receptor-encoding locus (*e.g.*, a human TCR or IgH locus). Such primer sets permit generation, in multiplexed (*e.g.*, using multiple forward and reverse primer pairs) PCR, of amplification products that have a first end that is encoded by a rearranged V region-encoding gene segment and a second end that is encoded by a J region-encoding gene segment.

[00130] Typically and in certain embodiments, such amplification products may include a CDR3-encoding sequence although the invention is not intended to be so limited and contemplates amplification products that do not include a CDR3-encoding sequence. The primers may be preferably designed to yield amplification products having sufficient portions of V and J sequences and/or of V-J barcode (B) sequences as described herein, such that by sequencing the products (amplicons), it is possible to identify on the basis of sequences that are unique to each gene segment (i) the particular V gene, and (ii) the particular J gene in the proximity of which the V gene underwent rearrangement to yield a functional adaptive immune receptor-encoding gene. Typically, and in preferred embodiments, the PCR amplification products will not be more than 600 base pairs in size, which according to non-limiting theory will exclude amplification products from non-rearranged adaptive immune receptor genes. In certain other preferred embodiments the amplification products will not be more than 500, 400, 300, 250, 200, 150, 125, 100, 90, 80, 70, 60, 50, 40, 30 or 20 base pairs in size, such as may advantageously provide rapid, high-throughput quantification of sequence-distinct amplicons by short sequence reads.

[00131] In certain preferred embodiments, the plurality of template oligonucleotides comprises at least a or at least b unique oligonucleotide sequences, whichever is larger, where a is the number of unique adaptive immune receptor V region-encoding gene segments in the subject and b is the number of unique adaptive immune receptor J region-encoding gene segments in the subject, and the composition comprises at least one template oligonucleotide for each unique V polynucleotide and at least one template oligonucleotide for each unique J polynucleotide. It will be appreciated that because the template oligonucleotides have a plurality of oligonucleotide sequences of general formula (I), which includes a V polynucleotide and which also includes a J polynucleotide, that the template composition may thus comprise fewer than $(a \times b)$ unique oligonucleotide sequences, but will comprise at least the larger of a or b unique oligonucleotide sequences. Accordingly, the composition may accommodate at least one occurrence of each unique V polynucleotide sequence and at least one occurrence of each unique J polynucleotide sequence, where in some instances the at least one occurrence of a particular unique V polynucleotide will be present in the same template oligonucleotide in which may be found the at least one occurrence of a particular unique J polynucleotide. Thus, for example, “at least one template oligonucleotide for each unique V polynucleotide and at least one template oligonucleotide for each unique J polynucleotide” may in certain instances refer to a single template oligonucleotide in which one unique V polynucleotide and one unique J polynucleotide are present.

[00132] As also disclosed elsewhere herein, in certain other preferred embodiments the template composition comprises at least one template oligonucleotide to which each oligonucleotide amplification primer in an amplification primer set can anneal. Hence, the composition may comprise fewer than a or b unique sequences, for example, where an amplification primer set may not include a unique primer for every possible V and/or J sequence.

[00133] It will be noted that certain embodiments contemplate a template composition for standardizing the amplification efficiency of an oligonucleotide primer set that is capable of amplifying productively rearranged DNA encoding one or a plurality of adaptive immune receptors in a biological sample that comprises DNA from lymphoid cells of a subject as provided herein, wherein the template composition comprises a plurality of template oligonucleotides having a plurality of oligonucleotide sequences of general formula 5'-U1-B1-V-B2-R-B3-J-B4-U2-3' (I) as described herein. According to these and related

embodiments and as also described elsewhere herein, the set of oligonucleotide amplification primers that is capable of amplifying productively rearranged DNA may exclude any oligonucleotide primers that specifically hybridize to a V-region pseudogene or orphon or to a J-region pseudogene or orphon. Hence, in such embodiments the template composition will desirably exclude template oligonucleotides of general formula (I) in which unique V oligonucleotide sequences and/or unique J oligonucleotide sequences are sequences that are, respectively, unique to a V-region pseudogene or orphon or to a J-region pseudogene or orphon.

[00134] An exemplary TCRB template composition comprising 858 distinct template oligonucleotides is disclosed in the Sequence Listing in SEQ ID NOS:3157-4014. Another exemplary TCRB template composition comprising 871 distinct template oligonucleotides is disclosed in the Sequence Listing in SEQ ID NOS:1-871. Another exemplary TCRB template composition comprising 689 distinct template oligonucleotides is disclosed in the Sequence Listing in SEQ ID NOS:872-1560.

[00135] An exemplary TCRG template composition comprising 70 distinct template oligonucleotides is disclosed in the Sequence Listing in SEQ ID NOS:4015-4084. An exemplary TCRG template composition comprising 70 distinct template oligonucleotides is also disclosed in the Sequence Listing in SEQ ID NOS:1561-1630.

[00136] An exemplary IGH template composition comprising 1116 distinct template oligonucleotides is disclosed in the Sequence Listing in SEQ ID NOS:4085-5200. An exemplary IGH template composition comprising 1116 distinct template oligonucleotides is also disclosed in the Sequence Listing in SEQ ID NOS:1805-2920.

[00137] Also disclosed herein are exemplary sets of V and J polynucleotides for inclusion in the herein described template oligonucleotides having a plurality of oligonucleotide sequences of general formula (I). For TCRB, the plurality of template oligonucleotides may have a plurality of oligonucleotide sequences of general formula (I) in which polynucleotides V and J have the TCRB V and J sequences set forth in at least one set of 68 TCRB V and J SEQ ID NOS, respectively, as set forth in Fig. 5 as TCRB V/J set 1, TCRB V/J set 2, TCRB V/J set 3, TCRB V/J set 4, TCRB V/J set 5, TCRB V/J set 6, TCRB V/J set 7, TCRB V/J set 8, TCRB V/J set 9, TCRB V/J set 10, TCRB V/J set 11, TCRB V/J set 12 and TCRB V/J set 13.

[00138] For TCRG, the plurality of template oligonucleotides may have a plurality of oligonucleotide sequences of general formula (I) in which polynucleotides V and J have the

TCRG V and J sequences set forth in at least one set of 14 TCRG V and J SEQ ID NOS, respectively, as set forth in Fig. 6 as TCRG V/J set 1, TCRG V/J set 2, TCRG V/J set 3, TCRG V/J set 4 and TCRG V/J set 5.

[00139] For IGH, the plurality of template oligonucleotides may have a plurality of oligonucleotide sequences of general formula (I) in which polynucleotides V and J have the IGH V and J sequences set forth in at least one set of 127 IGH V and J SEQ ID NOS, respectively, as set forth in Fig. 7 as IGH V/J set 1, IGH V/J set 2, IGH V/J set 3, IGH V/J set 4, IGH V/J set 5, IGH V/J set 6, IGH V/J set 7, IGH V/J set 8 and IGH V/J set 9.

PRIMERS

[00140] According to the present disclosure, oligonucleotide primers are provided in an oligonucleotide primer set that comprises a plurality of V-segment primers and a plurality of J-segment primers, where the primer set is capable of amplifying rearranged DNA encoding adaptive immune receptors in a biological sample that comprises lymphoid cell DNA.

Suitable primer sets are known in the art and disclosed herein, for example, the primer sets in U.S.A.N. 13/217,126; U.S.A.N. 12/794,507; PCT/US2011/026373; or PCT/US2011/049012; or the like; or those shown in Table 1. In certain embodiments the primer set is designed to include a plurality of V sequence-specific primers that includes, for each unique V region gene (including pseudogenes) in a sample, at least one primer that can specifically anneal to a unique V region sequence; and for each unique J region gene in the sample, at least one primer that can specifically anneal to a unique J region sequence.

[00141] Primer design may be achieved by routine methodologies in view of known TCR and BCR genomic sequences. Accordingly, the primer set is preferably capable of amplifying every possible V-J combination that may result from DNA rearrangements in the TCR or BCR locus. As also described below, certain embodiments contemplate primer sets in which one or more V primers may be capable of specifically annealing to a “unique” sequence that may be shared by two or more V regions but that is not common to all V regions, and/or in which one or more J primers may be capable of specifically annealing to a “unique” sequence that may be shared by two or more J regions but that is not common to all J regions.

[00142] In particular embodiments, oligonucleotide primers for use in the compositions and methods described herein may comprise or consist of a nucleic acid of at least about 15 nucleotides long that has the same sequence as, or is complementary to, a 15 nucleotide long contiguous sequence of the target V- or J- segment (*i.e.*, portion of genomic polynucleotide

encoding a V-region or J-region polypeptide). Longer primers, *e.g.*, those of about 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 45, or 50, nucleotides long that have the same sequence as, or sequence complementary to, a contiguous sequence of the target V- or J- region encoding polynucleotide segment, will also be of use in certain embodiments. All intermediate lengths of the presently described oligonucleotide primers are contemplated for use herein. As would be recognized by the skilled person, the primers may have additional sequence added (*e.g.*, nucleotides that may not be the same as or complementary to the target V- or J-region encoding polynucleotide segment), such as restriction enzyme recognition sites, adaptor sequences for sequencing, bar code sequences, and the like (see *e.g.*, primer sequences provided in the Tables and sequence listing herein). Therefore, the length of the primers may be longer, such as about 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 80, 85, 90, 95, 100 or more nucleotides in length or more, depending on the specific use or need.

[00143] Also contemplated for use in certain embodiments are adaptive immune receptor V-segment or J-segment oligonucleotide primer variants that may share a high degree of sequence identity to the oligonucleotide primers for which nucleotide sequences are presented herein, including those set forth in the Sequence Listing. Thus, in these and related embodiments, adaptive immune receptor V-segment or J-segment oligonucleotide primer variants may have substantial identity to the adaptive immune receptor V-segment or J-segment oligonucleotide primer sequences disclosed herein, for example, such oligonucleotide primer variants may comprise at least 70% sequence identity, preferably at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or higher sequence identity compared to a reference polynucleotide sequence such as the oligonucleotide primer sequences disclosed herein, using the methods described herein (*e.g.*, BLAST analysis using standard parameters). One skilled in this art will recognize that these values can be appropriately adjusted to determine corresponding ability of an oligonucleotide primer variant to anneal to an adaptive immune receptor segment-encoding polynucleotide by taking into account codon degeneracy, reading frame positioning and the like.

[00144] Typically, oligonucleotide primer variants will contain one or more substitutions, additions, deletions and/or insertions, preferably such that the annealing ability of the variant oligonucleotide is not substantially diminished relative to that of an adaptive immune receptor V-segment or J-segment oligonucleotide primer sequence that is specifically set forth herein.

[00145] Table 1 presents as a non-limiting example an oligonucleotide primer set that is capable of amplifying productively rearranged DNA encoding TCR β -chains (TCRB) in a biological sample that comprises DNA from lymphoid cells of a subject. In this primer set the J segment primers share substantial sequence homology, and therefore may cross-prime amongst more than one target J polynucleotide sequence, but the V segment primers are designed to anneal specifically to target sequences within the CDR2 region of V and are therefore unique to each V segment. An exception, however, is present in the case of several V primers where the within-family sequences of the closely related target genes are identical (*e.g.*, V6-2 and V6-3 are identical at the nucleotide level throughout the coding sequence of the V segment, and therefore may have a single primer, TRB2V6-2/3).

[00146] It will therefore be appreciated that in certain embodiments the number of different template oligonucleotides in the template composition, and/or the number of different oligonucleotide primers in the primer set, may be advantageously reduced by designing template and/or primers to exploit certain known similarities in V and/or J sequences. Thus, in these and related embodiments, “unique” oligonucleotide sequences as described herein may include specific V polynucleotide sequences that are shared by 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 distinct template oligonucleotides and/or specific J polynucleotide sequences that are shared by 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 or 13 distinct template oligonucleotides, where such templates differ in sequence from one another by other than the shared V and/or J sequences.

[00147] According to certain presently contemplated embodiments, it may be useful to decrease (*e.g.*, reduce in a statistically significant manner) template amplification bias such as non-uniform nucleic acid amplification potential among members of a set of amplification primers that can result from unequal primer efficiencies (*e.g.*, unequal primer utilization) only for a limited subset of all naturally occurring V and J genes. For example, in analyses of the TCR or BCR immune repertoire involved in an immune response, whether to a specific antigen, as in a vaccine, or to a tissue, as in an autoimmune disease, only the productive TCR or IG rearrangements may be of interest. In such circumstances, it may be economically advantageous to identify and correct non-uniform nucleic acid amplification potential only for those V and J segment primers that contribute to productive rearrangements of TCR or BCR encoding DNA, and to exclude efforts to correct non-uniform amplification of pseudogenes and orphans (*i.e.*, TCR or BCR V region-encoding segments that have been duplicated onto other chromosomes).

[00148] In the human IGH locus, for instance, the ImmunoGeneTics (IMGT) database (M.-P. LeFranc, Université Montpellier, Montpellier, France; www.imgt.org) annotates 165 V segment genes, of which 26 are orphans on other chromosomes and 139 are in the IGH locus at chromosome 14. Among the 139 V segments within the IGH locus, 51 have at least one functional allele, while 6 are ORFs (open-reading frames) which are missing at least one highly conserved amino-acid residue, and 81 are pseudogenes. Pseudogenes may include V segments that contain an in-frame stop codon within the V-segment coding sequence, a frameshift between the start codon and the CDR3 encoding sequence, one or more repeat-element insertions, and deletions of critical regions, such as the first exon or the RSS. To characterize functional IGH rearrangements in a sample while avoiding the time and expense of characterizing pseudogenes and/or orphans, it is therefore contemplated to use a subset of the herein described synthetic template oligonucleotides which is designed to include only those V segments that participate in a functional rearrangement to encode a TCR or BCR, without having to synthesize or calibrate amplification primers and template oligonucleotides specific to the pseudogene sequences. Advantageous efficiencies with respect, *inter alia*, to time and expense are thus obtained.

Table 1. Exemplary Oligonucleotide Primer Set (hsTCRB PCR Primers)

Name	Sequence	SEQ ID NO:
TRBJ1-1	TTACCTACAACGTGTGAGTCTGGTGCCTTGTCCTCAA	1631
TRBJ1-2	ACCTACAACGGTTAACCTGGTCCCCGAACCGAA	1632
TRBJ1-3	ACCTACAACAGTGAGCCAACTTCCCTCTCCAA	1633
TRBJ1-4	CCAAGACAGAGAGCTGGGTTCCTGCTCCAA	1634
TRBJ1-5	ACCTAGGATGGAGAGTCGAGTCCCATCACCAA	1635
TRBJ1-6	CTGTCACAGTGAGCCTGGTCCCGTTCCCAA	1636
TRBJ2-1	CGGTGAGCCGTGTCCCTGGCCCGAA	1637
TRBJ2-2	CCAGTACGGTCAGCCTAGAGCCTTCTCCAA	1638
TRBJ2-3	ACTGTCAGCCGGGTGCCTGGGCCAA	1639
TRBJ2-4	AGAGCCGGGTCCCGGCGCCGAA	1640
TRBJ2-5	GGAGCCGCGTGCCTGGCCCGAA	1641
TRBJ2-6	GTCAGCCTGCTGCCGGCCCCGAA	1642
TRBJ2-7	GTGAGCCTGGTGCCCGGCCCGAA	1643

Name	Sequence	SEQ ID NO:
TRB2V10-1	AACAAAGGAGAAGTCTCAGATGGCTACAG	1644
TRB2V10-2	GATAAAGGAGAAGTCCCCGATGGCTATGT	1645
TRB2V10-3	GACAAAGGAGAAGTCTCAGATGGCTATAG	1646
TRB2V6-2/3	GCCAAAGGAGAGGTCCCTGATGGCTACAA	1647
TRB2V6-8	CTCTAGATTAAACACAGAGGATTTCCCAC	1648
TRB2V6-9	AAGGAGAAGTCCCCGATGGCTACAATGTA	1649
TRB2V6-5	AAGGAGAAGTCCCCAATGGCTACAATGTC	1650
TRB2V6-6	GACAAAGGAGAAGTCCCGAATGGCTACAAC	1651
TRB2V6-7	GTTCCCAATGGCTACAATGTCTCCAGATC	1652
TRB2V6-1	GTCCCCAATGGCTACAATGTCTCCAGATT	1653
TRB2V6-4	GTCCCTGATGGTTATAGTGTCTCCAGAGC	1654
TRB2V24-1	ATCTCTGATGGATACAGTGTCTCTCGACA	1655
TRB2V25-1	TTTCCTCTGAGTCAACAGTCTCCAGAATA	1656
TRB2V27	TCCTGAAGGGTACAAAGTCTCTCGAAAAG	1657
TRB2V26	CTCTGAGAGGTATCATGTTTCTTGAAATA	1658
TRB2V28	TCCTGAGGGGTACAGTGTCTCTAGAGAGA	1659
TRB2V19	TATAGCTGAAGGGTACAGCGTCTCTCGGG	1660
TRB2V4-1	CTGAATGCCCCAACAGCTCTCTCTTAAAC	1661
TRB2V4-2/3	CTGAATGCCCCAACAGCTCTCACTTATTC	1662
TRB2V2P	CCTGAATGCCCTGACAGCTCTCGCTTATA	1663
TRB2V3-1	CCTAAATCTCCAGACAAAGCTCACTTAAA	1664
TRB2V3-2	CTCACCTGACTCTCCAGACAAAGCTCAT	1665
TRB2V16	TTCAGCTAAGTGCCTCCCAAATTCACCCT	1666
TRB2V23-1	GATTCTCATCTCAATGCCCCAAGAACGC	1667
TRB2V18	ATTTTCTGCTGAATTTCCCAAAGAGGGCC	1668
TRB2V17	ATTCACAGCTGAAAGACCTAACGGAACGT	1669
TRB2V14	TCTTAGCTGAAAGGACTGGAGGGACGTAT	1670
TRB2V2	TTCGATGATCAATTCTCAGTTGAAAGGCC	1671
TRB2V12-1	TTGATTCTCAGCACAGATGCCTGATGT	1672
TRB2V12-2	GCGATTCTCAGCTGAGAGGCCTGATGG	1673

Name	Sequence	SEQ ID NO:
TRB2V12-3/4	TCGATTCTCAGCTAAGATGCCTAATGC	1674
TRB2V12-5	TTCTCAGCAGAGATGCCTGATGCAACTTTA	1675
TRB2V7-9	GGTTCTCTGCAGAGAGGCCTAAGGGATCT	1676
TRB2V7-8	GCTGCCCAGTGATCGCTTCTTTGCAGAAA	1677
TRB2V7-4	GGCGGCCAGTGGTGCGTTCTCTGCAGAG	1678
TRB2V7-6/7	ATGATCGGTTCTCTGCAGAGAGGCCTGAGG	1679
TRB2V7-2	AGTGATCGCTTCTCTGCAGAGAGGACTGG	1680
TRB2V7-3	GGCTGCCCCAACGATCGGTTCTTTGCAGT	1681
TRB2V7-1	TCCCCGTGATCGGTTCTCTGCACAGAGGT	1682
TRB2V11-123	CTAAGGATCGATTTTCTGCAGAGAGGCTC	1683
TRB2V13	CTGATCGATTCTCAGCTCAACAGTTCAGT	1684
TRB2V5-1	TGGTCGATTCTCAGGGCGCCAGTTCTCTA	1685
TRB2V5-3	TAATCGATTCTCAGGGCGCCAGTTCCATG	1686
TRB2V5-4	TCCTAGATTCTCAGGTCTCCAGTTCCCTA	1687
TRB2V5-8	GGAAACTTCCCTCCTAGATTTTCAGGTCTG	1688
TRB2V5-5	AAGAGGAAACTTCCCTGATCGATTCTCAGC	1689
TRB2V5-6	GGCAACTTCCCTGATCGATTCTCAGGTCA	1690
TRB2V9	GTTCCCTGACTTGCACTCTGAACTAAAC	1691
TRB2V15	GCCGAACACTTCTTTCTGCTTTCTTGAC	1692
TRB2V30	GACCCCAGGACCGGCAGTTCATCCTGAGT	1693
TRB2V20-1	ATGCAAGCCTGACCTTGTCCACTCTGACA	1694
TRB2V29-1	CATCAGCCGCCCAAACCTAACATTCTCAA	1695

[00149] In certain embodiments, the V-segment and J-segment oligonucleotide primers as described herein are designed to include nucleotide sequences such that adequate information is present within the sequence of an amplification product of a rearranged adaptive immune receptor (TCR or Ig) gene to identify uniquely both the specific V and the specific J genes that give rise to the amplification product in the rearranged adaptive immune receptor locus (e.g., at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 base pairs of

sequence upstream of the V gene recombination signal sequence (RSS), preferably at least about 22, 24, 26, 28, 30, 32, 34, 35, 36, 37, 38, 39 or 40 base pairs of sequence upstream of the V gene recombination signal sequence (RSS), and in certain preferred embodiments greater than 40 base pairs of sequence upstream of the V gene recombination signal sequence (RSS), and at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 base pairs downstream of the J gene RSS, preferably at least about 22, 24, 26, 28 or 30 base pairs downstream of the J gene RSS, and in certain preferred embodiments greater than 30 base pairs downstream of the J gene RSS).

[00150] This feature stands in contrast to oligonucleotide primers described in the art for amplification of TCR-encoding or Ig-encoding gene sequences, which rely primarily on the amplification reaction merely for detection of presence or absence of products of appropriate sizes for V and J segments (*e.g.*, the presence in PCR reaction products of an amplicon of a particular size indicates presence of a V or J segment but fails to provide the sequence of the amplified PCR product and hence fails to confirm its identity, such as the common practice of spectratyping).

[00151] Oligonucleotides (*e.g.*, primers) can be prepared by any suitable method, including direct chemical synthesis by a method such as the phosphotriester method of Narang et al., 1979, *Meth. Enzymol.* 68:90-99; the phosphodiester method of Brown et al., 1979, *Meth. Enzymol.* 68:109-151; the diethylphosphoramidite method of Beaucage et al., 1981, *Tetrahedron Lett.* 22:1859-1862; and the solid support method of U.S. Pat. No. 4,458,066, each incorporated herein by reference. A review of synthesis methods of conjugates of oligonucleotides and modified nucleotides is provided in Goodchild, 1990, *Bioconjugate Chemistry* 1(3): 165-187, incorporated herein by reference.

[00152] The term "primer," as used herein, refers to an oligonucleotide capable of acting as a point of initiation of DNA synthesis under suitable conditions. Such conditions include those in which synthesis of a primer extension product complementary to a nucleic acid strand is induced in the presence of four different nucleoside triphosphates and an agent for extension (*e.g.*, a DNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature.

[00153] A primer is preferably a single-stranded DNA. The appropriate length of a primer depends on the intended use of the primer but typically ranges from 6 to 50 nucleotides, or in certain embodiments, from 15-35 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer

need not reflect the exact sequence of the template nucleic acid, but must be sufficiently complementary to hybridize with the template. The design of suitable primers for the amplification of a given target sequence is well known in the art and described in the literature cited herein.

[00154] As described herein, primers can incorporate additional features which allow for the detection or immobilization of the primer but do not alter the basic property of the primer, that of acting as a point of initiation of DNA synthesis. For example, primers may contain an additional nucleic acid sequence at the 5' end which does not hybridize to the target nucleic acid, but which facilitates cloning, detection, or sequencing of the amplified product. The region of the primer which is sufficiently complementary to the template to hybridize is referred to herein as the hybridizing region.

[00155] As used herein, a primer is "specific," for a target sequence if, when used in an amplification reaction under sufficiently stringent conditions, the primer hybridizes primarily to the target nucleic acid. Typically, a primer is specific for a target sequence if the primer-target duplex stability is greater than the stability of a duplex formed between the primer and any other sequence found in the sample. One of skill in the art will recognize that various factors, such as salt conditions as well as base composition of the primer and the location of the mismatches, will affect the specificity of the primer, and that routine experimental confirmation of the primer specificity will be needed in many cases. Hybridization conditions can be chosen under which the primer can form stable duplexes only with a target sequence. Thus, the use of target-specific primers under suitably stringent amplification conditions enables the selective amplification of those target sequences which contain the target primer binding sites.

[00156] In particular embodiments, primers for use in the methods described herein comprise or consist of a nucleic acid of at least about 15 nucleotides long that has the same sequence as, or is complementary to, a 15 nucleotide long contiguous sequence of the target V or J segment. Longer primers, *e.g.*, those of about 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 45, or 50, nucleotides long that have the same sequence as, or sequence complementary to, a contiguous sequence of the target V or J segment, will also be of use in certain embodiments. All intermediate lengths of the aforementioned primers are contemplated for use herein. As would be recognized by the skilled person, the primers may have additional sequence added (*e.g.*, nucleotides that may not be the same as or complementary to the target V or J segment), such as restriction

enzyme recognition sites, adaptor sequences for sequencing, bar code sequences, and the like (see *e.g.*, primer sequences provided herein and in the sequence listing). Therefore, the length of the primers may be longer, such as 55, 56, 57, 58, 59, 60, 65, 70, 75, nucleotides in length or more, depending on the specific use or need. For example, in one embodiment, the forward and reverse primers are both modified at the 5' end with the universal forward primer sequence compatible with a DNA sequencer.

[00157] Also contemplated for use in certain embodiments are adaptive immune receptor V-segment or J-segment oligonucleotide primer variants that may share a high degree of sequence identity to the oligonucleotide primers for which nucleotide sequences are presented herein, including those set forth in the Sequence Listing. Thus, in these and related embodiments, adaptive immune receptor V-segment or J-segment oligonucleotide primer variants may have substantial identity to the adaptive immune receptor V-segment or J-segment oligonucleotide primer sequences disclosed herein, for example, such oligonucleotide primer variants may comprise at least 70% sequence identity, preferably at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or higher sequence identity compared to a reference polynucleotide sequence such as the oligonucleotide primer sequences disclosed herein, using the methods described herein (*e.g.*, BLAST analysis using standard parameters). One skilled in this art will recognize that these values can be appropriately adjusted to determine corresponding ability of an oligonucleotide primer variant to anneal to an adaptive immune receptor segment-encoding polynucleotide by taking into account codon degeneracy, reading frame positioning and the like.

[00158] Typically, oligonucleotide primer variants will contain one or more substitutions, additions, deletions and/or insertions, preferably such that the annealing ability of the variant oligonucleotide is not substantially diminished relative to that of an adaptive immune receptor V-segment or J-segment oligonucleotide primer sequence that is specifically set forth herein. As also noted elsewhere herein, in preferred embodiments adaptive immune receptor V-segment and J-segment oligonucleotide primers are designed to be capable of amplifying a rearranged TCR or IGH sequence that includes the coding region for CDR3.

[00159] According to certain embodiments contemplated herein, the primers for use in the multiplex PCR methods of the present disclosure may be functionally blocked to prevent non-specific priming of non-T or B cell sequences. For example, the primers may be blocked with chemical modifications as described in U.S. patent application publication US2010/0167353. According to certain herein disclosed embodiments, the use of such

blocked primers in the present multiplex PCR reactions involves primers that may have an inactive configuration wherein DNA replication (*i.e.*, primer extension) is blocked, and an activated configuration wherein DNA replication proceeds. The inactive configuration of the primer is present when the primer is either single-stranded, or when the primer is specifically hybridized to the target DNA sequence of interest but primer extension remains blocked by a chemical moiety that is linked at or near to the 3' end of the primer.

[00160] The activated configuration of the primer is present when the primer is hybridized to the target nucleic acid sequence of interest and is subsequently acted upon by RNase H or another cleaving agent to remove the 3' blocking group, thereby allowing an enzyme (*e.g.*, a DNA polymerase) to catalyze primer extension in an amplification reaction. Without wishing to be bound by theory, it is believed that the kinetics of the hybridization of such primers are akin to a second order reaction, and are therefore a function of the T cell or B cell gene sequence concentration in the mixture. Blocked primers minimize non-specific reactions by requiring hybridization to the target followed by cleavage before primer extension can proceed. If a primer hybridizes incorrectly to a sequence that is related to the desired target sequence but which differs by having one or more non-complementary nucleotides that result in base-pairing mismatches, cleavage of the primer is inhibited, especially when there is a mismatch that lies at or near the cleavage site. This strategy to improve the fidelity of amplification reduces the frequency of false priming at such locations, and thereby increases the specificity of the reaction. As would be recognized by the skilled person, reaction conditions, particularly the concentration of RNase H and the time allowed for hybridization and extension in each cycle, can be optimized to maximize the difference in cleavage efficiencies between highly efficient cleavage of the primer when it is correctly hybridized to its true target sequence, and poor cleavage of the primer when there is a mismatch between the primer and the template sequence to which it may be incompletely annealed.

[00161] As described in US2010/0167353, a number of blocking groups are known in the art that can be placed at or near the 3' end of the oligonucleotide (*e.g.*, a primer) to prevent extension. A primer or other oligonucleotide may be modified at the 3'-terminal nucleotide to prevent or inhibit initiation of DNA synthesis by, for example, the addition of a 3' deoxyribonucleotide residue (*e.g.*, cordycepin), a 2',3'-dideoxyribonucleotide residue, non-nucleotide linkages or alkane-diol modifications (U.S. Pat. No. 5,554,516). Alkane diol modifications which can be used to inhibit or block primer extension have also been

described by Wilk et al., (1990 *Nucleic Acids Res.* 18 (8):2065), and by Arnold et al. (U.S. Pat. No. 6,031,091). Additional examples of suitable blocking groups include 3' hydroxyl substitutions (*e.g.*, 3'-phosphate, 3'-triphosphate or 3'-phosphate diesters with alcohols such as 3-hydroxypropyl), 2'3'-cyclic phosphate, 2' hydroxyl substitutions of a terminal RNA base (*e.g.*, phosphate or sterically bulky groups such as triisopropyl silyl (TIPS) or tert-butyl dimethyl silyl (TBDMS)). 2'-alkyl silyl groups such as TIPS and TBDMS substituted at the 3'-end of an oligonucleotide are described by Laikhter et al., U.S. patent application Ser. No. 11/686,894, which is incorporated herein by reference. Bulky substituents can also be incorporated on the base of the 3'-terminal residue of the oligonucleotide to block primer extension.

[00162] In certain embodiments, the oligonucleotide may comprise a cleavage domain that is located upstream (*e.g.*, 5' to) of the blocking group used to inhibit primer extension. As examples, the cleavage domain may be an RNase H cleavage domain, or the cleavage domain may be an RNase H2 cleavage domain comprising a single RNA residue, or the oligonucleotide may comprise replacement of the RNA base with one or more alternative nucleosides. Additional illustrative cleavage domains are described in US2010/0167353.

[00163] Thus, a multiplex PCR system may use 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, or more forward primers, wherein each forward primer is complementary to a single functional TCR or Ig V segment or a small family of functional TCR or Ig V segments, *e.g.*, a TCR V β segment, (see *e.g.*, the TCRBV primers as shown in Table 1, SEQ ID NOS:1644-1695), and, for example, thirteen reverse primers, each specific to a TCR or Ig J segment, such as TCR J β segment (see *e.g.*, TCRBJ primers in Table 1, SEQ ID NOS:1631-1643). In another embodiment, a multiplex PCR reaction may use four forward primers each specific to one or more functional TCR γ V segment and four reverse primers each specific for one or more TCR γ J segments. In another embodiment, a multiplex PCR reaction may use 84 forward primers each specific to one or more functional V segments and six reverse primers each specific for one or more J segments.

[00164] Thermal cycling conditions may follow methods of those skilled in the art. For example, using a PCR Express™ thermal cycler (Hybaid, Ashford, UK), the following cycling conditions may be used: 1 cycle at 95°C for 15 minutes, 25 to 40 cycles at 94°C for 30 seconds, 59°C for 30 seconds and 72°C for 1 minute, followed by one cycle at 72°C for 10 minutes. As will be recognized by the skilled person, thermal cycling conditions may be optimized, for example, by modifying annealing temperatures, annealing times, number of

cycles and extension times. As would be recognized by the skilled person, the amount of primer and other PCR reagents used, as well as PCR parameters (e.g., annealing temperature, extension times and cycle numbers), may be optimized to achieve desired PCR amplification efficiency.

[00165] Alternatively, in certain related embodiments also contemplated herein, "digital PCR" methods can be used to quantitate the number of target genomes in a sample, without the need for a standard curve. In digital PCR, the PCR reaction for a single sample is performed in a multitude of more than 100 microcells or droplets, such that each droplet either amplifies (e.g., generation of an amplification product provides evidence of the presence of at least one template molecule in the microcell or droplet) or fails to amplify (evidence that the template was not present in a given microcell or droplet). By simply counting the number of positive microcells, it is possible directly to count the number of target genomes that are present in an input sample.

[00166] Digital PCR methods typically use an endpoint readout, rather than a conventional quantitative PCR signal that is measured after each cycle in the thermal cycling reaction (see, e.g., Pekin et al., 2011 *Lab. Chip* 11(13):2156; Zhong et al., 2011 *Lab. Chip* 11(13):2167; Tewhey et al., 2009 *Nature Biotechnol.* 27:1025; 2010 *Nature Biotechnol.* 28:178; Vogelstein and Kinzler, 1999 *Proc. Natl. Acad. Sci. USA* 96:9236-41; Pohl and Shih, 2004 *Expert Rev. Mol. Diagn.* 4(1);41-7, 2004). Compared with traditional PCR, dPCR has the following advantages: (1) there is no need to rely on references or standards, (2) desired precision may be achieved by increasing the total number of PCR replicates, (3) it is highly tolerant to inhibitors, (4) it is capable of analyzing complex mixtures, and (5) it provides a linear response to the number of copies present in a sample to allow for small change in the copy number to be detected. Accordingly, any of the herein described compositions (e.g., template compositions and adaptive immune receptor gene-specific oligonucleotide primer sets) and methods may be adapted for use in such digital PCR methodology, for example, the ABI QuantStudio™ 12K Flex System (Life Technologies, Carlsbad, CA), the QX100™ Droplet Digital™ PCR system (BioRad, Hercules, CA), the QuantaLife™ digital PCR system (BioRad, Hercules, CA) or the RainDance™ microdroplet digital PCR system (RainDance Technologies, Lexington, MA).

[00167] ADAPTORS

[00168] The herein described template oligonucleotides of general formula (I) also may in certain embodiments comprise first (U1) and second (U2) universal adaptor oligonucleotide sequences, or may lack either or both of U1 and U2. U1 thus may comprise either nothing or an oligonucleotide having a sequence that is selected from (i) a first universal adaptor oligonucleotide sequence, and (ii) a first sequencing platform-specific oligonucleotide sequence that is linked to and positioned 5' to a first universal adaptor oligonucleotide sequence, and U2 may comprise either nothing or an oligonucleotide having a sequence that is selected from (i) a second universal adaptor oligonucleotide sequence, and (ii) a second sequencing platform-specific oligonucleotide sequence that is linked to and positioned 5' to a second universal adaptor oligonucleotide sequence.

[00169] U1 and/or U2 may, for example, comprise universal adaptor oligonucleotide sequences and/or sequencing platform-specific oligonucleotide sequences that are specific to a single-molecule sequencing technology being employed, for example the HiSeq™ or GeneAnalyzer™-2 (GA-2) systems (Illumina, Inc., San Diego, CA) or another suitable sequencing suite of instrumentation, reagents and software. Inclusion of such platform-specific adaptor sequences permits direct quantitative sequencing of the presently described template composition, which comprises a plurality of different template oligonucleotides of general formula (I), using a nucleotide sequencing methodology such as the HiSeq™ or GA2 or equivalent. This feature therefore advantageously permits qualitative and quantitative characterization of the template composition.

[00170] In particular, the ability to sequence all components of the template composition directly allows for verification that each template oligonucleotide in the plurality of template oligonucleotides is present in a substantially equimolar amount. For example, a set of the presently described template oligonucleotides may be generated that have universal adaptor sequences at both ends, so that the adaptor sequences can be used to further incorporate sequencing platform-specific oligonucleotides at each end of each template.

[00171] Without wishing to be bound by theory, platform-specific oligonucleotides may be added onto the ends of such modified templates using 5' (5'-platform sequence-universal adaptor-1 sequence-3') and 3' (5'-platform sequence-universal adaptor-2 sequence-3') oligonucleotides in as little as two cycles of denaturation, annealing and extension, so that the relative representation in the template composition of each of the component template oligonucleotides is not quantitatively altered. Unique identifier sequences (*e.g.*, barcode sequences B comprising unique V and B oligonucleotide sequences that are associated with

and thus identify, respectively, individual V and J regions, as described herein) are placed adjacent to the adaptor sequences, thus permitting quantitative sequencing in short sequence reads, in order to characterize the template population by the criterion of the relative amount of each unique template sequence that is present.

[00172] Where such direct quantitative sequencing indicates that one or more particular oligonucleotides may be over- or underrepresented in a preparation of the template composition, adjustment of the template composition can be made accordingly to obtain a template composition in which all oligonucleotides are present in substantially equimolar amounts. The template composition in which all oligonucleotides are present in substantially equimolar amounts may then be used as a calibration standard for amplification primer sets, such as in the presently disclosed methods for determining and correcting non-uniform amplification potential among members of a primer set.

In addition to adaptor sequences described in the Examples and included in the exemplary template sequences in the Sequence Listing (*e.g.*, at the 5' and 3' ends of SEQ ID NOS:1-1630), other oligonucleotide sequences that may be used as universal adaptor sequences will be known to those familiar with the art in view of the present disclosure, including selection of adaptor oligonucleotide sequences that are distinct from sequences found in other portions of the herein described templates. Non-limiting examples of additional adaptor sequences are shown in Table 2 and set forth in SEQ ID NOS:1710-1731.

Table 2. Exemplary Adaptor Sequences

Adaptor (primer) name	Sequence	SEQ ID NO:
T7 Promotor	AATACGACTCACTATAGG	1710
T7 Terminator	GCTAGTTATTGCTCAGCGG	1711
T3	ATTAACCCTCACTAAAGG	1712
SP6	GATTTAGGTGACACTATAG	1713
M13F(-21)	TGTAAAACGACGGCCAGT	1714
M13F(-40)	GTTTTCCCAGTCACGAC	1715
M13R Reverse	CAGGAAACAGCTATGACC	1716
AOX1 Forward	GACTGGTTCCAATTGACAAGC	1717
AOX1 Reverse	GCAAATGGCATTCTGACATCC	1718
pGEX Forward (GST 5,	GGGCTGGCAAGCCACGTTTGGTG	1719

Adaptor (primer) name	Sequence	SEQ ID NO:
pGEX 5')		
pGEX Reverse (GST 3, pGEX 3')	CCGGGAGCTGCATGTGTCAGAGG	1720
BGH Reverse	AACTAGAAGGCACAGTCGAGGC	1721
GFP (C' terminal, CFP, YFP or BFP)	CACTCTCGGCATGGACGAGC	1722
GFP Reverse	TGGTGCAGATGAACTTCAGG	1723
GAG	GTTCGACCCCGCCTCGATCC	1724
GAG Reverse	TGACACACATTCCACAGGGTC	1725
CYC1 Reverse	GCGTGAATGTAAGCGTGAC	1726
pFastBacF	5' -d (GGATTATTCATACCGTCCCA) -3'	1727
pFastBacR	5' -d (CAAATGTGGTATGGCTGATT) -3'	1728
pBAD Forward	5' -d (ATGCCATAGCATTTTATCC) -3'	1729
pBAD Reverse	5' -d (GATTTAATCTGTATCAGG) -3'	1730
CMV-Forward	5' -d (CGCAAATGGGCGGTAGGCGTG) -3'	1731

BARCODES

[00173] As described herein, certain embodiments contemplate designing the template oligonucleotide sequences to contain short signature sequences that permit unambiguous identification of the template sequence, and hence of at least one primer responsible for amplifying that template, without having to sequence the entire amplification product. In the herein described template oligonucleotides of general formula (I), B1, B2, B3, and B4 are each independently either nothing or each comprises an oligonucleotide B that comprises an oligonucleotide barcode sequence of 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500, 600, 700, 800, 900 or 1000 or more contiguous nucleotides (including all integer values therebetween), wherein in each of the plurality of template oligonucleotide sequences B comprises a unique oligonucleotide sequence that uniquely identifies, as a paired combination, (i) the unique V oligonucleotide sequence of the template oligonucleotide and (ii) the unique J oligonucleotide sequence of the template oligonucleotide.

[00174] Thus, for instance, template oligonucleotides having barcode identifier sequences may permit relatively short amplification product sequence reads, such as barcode sequence reads of no more than 1000, 900, 800, 700, 600, 500, 400, 300, 200, 100, 90, 80, 70, 60, 55, 50, 45, 40, 35, 30, 25, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4 or fewer nucleotides, followed by matching this barcode sequence information to the associated V and J sequences that are incorporated into the template having the barcode as part of the template design. By this approach, a large number of amplification products can be simultaneously partially sequenced by high throughput parallel sequencing, to identify primers that are responsible for amplification bias in a complex primer set.

[00175] Exemplary barcodes may comprise a first barcode oligonucleotide of 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or 16 nucleotides that uniquely identifies each V polynucleotide in the template and a second barcode oligonucleotide of 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or 16 nucleotides that uniquely identifies each J polynucleotide in the template, to provide barcodes of, respectively, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32 nucleotides in length, but these and related embodiments are not intended to be so limited. Barcode oligonucleotides may comprise oligonucleotide sequences of any length, so long as a minimum barcode length is obtained that precludes occurrence of a given barcode sequence in two or more template oligonucleotides having otherwise distinct sequences (*e.g.*, V and J sequences).

[00176] Thus, the minimum barcode length, to avoid such redundancy amongst the barcodes that are used to uniquely identify different V-J sequence pairings, is X nucleotides, where 4^X is greater than the number of distinct template species that are to be differentiated on the basis of having non-identical sequences. For example, for the set of 871 template oligonucleotides set forth herein as SEQ ID NOS:1-871, the minimum barcode length would be five nucleotides, which would permit a theoretical total of 1024 (*i.e.*, greater than 871) different possible pentanucleotide sequences. In practice, barcode oligonucleotide sequence read lengths may be limited only by the sequence read-length limits of the nucleotide sequencing instrument to be employed. For certain embodiments, different barcode oligonucleotides that will distinguish individual species of template oligonucleotides should have at least two nucleotide mismatches (*e.g.*, a minimum hamming distance of 2) when aligned to maximize the number of nucleotides that match at particular positions in the barcode oligonucleotide sequences.

[00177] In preferred embodiments, for each distinct template oligonucleotide species having a unique sequence within the template composition of general formula (I), B1, B2, B3, and B4 will be identical.

[00178] The skilled artisan will be familiar with the design, synthesis, and incorporation into a larger oligonucleotide or polynucleotide construct, of oligonucleotide barcode sequences of, for instance, at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 55, 60, 70, 80, 90, 100, 200, 300, 500 or more contiguous nucleotides, including all integer values therebetween. For non-limiting examples of the design and implementation of oligonucleotide barcode sequence identification strategies, see, *e.g.*, de Carcer et al., 2011 *Adv. Env. Microbiol.* 77:6310; Parameswaran et al., 2007 *Nucl. Ac. Res.* 35(19):330; Roh et al., 2010 *Trends Biotechnol.* 28:291.

[00179] Typically, barcodes are placed in templates at locations where they are not found naturally, *i.e.*, barcodes comprise nucleotide sequences that are distinct from any naturally occurring oligonucleotide sequences that may be found in the vicinity of the sequences adjacent to which the barcodes are situated (*e.g.*, V and/or J sequences). Such barcode sequences may be included, according to certain embodiments described herein, as elements B1, B2 and/or B3 of the presently disclosed template oligonucleotide of general formula (I). Accordingly, certain of the herein described template oligonucleotides of general formula (I) may also in certain embodiments comprise one, two or all three of barcodes B1, B2 and B3, while in certain other embodiments some or all of these barcodes may be absent. In certain embodiments all barcode sequences will have identical or similar GC content (*e.g.*, differing in GC content by no more than 20%, or by no more than 19, 18, 17, 16, 15, 14, 13, 12, 11 or 10%).

[00180] In the template compositions according to certain herein disclosed embodiments the barcode-containing element B (*e.g.*, B1, B2, B3, and/or B4) comprises the oligonucleotide sequence that uniquely identifies a single paired V-J combination. Optionally and in certain embodiments the barcode-containing element B may also include a random nucleotide, or a random polynucleotide sequence of at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 45, 50, 55, 60, 70, 80, 90, 100, 200, 300, 500 or more contiguous nucleotides, situated upstream and/or downstream of the specific barcode sequence that uniquely identifies each specific paired V-J combination. When present both upstream and downstream of the specific barcode sequence, the random nucleotide or random

polynucleotide sequence are independent of one another, that is, they may but need not comprise the same nucleotide or the same polynucleotide sequence.

RESTRICTION ENZYME SITES

[00181] According to certain embodiments disclosed herein, the template oligonucleotide may comprise a restriction endonuclease (RE) recognition site that is situated between the V and J sequences and does not occur elsewhere in the template oligonucleotide sequence. The RE recognition site may optionally be adjacent to a barcode site that identifies the V region sequence. The RE site may be included for any of a number of purposes, including without limitation as a structural feature that may be exploited to destroy templates selectively by contacting them with the appropriate restriction enzyme. It may be desirable to degrade the present template oligonucleotides selectively by contacting them with a suitable RE, for example, to remove template oligonucleotides from other compositions into which they may have been deliberately or accidentally introduced. Alternatively, the RE site may be usefully exploited in the course of sequencing template oligonucleotides in the template composition, and/or as a positional sequence marker in a template oligonucleotide sequence regardless of whether or not it is cleaved with a restriction enzyme. An exemplary RE site is the oligonucleotide motif GTCGAC, which is recognized by the restriction enzyme Sal I. A large number of additional restriction enzymes and their respective RE recognition site sequences are known in the art and are available commercially (*e.g.*, New England Biolabs, Beverly, MA). These include, for example, EcoRI (GAATTC) and SphI (GCATGC). Those familiar with the art will appreciate that any of a variety of such RE recognition sites may be incorporated into particular embodiments of the presently disclosed template oligonucleotides.

Sequencing

[00182] Sequencing may be performed using any of a variety of available high throughput single molecule sequencing machines and systems. Illustrative sequence systems include sequence-by-synthesis systems such as the Illumina Genome Analyzer and associated instruments (Illumina, Inc., San Diego, CA), Helicos Genetic Analysis System (Helicos BioSciences Corp., Cambridge, MA), Pacific Biosciences PacBio RS (Pacific Biosciences, Menlo Park, CA), or other systems having similar capabilities. Sequencing is achieved using a set of sequencing oligonucleotides that hybridize to a defined region within the amplified DNA molecules. The sequencing oligonucleotides are designed such that the V- and J-encoding gene segments can be uniquely identified by the sequences that are generated,

based on the present disclosure and in view of known adaptive immune receptor gene sequences that appear in publicly available databases. See, *e.g.*, U.S.A.N. 13/217,126; U.S.A.N. 12/794,507; PCT/US2011/026373; or PCT/US2011/049012. Exemplary TCRB J-region sequencing primers are set forth in Table 3:

Table 3: TCRBJ Sequencing Primers

PRIMER	SEQUENCE	SEQ ID NO:
>Jseq1-1	ACAACCTGTGAGTCTGGTGCCTTGTCCAAAGAAA	1696
>Jseq1-2	ACAACGGTTAACCTGGTCCCCGAACCGAAGGTG	1697
>Jseq1-3	ACAACAGTGAGCCAACTTCCCTCTCCAAAATAT	1698
>Jseq1-4	AAGACAGAGAGCTGGGTTCCTGCCCCAAAAC	1699
>Jseq1-5	AGGATGGAGAGTCGAGTCCCATCACCAAAATGC	1700
>Jseq1-6	GTCACAGTGAGCCTGGTCCCGTTCCCAAAGTGG	1701
>Jseq2-1	AGCACGGTGAGCCGTGTCCCTGGCCCCGAAGAAC	1702
>Jseq2-2	AGTACGGTCAGCCTAGAGCCTTCTCCAAAAAAC	1703
>Jseq2-3	AGCACTGTCAGCCGGGTGCCTGGGCCAAAATAC	1704
>Jseq2-4	AGCACTGAGAGCCGGGTCCCGGCGCCGAAGTAC	1705
>Jseq2-5	AGCACCAGGAGCCGCGTGCCTGGCCCCGAAGTAC	1706
>Jseq2-6	AGCACGGTCAGCCTGCTGCCGGCCCCGAAAGTC	1707
>Jseq2-7	GTGACCGTGAGCCTGGTGCCCGGCCCGAAGTAC	1708

[00183] The term “gene” means the segment of DNA involved in producing a polypeptide chain such as all or a portion of a TCR or Ig polypeptide (*e.g.*, a CDR3-containing polypeptide); it includes regions preceding and following the coding region “leader and trailer” as well as intervening sequences (introns) between individual coding segments (exons), and may also include regulatory elements (*e.g.*, promoters, enhancers, repressor binding sites and the like), and may also include recombination signal sequences (RSSs) as described herein.

[00184] The nucleic acids of the present embodiments, also referred to herein as polynucleotides, may be in the form of RNA or in the form of DNA, which DNA includes cDNA, genomic DNA, and synthetic DNA. The DNA may be double-stranded or single-stranded, and if single stranded may be the coding strand or non-coding (anti-sense) strand. A coding sequence which encodes a TCR or an immunoglobulin or a region thereof (*e.g.*, a V

region, a D segment, a J region, a C region, etc.) for use according to the present embodiments may be identical to the coding sequence known in the art for any given TCR or immunoglobulin gene regions or polypeptide domains (e.g., V-region domains, CDR3 domains, etc.), or may be a different coding sequence, which, as a result of the redundancy or degeneracy of the genetic code, encodes the same TCR or immunoglobulin region or polypeptide.

[00185] In certain embodiments, the amplified J-region encoding gene segments may each have a unique sequence-defined identifier tag of 2, 3, 4, 5, 6, 7, 8, 9, 10 or about 15, 20 or more nucleotides, situated at a defined position relative to a RSS site. For example, a four-base tag may be used, in the J β -region encoding segment of amplified TCR β CDR3-encoding regions, at positions +11 through +14 downstream from the RSS site. However, these and related embodiments need not be so limited and also contemplate other relatively short nucleotide sequence-defined identifier tags that may be detected in J-region encoding gene segments and defined based on their positions relative to an RSS site. These may vary between different adaptive immune receptor encoding loci.

[00186] The recombination signal sequence (RSS) consists of two conserved sequences (heptamer, 5'-CACAGTG-3', and nonamer, 5'-ACAAAAACC-3'), separated by a spacer of either 12 +/- 1 bp ("12-signal") or 23 +/- 1 bp ("23-signal"). A number of nucleotide positions have been identified as important for recombination including the CA dinucleotide at position one and two of the heptamer, and a C at heptamer position three has also been shown to be strongly preferred as well as an A nucleotide at positions 5, 6, 7 of the nonamer. (Ramsden et. al 1994; Akamatsu et. al. 1994; Hesse et. al. 1989). Mutations of other nucleotides have minimal or inconsistent effects. The spacer, although more variable, also has an impact on recombination, and single-nucleotide replacements have been shown to significantly impact recombination efficiency (Fanning et. al. 1996, Larijani et. al 1999; Nadel et. al. 1998). Criteria have been described for identifying RSS polynucleotide sequences having significantly different recombination efficiencies (Ramsden et. al 1994; Akamatsu et. al. 1994; Hesse et. al. 1989 and Cowell et. al. 1994). Accordingly, the sequencing oligonucleotides may hybridize adjacent to a four base tag within the amplified J-encoding gene segments at positions +11 through +14 downstream of the RSS site. For example, sequencing oligonucleotides for TCRB may be designed to anneal to a consensus nucleotide motif observed just downstream of this "tag", so that the first four bases of a

sequence read will uniquely identify the J-encoding gene segment (see, *e.g.*, WO/2012/027503).

[00187] The average length of the CDR3-encoding region, for the TCR, defined as the nucleotides encoding the TCR polypeptide between the second conserved cysteine of the V segment and the conserved phenylalanine of the J segment, is 35+/-3 nucleotides. Accordingly and in certain embodiments, PCR amplification using V-segment oligonucleotide primers with J-segment oligonucleotide primers that start from the J segment tag of a particular TCR or IgH J region (*e.g.*, TCR J β , TCR J γ or IgH JH as described herein) will nearly always capture the complete V-D-J junction in a 50 base pair read. The average length of the IgH CDR3 region, defined as the nucleotides between the conserved cysteine in the V segment and the conserved phenylalanine in the J segment, is less constrained than at the TCR β locus, but will typically be between about 10 and about 70 nucleotides. Accordingly and in certain embodiments, PCR amplification using V-segment oligonucleotide primers with J-segment oligonucleotide primers that start from the IgH J segment tag will capture the complete V-D-J junction in a 100 base pair read.

[00188] PCR primers that anneal to and support polynucleotide extension on mismatched template sequences are referred to as promiscuous primers. In certain embodiments, the TCR and Ig J-segment reverse PCR primers may be designed to minimize overlap with the sequencing oligonucleotides, in order to minimize promiscuous priming in the context of multiplex PCR. In one embodiment, the TCR and Ig J-segment reverse primers may be anchored at the 3' end by annealing to the consensus splice site motif, with minimal overlap of the sequencing primers. Generally, the TCR and Ig V and J-segment primers may be selected to operate in PCR at consistent annealing temperatures using known sequence/primer design and analysis programs under default parameters.

[00189] For the sequencing reaction, the exemplary IGHJ sequencing primers extend three nucleotides across the conserved CAG sequences as described in WO/2012/027503.

SAMPLES

[00190] The subject or biological source, from which a test biological sample may be obtained, may be a human or non-human animal, or a transgenic or cloned or tissue-engineered (including through the use of stem cells) organism. In certain preferred embodiments of the invention, the subject or biological source may be known to have, or may be suspected of having or being at risk for having, a circulating or solid tumor or other

malignant condition, or an autoimmune disease, or an inflammatory condition, and in certain preferred embodiments of the invention the subject or biological source may be known to be free of a risk or presence of such disease.

[00191] Certain preferred embodiments contemplate a subject or biological source that is a human subject such as a patient that has been diagnosed as having or being at risk for developing or acquiring cancer according to art-accepted clinical diagnostic criteria, such as those of the U.S. National Cancer Institute (Bethesda, MD, USA) or as described in *DeVita, Hellman, and Rosenberg's Cancer: Principles and Practice of Oncology* (2008, Lippincott, Williams and Wilkins, Philadelphia/ Ovid, New York); Pizzo and Poplack, *Principles and Practice of Pediatric Oncology* (Fourth edition, 2001, Lippincott, Williams and Wilkins, Philadelphia/ Ovid, New York); and Vogelstein and Kinzler, *The Genetic Basis of Human Cancer* (Second edition, 2002, McGraw Hill Professional, New York); certain embodiments contemplate a human subject that is known to be free of a risk for having, developing or acquiring cancer by such criteria.

[00192] Certain other embodiments contemplate a non-human subject or biological source, for example a non-human primate such as a macaque, chimpanzee, gorilla, vervet, orangutan, baboon or other non-human primate, including such non-human subjects that may be known to the art as preclinical models, including preclinical models for solid tumors and/or other cancers. Certain other embodiments contemplate a non-human subject that is a mammal, for example, a mouse, rat, rabbit, pig, sheep, horse, bovine, goat, gerbil, hamster, guinea pig or other mammal; many such mammals may be subjects that are known to the art as preclinical models for certain diseases or disorders, including circulating or solid tumors and/or other cancers (*e.g.*, Talmadge et al., 2007 *Am. J. Pathol.* 170:793; Kerbel, 2003 *Canc. Biol. Therap.* 2(4 Suppl 1):S134; Man et al., 2007 *Canc. Met. Rev.* 26:737; Cespedes et al., 2006 *Clin. Transl. Oncol.* 8:318). The range of embodiments is not intended to be so limited, however, such that there are also contemplated other embodiments in which the subject or biological source may be a non-mammalian vertebrate, for example, another higher vertebrate, or an avian, amphibian or reptilian species, or another subject or biological source.

[00193] Biological samples may be provided by obtaining a blood sample, biopsy specimen, tissue explant, organ culture, biological fluid or any other tissue or cell preparation from a subject or a biological source. Preferably the sample comprises DNA from lymphoid cells of the subject or biological source, which, by way of illustration and not limitation, may

contain rearranged DNA at one or more TCR or BCR loci. In certain embodiments a test biological sample may be obtained from a solid tissue (*e.g.*, a solid tumor), for example by surgical resection, needle biopsy or other means for obtaining a test biological sample that contains a mixture of cells.

[00194] According to certain embodiments, it may be desirable to isolate lymphoid cells (*e.g.*, T cells and/or B cells) according to any of a large number of established methodologies, where isolated lymphoid cells are those that have been removed or separated from the tissue, environment or milieu in which they naturally occur. B cells and T cells can thus be obtained from a biological sample, such as from a variety of tissue and biological fluid samples including bone marrow, thymus, lymph glands, lymph nodes, peripheral tissues and blood, but peripheral blood is most easily accessed. Any peripheral tissue can be sampled for the presence of B and T cells and is therefore contemplated for use in the methods described herein. Tissues and biological fluids from which adaptive immune cells, may be obtained include, but are not limited to skin, epithelial tissues, colon, spleen, a mucosal secretion, oral mucosa, intestinal mucosa, vaginal mucosa or a vaginal secretion, cervical tissue, ganglia, saliva, cerebrospinal fluid (CSF), bone marrow, cord blood, serum, serosal fluid, plasma, lymph, urine, ascites fluid, pleural fluid, pericardial fluid, peritoneal fluid, abdominal fluid, culture medium, conditioned culture medium or lavage fluid. In certain embodiments, adaptive immune cells may be isolated from an apheresis sample. Peripheral blood samples may be obtained by phlebotomy from subjects. Peripheral blood mononuclear cells (PBMC) are isolated by techniques known to those of skill in the art, *e.g.*, by Ficoll-Hypaque[®] density gradient separation. In certain embodiments, whole PBMCs are used for analysis.

[00195] For nucleic acid extraction, total genomic DNA may be extracted from cells using methods known in the art and/or commercially available kits, *e.g.*, by using the QIAamp[®] DNA blood Mini Kit (QIAGEN[®]). The approximate mass of a single haploid genome is 3 pg. Preferably, at least 100,000 to 200,000 cells are used for analysis, *i.e.*, about 0.6 to 1.2 μ g DNA from diploid T or B cells. Using PBMCs as a source, the number of T cells can be estimated to be about 30% of total cells. The number of B cells can also be estimated to be about 30% of total cells in a PBMC preparation.

[00196] The Ig and TCR gene loci contain many different variable (V), diversity (D), and joining (J) gene segments, which are subjected to rearrangement processes during early lymphoid differentiation. Ig and TCR V, D and J gene segment sequences are known in the art and are available in public databases such as GENBANK. The V-D-J rearrangements are

mediated via a recombinase enzyme complex in which the RAG1 and RAG2 proteins play a key role by recognizing and cutting the DNA at the recombination signal sequences (RSS), which are located downstream of the V gene segments, at both sides of the D gene segments, and upstream of the J gene segments. Inappropriate RSS reduce or even completely prevent rearrangement. The recombination signal sequence (RSS) includes two consensus sequences (heptamer, 5'-CACAGTG-3', and nonamer, 5'-ACAAAAACC-3'), separated by a spacer of either 12 +/- 1 bp ("12-signal") or 23 +/- 1 bp ("23-signal"). At the 3' end of the V segment and D segment the RSS sequence is heptamer (CACAGTG)-spacer-nonamer (ACAAAAACC). At the 5' end of the J segment and D segment the RSS sequence is nonamer (GGTTTTTGT)-spacer-heptamer (CACTGTG), with substantial sequence variation in the heptamer and nonamer sequence of each specific gene segment.

[00197] A number of nucleotide positions have been identified as important for recombination including the CA dinucleotide at position one and two of the heptamer, and a C at heptamer position three has also been shown to be strongly preferred as well as an A nucleotide at positions 5, 6, 7 of the nonamer. (Ramsden et. al 1994 *Nucl. Ac. Res.* 22:1785; Akamatsu et. al. 1994 *J. Immunol.* 153:4520; Hesse et. al. 1989 *Genes Dev.* 3:1053). Mutations of other nucleotides have minimal or inconsistent effects. The spacer, although more variable, also has an impact on recombination, and single-nucleotide replacements have been shown to significantly impact recombination efficiency (Fanning et. al. 1996 *Cell. Immunol. Immunopath.* 79:1, Larijani et. al 1999 *Nucl. Ac. Res.* 27:2304; Nadel et. al. 1998 *J. Immunol.* 161:6068; Nadel et al., 1998 *J. Exp. Med.* 187:1495). Criteria have been described for identifying RSS polynucleotide sequences having significantly different recombination efficiencies (Ramsden et. al 1994 *Nucl. Ac. Res.* 22:1785; Akamatsu et. al. 1994 *J. Immunol.* 153:4520; Hesse et. al. 1989 *Genes Dev.* 3:1053, and Lee et al., 2003 *PLoS* 1(1):E1).

[00198] The rearrangement process at the Ig heavy chain (IgH), TCR beta (TCRB), and TCR delta (TCRD) genes generally starts with a D to J rearrangement followed by a V to D-J rearrangement, while direct V to J rearrangements occur at Ig kappa (IgK), Ig lambda (IgL), TCR alpha (TCRA), and TCR gamma (TCRG) genes. The sequences between rearranging gene segments are generally deleted in the form of a circular excision product, also called TCR excision circle (TREC) or B cell receptor excision circle (BREC).

[00199] The many different combinations of V, D, and J gene segments represent the so-called combinatorial repertoire, which is estimated to be $\sim 2 \times 10^6$ for Ig molecules, $\sim 3 \times 10^6$ for

TCR $\alpha\beta$ and $\sim 5 \times 10^3$ for TCR $\gamma\delta$ molecules. At the junction sites of the V, D, and J gene segments, deletion and random insertion of nucleotides occurs during the rearrangement process, resulting in highly diverse junctional regions, which significantly contribute to the total repertoire of Ig and TCR molecules, estimated to be $> 10^{12}$ possible amino acid sequences.

[00200] Mature B-lymphocytes further extend their Ig repertoire upon antigen recognition in germinal centers via somatic hypermutation, a process leading to affinity maturation of the Ig molecules. The somatic hypermutation process focuses on the V- (D-) J exon of IgH and Ig light chain genes and primarily generates single nucleotide mutations but sometimes also insertions or deletions of nucleotides. Somatic-mutated Ig genes are also typically found in mature B-cell malignancies.

[00201] In certain embodiments described herein, V-segment and J-segment primers may be employed in a PCR reaction to amplify rearranged TCR or BCR CDR3-encoding DNA regions in a test biological sample, wherein each functional TCR or Ig V-encoding gene segment comprises a V gene recombination signal sequence (RSS) and each functional TCR or Ig J-encoding gene segment comprises a J gene RSS. In these and related embodiments, each amplified rearranged DNA molecule may comprise (i) at least about 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000 (including all integer values therebetween) or more contiguous nucleotides of a sense strand of the TCR or Ig V-encoding gene segment, with the at least about 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000 or more contiguous nucleotides being situated 5' to the V gene RSS and/or each amplified rearranged DNA molecule may comprise (ii) at least about 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500 (including all integer values therebetween) or more contiguous nucleotides of a sense strand of the TCR or Ig J-encoding gene segment, with the at least about 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500 or more contiguous nucleotides being situated 3' to the J gene RSS.

Amplification Factor Determination

[00202] In addition to the use of the presently disclosed template compositions for standardizing amplification efficiency of oligonucleotide amplification primer sets as described herein, certain other embodiments contemplate use of the template composition to determine amplification factors for estimating the number of rearranged adaptive immune receptor encoding sequences in a sample. These and related embodiments may find use to

quantify the number of adaptive immune receptor encoding sequences in a DNA sample that has been obtained from lymphoid cells, including lymphoid cells that are present in a mixture of cells that comprises cells in which DNA encoding an adaptive immune receptor has undergone DNA rearrangement, but where the sample also contains DNA from cells in which no such rearrangement has taken place (*e.g.*, non-lymphoid cells, immature cells, mesenchymal cells, cancer cells, etc.).

[00203] The total number of different members of a given class of adaptive immune receptors (*e.g.*, TCRs or IGs) in a subject may be estimated by multiplexed PCR using a comprehensive V-J amplification primer set followed by quantitative sequencing of amplification products. Multiplexed amplification and high throughput sequencing of rearranged TCR and BCR (IG) encoding DNA sequences are described, for example, in Robins et al., 2009 *Blood* 114, 4099; Robins et al., 2010 *Sci. Translat. Med.* 2:47ra64; Robins et al., 2011 *J. Immunol. Meth.* doi:10.1016/j.jim.2011.09.001; Sherwood et al. 2011 *Sci. Translat. Med.* 3:90ra61; U.S.A.N. 13/217,126 (US Pub. No. 2012/0058902), U.S.A.N. 12/794,507 (US Pub. No. 2010/0330571), WO/2010/151416, WO/2011/106738 (PCT/US2011/026373), WO2012/027503 (PCT/US2011/049012), U.S.A.N. 61/550,311, and U.S.A.N. 61/569,118.

[00204] This methodology typically involves sampling DNA from a subpopulation of lymphoid cells, such as lymphoid cells that are present in a blood sample, which is known also to contain nucleated cells that lack rearranged TCR or IG encoding DNA. The present compositions and methods may permit improved accuracy and precision in the determination of the number of rearranged TCR and IG encoding DNA molecules in such a sample. As described herein, for instance, by spiking the DNA sample with the present template composition, an internal amplification template standard is provided for assessing the relative efficiencies across the range of oligonucleotide primers that are present in the multiplexed amplification primer set. By so assessing the amplification products of the present artificial template composition, which is added to the amplification reaction in known amounts, an amplification factor (*e.g.*, a multiplicative, normalizing, scaling or geometric factor, etc.) can be determined for the oligonucleotide amplification primer set and can then be used to calculate the number of natural DNA templates in the sample.

[00205] As another example, these and related embodiments permit quantification of Minimal Residual Disease (MRD) in lymphoma or leukemia, by quantitative detection of rearranged TCR or IG encoding DNA in samples obtained from mixed preparations of

lymphoid and non-lymphoid cells, including persistent lymphoma or leukemia cells. Prior methods determine MRD as the number of malignant cells that are detectable as a proportion of the total number of cells in a sample. In contrast, the present methods permit estimation of the total number of cells in a sample that have rearranged TCR or IG encoding DNA, so that malignant cells (*e.g.*, those having a particular TCR or IG rearrangement, such as a clonotype) can be quantified as a proportion of such rearranged cells instead of as a proportion of all cells. By way of non-limiting theory, it is believed that because the representation of all rearranged cells in a clinical sample from a subject having or suspected of having MRD is typically very low, the present methods will dramatically improve the sensitivity with which MRD can be detected, including improving such sensitivity by increasing the signal-to-noise ratio.

[00206] Accordingly certain embodiments thus provide a method for quantifying rearranged DNA molecules encoding one or a plurality of adaptive immune receptors in a biological sample that comprises DNA from lymphoid cells of a subject, each adaptive immune receptor comprising a variable region and a joining region. Briefly, the method comprises the steps of:

[00207] (A) in a multiplexed amplification reaction using the herein described oligonucleotide amplification primer set that is capable of amplifying substantially all V-J encoding combinations for a given adaptive immune receptor, amplifying DNA from the sample to which has been added a known amount of the herein described template composition for standardizing amplification efficiency, to obtain amplification products;

[00208] (B) quantitatively sequencing the amplification products of (A) to quantify (i) template amplification products, which are amplification products of the herein described template composition and will be identifiable because they contain at least one barcode oligonucleotide sequence, and (ii) amplification products of rearranged adaptive immune receptor encoding DNA sequences in the sample, which will be identifiable because they contain specific V and J sequences but lack an oligonucleotide barcode sequence;

[00209] (C) calculating an amplification factor based on quantitative information obtained in step (B); and

[00210] (D) using the amplification factor of (C) to determine, by calculation, the number of unique adaptive immune receptor encoding DNA molecules in the sample.

[00211] Without wishing to be bound by theory, according to these and related methods, the number of rearranged TCR or IG encoding DNA molecules that are sampled in a

multiplexed amplification reaction is measured. To do so, a sequence coverage value, *e.g.*, the number of output sequence reads that are determined for each input (template) molecule, is determined and averaged across the entire number of different template oligonucleotides that are present, to obtain an average sequence coverage value. By dividing (i) the number of reads that are obtained for a given sequence by (ii) the average sequence coverage value, the number of rearranged molecules that are present as templates at the start of the amplification reaction can be calculated.

[00212] Thus, for example, to calculate the sequence coverage value, a known quantity of a set of synthetic molecules of the presently disclosed template composition is added to each PCR amplification, the synthetic templates having the basic structure of formula (I) 5' U-B1-V-B2-R-(B3)-J-B4-U 3' where each V is a 300 base pair segment having a sequence that matches a TCR or IG V gene sequence and J is a 100 base pair segment having a sequence that matches a TCR or IG J gene. B2 is a unique barcode oligonucleotide sequence that uniquely identifies each VJ pair and that also differentiates amplification products of the synthetic DNA templates (which will contain the barcode sequence) from amplification products of naturally occurring biologic template DNA molecules that are contributed by the lymphoid DNA sample (which will lack the barcode sequence). In this example, B3 of formula (I) is nothing. After PCR amplification and sequencing, the numbers of each sequenced synthetic molecule (*i.e.*, amplification products containing the barcode sequence) are counted. The sequence coverage of the synthetic molecules is then calculated based on the known number of starting synthetic template molecules used to spike the amplification reaction.

[00213] For example, a pool of 5000 synthetic, barcode-containing template molecules comprising 4-5 copies each of 1100 unique synthetic template oligonucleotide sequences (representing every possible VJ pair) may be added to the amplification reaction. If the amplification products include 50,000 sequences that match the synthetic template molecules, a sequence coverage value of 10X has been obtained and the amplification factor is 10. To estimate the number of natural VDJ-rearranged template molecules in the DNA obtained from the sample, the number of amplification products of the natural templates (*i.e.*, amplification products that lack any barcode sequence) is then divided by the amplification factor. For added accuracy, because in this example the 5000 synthetic molecules are a complex pool of 1100 molecules representing every VJ pair, the amplification factor for every VJ pair can be individually calculated. The amplification factor can then be averaged

across all of the synthetic molecules (Fig. 8). The accuracy and robustness of the method is shown in Fig. 9 and details are described below in Example 5.

[00214] In an alternative embodiment, identical to what is described above and below in this section, except differing in the use of a subset of the total pool of synthetic template molecules is used in a manner resulting in the addition to a sample of not more than 1 copy of a subset of distinct template molecules to the sample. Application of Poisson statistical methods well known to the ordinarily skilled artisan are used to determine the amount of template to add based upon the known properties of the pool (e.g., the total number of distinct sequences and the concentration of template molecules). For example, 200-500 template molecules are added to the amplification reaction, such that there is on average not more than one copy each of a subset of template molecules present in the pool.

[00215] Accordingly, in these embodiments the method comprises: (A) amplifying DNA in a multiplex polymerase chain reaction (PCR) that comprises: (1) DNA from the biological sample that comprises lymphoid cells of the subject, (2) the template composition of claim 1 in which a known number of each of the plurality of template oligonucleotides having a unique oligonucleotide sequence is present, (3) an oligonucleotide amplification primer set that is capable of amplifying rearranged DNA encoding one or a plurality of adaptive immune receptors in the DNA from the biological sample, the primer set comprising: (a) in substantially equimolar amounts, a plurality of V-segment oligonucleotide primers that are each independently capable of specifically hybridizing to at least one polynucleotide encoding an adaptive immune receptor V-region polypeptide or to the complement thereof, wherein each V-segment primer comprises a nucleotide sequence of at least 15 contiguous nucleotides that is complementary to at least one functional adaptive immune receptor V region-encoding gene segment and wherein the plurality of V-segment primers specifically hybridize to substantially all functional adaptive immune receptor V region-encoding gene segments that are present in the template composition, and (b) in substantially equimolar amounts, a plurality of J-segment oligonucleotide primers that are each independently capable of specifically hybridizing to at least one polynucleotide encoding an adaptive immune receptor J-region polypeptide or to the complement thereof, wherein each J-segment primer comprises a nucleotide sequence of at least 15 contiguous nucleotides that is complementary to at least one functional adaptive immune receptor J region-encoding gene segment and wherein the plurality of J-segment primers specifically hybridize to substantially all functional adaptive immune receptor J region-encoding gene segments that are present in

the template composition, wherein the V-segment and J-segment oligonucleotide primers are capable of promoting amplification in said multiplex polymerase chain reaction (PCR) of (i) substantially all template oligonucleotides in the template composition to produce a multiplicity of amplified template DNA molecules, said multiplicity of amplified template DNA molecules being sufficient to quantify diversity of the template oligonucleotides in the template composition, and (ii) substantially all rearranged DNA molecules encoding adaptive immune receptors in the biological sample to produce a multiplicity of amplified rearranged DNA molecules, said multiplicity of amplified rearranged DNA molecules being sufficient to quantify diversity of the rearranged DNA molecules in the DNA from the biological sample, and wherein each amplified DNA molecule in the multiplicity of amplified template DNA molecules and in the multiplicity of amplified rearranged DNA molecules is less than 1000, 900, 800, 700, 600, 500, 400, 300, 200, 100, 90, 80 or 70 nucleotides in length;

[00216] (B) quantitatively sequencing all or a sufficient portion of each of said amplified template DNA molecules and each of said amplified rearranged DNA molecules to quantify (i) a template product number of amplified template DNA molecules which contain at least one oligonucleotide barcode sequence, and (ii) a rearranged product number of amplified rearranged DNA molecules which lack an oligonucleotide barcode sequence;

[00217] (C) calculating an amplification factor by dividing the template product number of (B)(i) by the known number of each of the plurality of template oligonucleotides having a unique oligonucleotide sequence of (A)(2); and

[00218] (D) dividing the rearranged product number of (B)(ii) by the amplification factor calculated in (C) to quantify unique adaptive immune receptor encoding DNA molecules in the sample.

[00219] The contemplated embodiments are not intended to be limited to the above described method, such that from the present disclosure the skilled person will appreciate variations that may be employed. An alternative approach, for example, may not use the herein described synthetic template composition as a spiked-in control template in multiplexed PCR amplification of a DNA sample that contains rearranged lymphoid cell TCR and/or IG encoding DNA as well as non-rearranged DNA. Instead, according to one such alternative, to the amplification reaction using V and J amplification primers may be added a known set of oligonucleotide amplification primers that amplify a distinct, highly conserved genomic sequence region. These genomic control primers may amplify every genome that is present in the DNA sample regardless of whether or not it contains rearranged TCR and/or IG

encoding sequences, whereas the V and J primers may amplify products only from genomes with a rearranged VDJ region. The ratio between these two classes of amplification product molecules permits estimation of the total number of B cell genomes in the sample.

[00220] The practice of certain embodiments of the present invention will employ, unless indicated specifically to the contrary, conventional methods in microbiology, molecular biology, biochemistry, molecular genetics, cell biology, virology and immunology techniques that are within the skill of the art, and reference to several of which is made below for the purpose of illustration. Such techniques are explained fully in the literature. See, *e.g.*, Sambrook, et al., *Molecular Cloning: A Laboratory Manual* (3rd Edition, 2001); Sambrook, et al., *Molecular Cloning: A Laboratory Manual* (2nd Edition, 1989); Maniatis et al., *Molecular Cloning: A Laboratory Manual* (1982); Ausubel et al., *Current Protocols in Molecular Biology* (John Wiley and Sons, updated July 2008); *Short Protocols in Molecular Biology: A Compendium of Methods from Current Protocols in Molecular Biology*, Greene Pub. Associates and Wiley-Interscience; Glover, *DNA Cloning: A Practical Approach*, vol. I & II (IRL Press, Oxford Univ. Press USA, 1985); *Current Protocols in Immunology* (Edited by: John E. Coligan, Ada M. Kruisbeek, David H. Margulies, Ethan M. Shevach, Warren Strober 2001 John Wiley & Sons, NY, NY); *Real-Time PCR: Current Technology and Applications*, Edited by Julie Logan, Kirstin Edwards and Nick Saunders, 2009, Caister Academic Press, Norfolk, UK; Anand, *Techniques for the Analysis of Complex Genomes*, (Academic Press, New York, 1992); Guthrie and Fink, *Guide to Yeast Genetics and Molecular Biology* (Academic Press, New York, 1991); *Oligonucleotide Synthesis* (N. Gait, Ed., 1984); *Nucleic Acid Hybridization* (B. Hames & S. Higgins, Eds., 1985); *Transcription and Translation* (B. Hames & S. Higgins, Eds., 1984); *Animal Cell Culture* (R. Freshney, Ed., 1986); Perbal, *A Practical Guide to Molecular Cloning* (1984); *Next-Generation Genome Sequencing* (Janitz, 2008 Wiley-VCH); *PCR Protocols (Methods in Molecular Biology)* (Park, Ed., 3rd Edition, 2010 Humana Press); *Immobilized Cells And Enzymes* (IRL Press, 1986); the treatise, *Methods In Enzymology* (Academic Press, Inc., N.Y.); *Gene Transfer Vectors For Mammalian Cells* (J. H. Miller and M. P. Calos eds., 1987, Cold Spring Harbor Laboratory); Harlow and Lane, *Antibodies*, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1998); *Immunochemical Methods In Cell And Molecular Biology* (Mayer and Walker, eds., Academic Press, London, 1987); *Handbook Of Experimental Immunology*, Volumes I-IV (D. M. Weir and CC Blackwell, eds., 1986); Riott, *Essential Immunology*, 6th Edition, (Blackwell Scientific Publications, Oxford, 1988);

Embryonic Stem Cells: Methods and Protocols (Methods in Molecular Biology) (Kurstad Turksen, Ed., 2002); *Embryonic Stem Cell Protocols: Volume I: Isolation and Characterization* (Methods in Molecular Biology) (Kurstad Turksen, Ed., 2006); *Embryonic Stem Cell Protocols: Volume II: Differentiation Models* (Methods in Molecular Biology) (Kurstad Turksen, Ed., 2006); *Human Embryonic Stem Cell Protocols* (Methods in Molecular Biology) (Kurstad Turksen Ed., 2006); *Mesenchymal Stem Cells: Methods and Protocols* (Methods in Molecular Biology) (Darwin J. Prockop, Donald G. Phinney, and Bruce A. Bunnell Eds., 2008); *Hematopoietic Stem Cell Protocols* (Methods in Molecular Medicine) (Christopher A. Klug, and Craig T. Jordan Eds., 2001); *Hematopoietic Stem Cell Protocols* (Methods in Molecular Biology) (Kevin D. Bunting Ed., 2008) *Neural Stem Cells: Methods and Protocols* (Methods in Molecular Biology) (Leslie P. Weiner Ed., 2008).

[00221] Unless specific definitions are provided, the nomenclature utilized in connection with, and the laboratory procedures and techniques of, molecular biology, analytical chemistry, synthetic organic chemistry, and medicinal and pharmaceutical chemistry described herein are those well known and commonly used in the art. Standard techniques may be used for recombinant technology, molecular biological, microbiological, chemical syntheses, chemical analyses, pharmaceutical preparation, formulation, and delivery, and treatment of patients.

[00222] Unless the context requires otherwise, throughout the present specification and claims, the word “comprise” and variations thereof, such as, “comprises” and “comprising” are to be construed in an open, inclusive sense, that is, as “including, but not limited to”. By “consisting of” is meant including, and typically limited to, whatever follows the phrase “consisting of.” By “consisting essentially of” is meant including any elements listed after the phrase, and limited to other elements that do not interfere with or contribute to the activity or action specified in the disclosure for the listed elements. Thus, the phrase “consisting essentially of” indicates that the listed elements are required or mandatory, but that no other elements are required and may or may not be present depending upon whether or not they affect the activity or action of the listed elements.

[00223] In this specification and the appended claims, the singular forms “a,” “an” and “the” include plural references unless the content clearly dictates otherwise. As used herein, in particular embodiments, the terms “about” or “approximately” when preceding a numerical value indicates the value plus or minus a range of 5%, 6%, 7%, 8% or 9%. In other embodiments, the terms “about” or “approximately” when preceding a numerical value

indicates the value plus or minus a range of 10%, 11%, 12%, 13% or 14%. In yet other embodiments, the terms “about” or “approximately” when preceding a numerical value indicates the value plus or minus a range of 15%, 16%, 17%, 18%, 19% or 20%.

[00224] Reference throughout this specification to “one embodiment” or “an embodiment” or “an aspect” means that a particular feature, structure or characteristic described in connection with the embodiment is included in at least one embodiment of the present invention. Thus, the appearances of the phrases “in one embodiment” or “in an embodiment” in various places throughout this specification are not necessarily all referring to the same embodiment. Furthermore, the particular features, structures, or characteristics may be combined in any suitable manner in one or more embodiments.

EXAMPLES

EXAMPLE 1: DESIGN OF TEMPLATE OLIGONUCLEOTIDES FOR CALIBRATING AMPLIFICATION PRIMER BIAS CONTROL

[00225] In this and the following Examples, standard molecular biology and biochemistry materials and methodologies were employed, including techniques described in , *e.g.*, Sambrook, et al., *Molecular Cloning: A Laboratory Manual* (3rd Edition, 2001); Sambrook, et al., *Molecular Cloning: A Laboratory Manual* (2nd Edition, 1989); Maniatis et al., *Molecular Cloning: A Laboratory Manual* (1982); Ausubel et al., *Current Protocols in Molecular Biology* (John Wiley and Sons, updated July 2008); *Short Protocols in Molecular Biology: A Compendium of Methods from Current Protocols in Molecular Biology*, Greene Pub. Associates and Wiley-Interscience; Glover, *DNA Cloning: A Practical Approach*, vol. I & II (IRL Press, Oxford Univ. Press USA, 1985); Anand, *Techniques for the Analysis of Complex Genomes*, (Academic Press, New York, 1992); *Oligonucleotide Synthesis* (N. Gait, Ed., 1984); *Nucleic Acid Hybridization* (B. Hames & S. Higgins, Eds., 1985); *Transcription and Translation* (B. Hames & S. Higgins, Eds., 1984); Perbal, *A Practical Guide to Molecular Cloning* (1984); *Next-Generation Genome Sequencing* (Janitz, 2008 Wiley-VCH); *PCR Protocols (Methods in Molecular Biology)* (Park, Ed., 3rd Edition, 2010 Humana Press).

[00226] A set of double-stranded DNA (dsDNA) template oligonucleotides was designed as a calibration standard for use as a control template that simulated all possible V/J combinations at a specified adaptive immune receptor (TCR or BCR) locus. For each human TCR and BCR locus, a list was compiled of the known genomic V segment sequences 5' of the RSS, and a list of the known genomic J segments 3' of the RSS. The coding strand

sequences of the dsDNA template are presented here for ease of interpretation, according to the convention by which the 5'-to-3' orientation is read left-to-right.

[00227] A schematic representation of the general structure of the template oligonucleotides is shown in Fig. 1. For use in cross-validation of each unique template oligonucleotide's identity in multiple contexts, a different 16 bp barcode oligonucleotide (B) was incorporated into each template that uniquely identified the V segment polynucleotide of the template with the first 8 bp of the barcode, and the J segment with the second 8 bp of the barcode. Copies of this barcode were incorporated thrice: (B3) between the external adapter (U2) and the J segment sequence (J) so that a short single-end read with standard Illumina or Ion primers can reveal the identity of the unique combination of V and J sequences in each template oligonucleotide, (B2) between the V and J segments so that a standard sequencing strategy (*e.g.*, Illumina GA-2 or HiSeq™ or MiSEQ®) will capture the unique combination of V and J sequences in each template oligonucleotide, and (B3) between the V segment and the other external adapter (U1), so that a short paired-end read can confirm the identity of the unique combination of V and J sequences in each template oligonucleotide if so desired.

[00228] As shown in Fig. 1, the template oligonucleotide sequences started with an adapter sequence (U1) that was capable of incorporating sequencing platform-specific short oligonucleotide sequences at the ends of the molecule. In this example the Illumina Nextera™ adaptors were used, but it should be noted that essentially any pair of robust PCR primers would work equally well. As an exemplary adapter, the oligonucleotide sequence GCCTTGCCAGCCCGCTCAG [SEQ ID NO:1746] was attached at the V segment end of U1 (Fig. 1), in order to maintain compatibility with the Nextera™ Illumina Adaptor (Illumina, Inc., San Diego, CA)

(CAAGCAGAAGACGGCATACGAGATCGGTCTGCCTTGCCAGCCCGCTCAG) [SEQ ID NO:1747] to add on the standard Illumina oligonucleotide, which was compatible with either single or paired end Illumina sequencing flowcells.

[00229] Immediately downstream from (3' to) U1 was the first copy (B1) of the barcode oligonucleotide ACACACGTGACACTCT [SEQ ID NO:1748]. Next, a fixed length of V segment sequence was incorporated into the template oligonucleotide, with all templates in the template set ending a given number of bases before the natural RSS, in order to mimic a natural TCR or BCR gene rearrangement having a fixed number of bases deleted at the V segment. In this example zero bases were initially deleted before the RSS. To maximize the recognizability of these sequences, all V segment polynucleotide sequences were then

trimmed to remove partial codons adjacent to the RSS, so that the residual V segment sequences were in frame with the start codon. Diverse V segment sequences were those shown in the exemplary template oligonucleotide sets presented in the Sequence Listing (*e.g.*, a set of TCRB V segments within the formula (I) sequences of the TCRB template oligonucleotide set in SEQ ID NOS:1-871; a distinct set of TCRB V segments within the formula (I) sequences of the TCRB template oligonucleotide set in SEQ ID NOS:872-1560; a set of TCRG V segments within the formula (I) sequences of the TCRG template oligonucleotide set in SEQ ID NOS:1561-1630); a single exemplary V polynucleotide was as follows:

[00230] TCTTATTTTCATAGGCTCCATGGATACTGGAATTACCCAGACACCAAAA
TACCTGGTCACAGCAATGGGGAGTAAAAGGACAATGAAACGTGAGCATCTGGGA
CATGATTCTATGTATTGGTACAGACAGAAAGCTAAGAAATCCCTGGAGTTCATGT
TTTACTACAACGTAAAGGAATTCATTGAAAACAAGACTGTGCCAAATCACTTCAC
ACCTGAATGCCCTGACAGCTCTCGCTTATACCTTCATGTGGTCGCACTGCAGCAA
GAAGACTCAGCTGCGTATCTCTGCACCAGCAG [SEQ ID NO:1749].

[00231] The stop codon TGA was incorporated in-frame at the 3' end of the V polynucleotide sequence in each template oligonucleotide, to ensure that the template oligonucleotide sequences would not be considered relevant in the event they contaminated a biological sample. Downstream from the stop codon, between the V segment and J segment where the NDN would normally be, the second copy of the V/J identifier barcode sequence B2 (SEQ ID NO:1748) was inserted. Next the SalI restriction enzyme recognition site (R) sequence GTCGAC was incorporated; this sequence was selected on the basis of being a sequence that was not naturally present in any of the TCRB V or J segment genomic sequences, conferring the ability to specifically destroy the synthetic template if desired, or for use as an informatic marker to identify the synthetic sequences. The B3 site, in this version of the template is empty.

[00232] The J polynucleotide (J) was incorporated as a fixed length of sequence from a J gene segment, measured from a fixed number of bases after the natural RSS to mimic a natural rearrangement, and in the present example extending into the J-C intron. In this example zero bases were deleted bases from the J segment, but in other template oligonucleotide designs a deletion of 5 bp was used to make room for the VJ barcode (B2) at the V-J junction while maintaining an overall J segment length in the natural range. An exemplary J polynucleotide was

[00233] ACTGAAGCTTTCTTTGGACAAGGCACCAGACTCACAGTTGTAGGTAAG
ACATTTTTCAGGTTCTTTTGCAGATCCGTCACAGGGAAAAGTGGGTCCACAG
[SEQ ID NO:1750].

[00234] Downstream from the J segment polynucleotide was the third copy (B4) of the V/J barcode identifier oligonucleotide (SEQ ID NO:1748). The exemplary template oligonucleotide sequence the sequence ended with a second adapter sequence (U2) that was capable of incorporating platform-specific sequences at the ends of the molecule. As noted above, a Nextera™-compatible adaptor (CTGATGGCGCGAGGGAGGC) [SEQ ID NO:1751] was used on the J segment end of U2, for use with the Nextera™ Illumina Adaptor (AATGATACGGCGACCACCGAGATCTACACGCCTCCCTCGCGCCATCAG) [SEQ ID NO:1752] to permit adding on the standard Illumina sequencing oligonucleotide, which is compatible with either single or paired end flowcells.

[00235] Exemplary TCRB and TCRG template oligonucleotide sets according to the present disclosure were prepared and had the nucleotide sequences set forth in SEQ ID NOS:1-1630. The sets of template oligonucleotides having sequences set forth in SEQ ID NOS:1-871 and 1561-1630 were custom synthesized, based on the sequence design information disclosed herein, by Integrated DNA Technologies, Inc. (Coralville, IA) using gBlocks™ Gene Fragments chemistry. The set of template oligonucleotides having sequences set forth in SEQ ID NOS:872-1560 was generated by a PCR tiling approach described in Example 2.

[00236] TCRB Template Oligonucleotides (SEQ ID NOS:1-871). A set of 871 template oligonucleotides of general formula (I) (in which B3 is nothing) was designed using human TCRB V and J polynucleotide sequences:

[00237] 5'-U1-B1-V-B2-R-(B3)-J-B4-U2-3' (I).

[00238] Each template oligonucleotide consisted of a 495 base pair DNA molecule. Sense strand sequences are presented as SEQ ID NOS:1-871.

[00239] A schematic diagram depicting the design of this template set is shown in Fig. 1. By convention, the diagram depicts the oligonucleotide design in the 5'-to-3' (left-to-right) direction. "V segment" represents an adaptive immune receptor variable (V) region encoding gene sequence, or the complement thereof. "J segment" represents an adaptive immune receptor joining (J) region encoding gene sequence, or the complement thereof. U1 and U2 represent, respectively, first and second universal adaptor oligonucleotide sequences, which may optionally further comprise, respectively, first and second sequencing platform-specific

oligonucleotide sequences linked to and positioned 5' to the first and second universal adaptor oligonucleotide sequences. B1, B2 and B4 represent oligonucleotide barcode sequences that each comprise an oligonucleotide barcode sequence comprising a unique oligonucleotide sequence that uniquely identifies, as a paired combination, (i) a unique V segment sequence, and (ii) a unique J segment sequence; in this Example, B3 was nothing.

[00240] S represents an optional stop codon that may be in-frame or out of frame at the 3' end of V. R represents an optional restriction enzyme recognition site. In SEQ ID NOS:1-871 the U1 and U2 adapters included the 19-mers as described above (SEQ ID NOS:1746 and 1751, respectively) and all (V+J)-identifying barcode (B) sequences (B1, B2, B4) were 16 nucleotides in length; the stop codon TGA and the SalI restriction enzyme recognition site (GTCGAC) were included.

[00241] TCRB Template Oligonucleotides (SEQ ID NOS:872-1560). A second set of 689 template oligonucleotides was designed in which, according to general formula (I), V and J comprised, respectively, human TCRB V and J polynucleotide sequences, U1 and U2 independently comprised distinct restriction enzyme recognition sites (R1 and R3), and B1, B3, and B4 were independently nothing, to arrive at general formula (II):

[00242] R1-V-B2-R2-J-R3(II)

[00243] wherein B2 was an 8-nucleotide barcode identifier (*e.g.*, a barcode sequence as set forth in Table 7); R1, R2 and R3 were, respectively, the restriction enzyme recognition sites EcoRI (GAATTC), SalI (GTCGAC) and SphI (GCATGC); and V and J were, respectively, V region and J region polynucleotides as described herein. Each template oligonucleotide consisted of a 239 base pair DNA molecule. Sense strand sequences are presented as SEQ ID NOS:872-1560.

[00244] TCRG Template Oligonucleotides (SEQ ID NOS:1561-1630). A third set of 70 template oligonucleotides of general formula (I) was designed using human TCRG V and J polynucleotide sequences. Each template oligonucleotide consisted of a 495 base pair DNA molecule. Sense strand sequences are presented as SEQ ID NOS:1561-1630. Details for the 70-oligonucleotide set of TCRG templates (SEQ ID NOS:1561-1630) are representative and were as follows:

[00245] Based on previously determined genomic sequences the human TCRG locus was shown to contain 14 V γ segments that each had a RSS sequence and were therefore regarded as rearrangement-competent. These 14 V γ segments included six gene segments known to be expressed, three V segments that were classified as having open reading frames, and five V

pseudogenes. The V γ gene segments were linked to five J γ gene segments. In order to include all possible V+J gene combinations for the 14 V and 5 J segments, 70 (5 x 14) templates were designed that represented all possible VJ combinations. Each template conformed to the general formula (I) (5'-U1-B1-V-B2-R-(B3)-J-B4-U2-3')(Fig. 1) and thus included nine sections, a 19 base pair (bp) universal adapter (U1), a 16 bp nucleotide tag uniquely identifying each paired combination of V gene and J gene segments (B1), 300 bp of V gene specific sequence (V), a 3 bp stop codon (S), another copy of the 16 bp nucleotide tag (B2), a 6 bp junction tag shared by all molecules (R), nothing for B3, 100 bp of J gene specific sequence (J), a third copy of the 16 bp nucleotide tag (B4), and a 19 bp universal adapter sequence (U2).

[00246] Each of the 70 templates (SEQ ID NOS:1561-1630) was amplified individually using oligonucleotide primers (Table 4; SEQ ID NOS:1732-1745) designed to anneal to the universal adapter sequences (U1, U2).

Table 4. TCRG Amplification Primers

Primer Name	5' Adapter	Sequence	SEQ ID NO:
TCRGV01_dev10	pGEXf	GGAGGGGAAGGCCCCACAGTGTCTTC	1732
TCRGV02/3/4/5/8_dev10	pGEXf	GGAGGGGAAGGCCCCACAGCGTCTTC	1733
TCRGV05P_dev10	pGEXf	GGAGGGGAAGACCCCCACAGCATCTTC	1734
TCRGV06_dev10	pGEXf	GGAGGGGAAGGCCCCACAGCATCTTC	1735
TCRGV07_dev10	pGEXf	GGCGGGGAAGGCCCCACAGCATCTTC	1736
TCRGV09_dev10	pGEXf	TGAAGTCATACAGTTCCTGGTGTCCAT	1737
TCRGV10_dev10	pGEXf	CCAAATCAGGCTTTGGAGCACCTGATCT	1738
TCRGV11_dev10	pGEXf	CAAAGGCTTAGAATATTTATTACATGT	1739
TCRGVA_dev10	pGEXf	CCAGGTCCCTGAGGCACTCCACCAGCT	1740
TCRGVB_dev10	pGEXf	CTGAATCTAAATTATGAGCCATCTGACA	1741
TCRGJP1_dev10	pGEXr	GTGAAGTTACTATGAGCTTAGTCCCTTC AGCAA	1742
TCRGJP2_dev10	pGEXr	CGAAGTTACTATGAGCCTAGTCCCTTTT GCAA	1743
TCRGJ1/2_dev10	pGEXr	TGACAACAAGTGTTGTTCCACTGCCAAA	1744

Primer Name	5' Adapter	Sequence	SEQ ID NO:
TCRGJP_dev10	pGEXr	CTGTAATGATAAGCTTTGTTCCGGGACC AAA	1745

[00247] The resulting concentration of each amplified template oligonucleotide product was quantified using a LabChip GX™ capillary electrophoresis system (Caliper Life Sciences, Inc., Hopkinton, MA) according to the manufacturer's instructions. The frequencies of occurrence for each of the 70 possible V-J combinations, as determined by sequencing barcodes B1, are shown in Table 5. The 70 amplified template oligonucleotide preparations were normalized to a standard concentration and then pooled.

[00248] To verify that all 70 template oligonucleotides were present at substantially equimolar concentrations, the pool was sequenced using the Illumina HiSeq™ sequencing platform according to the manufacturer's recommendations. Briefly, to incorporate platform-specific oligonucleotide sequences into the pooled template oligonucleotides, tailed primers were designed that annealed to the universal priming sites (U1, U2) and that had Illumina Nextera™ adapter sequence tails as the 5' ends. A seven-cycle PCR reaction was then performed to anneal the Illumina adapters to the template oligonucleotides. The PCR reaction product mixture was then purified using Agencourt® AMPure® XP beads (Beckman Coulter, Inc., Fullerton, CA) under the conditions recommended by the manufacturer. The first 60 bp of the PCR reaction products were sequenced using an Illumina HiSEQ™ sequencer (Illumina, Inc., San Diego, CA) and analyzed by assessing the frequency of each 16 bp molecular barcode tag (B1).

[00249] A substantially equimolar preparation for the set of 70 distinct template oligonucleotides was calculated to contain approximately 1.4% of each member of the set, and a threshold tolerance of plus or minus ten-fold frequency (0.14-14%) for all species was desired. The quantitative sequencing revealed that the 70 species of adapter-modified template oligonucleotides within the initial pool were not evenly represented.

[00250] Accordingly, adjustment of the concentrations of individual template oligonucleotides and reiteration of the quantitative sequencing steps are conducted until each molecule is present within the threshold tolerance concentration (0.14-14%).

Table 5: Relative Representation (number of occurrences of indicated V-J combination) of amplification products of each TCRG VJ pair (14 V x 5 J) in pre-amplification Template Pool

Count of Jseg							
B Labels	TCRGJ	TCRGJ2	TCRGJ P	TCRGJP1	TCRGJP2	#N/A	GrandTotal
TCRGV01	17	308	1315	741	822	44	3247
TCRGV02	630	781	2394	2009	122	65	6001
TCRGV03	250	166	2119	157	1105	51	3848
TCRGV04	777	37	2031	1490	1443	76	5854
TCRGV05	323	93	2571	716	150	63	3916
TCRGV05P	294	1161	2946	1552	530	111	6594
TCRGV06	164	1280	1809	401	23	40	3717
TCRGV07	16	234	1849	1697	93	78	3967
TCRGV08	2523	653	944	170	134	57	4481
TCRGV09	55	1004	2057	124	228	42	3510
TCRGV10	351	690	814	384	466	36	2741
TCRGV11	505	648	639	330	181	39	2342
TCRGVA	199	475	112	272	437	12	1507
TCRGVB	210	20	423	874	917	24	2468
#N/A	77	118	309	150	106	531	1291
Grand Total	6391	7668	22332	11067	6757	1269	55484

EXAMPLE 2: DETECTION OF TCRB V GENE AMPLIFICATION BIAS

[00251] This example describes how a set of 689 human TCRB template oligonucleotides of general formula (I) was assembled by tiling together four single stranded oligonucleotides of 50-90 nucleotides each to generate a template set containing hybridization targets for all possible V-J combinations in a set of oligonucleotide primers that was capable of amplifying human TCRB sequences. The set of template oligonucleotides was then used to characterize the relative amplification efficiencies of a set of TCRB V and J amplification primers.

[00252] A set of TCRB 689 template oligonucleotides containing polynucleotide sequences representing all possible productively rearranged V and J combinations for human TCRB chains was synthesized by “tiling” together four single-stranded DNA primers in a standard PCR reaction. Briefly, two 90 bp fragments (one in “forward” orientation and the other in “reverse”) were designed for each TCRB V gene segment, one 90 bp fragment (in “reverse” orientation) was designed for each TCRB J gene segment, and a 50 bp (forward) linker molecule was designed to link together the V and J gene fragments. In total, 52 V forward and 52 V reverse, 13 J reverse, and 689 linker molecules were designed. The two 90 bp fragments (one forward, one reverse) that corresponded to each of the V gene segments had 39 bp of complementary overlapping sequence. One end of each V reverse fragment had 25 bp of complementary sequence which overlapped with the 50 bp linker molecule. The remaining 25 bp in each of the linker molecules was a sequence that complementarily overlapped with one end of the J molecule. The molecules were designed so that the complementary sequences would anneal to one another and form double stranded DNA to which *Taq* polymerase could bind and enzymatically extend the molecule.

[00253] Each PCR reaction to assemble the tiled molecules used QIAGEN Multiplex PCR master mix (QIAGEN part number 206145, Qiagen, Valencia, CA), 10% Q- solution (QIAGEN), and the four single-stranded oligonucleotide sequences (two TCRB V, a TCRB J and a linker, as described above). The two external molecules (one V forward and one J reverse) were added at a final concentration of 1 μ M each while the two internal molecules, (one V reverse and the forward linker), were each added at a final concentration of 0.01 μ M. The thermocycler conditions were: 95°C for 15 minutes, followed by 35 cycles of 94°C for 30 seconds, 59°C for 30 seconds, and 72°C for 1 minute, followed by 1 cycle at 72°C for 10 minutes. After synthesis, the molecules were quantified by the LabChip GX™ capillary electrophoresis system (Caliper Life Sciences, Inc., Hopkinton, MA) according to the manufacturer’s instructions and the concentration (in ng/ μ l) of each resulting band was calculated using Caliper LabChip GX software.

[00254] The nucleotide sequences for the resulting set of 689 TCRB template oligonucleotides are set forth in SEQ ID NOS:872-1560. In SEQ ID NOS:872-1560, each distinct V region sequence was identified by a unique barcode sequence of eight nucleotides, as shown in Table 7. All 689 templates were normalized to a standard concentration of 25 ng/ μ l, and then pooled. The resulting pool was used for the TCRB assays described herein to

detect biased (non-uniform) utilization of TCRB amplification primers during amplification of the 689-template oligonucleotide set (SEQ ID NOS:872-1560).

[00255] Each of the 689 templates was present in the template oligonucleotide pool at experimentally as close as possible to equal molar concentration, and the pool was used as template for the TCRB amplification PCR reaction using an equimolar mixture of 52 TCRB V region primers that included an Illumina adapter-compatible sequence (SEQ ID NOS:1753-1804, Table 6) and an equimolar mix of 13 TCRB J region primers (SEQ ID NOS:1631-1643, Table 1). The members of the pool of 689 templates were amplified using an equimolar pool of the 52 TCRB V β F (forward) primers (the “VF pool”) and an equimolar pool of the 13 TCRB J β R (reverse) primers (the “JR pool”) as shown in Table 1 (SEQ ID NOS:1631-1695). Polymerase chain reactions (PCR) (50 μ L each) were set up at 1.0 μ M VF pool (22 nM for each unique TCRB V β F primer), 1.0 μ M JR pool (77 nM for each unique TCRB J β R primer), 1 μ M QIAGEN Multiplex PCR master mix (QIAGEN part number 206145, Qiagen Corp., Valencia, CA), 10% Q- solution (QIAGEN), and 16 ng/ μ L genomic DNA (gDNA). The following thermal cycling conditions were used in a C100 thermal cycler (Bio-Rad Laboratories, Hercules, CA, USA): one cycle at 95°C for 15 minutes, 25 to 40 cycles at 94°C for 30 seconds, 59°C for 30 seconds, and 72°C for one minute, followed by one cycle at 72°C for 10 minutes. To sample millions of rearranged *TCR β* CDR3 loci, 12 to 20 wells of PCR were performed for each library. As noted above, the V and J primers included a tail that corresponded to, and was compatible with, Illumina adapters for sequencing.

[00256] Amplification products were quantitatively sequenced on an Illumina HiSeq™ sequencer. A 60-base pair region of each product molecule was sequenced using standard J sequencing primers (Table 3) starting from the J molecules. The frequencies of occurrence of each TCRB sequence in the reaction products are shown in Fig. 2, from which it was apparent that not all TCRB sequences had been amplified to a comparable degree.

Table 6. TCRB Amplification Primers

Primer Name	Primer Sequence	Adjusted Relative Primer Molar Ratio	SEQ ID NO:
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Primer Name	Primer Sequence	Adjusted Relative Primer Molar Ratio	SEQ ID NO:
TRB2V10-1	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TAA CAA AGG AGA AGT CTC AGA TGG CTA CAG	0.77	1753
TRB2V10-2	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TGA TAA AGG AGA AGT CCC CGA TGG CTA TGT	1.57	1754
TRB2V10-3	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TGA CAA AGG AGA AGT CTC AGA TGG CTA TAG	2.76	1755
TRB2V11-123	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TCT AAG GAT CGA TTT TCT GCA GAG AGG CTC	1.88	1756
TRB2V12-1	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TTT GAT TCT CAG CAC AGA TGC CTG ATG T	1	1757
TRB2V12-2	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TGC GAT TCT CAG CTG AGA GGC CTG ATG G	1	1758
TRB2V12-3/4	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TTC GAT TCT CAG CTA AGA TGC CTA ATG C	3.24	1759
TRB2V12-5	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TTT CTC AGC AGA GAT GCC TGA TGC AAC TTT A	1.82	1760
TRB2V13	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TCT GAT CGA TTC TCA GCT CAA CAG TTC AGT	2.14	1761

Primer Name	Primer Sequence	Adjusted Relative Primer Molar Ratio	SEQ ID NO:
TRB2V14	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TTC TTA GCT GAA AGG ACT GGA GGG ACG TAT	1.65	1762
TRB2V15	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TGC CGA ACA CTT CTT TCT GCT TTC TTG AC	3.77	1763
TRB2V16	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TTT CAG CTA AGT GCC TCC CAA ATT CAC CCT	1.40	1764
TRB2V17	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TAT TCA CAG CTG AAA GAC CTA ACG GAA CGT	2.87	1765
TRB2V18	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TAT TTT CTG CTG AAT TTC CCA AAG AGG GCC	0.80	1766
TRB2V19	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TTA TAG CTG AAG GGT ACA GCG TCT CTC GGG	0.84	1767
TRB2V2	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TTT CGA TGA TCA ATT CTC AGT TGA AAG GCC	1.02	1768
TRB2V20-1	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TAT GCA AGC CTG ACC TTG TCC ACT CTG ACA	1.66	1769
TRB2V23-1	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TGA TTC TCA TCT CAA TGC CCC AAG AAC GC	1	1770
TRB2V24-1	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TAT CTC TGA TGG ATA CAG TGT CTC TCG ACA	4.01	1771

Primer Name	Primer Sequence	Adjusted Relative Primer Molar Ratio	SEQ ID NO:
TRB2V25-1	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TTT TCC TCT GAG TCA ACA GTC TCC AGA ATA	1.29	1772
TRB2V26	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TCT CTG AGA GGT ATC ATG TTT CTT GAA ATA	1	1773
TRB2V27	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TTC CTG AAG GGT ACA AAG TCT CTC GAA AAG	4.22	1774
TRB2V28	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TTC CTG AGG GGT ACA GTG TCT CTA GAG AGA	2.37	1775
TRB2V29-1	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TCA TCA GCC GCC CAA ACC TAA CAT TCT CAA	1.50	1776
TRB2V2P	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TCC TGA ATG CCC TGA CAG CTC TCG CTT ATA	1	1777
TRB2V3-1	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TCC TAA ATC TCC AGA CAA AGC TCA CTT AAA	3.35	1778
TRB2V3-2	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TCT CAC CTG ACT CTC CAG ACA AAG CTC AT	1	1779
TRB2V30	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TGA CCC CAG GAC CGG CAG TTC ATC CTG AGT	1.48	1780
TRB2V4-1	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TCT GAA TGC CCC AAC AGC TCT CTC TTA AAC	3.32	1781

Primer Name	Primer Sequence	Adjusted Relative Primer Molar Ratio	SEQ ID NO:
TRB2V4-2/3	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TCT GAA TGC CCC AAC AGC TCT CAC TTA TTC	3.11	1782
TRB2V5-1	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TTG GTC GAT TCT CAG GGC GCC AGT TCT CTA	1.27	1783
TRB2V5-3	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TTA ATC GAT TCT CAG GGC GCC AGT TCC ATG	1.75	1784
TRB2V5-4	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TTC CTA GAT TCT CAG GTC TCC AGT TCC CTA	1.58	1785
TRB2V5-5	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TAA GAG GAA ACT TCC CTG ATC GAT TCT CAG C	0.99	1786
TRB2V5-6	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TGG CAA CTT CCC TGA TCG ATT CTC AGG TCA	0.69	1787
TRB2V5-8	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TGG AAA CTT CCC TCC TAG ATT TTC AGG TCG	3.30	1788
TRB2V6-1	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TGT CCC CAA TGG CTA CAA TGT CTC CAG ATT	1.74	1789
TRB2V6-2/3	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TGC CAA AGG AGA GGT CCC TGA TGG CTA CAA	1.59	1790

Primer Name	Primer Sequence	Adjusted Relative Primer Molar Ratio	SEQ ID NO:
TRB2V6-4	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TGT CCC TGA TGG TTA TAG TGT CTC CAG AGC	1.48	1791
TRB2V6-5	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TAA GGA GAA GTC CCC AAT GGC TAC AAT GTC	0.45	1792
TRB2V6-6	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TGA CAA AGG AGA AGT CCC GAA TGG CTA CAA C	0.41	1793
TRB2V6-7	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TGT TCC CAA TGG CTA CAA TGT CTC CAG ATC	2.23	1794
TRB2V6-8	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TCT CTA GAT TAA ACA CAG AGG ATT TCC CAC	1.18	1795
TRB2V6-9	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TAA GGA GAA GTC CCC GAT GGC TAC AAT GTA	0.96	1796
TRB2V7-1	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TTC CCC GTG ATC GGT TCT CTG CAC AGA GGT	0.85	1797
TRB2V7-2	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TAG TGA TCG CTT CTC TGC AGA GAG GAC TGG	0.64	1798
TRB2V7-3	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TGG CTG CCC AAC GAT CGG TTC TTT GCA GT	0.84	1799

Primer Name	Primer Sequence	Adjusted Relative Primer Molar Ratio	SEQ ID NO:
TRB2V7-4	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TGG CGG CCC AGT GGT CGG TTC TCT GCA GAG	0.48	1800
TRB2V7-6/7	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TAT GAT CGG TTC TCT GCA GAG AGG CCT GAG G	1.01	1801
TRB2V7-8	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TGC TGC CCA GTG ATC GCT TCT TTG CAG AAA	1.57	1802
TRB2V7-9	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TGG TTC TCT GCA GAG AGG CCT AAG GGA TCT	0.49	1803
TRB2V9	CAA GCA GAA GAC GGC ATA CGA GCT CTT CCG ATC TGT TCC CTG ACT TGC ACT CTG AAC TAA AC	3.46	1804

Table 7: Barcode sequences used to identify TCRB V Regions in SEQ ID NOS:872-1560

TCRBV region name of 8 bp barcode	Nucleotide Sequence	SEQ ID NO
TCRBV2_8bpBC	CAAGGTCA	SEQ ID NO: 6375
TCRBV3-1_8bpBC	TACGTACG	SEQ ID NO: 6376
TCRBV4-1_8bpBC	TACGCGTT	SEQ ID NO: 6377
TCRBV4-2_8bpBC	CTCAGTGA	SEQ ID NO: 6378
TCRBV4-3_8bpBC	GTGTCTAC	SEQ ID NO: 6379
TCRBV5-1_8bpBC	AGTACCGA	SEQ ID NO: 6380
TCRBV5-3_8bpBC	TTGCCTCA	SEQ ID NO: 6381
TCRBV5-4_8bpBC	TCGTTAGC	SEQ ID NO: 6382

TCRBV region name of 8 bp barcode	Nucleotide Sequence	SEQ ID NO
TCRBV5-5_8bpBC	TGGACATG	SEQ ID NO: 6383
TCRBV5-6_8bpBC	AGGTTGCT	SEQ ID NO: 6384
TCRBV5-7_8bpBC	GTACAGTG	SEQ ID NO: 6385
TCRBV5-8_8bpBC	ATCCATGG	SEQ ID NO: 6386
TCRBV6-1_8bpBC	TGATGCGA	SEQ ID NO: 6387
TCRBV6-2_8bpBC	GTAGCAGT	SEQ ID NO: 6388
TCRBV6-3_8bpBC	GGATCATC	SEQ ID NO: 6389
TCRBV6-4_8bpBC	GTGAACGT	SEQ ID NO: 6390
TCRBV6-5_8bpBC	TGTCATCG	SEQ ID NO: 6391
TCRBV6-6_8bpBC	AGGCTTGA	SEQ ID NO: 6392
TCRBV6-7_8bpBC	ACACACGT	SEQ ID NO: 6393
TCRBV6-8_8bpBC	TCCACAGT	SEQ ID NO: 6394
TCRBV6-9_8bpBC	CAGTCTGT	SEQ ID NO: 6395
TCRBV7-1_8bpBC	TCCATGTG	SEQ ID NO: 6396
TCRBV7-2_8bpBC	TCACTGCA	SEQ ID NO: 6397
TCRBV7-3_8bpBC	CAAGTCAC	SEQ ID NO: 6398
TCRBV7-4_8bpBC	TAGACGGA	SEQ ID NO: 6399
TCRBV7-6_8bpBC	GAGCGATA	SEQ ID NO: 6400
TCRBV7-7_8bpBC	CTCGAGAA	SEQ ID NO: 6401
TCRBV7-8_8bpBC	ATGACACC	SEQ ID NO: 6402
TCRBV7-9_8bpBC	CTTCACGA	SEQ ID NO: 6403
TCRBV9_8bpBC	CGTAGAGT	SEQ ID NO: 6404
TCRBV10-1_8bpBC	TCGTCGAT	SEQ ID NO: 6405
TCRBV10-2_8bpBC	AGCTAGTG	SEQ ID NO: 6406
TCRBV10-3_8bpBC	TGAGACCT	SEQ ID NO: 6407
TCRBV11-1_8bpBC	GATGGCTT	SEQ ID NO: 6408
TCRBV11-2_8bpBC	GCATCTGA	SEQ ID NO: 6409
TCRBV11-3_8bpBC	GACACTCT	SEQ ID NO: 6410
TCRBV12-3_8bpBC	TGCTACAC	SEQ ID NO: 6411
TCRBV12-4_8bpBC	TCAGCTTG	SEQ ID NO: 6412

TCRBV region name of 8 bp barcode	Nucleotide Sequence	SEQ ID NO
TCRBV12-5_8bpBC	TTCGGAAC	SEQ ID NO: 6413
TCRBV13_8bpBC	GCAATTCG	SEQ ID NO: 6414
TCRBV14_8bpBC	CAAGAGGT	SEQ ID NO: 6415
TCRBV15_8bpBC	GAATGGAC	SEQ ID NO: 6416
TCRBV16_8bpBC	AACTGCCA	SEQ ID NO: 6417
TCRBV17p_8bpBC	CCTAGTAG	SEQ ID NO: 6418
TCRBV18_8bpBC	CTGACGTT	SEQ ID NO: 6419
TCRBV19_8bpBC	TGCAGACA	SEQ ID NO: 6420
TCRBV20-1_8bpBC	AGTTGACC	SEQ ID NO: 6421
TCRBV24-1_8bpBC	GTCTCCTA	SEQ ID NO: 6422
TCRBV25-1_8bpBC	CTGCAATC	SEQ ID NO: 6423
TCRBV27-1_8bpBC	TGAGCGAA	SEQ ID NO: 6424
TCRBV28_8bpBC	TTGGACTG	SEQ ID NO: 6425
TCRBV29-1_8bpBC	AGCAATCC	SEQ ID NO: 6426
TCRBV30_8bpBC	CGAACTAC	SEQ ID NO: 6427

[00257] Using the data that were obtained to generate Fig. 2, as described above, the cross-amplification capability (ability to amplify a V gene segment other than the one for which the primer was specifically designed on the basis of annealing sequence complementarity) was assessed for each amplification primer that had been designed to anneal to a specific V gene segment. 52 independent amplification primer pools were prepared, where each primer pool had 51 of the 52 TCRB V region primers of Table 6 pooled at equimolar concentrations, and the 52nd TCRB V region primer present in the pool at twice the molar concentration of the other 51 primers. A separate amplification primer pool was prepared so that there was one pool for each of the 52 V primers in which a single primer was present at twice the concentration of the other primers, resulting in 52 unique primer pools. 52 separate amplification reactions were then set up, one for each of the unique amplification primer pools, with each reaction using the set of 689 template oligonucleotides (SEQ ID NOS:872-1560) described above. Template oligonucleotides were present at equimolar concentration relative to one another. Amplification and sequencing were conducted using the conditions described above. The results are shown in Fig. 3.

[00258] In Fig. 3, black squares indicated no change in the degree of amplification with the respective indicated TCRB V region-specific primer present at twice the concentration relative to equimolar concentrations of all other primers; white squares indicated a 10-fold increase in amplification; grey squares indicated intermediate degrees (on a greyscale gradient) of amplification between zero and 10-fold. The diagonal line indicated that doubling the molar concentration for a given primer resulted in about a 10-fold increase in the amplification of the respective template oligonucleotide having the specific annealing target sequence, in the case of most of the TCRB V regions primers that were tested. The off-diagonal white squares indicated non-corresponding templates to which certain primers were able to anneal and amplify.

[00259] Where one or more primers exhibited amplification potential that was significantly greater or lower than an acceptable range of amplification potential (*e.g.*, a designated uniform amplification potential range), further adjustment of the concentrations of individual primer oligonucleotides and reiteration of the template amplification and quantitative sequencing steps were conducted, until each species of product molecule was present within a desired range that was indicative of correction of the non-uniform amplification potential among the primers within an amplification primer set.

[00260] Accordingly, primer concentrations were adjusted as indicated in Table 6, in order to determine whether biased amplification results that were apparent in Figs. 2 and 3 could be reduced in severity by increasing or decreasing the relative presence of, respectively, highly efficient or poorly efficient amplification primers. For multiplexed PCR using an adjusted primer set, the V gene primer sequences remained the same (sequence reported in table 6), however the relative concentration of each primer was either increased, if the primer under-amplified its template (Fig. 3), or decreased if the primer over-amplified its template (Fig. 3). The adjusted mixture of amplification primers was then used in a PCR to amplify the template composition containing, in equimolar amounts, the set of 689 template oligonucleotides (SEQ ID NOS:872-1560) that were used to generate the data in Figs. 2 and 3.

[00261] Amplification and quantitative sequencing were performed as described above and the results are shown in Fig. 4, which compares the frequency at which each indicated amplified V region sequence-containing product was obtained when all amplification primers were present at equimolar concentrations (black bars) to the frequency at which each such

product was obtained after the concentrations of the amplification primers were adjusted (grey bars) to the concentrations as indicated in Table 6.

[00262] Additional hs-TCRB primer sequences are found at SEQ ID NOs. 6192-6264.

**EXAMPLE 3: CORRECTING NON-UNIFORM AMPLIFICATION
POTENTIAL (PCR BIAS) IN TCR-AMPLIFYING OLIGONUCLEOTIDE
PRIMER SETS**

[00263] Diverse TCR amplification primers are designed to amplify every possible combination of rearranged TCR V and J gene segments in a biological sample that contains lymphoid cell DNA from a subject. A preparation containing equimolar concentrations of the diverse amplification primers is used in multiplexed PCR to amplify a diverse template composition that comprises equimolar concentrations of TCR-specific template oligonucleotides according to formula (I) with at least one template representing every possible V-J combination for the TCR locus. The amplification products are quantitatively sequenced and the frequency of occurrence of each unique V-J product sequence is obtained from the frequency of occurrence of each 16 bp molecular barcode sequence (B in formula (I)) that uniquely identifies each V-J combination.

[00264] For TCRG, the TCRG template oligonucleotides (SEQ ID NOS:1561-1630) are amplified using TCRG V- and J-specific primers (SEQ ID NOS:1732-1745, Table 4). J primer independence of respectively paired V primers is identified by separately amplifying each of the eight TCRG V gene segment specific primers with a pool of the five J gene segment specific primers. The amplification products are quantitatively sequenced on an Illumina HiSeq™ sequencing platform and the frequency of occurrence of the internal 16 bp barcode sequences (B) that uniquely identify specific V-J combinations permit quantification of each V-J pair. V primer independence of respectively paired J primers is identified by performing the inverse reaction, *i.e.*, by separately amplifying each of the five TCRG J gene segment primers with a pool of the eight V gene segment specific primers.

[00265] To test if TCRG V primers or J primers cross-amplify (*e.g.*, whether gene segment specific primers amplify non-specifically, for instance, to test if the V primer specifically designed to amplify TCRG V7 segments is able to amplify both TCRG V6 and TCRG V7 V gene segments), independent primer pools are generated that contain equimolar concentrations of all but one of the primers, and the omitted primer is then added to the pool at twice the molar concentration of all other primers. The primers are then used to amplify a

template composition that comprises a plurality of template oligonucleotides of general formula (I) as described herein, using TCRG V and J gene sequences in, respectively, the V and J polynucleotides of formula (I). Quantitative sequencing reveals the identities of any one or more templates that are overrepresented among the amplification products when a single amplification primer is present at twice the concentration of all other primers in the pool of primers. The primer mixture is then adjusted to increase or decrease the relative concentrations of one or more primers, to obtain amplification frequencies in iterative rounds that are within acceptable quantitative tolerances. The adjusted primer mixture so obtained is regarded as having been corrected to reduce non-uniform amplification potential among the members of the primer set.

[00266] To determine whether a corrected primer mixture exhibits unbiased amplification potential when used to amplify rearranged TCR template DNA in a biological sample from lymphoid cells of a subject, the artificial template compositions as described herein are prepared with all VJ pairs present at similar frequency, and also with varying ratios of the relative representation of certain VJ pairs. Each type of template preparation is separately tested as an amplification template for an amplification primer set that has been corrected to reduce non-uniform amplification potential among certain members of the primer set.

Quantitative sequence determination of amplification products identifies that the relative quantitative representation of specific sequences in the template preparation is reflected in the relative quantitative representation of specific sequences among the amplification products.

[00267] As an alternative to the iterative process described above, or in addition to such iterative amplification steps followed by quantitative sequencing, amplification bias can also be corrected computationally. According to this computational approach, the starting frequency of each of the species of template oligonucleotide sequences in the synthesized template composition is known. The frequency of each of these species of oligonucleotide sequences among the amplification products that are obtained following PCR amplification is determined by quantitative sequencing. The difference between the relative frequencies of the template oligonucleotide sequences prior to PCR amplification and their frequencies following PCR amplification is the "PCR bias." This difference is the amplification bias introduced during amplification, for example, as a consequence of different amplification efficiencies among the various amplification primers.

[00268] As quantitatively determined for each known template oligonucleotide sequence, the PCR bias for each primer is used to calculate an amplification bias (normalization) factor

by which the observed frequency for each amplification product is corrected to reflect the actual frequency of the respective template sequence in the template composition. If PCR bias for an amplification primer set is empirically detected using the present template composition as being within a factor of 10, then the bias can be computationally corrected in amplification products obtained when the same amplification primer set is used to amplify a DNA sample of unknown composition. Improved accuracy in the quantification of template species in the DNA sample is thereby obtained.

[00269] Because V and J primers are empirically tested and shown to be independent, an amplification bias factor can be derived for each V species and for each J species, and an amplification factor for each VJ species pair is not necessary. Accordingly, the amplification bias factor for each V species and J species is derived using the present template composition. By the present method, the frequencies of the V and J gene sequences in the template composition are known (or can be calculated based on knowledge of the concentrations of each template oligonucleotide species in the template composition as synthesized) prior to PCR amplification. After PCR amplification, quantitative sequencing is used to detect the frequency of each V and J gene segment sequence in the amplification products. For each sequence, the difference in gene segment frequency is the amplification bias:

[00270] Initial Frequency /final frequency = amplification bias factor

[00271] Amplification bias factors are calculated for every V gene segment and every J gene segment. These amplification factors, once calculated, can be applied to samples for which the starting frequency of V and J genes is unknown.

[00272] In a mixed template population (such as a complex DNA sample obtained from a biological source that comprises DNA from lymphoid cells that are presumed to contain rearranged adaptive immune receptor encoding DNA, or a complex DNA sample which additionally comprises DNA from other cells lacking such rearrangements), where the starting frequency of each V and J gene segment is unknown, the calculated amplification factors for a primer set that has been characterized using the present template composition can be used to correct for residual PCR amplification bias. For each species of sequenced amplification product molecule, the V and J genes that are used by the molecule are determined based on sequence similarity. To correct for amplification bias, the number of times the molecule was sequenced is multiplied by both the correct V and J amplification factors. The resulting sequence count is the computationally “normalized” set.

EXAMPLE 4: GENERATION OF ADDITIONAL TEMPLATE COMPOSITIONS

[00273] Additional template compositions were designed and produced essentially according to the methodologies described above.

[00274] V and J Polynucleotides. TCRB V and J polynucleotide sequences were generated for inclusion in the herein described plurality of template oligonucleotides and are set forth in sets of 68 TCRB V and J SEQ ID NOS, respectively, as shown in Figs. 5a-5l as TCRB V/J set 1, TCRB V/J set 2, TCRB V/J set 3, TCRB V/J set 4, TCRB V/J set 5, TCRB V/J set 6, TCRB V/J set 7, TCRB V/J set 8, TCRB V/J set 9, TCRB V/J set 10, TCRB V/J set 11, TCRB V/J set 12 and TCRB V/J set 13.

[00275] TCRG V and J polynucleotide sequences were generated for inclusion in the herein described plurality of template oligonucleotides and are set forth in sets of 14 TCRG V and J SEQ ID NOS, respectively, as set forth in Figs. 6a-6b as TCRG V/J set 1, TCRG V/J set 2, TCRG V/J set 3, TCRG V/J set 4 and TCRG V/J set 5.

[00276] IGH V and J polynucleotide sequences were generated for inclusion in the herein described plurality of template oligonucleotides and are set forth in sets of 127 IGH V and J SEQ ID NOS, respectively, as set forth in Figs. 7a-7m as IGH V/J set 1, IGH V/J set 2, IGH V/J set 3, IGH V/J set 4, IGH V/J set 5, IGH V/J set 6, IGH V/J set 7, IGH V/J set 8 and IGH V/J set 9.

[00277] Template Compositions. A template composition was prepared for standardizing the amplification efficiency of TCRB amplification primer sets. The composition comprised a plurality of template oligonucleotides having a plurality of oligonucleotide sequences of general formula (I). The TCRB template composition comprising 858 distinct template oligonucleotides is disclosed in the Sequence Listing in SEQ ID NOS:3157-4014.

[00278] A template composition was prepared for standardizing the amplification efficiency of TCRG amplification primer sets. The composition comprised a plurality of template oligonucleotides having a plurality of oligonucleotide sequences of general formula (I). The TCRG template composition comprising 70 distinct template oligonucleotides is disclosed in the Sequence Listing in SEQ ID NOS:4015-4084.

[00279] A template composition was prepared for standardizing the amplification efficiency of IGH amplification primer sets. The composition comprised a plurality of template oligonucleotides having a plurality of oligonucleotide sequences of general formula (I). The IGH template composition comprising 1116 distinct template oligonucleotides is

disclosed in the Sequence Listing in SEQ ID NOS:4085-5200. An IGH template composition comprising a set of 1116 template oligonucleotides is also disclosed in the Sequence Listing in SEQ ID NOS:1805-2920.

**EXAMPLE 5: USE OF THE TEMPLATE COMPOSITION TO DETERMINE
AMPLIFICATION FACTOR**

[00280] This example describes quantification of rearranged DNA molecules encoding a plurality of IG molecules, using the presently described template oligonucleotide composition as a “spiked-in” synthetic template in a multiplexed PCR amplification of a DNA sample containing B cell and fibroblast DNA.

[00281] Biological Template DNA: Eight biological samples were used as sources of template DNA, with each biological sample containing the same amount of total genomic DNA (gDNA), 300ng, but in a different proportion of (i) DNA extracted from B cells to (ii) DNA extracted from human fibroblast cells, a cell type in which IG and TCR encoding genes do not rearrange. The samples contained 0, 0.07, 0.3, 1, 4, 18, 75 or 300 ng B cell gDNA, with fibroblast gDNA supplying the balance of each 300 ng gDNA preparation. Four replicates of each sample were made.

[00282] Synthetic Template DNA: To each PCR reaction (below) were added 5000 molecules (4-5 molecules of each sequence) from an oligonucleotide template composition comprising a pool of 1116 synthetic IGH template oligonucleotide molecules (SEQ ID NOS:4085-5200). An IGH template composition comprising a set of 1116 template oligonucleotides is also disclosed in the Sequence Listing as SEQ ID NOS:1805-2920.

[00283] PCR Reaction: The PCR reaction used QIAGEN Multiplex Plus™ PCR master mix (QIAGEN part number 206152, Qiagen, Valencia, CA), 10% Q- solution (QIAGEN), and 300 ng of biological template DNA (described above). The pooled amplification primers were added so the final reaction had an aggregate forward primer concentration of 2 μ M and an aggregate reverse primer concentration of 2 μ M. The forward primers (SEQ ID NOS:5201-5286) included 86 primers that had at the 3' end an approximately 20 bp segment that annealed to the IGH V segment encoding sequence and at the 5' end an approximately 20 bp universal primer pGEXf. The reverse primers (SEQ ID NOS:5287-5293) included an aggregate of J segment specific primers that at the 3' end had an approximately 20 bp segment that annealed to the IGH J segment encoding sequence and at the 5' end of the J primers was a universal primer pGEXr. The following thermal cycling conditions were used in a C100 thermal cycler (Bio-Rad Laboratories, Hercules, CA, USA): one cycle at 95°C for

10 minutes, 30 cycles at 94°C for 30 seconds, 63°C for 30 seconds, and 72°C for one minute, followed by one cycle at 72°C for 10 minutes. Each reaction was run in quadruplicates.

[00284] For sequencing, Illumina adapters (Illumina Inc., San Diego, CA), which also included a 8 bp tag and a 6bp random set of nucleotides, were incorporated onto the ends of the PCR reaction products in a 7 cycle PCR reaction. The PCR reagents and conditions were as described above, except for the thermocycle conditions, which were: 95° C for 5 minutes, followed by 7 cycles of 95° for 30 sec, 68° for 90 sec, and 72° for 30 sec. Following thermal cycling, the reactions were held for 10 minutes at 72° and the primers were the Illumina adaptor tailing primers (SEQ ID NOS:5387-5578). Samples were sequenced on an Illumina MiSEQ™ sequencer using the Illumina_PE_RD2 primer.

[00285] Results: Sequence data were obtained for each sample and amplification products of synthetic templates were identified by the presence of the barcode oligonucleotide sequence. For each sample, the number of template products was divided by the number of unique synthetic template oligonucleotide sequences (1116) to arrive at a sample amplification factor. The total number of amplification products of the biological templates for each sample was then divided by the amplification factor to calculate the number of rearranged biological template molecules (*e.g.*, VDJ recombinations) in the starting amplification reaction as an estimate of the number of unique B cell genome templates. The average values with standard deviations were plotted against the known number of rearranged biological template molecules based on B cell input (Fig. 9). In Fig. 9, the dots represent the average amplification factor and the bars represent the standard deviation across the four replicates. The use of amplification factors calculated as described herein to estimate the number of VJ-rearranged IG encoding molecules (as a proxy value for the number of B cells) yielded determinations that were consistent with known B cell numbers at least down to an input of 100 B cells. The estimated amplification factor values and the observed amplification factor were highly correlated (Fig. 9, $R^2 = 0.9988$).

EXAMPLE 6: IgH, IgL, and IgK BIAS CONTROL TEMPLATES

IgH VJ Template Oligonucleotides

[00286] In one embodiment, IgH VJ template oligonucleotides were generated and analyzed. A set of 1134 template oligonucleotides of general formula (I) was designed using human IgH V and J polynucleotide sequences. Each template oligonucleotide consisted of a 495 base pair DNA molecule. Details for the 1134-oligonucleotide set of IgH templates are representative and were as follows.

[00287] Based on previously determined genomic sequences, the human IgH locus was shown to contain 126 Vh segments that each had a RSS sequence and were therefore regarded as rearrangement-competent. These 126 Vh segments included 52 gene segments known to be expressed, five V segments that were classified as having open reading frames, and 69 V pseudogenes. The Vh gene segments were linked to 9 Jh gene segments. In order to include all possible V+J gene combinations for the 126 V and 9 J segments, 1134 (9 x 126) templates were designed that represented all possible VJ combinations. Each template conformed to the general formula (I) (5'-U1-B1-V-B2-R-J-B4-U2-3')(Fig. 1) and thus included nine sections, a 19 base pair (bp) universal adapter (U1), a 16 bp nucleotide tag uniquely identifying each paired combination of V gene and J gene segments (B1), 300 bp of V gene specific sequence (V), a 3 bp stop codon (S), another copy of the 16 bp nucleotide tag (B2), a 6 bp junction tag shared by all molecules (R), nothing for B3, 100 bp of J gene specific sequence (J), a third copy of the 16 bp nucleotide tag (B4), and a 19 bp universal adapter sequence (U2). Two V segments were nucleotide identical to another two V segments – and thus were not ordered. This reduced the number of included segments from 1134 to 1116. The IGH template composition comprising 1116 distinct template oligonucleotides is disclosed in the Sequence Listing in SEQ ID NOS:4085-5200.

[00288] Each of the 1116 templates was amplified individually using oligonucleotide primers designed to anneal to the universal adapter sequences (U1, U2). These oligonucleotide sequences can be any universal primer. For this application a universal primer coded Nextera was used.

Table 8: Universal Primer sequences included in bias control templates

Primer Name	Primer Sequence	SEQ ID NO
pGEXF	GGGCTGGCAAGCCACGTTTGGTG	SEQ ID NO: 6428
pGEXR	CCGGGAGCTGCATGTGTCAGAGG	SEQ ID NO: 6429

[00289] The universal primer sequences can be annealed to any primer sequence disclosed herein. An example of the PCR primers including the universal primer sequence are shown below:

Table 9: Example IGH PCR primers with Universal Sequences (Bold and Underlined)

Primer Name	Primer Sequence	SEQ ID NO
pGEXf_IGHV(II)-	<u>GGGCTGGCAAGCCACGTTTGGTG</u> AGCCCCCAGGGAAGAAGCT	SEQ ID

15-1_ver10_01	GAAGTGG	NO:6430
pGEXr_IGHJ1/4/5_ ver10_03	<u>CCGGGAGCTGCATGTGTCAGAGG</u> CACCTGAGGAGACGGTGAC CAGGGT	SEQ ID NO: 6431

[00290] The resulting concentration of each amplified template oligonucleotide product was quantified using a LabChip GX™ capillary electrophoresis system (Caliper Life Sciences, Inc., Hopkinton, MA) according to the manufacturer's instructions. The 1116 amplified template oligonucleotide preparations were normalized to a standard concentration and then pooled.

[00291] To verify that all 1116 template oligonucleotides were present at substantially equimolar concentrations, the pool was sequenced using the Illumina MiSeq™ sequencing platform according to the manufacturer's recommendations. To incorporate platform-specific oligonucleotide sequences into the pooled template oligonucleotides, tailed primers were designed that annealed to the universal priming sites (U1, U2) and that had Illumina™ adapter sequence tails as the 5' ends. A seven-cycle PCR reaction was then performed to anneal the Illumina adapters to the template oligonucleotides. The PCR reaction product mixture was then purified using Agencourt® AMPure® XP beads (Beckman Coulter, Inc., Fullerton, CA) under the conditions recommended by the manufacturer. The first 29 bp of the PCR reaction products were sequenced using an Illumina MiSEQ™ sequencer (Illumina, Inc., San Diego, CA) and analyzed by assessing the frequency of each 16 bp molecular barcode tag (B1).

[00292] A substantially equimolar preparation for the set of 1116 distinct template oligonucleotides was calculated to contain approximately ~0.09% of each member of the set, and a threshold tolerance of plus or minus ten-fold frequency (0.009% - 0.9%) for all species was desired. The quantitative sequencing revealed that the 1116 species of adapter-modified template oligonucleotides within the initial pool were not evenly represented.

[00293] Accordingly, adjustment of the concentrations of individual template oligonucleotides and reiteration of the quantitative sequencing steps are conducted until each molecule is present within the threshold tolerance concentration (0.009 – 0.9 %).

IgH DJ Template Oligonucleotides

[00294] In another embodiment, IgH DJ template oligonucleotides were generated and analyzed. A set of 243 template oligonucleotides of general formula (I) was designed using human IgH D and J polynucleotide sequences. Each template oligonucleotide consisted of a

382 base pair DNA molecule. The IgH DJ template oligonucleotide sequences are presented in SEQ ID NOs: 5579-5821. Details for the 243-oligonucleotide set of IgH templates are representative and were as follows.

[00295] Based on previously determined genomic sequences, the human IgH locus was shown to contain 27 Dh segments. The 27 Dh gene segments were linked to 9 Jh gene segments. To include all possible D+J gene combinations for the 27 D and 9 J segments, 243 (9 x 27) templates were designed that represented all possible DJ combinations. Each template conformed to the general formula (I) (5'-U1-B1-V-B2-R-J-B4-U2-3') (Fig. 1) and thus included nine sections, a 19 base pair (bp) universal adapter (U1), a 16 bp nucleotide tag uniquely identifying each paired combination of D gene and J gene segments (B1). However, for these molecules, the 300 bp of V gene specific sequence (V) was replaced with a segment of 182 bp of D gene specific sequence. This segment included both exonic and intronic nucleotide segments. Like the other molecules, these included a 3 base pair (bp) stop codon (S), another copy of the 16 bp nucleotide tag (B2), a 6 bp junction tag shared by all molecules (R), nothing for B3, 100 bp of J gene specific sequence (J), a third copy of the 16 bp nucleotide tag (B4), and a 19 bp universal adapter sequence (U2).

[00296] Each of the 243 templates (SEQ ID NOs: 5579-5821) was amplified individually using oligonucleotide primers designed to anneal to the universal adapter sequences (U1, U2; See Table 8). These oligonucleotide sequences can be any universal primer; for this application a universal primer coded Nextera was used.

[00297] An example of the PCR primers with the universal adapter sequences are shown in Table 10.

Table 10: Example IgH DJ PCR primers with Universal Sequences (Bold and Underlined)

Primer Name	Primer Sequence	SEQ ID NO
pGEXf_IGHV(I I)-15- 1_ver10_01	<u>GGGCTGGCAAGCCACGTTTGGT</u> GAGCCCCAGGG AAGAAGCTGAAGTGG	SEQ ID NO: 6432
pGEXr_IGHJ1/ 4/5_ver10_03	<u>CCGGGAGCTGCATGTGTCAGAGG</u> CACCTGAGGAG ACGGTGACCAGGGT	SEQ ID NO: 6433

[00298] The resulting concentration of each amplified template oligonucleotide product was quantified using a LabChip GX™ capillary electrophoresis system (Caliper Life

Sciences, Inc., Hopkinton, MA) according to the manufacturer's instructions. The 243 amplified template oligonucleotide preparations were normalized to a standard concentration and then pooled.

[00299] To verify that all 243 template oligonucleotides were present at substantially equimolar concentrations, the pool was sequenced using the Illumina MiSeq™ sequencing platform according to the manufacturer's recommendations. To incorporate platform-specific oligonucleotide sequences into the pooled template oligonucleotides, tailed primers were designed that annealed to the universal priming sites (U1, U2) and that had Illumina™ adapter sequence tails as the 5' ends. A seven-cycle PCR reaction was then performed to anneal the Illumina adapters to the template oligonucleotides. The PCR reaction product mixture was then purified using Agencourt® AMPure® XP beads (Beckman Coulter, Inc., Fullerton, CA) under the conditions recommended by the manufacturer. The first 29 bp of the PCR reaction products were sequenced using an Illumina MiSEQ™ sequencer (Illumina, Inc., San Diego, CA) and analyzed by assessing the frequency of each 16 bp molecular barcode tag (B1).

[00300] A substantially equimolar preparation for the set of 243 distinct template oligonucleotides was calculated to contain approximately ~0.4% of each member of the set, and a threshold tolerance of plus or minus ten-fold frequency (0.04% - 4.0%) for all species was desired. The quantitative sequencing revealed that the 243 species of adapter-modified template oligonucleotides within the initial pool were not evenly represented.

[00301] Accordingly, adjustment of the concentrations of individual template oligonucleotides and reiteration of the quantitative sequencing steps are conducted until each molecule is present within the threshold tolerance concentration (0.04 – 4.0 %). Following normalization, this set was combined with 1116 IgH VJ bias control set for a pool of 1359 templates.

[00302] Fig. 10 shows results for a pre-PCR amplification sequencing count for each of the 1116 IGH VJ bias control molecules and 243 IGH DJ bias control molecules. Individual bias control molecules are along the x-axis. The set includes the 1116 IGH VJ bias control molecules and 243 IGH DJ bias control molecules for a total of 1359 gblocks. The Y axis is the sequence count for each individual gblock. This calculation provides the quantification of the composition of the pre-amplification representation of each VJ pair. This data is used to estimate the change in frequency between the pre-sample and post-PCR amplification sample to calculate the amplification bias introduced by the primers.

IgL VJ Template Oligonucleotides

[00303] In another embodiment, IgL VJ template oligonucleotides were generated and analyzed. A set of 245 template oligonucleotides of general formula (I) was designed using human IgL V and J polynucleotide sequences. Each template oligonucleotide consisted of a 495 base pair DNA molecule. The IgL template oligonucleotides are presented as SEQ ID NOs: 5822-6066. Details for the 245-oligonucleotide set of IgL templates are representative and were as follows.

[00304] Based on previously determined genomic sequences, the human IgL locus was shown to contain 75 VL segments that each had a RSS sequence and were therefore regarded as rearrangement-competent. These 33 VL segments included gene segments known to be expressed, 5 V segments that were classified as having open reading frames, and 37 V pseudogenes. The VL gene segments were linked to five 6 JL gene segments. To include all possible functional and expressed V+J gene combinations for the 33 functional V and 6 J segments, 204 (6 x 33) templates were designed that represented all possible expressed VJ combinations. In addition, two of the V pseudogenes were questionable; an additional 12 (2 x 6) VJ templates were designed, resulting in a total of 216. Each template conformed to the general formula (I) (5'-U1-B1-V-B2-R-J-B4-U2-3') (Fig. 1) and thus included nine sections, a 19 base pair (bp) universal adapter (U1), a 16 bp nucleotide tag uniquely identifying each paired combination of V gene and J gene segments (B1), 300 bp of V gene specific sequence (V), a 3 bp stop codon (S), another copy of the 16 bp nucleotide tag (B2), a 6 bp junction tag shared by all molecules (R), nothing for B3, 100 bp of J gene specific sequence (J), a third copy of the 16 bp nucleotide tag (B4), and a 19 bp universal adapter sequence (U2).

[00305] Each of the 216 templates was amplified individually using oligonucleotide primers designed to anneal to the universal adapter sequences (U1, U2). These oligonucleotide sequences can be any universal primer; for this application, a universal primer coded Nextera was used.

[00306] The resulting concentration of each amplified template oligonucleotide product was quantified using a LabChip GX™ capillary electrophoresis system (Caliper Life Sciences, Inc., Hopkinton, MA) according to the manufacturer's instructions. The 216 amplified template oligonucleotide preparations were normalized to a standard concentration and then pooled.

[00307] To verify that all 216 template oligonucleotides were present at substantially equimolar concentrations, the pool was sequenced using the Illumina MiSeq™ sequencing

platform according to the manufacturer's recommendations. To incorporate platform-specific oligonucleotide sequences into the pooled template oligonucleotides, tailed primers were designed that annealed to the universal priming sites (U1, U2) and that had Illumina™ adapter sequence tails as the 5' ends. A seven-cycle PCR reaction was then performed to anneal the Illumina adapters to the template oligonucleotides. The PCR reaction product mixture was then purified using Agencourt® AMPure® XP beads (Beckman Coulter, Inc., Fullerton, CA) under the conditions recommended by the manufacturer. The first 29 bp of the PCR reaction products were sequenced using an Illumina MiSEQ™ sequencer (Illumina, Inc., San Diego, CA) and analyzed by assessing the frequency of each 16 bp molecular barcode tag (B1).

[00308] A substantially equimolar preparation for the set of 216 distinct template oligonucleotides was calculated to contain approximately ~0.46% of each member of the set, and a threshold tolerance of plus or minus ten-fold frequency (0.046% - 4.6%) for all species was desired. The quantitative sequencing revealed that the 216 species of adapter-modified template oligonucleotides within the initial pool evenly represented.

IgK VJ Template Oligonucleotides

[00309] In one embodiment, IgK VJ template oligonucleotides were generated and analyzed. A set of 560 template oligonucleotides of general formula (I) was designed using human IgK V and J polynucleotide sequences. Each template oligonucleotide consisted of a 495 base pair DNA molecule. Examples of IgK template oligonucleotides are found at SEQ ID NOs: 6067-6191. Details for the 560-oligonucleotide set of IgK templates are representative and were as follows.

[00310] Based on previously determined genomic sequences, the human IgK locus was shown to contain 112 Vk segments that each had a RSS sequence and were therefore regarded as rearrangement-competent. These 112 Vk segments included 46 gene segments known to be expressed, 8 V segments that were classified as having open reading frames, and 50 V pseudogenes. For this IgK, only expressed IgK VJ rearrangements were analyzed. Genes classified as pseudogenes and open reading frames were excluded. The Vk gene segments were linked to five Jk gene segments. This left us with 230 VJ gene rearrangements (46 x 5). To include all possible functional V+J gene combinations for the 46 functional V and 5 J segments, 230 (5 x 46) templates were designed that represented all possible VJ combinations. Each template conformed to the general formula (I) (5'-U1-B1-V-B2-R-J-B4-U2-3') (Fig. 1) and thus included nine sections, a 19 base pair (bp) universal

adapter (U1), a 16 bp nucleotide tag uniquely identifying each paired combination of V gene and J gene segments (B1), 300 bp of V gene specific sequence (V), a 3 bp stop codon (S), another copy of the 16 bp nucleotide tag (B2), a 6 bp junction tag shared by all molecules (R), nothing for B3, 100 bp of J gene specific sequence (J), a third copy of the 16 bp nucleotide tag (B4), and a 19 bp universal adapter sequence (U2).

[00311] Each of the 230 templates was amplified individually using oligonucleotide primers designed to anneal to the universal adapter sequences (U1, U2). These oligonucleotide sequences can be any universal primer – for this application a universal primer coded Nextera was used.

[00312] The resulting concentration of each amplified template oligonucleotide product was quantified using a LabChip GX™ capillary electrophoresis system (Caliper Life Sciences, Inc., Hopkinton, MA) according to the manufacturer's instructions. The 230 amplified template oligonucleotide preparations were normalized to a standard concentration and then pooled.

[00313] To verify that all 230 template oligonucleotides were present at substantially equimolar concentrations, the pool was sequenced using the Illumina MiSeq™ sequencing platform according to the manufacturer's recommendations. Briefly, to incorporate platform-specific oligonucleotide sequences into the pooled template oligonucleotides, tailed primers were designed that annealed to the universal priming sites (U1, U2) and that had Illumina™ adapter sequence tails as the 5' ends. A seven-cycle PCR reaction was then performed to anneal the Illumina adapters to the template oligonucleotides. The PCR reaction product mixture was then purified using Agencourt® AMPure® XP beads (Beckman Coulter, Inc., Fullerton, CA) under the conditions recommended by the manufacturer. The first 29 bp of the PCR reaction products were sequenced using an Illumina MiSEQ™ sequencer (Illumina, Inc., San Diego, CA) and analyzed by assessing the frequency of each 16 bp molecular barcode tag (B1).

[00314] A substantially equimolar preparation for the set of 230 distinct template oligonucleotides was calculated to contain approximately ~0.4% of each member of the set, and a threshold tolerance of plus or minus ten-fold frequency (4.0% - 0.04%) for all species was desired. The quantitative sequencing revealed that the 230 species of adapter-modified template oligonucleotides within the initial pool were evenly represented.

EXAMPLE 7: COMBINED ASSAYS

IgH DJ and IgH VJ Combined Assay

[00315] In some embodiments, it is desired to co-amplify and sequence rearranged IgH VDJ CDR3 chains and rearranged IgH DJ chains. To generate a pool of templates to test a combined IgH DJ and IgH VJ assay using the IgH DJ and IgH VJ templates. When pooled—, the final pool includes 1116 VJ and 243 DJ templates, resulting in a total of 1359 individual templates. The IgH VJ template composition comprising 1116 distinct template oligonucleotides is disclosed in the Sequence Listing in SEQ ID NOs: 4085-5200. The IgH DJ template oligonucleotide sequences are presented in SEQ ID NOs: 5579-5821.

[00316] To verify that all 1359 template oligonucleotides were present at substantially equimolar concentrations, the pool was sequenced using the Illumina MiSeq™ sequencing platform according to the manufacturer's recommendations. To incorporate platform-specific oligonucleotide sequences into the pooled template oligonucleotides, tailed primers were designed that annealed to the universal priming sites (U1, U2) and that had Illumina™ adapter sequence tails as the 5' ends. A seven-cycle PCR reaction was then performed to anneal the Illumina adapters to the template oligonucleotides. The PCR reaction product mixture was then purified using Agencourt® AMPure® XP beads (Beckman Coulter, Inc., Fullerton, CA) under the conditions recommended by the manufacturer. The first 29 bp of the PCR reaction products were sequenced using an Illumina MiSEQ™ sequencer (Illumina, Inc., San Diego, CA) and analyzed by assessing the frequency of each 16 bp molecular barcode tag (B1).

[00317] A substantially equimolar preparation for the set of 1359 distinct template oligonucleotides was calculated to contain approximately ~0.073% of each member of the set, and a threshold tolerance of plus or minus ten-fold frequency (0.73% - 0.0073%) for all species was desired. The quantitative sequencing revealed that the 1359 species of adapter-modified template oligonucleotides within the initial pool were evenly represented.

IgL and IgK Combined Assay

[00318] In other embodiments, it is desired to co-amplify and sequence rearranged IgL and IgK rearranged CDR3 chains. To generate a pool of templates to test a combined IgL and IgK assay (the IgL and IgK templates were combined). When pooled, the final pool includes 216 IgL and 230 IgK templates, for a total of 446 individual templates. The IgL template oligonucleotides are presented as SEQ ID NOs: 5822-6066.

[00319] To verify that all 446 template oligonucleotides were present at substantially equimolar concentrations, the pool was sequenced using the Illumina MiSeq™ sequencing platform according to the manufacturer's recommendations. Briefly, to incorporate platform-specific oligonucleotide sequences into the pooled template oligonucleotides, tailed primers were designed that annealed to the universal priming sites (U1, U2) and that had Illumina™ adapter sequence tails as the 5' ends. A seven-cycle PCR reaction was then performed to anneal the Illumina adapters to the template oligonucleotides. The PCR reaction product mixture was then purified using Agencourt® AMPure® XP beads (Beckman Coulter, Inc., Fullerton, CA) under the conditions recommended by the manufacturer. The first 29 bp of the PCR reaction products were sequenced using an Illumina MiSeq™ sequencer (Illumina, Inc., San Diego, CA) and analyzed by assessing the frequency of each 16 bp molecular barcode tag (B1).

[00320] A substantially equimolar preparation for the set of 446 distinct template oligonucleotides was calculated to contain approximately ~0.22% of each member of the set, and a threshold tolerance of plus or minus ten-fold frequency (2.2% - 0.022%) for all species was desired. The quantitative sequencing revealed that the 446 species of adapter-modified template oligonucleotides within the initial pool were evenly represented.

**EXAMPLE 8: CORRECTING NON-UNIFORM AMPLIFICATION
POTENTIAL (PCR BIAS) IN IGH-AMPLIFYING OLIGONUCLEOTIDE
PRIMER SETS**

[00321] Diverse IgH amplification primers were designed to amplify every possible combination of rearranged IgH V and J gene segments in a biological sample that contains lymphoid cell DNA from a subject. A preparation containing equimolar concentrations of the diverse amplification primers was used in multiplexed PCR to amplify a diverse template composition that comprises equimolar concentrations of IgH-specific template oligonucleotides according to formula (I) with at least one template representing every possible V-J combination for the IgH locus. The amplification products were quantitatively sequenced and the frequency of occurrence of each unique V-J product sequence was obtained from the frequency of occurrence of each 16 bp molecular barcode sequence (B in formula (I)) that uniquely identified each V-J combination.

[00322] The multiplex PCR reaction was designed to amplify all possible V and J gene rearrangements of the *IgH* locus, as annotated by the IMGT collaboration. See Yousfi Monod M, Giudicelli V, Chaume D, Lefranc. MP. IMGT/JunctionAnalysis: the first tool for

the analysis of the immunoglobulin and T cell receptor complex V-J and V-D-J JUNCTIONS. *Bioinformatics*. 2004;20(suppl 1):i379-i385. The locus included 126 unique V genes; 52 functional genes, 6 putative open reading frames lacking critical amino acids for function and 69 pseudogenes; and 9 J genes, 6 functional and 3 pseudogenes. The target sequence for primer annealing was identical for some V segments, allowing amplification of all 126 V segments with 86 unique forward primers. Similarly, 7 unique reverse primers annealed to all 9 J genes. As a baseline for bias assessment, the pool of 1116 templates was amplified using an equimolar pool of the 86 V forward primers (VF; specific to V genes) and an equimolar pool of the 7 J reverse primers (JR; specific to J genes).

[00323] Polymerase chain reactions (PCR) (25 μ L each) were set up at 2.0 μ M VF, 2.0 μ M JR pool (Integrated DNA Technologies), 1 μ M QIAGEN Multiplex Plus PCR master mix (QIAGEN, Valencia, CA), 10% Q- solution (QIAGEN), and 200,000 target molecules from our synthetic IgH repertoire mix. The following thermal cycling conditions were used in a C100 thermal cycler (Bio-Rad Laboratories, Hercules, CA): one cycle at 95°C for 6 minutes, 31 cycles at 95°C for 30 sec, 64°C for 120 sec, and 72°C for 90 sec, followed by one cycle at 72°C for 3 minutes. For all experiments, each PCR condition was replicated three times.

[00324] Following initial bias assessment, experiments were performed to define all individual primer amplification characteristics. To determine the specificity of VF and JR primers, 86 mixtures were prepared containing a single VF primer with all JR primers, and 7 mixtures containing a single JR primer with all VF primers. These primer sets were used to amplify the synthetic template and sequenced the resulting libraries to measure the specificity of each primer for the targeted V or J gene segments, and to identify instances of off-target priming. Titration experiments were performed using pools of 2-fold and 4-fold concentrations of each individual VF or JF within the context of all other equimolar primers (e.g. 2x-fold IgHV1-01+ all other equimolar VF and JR primers) to estimate scaling factors relating primer concentration to observed template frequency.

Primer Mix Optimization

[00325] Using the scaling factors derived by titrating primers one at a time, alternative primer mixes were developed in which the primers were combined at uneven concentrations to minimize amplification bias. The revised primer mixes were then used to amplify the template pool and measure the residual amplification bias. This process was reiterated, reducing or increasing each primer concentration appropriately based on whether templates

amplified by that primer were over or under-represented in the previous round of results. At each stage of this iterative process, the overall degree of amplification bias was determined by calculating metrics for the dynamic range (max bias/min bias) and sum of squares (SS, calculated on log(bias) values), and iterated the process of adjusting primer concentrations until there was minimal improvement between iterations. To assess the robustness of the final optimized primer mix and scaling factors to deviations from equimolar template input, we used a highly uneven mixture of IgH reference templates to determine the effect on sequencing output. The final mix was substantially better than an equimolar mix.

EXAMPLE 9: CORRECTING NON-UNIFORM AMPLIFICATION
POTENTIAL (PCR BIAS) IN TCRB-AMPLIFYING OLIGONUCLEOTIDE
PRIMER SETS

[00326] Diverse TCRB amplification primers were designed to amplify every possible combination of rearranged TCRB V and J gene segments in a biological sample that contains lymphoid cell DNA from a subject. A preparation containing equimolar concentrations of the diverse amplification primers was used in multiplexed PCR to amplify a diverse template composition that comprises equimolar concentrations of TCRB-specific template oligonucleotides according to formula (I) with at least one template representing every possible V-J combination for the TCRB locus. The amplification products were quantitatively sequenced and the frequency of occurrence of each unique V-J product sequence was obtained from the frequency of occurrence of each 16 bp molecular barcode sequence (B in formula (I)) that uniquely identifies each V-J combination.

[00327] The multiplex PCR reaction was designed to amplify all possible V and J gene rearrangements of the *TCRB* locus, as annotated by the IMGT collaboration. See Yousfi Monod M, Giudicelli V, Chaume D, Lefranc. MP. IMGT/JunctionAnalysis: the first tool for the analysis of the immunoglobulin and T cell receptor complex V-J and V-D-J JUNCTIONS. Bioinformatics. 2004;20(suppl 1):i379-i385. The locus includes 67 unique V genes. The target sequence for primer annealing was identical for some V segments, allowing us to amplify all 67 V segments with 60 unique forward primers. For the J locus, 13 unique reverse primers annealed to 13 J genes. As a baseline for bias assessment, the pool of 868 templates was amplified using an equimolar pool of the 60 V forward primers (VF; specific to V genes) and an equimolar pool of the 13 J reverse primers (JR; specific to J genes). Polymerase chain reactions (PCR) (25 μ L each) were set up at 3.0 μ M VF, 3.0 μ M JR pool (Integrated DNA Technologies), 1 μ M QIAGEN Multiplex Plus PCR master mix (QIAGEN,

Valencia, CA), 10% Q- solution (QIAGEN), and 200,000 target molecules from our synthetic TCRB repertoire mix. The following thermal cycling conditions were used in a C100 thermal cycler (Bio-Rad Laboratories, Hercules, CA): one cycle at 95°C for 5 minutes, 31 cycles at 95°C for 30 sec, 62°C for 90 sec, and 72°C for 90 sec, followed by one cycle at 72°C for 3 minutes. For all experiments, each PCR condition was replicated three times.

[00328] Following initial bias assessment, experiments were performed to define all individual primer amplification characteristics. To determine the specificity of our VF and JR primers, 60 mixtures were prepared containing a single VF primer with all JR primers, and 13 mixtures containing a single JR primer with all VF primers. These primer sets were used to amplify the synthetic template and sequenced the resulting libraries to measure the specificity of each primer for the targeted V or J gene segments and to identify instances of off-target priming. Titration experiments were performed using pools of 2-fold and 4-fold concentrations of each individual VF or JF within the context of all other equimolar primers (e.g. 2x-fold TCRBV07-6 + all other equimolar VF and JR primers) to allow us to estimate scaling factors relating primer concentration to observed template frequency.

Primer Mix Optimization

[00329] Using the scaling factors derived by titrating primers one at a time, alternative primer mixes were developed in which the primers were combined at uneven concentrations to minimize amplification bias. The revised primer mixes were then used to amplify the template pool and measure the residual amplification bias. This process was iterated, reducing or increasing each primer concentration appropriately based on whether templates amplified by that primer were over or under-represented in the previous round of results. At each stage of this iterative process, the overall degree of amplification bias was determined by calculating metrics for the dynamic range (max bias/min bias) and sum of squares (SS, calculated on log(bias) values), and iterated the process of adjusting primer concentrations until there was minimal improvement between iterations. The final mix was substantially better than an equimolar mix of primers.

[00330] Fig. 11 shows TCRB-primer iterations for synthetic TCRB VJ templates graphed against relative amplification bias. Relative amplification bias was determined for 858 synthetic TCRB VJ templates prior to chemical bias control correction (Equimolar Primers (black)), post chemical correction (Optimized Primers (dark grey)), and post chemical and computational correction (After computational adjustment (light grey)). The equimolar primers had a dynamic range of 264, an interquartile range of 0.841, and a sum of squares

(log bias) of 132. The optimized primers had a dynamic range of 147, an interquartile range of 0.581, and a sum of squares (log bias) of 50.7. The corrected primers (after computational adjustment) had a dynamic range of 90.8, an interquartile range of 0.248, and a sum of squares (log bias) of 12.8.

**EXAMPLE 10: CORRECTING NON-UNIFORM AMPLIFICATION
POTENTIAL (PCR BIAS) IN A COMBINED IGH VJ AND DJ-AMPLIFYING
OLIGONUCLEOTIDE PRIMER SETS**

[00331] Diverse IgH amplification primers were designed to amplify every possible combination of rearranged IgH V and J gene segments and IgH D and J gene segments in a biological sample that contained lymphoid cell DNA from a subject. A preparation containing equimolar concentrations of the diverse amplification primers was used in multiplexed PCR to amplify a diverse template composition that comprises equimolar concentrations of IgH-specific template oligonucleotides according to formula (I) with at least one template representing every possible V-J combination for the IgH locus and every possible D-J combination for the IgH locus. The amplification products were quantitatively sequenced and the frequency of occurrence of each unique V-J and D-J product sequence was obtained from the frequency of occurrence of each 16 bp molecular barcode sequence (B in formula (I)) that uniquely identifies each V-J and D-J combination.

[00332] The multiplex PCR reaction was designed to amplify all possible V and J gene rearrangements AND D and J gene rearrangements of the *IgH* locus, as annotated by the IMGT collaboration. The locus included 126 unique V genes; 52 functional genes, 6 putative open reading frames lacking critical amino acids for function and 69 pseudogenes; and 9 J genes, 6 functional and 3 pseudogenes. The locus also included 27 unique D genes. The target sequence for primer annealing was identical for some V segments, allowing amplification of all 126 V segments with 86 unique forward primers. Similarly, 7 unique reverse primers annealed to all 9 J genes. For the D-J assay, primers were designed to anneal to rearranged –DJ stems. During B cell development, both alleles undergo rearrangement between the D and J gene segments, resulting in two –DJ stems. A –DJ stem includes a J gene, one N region, and a D gene. Following DJ rearrangements, one of the two alleles V gene rearranges with the –DJ stem to code for the CDR3 gene region (VnDnJ). To amplify the –DJ stem, 27 unique primers were designed to anneal to each specific D genes in an intronic region upstream of the D gene exon. These segments, while present in –DJ stems.

are excised following V to -DJ recombination. However, J primers were not re-designed; the DJ assay used the same J primers as the VJ assay.

[00333] As a baseline for bias assessment, the pool of 1359 templates was amplified using an optimized (mix 2-1) pool of the 86 V forward primers (VF; specific to V genes), 27 D forward primers (DF; specific to D genes) and an equimolar pool of the 7 J reverse primers (JR; specific to J genes). Polymerase chain reactions (PCR) (25 μ L each) were set up at 1.0 μ M VF, 1.0 μ M DF, and 2.0 μ M JR pool (Integrated DNA Technologies), 1 X QIAGEN Multiplex Plus PCR master mix (QIAGEN, Valencia, CA), 10% Q- solution (QIAGEN), and 200,000 target molecules from our synthetic IgH VJ and DJ repertoire mix. The following thermal cycling conditions were used in a C100 thermal cycler (Bio-Rad Laboratories, Hercules, CA): one cycle at 95°C for 6 minutes, 31 cycles at 95°C for 30 sec, 64°C for 120 sec, and 72°C for 90 sec, followed by one cycle at 72°C for 3 minutes. For all experiments, each PCR condition was replicated three times.

[00334] Following initial bias assessment, experiments were performed to define all individual primer amplification characteristics. To determine the specificity of our DF and JR primers, 27 mixtures were prepared containing a single DF primer with all JR primers and the previously identified optimized VF pool, and 7 mixtures containing a single JR primer with all VF and DF primers. These primer sets were used to amplify the synthetic template and sequenced the resulting libraries to measure the specificity of each primer for the targeted V, D, or J gene segments, and to identify instances of off-target priming.

[00335] Titration experiments were performed using pools of 2-fold and 4-fold concentrations of each individual DF or JF within the context of all other primers – including the optimized mix of VF primers (e.g. 2x-fold IgHD2-08 + all other equimolar DF, optimal VF mix, and JR primers) to allow us to estimate scaling factors relating primer concentration to observed template frequency.

Primer mix optimization

[00336] Using the cross-amplification test, the DF primers were identified as cross amplified. 12 of the DF primers were removed, resulting in a final pool of 15 DF primers. Using the scaling factors derived by titrating primers one at a time, alternative primer mixes were developed in which the primers were combined at uneven concentrations to minimize amplification bias. The revised primer mixes were then used to amplify the template pool and measure the residual amplification bias. This process was iterated, reducing or increasing each primer concentration appropriately based on whether templates amplified by

that primer were over or under-represented in the previous round of results. At each stage of this iterative process, the overall degree of amplification bias was determined by calculating metrics for the dynamic range (max bias/min bias) and sum of squares (SS, calculated on log(bias) values), and iterated the process of adjusting primer concentrations until there was minimal improvement between iterations. The final primer mix has substantially less primer bias than an equimolar primer mix.

[00337] Fig. 12 shows IGH primer iterations for synthetic IGH VJ templates graphed against relative amplification bias. Relative amplification bias was determined for 1116 synthetic IGH VJ templates relative amplification bias prior to chemical bias control correction (equimolar primers (black)), post chemical correction (optimized primers (dark grey)), and post chemical and computational correction (After computational adjustment (light grey)). The equimolar primers had a dynamic range of 1130, an interquartile range of 0.991, and a sum of squares (log bias) of 233. The optimized primers had a dynamic range of 129, an interquartile range of 0.732, and a sum of squares (log bias) of 88.2. The after computational adjusted primers had a dynamic range of 76.9, an interquartile range of 0.545, and a sum of squares (log bias) of 37.9.

[00338] Fig. 13 shows the relative amplification bias for 27 synthetic IGH DJ templates of the V gene. Relative amplification bias of the V gene segment is shown in three primer iterations : 1) prior to chemical bias control correction (black), 2) a first iteration of chemical correction (white), and 3) a post second iteration of chemical correction (light grey).

EXAMPLE 11: TCRG VJ PRIMER ITERATIONS

[00339] In other embodiments, TCRG VJ primers were tested for relative amplification bias in multiple primer iterations. Figs. 14a-d show TCRG-primer iterations for 55 synthetic TCRG VJ templates. Relative amplification bias was determined for the TCRG VJ primers prior to chemical bias control correction (Fig. 14a), a first iteration of chemical correction (Fig. 14b), a second iteration of chemical correction (Fig. 14c), and final iteration of chemical correction (Fig. 14d).

EXAMPLE 12: ALTERNATIVE BIAS CONTROL AND SPIKE-IN METHOD

[00340] In other embodiments, alternative methods can be used to determine amplification bias. Two primary goals of the method are as follows: (1) to remove amplification bias in a multiplex PCR amplification of BCR or TCR genes and (2) to estimate the fraction of B or T cells in the starting template.

[00341] The method includes starting with a set of cells comprising DNA, or cDNA (mRNA) extracted from a sample that includes B and/or T cells. In a sample comprising cells, the DNA is extracted using methods standard in the art.

[00342] The extracted DNA is divided into multiple parts and put into different PCR wells. In some embodiments, one well is used to full capacity or thousands of wells can be used. In one embodiment, 188 wells are used for PCR (two 96 well plates). The number of TCR or BCR templates per well should be sparse, such that it is rare to have multiple molecules from the same clonotype in the same well.

[00343] The method then includes amplifying the DNA separately in each well using the same multiplex set of primers. The sets of primers described herein can be used. As described above, the bar coding method is applied to the amplified molecules in each well with the same barcode sequence. For example, each well gets its own barcode.

[00344] The molecules are then sequenced on a high throughput sequencing machine with a sufficient amount of the amplified BCR or TCR sequences to identify by sequence the V and the J chain used, as well as the bar code sequence.

[00345] Each well has an average copy count. Since each clonotype appears once in a well, the amount of that template relative to the average is the bias for that V-J combination. Since V and J bias are independent, not every V-J combination is necessary to determine the biases. These relative biases are then used to either re-design primers that are either highly under or over amplifying or to titrate the primer concentration to increase or decrease amplification. The entire process is repeated with a new primer lot and iterated to continue to decrease bias.

[00346] After any cycle of the iterations, a set of computational factors (the relative amplification factors) can be applied to remove bias. Bias can be reduced by both (or either) primer changes and computational correction.

[00347] The method includes computing a fraction of nucleated cells from a similar assay. For each well, each clonotype is identified, and the number of sequencing reads is determined for each clone. In some embodiments, the number of templates does not need to be sparse. The read counts for each clone are corrected by the bias control factors as described above.

[00348] A histogram is created of the corrected read counts, and the graph has a primary mode (the amplification factor). This mode is identified by inspection (based on identification of the first large peak), or by Fourier transform, or other known methods.

[00349] The total number of corrected reads in each well is divided by the amplification factor for that well. This is the estimated number of TCR or BCR genome templates that were in the well. The total number of BCR or TCRs from the sample is the sum of the number from all the wells. The total number of genomes in each well is measured prior to PCR. This can be done by nanodrop, or other known methods used to quantify DNA. The measured weight of the DNA is divided by the weight of a double stranded genome (for example, in humans ~6.2 pico grams).

[00350] The fraction of B cells or T cells in the sample is the total number of BCR or TCRs in the samples divided by the total number of double stranded DNA molecules added to the reaction. The result needs a minor correction as a small fraction of T cells have both alleles rearranged. This correction factor is approximately 15% for alpha beta T cells, 10% for B cells. For gamma delta T cells, almost all of the cells have both alleles rearranged, so the correction is a factor of two.

[00351] These additional methods can determine amplification bias in a multiplex PCR amplification of BCR or TCR genes and be used to estimate the fraction of B or T cells in the starting template.

[00352] The various embodiments described above can be combined to provide further embodiments. All of the U.S. patents, U.S. patent application publications, U.S. patent applications, foreign patents, foreign patent applications and non-patent publications referred to in this specification and/or listed in the Application Data Sheet are incorporated herein by reference, in their entirety. Aspects of the embodiments can be modified, if necessary to employ concepts of the various patents, applications and publications to provide yet further embodiments.

[00353] These and other changes can be made to the embodiments in light of the above-detailed description. In general, in the following claims, the terms used should not be construed to limit the claims to the specific embodiments disclosed in the specification and the claims, but should be construed to include all possible embodiments along with the full scope of equivalents to which such claims are entitled. Accordingly, the claims are not limited by the disclosure.

INFORMAL SEQUENCE LISTING

Bias Control Sequences for hs-IgH-DJ (243 Sequences)

Name	Sequence	SEQ ID NO
hsIGH_2001_ D001_J001_I GHD1- 01_IGHJ1	GCCTTGCCAGCCCGCTCAGGACACTCTGTACAGTGGCCCCGGTCTCTG TGGGTGTTCCGCTAACTGGGGCTCCCAGTGCTCACCCACAACTAAAG CGAGCCCCAGCCTCCAGAGCCCCCGAAGGAGATGCCGCCACAAAGCCC AGCCCCCATCCAGGAGGCCCCAGAGCTCAGGGCGCCGGGGCAGATTCT GAACAGCCCCGAGTCACGGTGGGTACAACCTGGAGACACTCTGTACAGT GGTCGACATACTTCCAGCACTGGGGCCAGGGCACCCCTGGTCACCGTCT CCTCAGGTGAGTCTGCTGTCTGGGGATAGCGGGGAGCCAGGTGTACTG GGCCAGGCAAGGACACTCTGTACAGTGTGATGGCGCGAGGGAGGC	SEQ ID NO: 5579
hsIGH_2002_ D002_J001_I GHD1- 07_IGHJ1	GCCTTGCCAGCCCGCTCAGTTCCGAACGTACAGTGGGCCTCGGTCTCT GTGGGTGTTCCGCTAGCTGGGGCTCACAGTGCTCACCCACACCTAAA ACGAGCCACAGCCTCAGAGCCCCCTGAAGGAGACCCCGCCCAAGCCC AGCCCCACCCAGGAGGCCCCAGAGCACAGGGCGCCCCGTGGATTCT GAACAGCCCCGAGTCACAGTGGGTATAACTGGATTCCGAACGTACAGT GGTCGACATACTTCCAGCACTGGGGCCAGGGCACCCCTGGTCACCGTCT CCTCAGGTGAGTCTGCTGTCTGGGGATAGCGGGGAGCCAGGTGTACTG GGCCAGGCAAGTTCGGAACGTACAGTGTGATGGCGCGAGGGAGGC	SEQ ID NO: 5580
hsIGH_2003_ D003_J001_I GHD1- 14_IGHJ1	GCCTTGCCAGCCCGCTCAGAAGTAACGGTACAGTGGGCCTCGGTCTCT GTGGGTGTTCCGCTAGCTGGGGCTCACAGTGCTCACCCACACCTAAA ATGAGCCACAGCCTCCGGAGCCCCCGCAGAGACCCCGCCCAAGCCC AGCCCCACCCAGGAGGCCCCAGAGCTCAGGGCGCCCCGTGGATTCC GAACAGCCCCGAGTCACAGCGGGTATAACCGGAAAGTAACGGTACAGT GGTCGACATACTTCCAGCACTGGGGCCAGGGCACCCCTGGTCACCGTCT CCTCAGGTGAGTCTGCTGTCTGGGGATAGCGGGGAGCCAGGTGTACTG GGCCAGGCAAGAAGTAACGGTACAGTGTGATGGCGCGAGGGAGGC	SEQ ID NO: 5581
hsIGH_2004_ D004_J001_I GHD1- 20_IGHJ1	GCCTTGCCAGCCCGCTCAGGTCTCCTAGTACAGTGGTCTCTGTGGGTG TTCCGCTAGCTGGGGCCCCCAGTGCTCACCCACACCTAAAGCGAGCC CCAGCCTCCAGAGCCCCCTAAGCATTCCCCGCCAGCAGCCAGCCCC TGCCCCACCCAGGAGGCCCCAGAGCTCAGGGCGCCTGGTCGGATTCT GAACAGCCCCGAGTCACAGTGGGTATAACTGGAGTCTCCTAGTACAGT GGTCGACATACTTCCAGCACTGGGGCCAGGGCACCCCTGGTCACCGTCT CCTCAGGTGAGTCTGCTGTCTGGGGATAGCGGGGAGCCAGGTGTACTG GGCCAGGCAAGGTCTCCTAGTACAGTGTGATGGCGCGAGGGAGGC	SEQ ID NO: 5582

Name	Sequence	SEQ ID NO
hsIGH_2005_ D005_J001_I GHD1- 26_IGHJ1	GCCTTGCCAGCCCGCTCAGAGAGTGTCGTACAGTGAGGCCTCAGGCTC TGTGGGTGCCGCTAGCTGGGGCTGCCAGTCCTCACCCACACCTAAGG TGAGCCACAGCCGCCAGAGCCTCCACAGGAGACCCACCCAGCAGCCC AGCCCCCTACCCAGGAGGCCCCAGAGCTCAGGGCGCCTGGGTGGATTCT GAACAGCCCCGAGTCACGGTGGGTATAGTGGGAGCTAGAGTGTCGTAC AGTGGTCGACATACTTCCAGCACTGGGGCCAGGGCACCTGGTCACCG TCTCCTCAGGTGAGTCTGCTGTCTGGGGATAGCGGGAGCCAGGTGTA CTGGGCCAGGCAAGAGAGTGTCGTACAGTGCTGATGGCGCGAGGGAGG C	SEQ ID NO: 5583
hsIGH_2006_ D006_J001_I GHD2- 02_IGHJ1	GCCTTGCCAGCCCGCTCAGGTTCCGAAGTACAGTGAAAGGAGGAGCCC CCTGTACAGCACTGGGCTCAGAGTCCTCTCCACACACCCTGAGTTTC AGACAAAAACCCCTGGAAATCATAGTATCAGCAGGAGAACTAGCCAG AGACAGCAAGAGGGGACTCAGTGACTCCCGCGGGGACAGGAGGATTTT GTGGGGGCTCGTGTCAGTGTGAGGATATTGTAGTAGTACCAGCTGCTG TTCCGAAGTACAGTGGTCGACATACTTCCAGCACTGGGGCCAGGGCAC CCTGGTCACCGTCTCCTCAGGTGAGTCTGCTGTCTGGGGATAGCGGGG AGCCAGGTGTACTGGGCCAGGCAAGGTTCCGAAGTACAGTGCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5584
hsIGH_2007_ D007_J001_I GHD2- 08_IGHJ1	GCCTTGCCAGCCCGCTCAGCGTTACTTGTACAGTGAAAGGAGGAGCCC CTTGTTTACAGCACTGGGCTCAGAGTCCTCTCCAAGACACCCAGAGTTTC AGACAAAAACCCCTGGAATGCACAGTCTCAGCAGGAGAGCCAGCCAG AGCCAGCAAGATGGGGCTCAGTGACACCCGACGGGACAGGAGGATTTT GTGGGGGCTCGTGTCAGTGTGAGGATATTGTACTAATGGTGTATGCTC GTTACTTGTACAGTGGTCGACATACTTCCAGCACTGGGGCCAGGGCAC CCTGGTCACCGTCTCCTCAGGTGAGTCTGCTGTCTGGGGATAGCGGGG AGCCAGGTGTACTGGGCCAGGCAAGCGTTACTTGTACAGTGCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5585
hsIGH_2008_ D008_J001_I GHD2- 15_IGHJ1	GCCTTGCCAGCCCGCTCAGTAGGAGACGTACAGTGAAAGGAGGAGCCC CCTATACAGCACTGGGCTCAGAGTCCTCTCTGAGACACCCTGAGTTTC AGACAACAACCCGCTGGAATGCACAGTCTCAGCAGGAGAACAGACCAA AGCCAGCAAAAGGGACCTCGGTGACACCAGTAGGGACAGGAGGATTTT GTGGGGGCTCGTGTCAGTGTGAGGATATTGTAGTGGTGGTAGCTGCTT AGGAGACGTACAGTGGTCGACATACTTCCAGCACTGGGGCCAGGGCAC CCTGGTCACCGTCTCCTCAGGTGAGTCTGCTGTCTGGGGATAGCGGGG AGCCAGGTGTACTGGGCCAGGCAAGTAGGAGACGTACAGTGCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5586

Name	Sequence	SEQ ID NO
hsIGH_2009_ D009_J001_I GHD2- 21_IGHJ1	GCCTTGCCAGCCCGCTCAGGTGTCTACGTACAGTGAGCCCCCTGTACA GCACTGGGCTCAGAGTCTCTCTGAGACAGGCTCAGTTTCAGACAACA ACCCGCTGGAATGCACAGTCTCAGCAGGAGAGCCAGGCCAGAGCCAGC AAGAGGAGACTCGGTGACACCAGTCTCCTGTAGGGACAGGAGGATTTT GTGGGGGTTCGTGTCACTGTGAGCATATTGTGGTGGTGACTGCTGTGT CTACGTACAGTGGTCGACATACTTCCAGCACTGGGGCCAGGGCACCCCT GGTCACCGTCTCCTCAGGTGAGTCTGCTGTCTGGGGATAGCGGGGAGC CAGGTGTACTGGGCCAGGCAAGGTGTCTACGTACAGTGCTGATGGCGC GAGGGAGGC	SEQ ID NO: 5587
hsIGH_2010_ D010_J001_I GHD3- 03_IGHJ1	GCCTTGCCAGCCCGCTCAGTGCTACACGTACAGTGGTGGGCACGGACA CTGTCCACCTAAGCCAGGGGCAGACCCGAGTGTCCCCGAGTAGACCT GAGAGCGCTGGGCCCACAGCCTCCCCTCGGTGCCCTGCTACCTCCTCA GGTCAGCCCTGGACATCCCGGGTTTCCCCAGGCTGGCGGTAGGTTTGG GGTGAGGTCTGTGTCACTGTGGTATTACGATTTTTGGAGTGGTTATTT GCTACACGTACAGTGGTCGACATACTTCCAGCACTGGGGCCAGGGCAC CCTGGTCACCGTCTCCTCAGGTGAGTCTGCTGTCTGGGGATAGCGGGG AGCCAGGTGTACTGGGCCAGGCAAGTGCTACACGTACAGTGCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5588
hsIGH_2011_ D011_J001_I GHD3- 09_IGHJ1	GCCTTGCCAGCCCGCTCAGAACTGCCAGTACAGTGTTGGGCACGGACAC TATCCACATAAGCGAGGGATAGACCCGAGTGTCCCCACAGCAGACCTG AGAGCGCTGGGCCCACAGCCTCCCCTCAGAGCCCTGCTGCCTCCTCCG GTCAGCCCTGGACATCCCAGGTTTCCCCAGGCCTGCCGGTAGGTTTAG AATGAGGTCTGTGTCACTGTGGTATTACGATATTTTACTGGTTATTA ACTGCCAGTACAGTGGTCGACATACTTCCAGCACTGGGGCCAGGGCAC CCTGGTCACCGTCTCCTCAGGTGAGTCTGCTGTCTGGGGATAGCGGGG AGCCAGGTGTACTGGGCCAGGCAAGAACTGCCAGTACAGTGCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5589
hsIGH_2012_ D012_J001_I GHD3- 10_IGHJ1	GCCTTGCCAGCCCGCTCAGTTGGACTGGTACAGTGCGATATTTTACT GGTTATTATAACCACAGTGTACAGAGTCCATCAAAAACCCATGCCTG GAAGCTTCCCCGCCACAGCCCTCCCCATGGGGCCCTGCTGCCTCCTCAG GTCAGCCCCGACATCCCGGGTTTCCCCAGGCTGGGCGGTAGGTTTGG GGTGAGGTCTGTGTCACTGTGGTATTACTATGGTTCGGGGAGTTATTT TGGACTGGTACAGTGGTCGACATACTTCCAGCACTGGGGCCAGGGCAC CCTGGTCACCGTCTCCTCAGGTGAGTCTGCTGTCTGGGGATAGCGGGG AGCCAGGTGTACTGGGCCAGGCAAGTTGGACTGGTACAGTGCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5590

Name	Sequence	SEQ ID NO
hsIGH_2013_ D013_J001_I GHD3- 16_IGHJ1	GCCTTGCCAGCCCGCTCAGGTAGACACGTACAGTGTGGACGCGGACAC TATCCACATAAGCGAGGGACAGACCCGAGTGTTCCTGCAGTAGACCTG AGAGCGCTGGGCCCACAGCCTCCCCTCGGTGCCCTGCTGCCTCCTCAG GTCAGCCCTGGACATCCCGGGTTTCCCCAGGCCAGATGGTAGGTTTGA AGTGAGGTCTGTGTCACTGTGGTATTATGATTACGTTTGGGGGAGTTA TCGTTGTAGACACGTACAGTGGTCGACATACTTCCAGCACTGGGGCCA GGGCACCTGGTCACCGTCTCCTCAGGTGAGTCTGCTGTCTGGGGATA GCGGGGAGCCAGGTGTACTGGGCCAGGCAAGGTAGACACGTACAGTGC TGATGGCGCGAGGGAGGC	SEQ ID NO: 5591
hsIGH_2014_ D014_J001_I GHD3- 22_IGHJ1	GCCTTGCCAGCCCGCTCAGCACTGTACGTACAGTGTGGGCATGGACAG TGTCCACCTAAGCGAGGGACAGACCCGAGTGTCCCTGCAGTAGACCTG AGAGCGCTGGGCCCACAGCCTCCCCTCGGGGCCCTGCTGCCTCCTCAG GTCAGCCCTGGACATCCCGGGTTTCCCCAGGCCCTGGCGGTAGGTTTGA AGTGAGGTCTGTGTCACTGTGGTATTACTATGATAGTAGTGTTATTC ACTGTACGTACAGTGGTCGACATACTTCCAGCACTGGGGCCAGGGCAC CCTGGTCACCGTCTCCTCAGGTGAGTCTGCTGTCTGGGGATAGCGGGG AGCCAGGTGTACTGGGCCAGGCAAGCACTGTACGTACAGTGCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5592
hsIGH_2015_ D015_J001_I GHD4- 04_IGHJ1	GCCTTGCCAGCCCGCTCAGGATGATCCGTACAGTGCAAGGGTGAGTCA GACCCTCCTGCCCTCGATGGCAGGCGGAGAAGATTAGAAAGGTCTGA GATCCCCAGGACGCAGCACCCTGTCAATGGGGGCCCCAGACGCCTGG ACCAGGGCCTGCGTGGGAAAGGCCTCTGGGCACACTCAGGGGCTTTTT GTGAAGGGTCCTCCTACTGTGTGACTACAGTAGATGATCCGTACAGTG GTCGACATACTTCCAGCACTGGGGCCAGGGCACCCCTGGTCACCGTCTC CTCAGGTGAGTCTGCTGTCTGGGGATAGCGGGGAGCCAGGTGTACTGG GCCAGGCAAGGATGATCCGTACAGTGCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5593
hsIGH_2016_ D016_J001_I GHD4- 11_IGHJ1	GCCTTGCCAGCCCGCTCAGCGCCAATAGTACAGTGTGCCTCTCTCCCC AGTGGACACCCTCTTCCAGGACAGTCCTCAGTGGCATCACAGCGGCCT GAGATCCCCAGGACGCAGCACCCTGTCAATAGGGGCCCCAAATGCCT GGACCAGGGCCTGCGTGGGAAAGGTCTCTGGCCACACTCGGGCTTTTT GTGAAGGGCCCTCCTGCTGTGTGACTACAGTACGCCAATAGTACAGTG GTCGACATACTTCCAGCACTGGGGCCAGGGCACCCCTGGTCACCGTCTC CTCAGGTGAGTCTGCTGTCTGGGGATAGCGGGGAGCCAGGTGTACTGG GCCAGGCAAGCGCCAATAGTACAGTGCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5594

Name	Sequence	SEQ ID NO
hsIGH_2017_ D017_J001_I GHD4- 17_IGHJ1	GCCTTGCCAGCCCGCTCAGTCAAGCCTGTACAGTGGGAGGGTGAGTCA GACCCACCTGCCCTCGATGGCAGGCGGGGAAGATTAGAAAAGGCCTGA GATCCCCAGGACGCAGCACCCTGTCAATGGGGGCCCCAGACGCCTGG ACCAGGGCCTGCGTGGGAAAAGGCCGCTGGGCACACTCAGGGGCTTTTT GTGAAGGCCCCCTCCTACTGTGTGACTACGGTGTCAAGCCTGTACAGTG GTCGACATACTTCCAGCACTGGGGCCAGGGCACCCCTGGTCACCGTCTC CTCAGGTGAGTCTGCTGTCTGGGGATAGCGGGGAGCCAGGTGTACTGG GCCAGGCAAGTCAAGCCTGTACAGTGCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5595
hsIGH_2018_ D018_J001_I GHD4- 23_IGHJ1	GCCTTGCCAGCCCGCTCAGACGTGTGTGTACAGTGGGAGGGTGAGTCA GACCCACCTGCCCTCAATGGCAGGCGGGGAAGATTAGAAAAGGCCTGA GATCCCCAGGACGCAGCACCCTGTCAATGGGGGCCCCAGACGCCTGG ACCAGGGCCTGTGTGGGAAAAGGCCCTCTGGCCACACTCAGGGGCTTTTT GTGAAGGCCCCCTCCTGCTGTGTGACTACGGTGGTAACGTGTGTGTACA GTGGTCGACATACTTCCAGCACTGGGGCCAGGGCACCCCTGGTCACCGT CTCCTCAGGTGAGTCTGCTGTCTGGGGATAGCGGGGAGCCAGGTGTAC TGGGCCAGGCAAGACGTGTGTGTACAGTGCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5596
hsIGH_2019_ D019_J001_I GHD5- 05_IGHJ1	GCCTTGCCAGCCCGCTCAGTCCGTCTAGTACAGTGAGAGGCCTCTCCA GGGGGACACTGTGCATGTCTGGTCCCTGAGCAGCCCCCATGTCCCCA GTCTGGGGGGCCCCCTGGCAGAGCTGTCTGGACCCTCTCTATTCCCT GGGAAGCTCCTCCTGACAGCCCCGCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGTGACACTGTGGTGGATACAGCTATGTCCGTCTAGTAC AGTGGTCGACATACTTCCAGCACTGGGGCCAGGGCACCCCTGGTCACCG TCTCCTCAGGTGAGTCTGCTGTCTGGGGATAGCGGGGAGCCAGGTGTA CTGGGCCAGGCAAGTCCGTCTAGTACAGTGCTGATGGCGCGAGGGAGG C	SEQ ID NO: 5597
hsIGH_2020_ D020_J001_I GHD5- 12_IGHJ1	GCCTTGCCAGCCCGCTCAGAAGAGCTGGTACAGTGGCAGAGGCCTCTC CAGGGAGACACTGTGCATGTCTGGTACCTAAGCAGCCCCCACGTCCC CAGTCTGGGGGGCCCCCTGGCTCAGCTGTCTGGACCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCTCCAGTTCCAGGTGTGGTTATT GTCAGGCGATGTGACACTGTGGTGGATATAGTGGCTACGAAGAGCTGG TACAGTGGTCGACATACTTCCAGCACTGGGGCCAGGGCACCCCTGGTCA CCGTCTCCTCAGGTGAGTCTGCTGTCTGGGGATAGCGGGGAGCCAGGT GTACTGGGCCAGGCAAGAAGAGCTGGTACAGTGCTGATGGCGCGAGGG AGGC	SEQ ID NO: 5598

Name	Sequence	SEQ ID NO
hsIGH_2021_ D021_J001_I GHD5- 18_IGHJ1	GCCTTGCCAGCCCGCTCAGTATCGCTCGTACAGTGGCAGAGGCCTCTC CAGGGGGACACTGTGCATGTCTGGTCCCTGAGCAGCCCCCACGTCCC CAGTCCTGGGGGCCCTGGCACAGCTGTCTGGACCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGTGAGTGTGGTGGATACAGCTATGTATCGCTCGTAC AGTGGTCGACATACTTCCAGCACTGGGGCCAGGGCACCCCTGGTCACCG TCTCCTCAGGTGAGTCTGCTGTCTGGGGATAGCGGGAGCCAGGTGTA CTGGGCCAGGCAAGTATCGCTCGTACAGTGCTGATGGCGCGAGGGAGG C	SEQ ID NO: 5599
hsIGH_2022_ D022_J001_I GHD5- 24_IGHJ1	GCCTTGCCAGCCCGCTCAGTCAGATGCGTACAGTGGCAGAGGCCTCTC CAGGGGGACACAGTGCATGTCTGGTCCCTGAGCAGCCCCCAGGCTCTC TAGCACTGGGGGCCCTGGCACAGCTGTCTGGACCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGCCAGGCCGTGGTAGAGATGGCTACATCAGATGCGTAC AGTGGTCGACATACTTCCAGCACTGGGGCCAGGGCACCCCTGGTCACCG TCTCCTCAGGTGAGTCTGCTGTCTGGGGATAGCGGGAGCCAGGTGTA CTGGGCCAGGCAAGTCAGATGCGTACAGTGCTGATGGCGCGAGGGAGG C	SEQ ID NO: 5600
hsIGH_2023_ D023_J001_I GHD6- 06_IGHJ1	GCCTTGCCAGCCCGCTCAGGTGTAGCAGTACAGTGAGGCAGCTGACTC CTGACTTGAGCGCTATTCCAGACACCAGACAGAGGGGCAGGCCCCC AGAACCAGGGATGAGGACGCCCCGTCAAGGCCAGAAAAGACCAAGTTG TGCTGAGCCCAGCAAGGGAAGGTCCCCAAACAAACCAGGAACGTTTCT GAAGGTGTCTGTGTACAGTGGAGTATAGCAGCTGTGTAGCAGTACAG TGGTCGACATACTTCCAGCACTGGGGCCAGGGCACCCCTGGTCACCGTC TCCTCAGGTGAGTCTGCTGTCTGGGGATAGCGGGAGCCAGGTGTACT GGGCCAGGCAAGGTGTAGCAGTACAGTGCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5601
hsIGH_2024_ D024_J001_I GHD6- 13_IGHJ1	GCCTTGCCAGCCCGCTCAGTGGCAGTTGTACAGTGAGGCAGCTGACCC CTGACTTGAGCCCTATTCCAGACACCAGACAGAGGCGCAGGCCCCC AGAACCAGGGTTGAGGGACGCCCCGTCAAAGCCAGACAAAACCAAGGG GTGTTGAGCCCAGCAAGGGAAGGCCCCCAACAGACCAGGAGGTTTCT GAAGGTGTCTGTGTACAGTGGGGTATAGCAGCAGCTTGGCAGTTGTA CAGTGGTCGACATACTTCCAGCACTGGGGCCAGGGCACCCCTGGTCACC GTCTCCTCAGGTGAGTCTGCTGTCTGGGGATAGCGGGAGCCAGGTGT ACTGGGCCAGGCAAGTGGCAGTTGTACAGTGCTGATGGCGCGAGGGAG GC	SEQ ID NO: 5602

Name	Sequence	SEQ ID NO
hsIGH_2025_ D025_J001_I GHD6- 19_IGHJ1	GCCTTGCCAGCCCGCTCAGCAGTCCAAGTACAGTGTGAGGTAGCTGGC CTCTGTCTCGGACCCCACTCCAGACACCAGACAGAGGGGACAGGCCCCC CAAAACCAGGGTTGAGGGATGATCCGTCAAGGCAGACAAGACCAAGGG GCACTGACCCCAAGCAAGGGAAGGCTCCCAAACAGACGAGGAGGTTTCT GAAGCTGTCTGTATCACAGTGGGGTATAGCAGTGGCTCAGTCCAAGTA CAGTGGTCGACATACTTCCAGCACTGGGGCCAGGGCACCCCTGGTCACC GTCTCCTCAGGTGAGTCTGCTGTCTGGGGATAGCGGGGAGCCAGGTGT ACTGGGCCAGGCAAGCAGTCCAAGTACAGTGCTGATGGCGCGAGGGAG GC	SEQ ID NO: 5603
hsIGH_2026_ D026_J001_I GHD6- 25_IGHJ1	GCCTTGCCAGCCCGCTCAGTACGTACGGTACAGTGCAGCTGGCCTCTG TCTCGGACCCCACTTCCAGACACCAGACAGAGGGACAGGCCCCCAGA ACCAAGTGTGAGGGACACCCCTGTCCAGGGCAGCCAAGTCCAAGAGGC GCGCTGAGCCCAGCAAGGGAAGGCCCCCAACAAACCAGGAGGTTTCT GAAGCTGTCTGTGTACAGTCCGGTATAGCAGCGTACGTACGGTACAG TGGTCGACATACTTCCAGCACTGGGGCCAGGGCACCCCTGGTCACCGTC TCCTCAGGTGAGTCTGCTGTCTGGGGATAGCGGGGAGCCAGGTGTACT GGGCCAGGCAAGTACGTACGGTACAGTGCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5604
hsIGH_2027_ D027_J001_I GHD7- 27_IGHJ1	GCCTTGCCAGCCCGCTCAGAGTACCGAGTACAGTGAGGGTTGAGGGCT GGGGTCTCCACGTGTTTTGGGGCTAACAGCGGAAGGGAGAGCACTGG CAAAGGTGCTGGGGGTCCCTGAACCCGACCCGCCCTGAGACCGCAGC CACATCAGCCCCAGCCCCACAGGCCCCCTACCAGCCGCAGGGTTTTT GGCTGAGCTGAGAACCACTGTGCTAACTAGTACCGAGTACAGTGGTCG ACATACTTCCAGCACTGGGGCCAGGGCACCCCTGGTCACCGTCTCCTCA GGTGAGTCTGCTGTCTGGGGATAGCGGGGAGCCAGGTGTACTGGGCCA GGCAAGAGTACCGAGTACAGTGCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5605
hsIGH_2028_ D001_J002_I GHD1- 01_IGHJ2	GCCTTGCCAGCCCGCTCAGGACACTCTGGATCATCGCCCCGGTCTCTG TGGGTGTTCCGCTAACTGGGGCTCCAGTGCTCACCACCACTAAAG CGAGCCCCAGCCTCCAGAGCCCCCGAAGGAGATGCCGCCACAAGCCC AGCCCCCATCCAGGAGGCCCCAGAGCTCAGGGCGCCGGGGCAGATTCT GAACAGCCCCGAGTCACGGTGGGTACAACGGAGACACTCTGGATCAT CGTCGACTGCTGGGGGCCCCCTGGACCCGACCCGCCCTGGAGACCGCAG CCACATCAGCCCCCAGCCCCACAGGCCCCCTACCAGCCGCAGGGTTTT GGCTGAGCTGAGACACTCTGGATCATCCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5606
hsIGH_2029_ D002_J002_I GHD1- 07_IGHJ2	GCCTTGCCAGCCCGCTCAGTTCCGAACGGATCATCGGCCTCGGTCTCT GTGGGTGTTCCGCTAGCTGGGGCTCAGAGTGCTCACCACACCTAAA ACGAGCCACAGCCTCAGAGCCCCCTGAAGGAGACCCGCCCCACAAGCCC AGCCCCCACCAGGAGGCCCCAGAGCACAGGGCGCCCCGTCGGATTCT GAACAGCCCCGAGTCACAGTGGGTATAACTGGATTTCGGAACGGATCAT CGTCGACTGCTGGGGGCCCCCTGGACCCGACCCGCCCTGGAGACCGCAG CCACATCAGCCCCCAGCCCCACAGGCCCCCTACCAGCCGCAGGGTTTT GGCTGAGCTGATTCCGAACGGATCATCCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5607

Name	Sequence	SEQ ID NO
hsIGH_2030_ D003_J002_I GHD1- 14_IGHJ2	GCCTTGCCAGCCCGCTCAGAAGTAACGGGATCATCGGCCTCGGTCTCT GTGGGTGTTCCGCTAGCTGGGGCTCACAGTGCTCACCCACACCTAAA ATGAGCCACAGCCTCCGAGCCCCCGCAGAGACCCCGCCACAAGCCC AGCCCCACCCAGGAGGCCCCAGAGCTCAGGGCGCCCCGTCGGATTCC GAACAGCCCCGAGTCACAGCGGGTATAACCGGAAAGTAACGGGATCAT CGTCGACTGCTGGGGGCCCTTGACCCGACCCGCCCTGGAGACCGCAG CCACATCAGCCCCCAGCCCCACAGGCCCCCTACCAGCCGCAGGGTTTT GGCTGAGCTGAAAGTAACGGGATCATCCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5608
hsIGH_2031_ D004_J002_I GHD1- 20_IGHJ2	GCCTTGCCAGCCCGCTCAGGTCTCCTAGGATCATCGTCTCTGTGGGTG TTCCGCTAGCTGGGGCCCCCAGTGCTCACCCACACCTAAAGCGAGCC CCAGCCTCCAGAGCCCCCTAAGCATTCCTCGCCAGCAGCCAGCCCC TGCCCCCACCAGGAGGCCCCAGAGCTCAGGGCGCCTGGTCGGATTCT GAACAGCCCCGAGTCACAGTGGGTATAACTGGAGTCTCTAGGATCAT CGTCGACTGCTGGGGGCCCTTGACCCGACCCGCCCTGGAGACCGCAG CCACATCAGCCCCCAGCCCCACAGGCCCCCTACCAGCCGCAGGGTTTT GGCTGAGCTGAGTCTCCTAGGATCATCCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5609
hsIGH_2032_ D005_J002_I GHD1- 26_IGHJ2	GCCTTGCCAGCCCGCTCAGAGAGTGTGGATCATCAGGCCTCAGGCTC TGTGGGTGCCGCTAGCTGGGGCTGCCAGTCCTCACCCACACCTAAGG TGAGCCACAGCCGCCAGAGCCTCCACAGGAGACCCACCCAGCAGCCC AGCCCCTACCAGGAGGCCCCAGAGCTCAGGGCGCCTGGGTGGATTCT GAACAGCCCCGAGTCACGGTGGGTATAGTGGGAGCTAGAGTGTCCGAT CATCGTCGACTGCTGGGGGCCCTTGACCCGACCCGCCCTGGAGACCG CAGCCACATCAGCCCCCAGCCCCACAGGCCCCCTACCAGCCGCAGGGT TTTGGCTGAGCTGAAGAGTGTCCGATCATCCTGATGGCGCGAGGGAGG C	SEQ ID NO: 5610
hsIGH_2033_ D006_J002_I GHD2- 02_IGHJ2	GCCTTGCCAGCCCGCTCAGGTTCGAAGGATCATCAAAGGAGGAGCCC CCTGTACAGCACTGGGCTCAGAGTCCTCTCCACACACCCTGAGTTTC AGACAAAAACCCCTGGAAATCATAGTATCAGCAGGAGAACTAGCCAG AGACAGCAAGAGGGGACTCAGTGACTCCCGCGGGGACAGGAGGATTTT GTGGGGGCTCGTGCTACTGTGAGGATATTGTAGTAGTACCAGCTGCTG TTCCGAAGGATCATCGTCGACTGCTGGGGGCCCTTGACCCGACCCGC CCTGGAGACCGCAGCCACATCAGCCCCCAGCCCCACAGGCCCCCTACC AGCCGCAGGGTTTTGGCTGAGCTGAGTTCCGAAGGATCATCCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5611

Name	Sequence	SEQ ID NO
hsIGH_2034_ D007_J002_I GHD2- 08_IGHJ2	GCCTTGCCAGCCCGCTCAGCGTTACTTGGATCATCAAAGGAGGAGCCC CTTGTTTCAGCACTGGGCTCAGAGTCCTCTCCAAGACACCCAGAGTTTC AGACAAAAACCCCTGGAATGCACAGTCTCAGCAGGAGAGCCAGCCAG AGCCAGCAAGATGGGGCTCAGTGACACCCGCAGGGACAGGAGGATTTT GTGGGGGCTCGTGTCAGTGTGAGGATATTGTACTAATGGTGTATGCTC GTTACTTGGATCATCGTCGACTGCTGGGGGCCCTGGACCCGACCCGC CCTGGAGACCGCAGCCACATCAGCCCCAGCCCCACAGGCCCCCTACC AGCCGCAGGGTTTTGGCTGAGCTGACGTTACTTGGATCATCCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5612
hsIGH_2035_ D008_J002_I GHD2- 15_IGHJ2	GCCTTGCCAGCCCGCTCAGTAGGAGACGGATCATCAAAGGAGGAGCCC CCTATACAGCACTGGGCTCAGAGTCCTCTCTGAGACACCCAGAGTTTC AGACAACAACCCGCTGGAATGCACAGTCTCAGCAGGAGAACAGACCAA AGCCAGCAAAAGGGACCTCGGTGACACCAGTAGGGACAGGAGGATTTT GTGGGGGCTCGTGTCAGTGTGAGGATATTGTAGTGGTGGTAGCTGCTT AGGAGACGGATCATCGTCGACTGCTGGGGGCCCTGGACCCGACCCGC CCTGGAGACCGCAGCCACATCAGCCCCAGCCCCACAGGCCCCCTACC AGCCGCAGGGTTTTGGCTGAGCTGATAGGAGACGGATCATCCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5613
hsIGH_2036_ D009_J002_I GHD2- 21_IGHJ2	GCCTTGCCAGCCCGCTCAGGTGTCTACGGATCATCAGCCCCCTGTACA GCACTGGGCTCAGAGTCCTCTCTGAGACAGGCTCAGTTTCAGACAACA ACCCGCTGGAATGCACAGTCTCAGCAGGAGAGCCAGGCCAGAGCCAGC AAGAGGAGACTCGGTGACACCAGTCTCCTGTAGGGACAGGAGGATTTT GTGGGGGTTCTGTGTCAGTGTGAGCATATTGTGGTGGTGAAGTGTGT CTACGGATCATCGTCGACTGCTGGGGGCCCTGGACCCGACCCGCCCT GGAGACCGCAGCCACATCAGCCCCAGCCCCACAGGCCCCCTACCAGC CGCAGGGTTTTGGCTGAGCTGAGTGTCTACGGATCATCCTGATGGCGC GAGGGAGGC	SEQ ID NO: 5614
hsIGH_2037_ D010_J002_I GHD3- 03_IGHJ2	GCCTTGCCAGCCCGCTCAGTGCTACACGGATCATCGTGGGCACGGACA CTGTCCACCTAAGCCAGGGGCAGACCCGAGTGTCCCCGAGTAGACCT GAGAGCGCTGGGCCCACAGCCTCCCTCGGTGCCCTGCTACCTCCTCA GGTCAGCCCTGGACATCCCGGGTTTCCCCAGGCTGGCGGTAGGTTTGG GGTGAGGTCTGTGTCACTGTGGTATTACGATTTTGGAGTGGTTATTT GCTACACGGATCATCGTCGACTGCTGGGGGCCCTGGACCCGACCCGC CCTGGAGACCGCAGCCACATCAGCCCCAGCCCCACAGGCCCCCTACC AGCCGCAGGGTTTTGGCTGAGCTGATGCTACACGGATCATCCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5615

Name	Sequence	SEQ ID NO
hsIGH_2038_ D011_J002_I GHD3- 09_IGHJ2	GCCTTGCCAGCCCGCTCAGAACTGCCAGGATCATCTGGGCACGGACAC TATCCACATAAGCGAGGGATAGACCCGAGTGTCCCCACAGCAGACCTG AGAGCGCTGGGCCCACAGCCTCCCCTCAGAGCCCTGCTGCCTCCTCCG GTCAGCCCTGGACATCCCAGGTTTCCCCAGGCCTGCCGGTAGGTTTAG AATGAGGTCTGTGTCAGTGTGGTATTACGATATTTTGAAGTGGTTATTA ACTGCCAGGATCATCGTCGACTGCTGGGGGCCCCCTGGACCCGACCCGC CCTGGAGACCGCAGCCACATCAGCCCCCAGCCCCACAGGCCCCCTACC AGCCGCAGGGTTTTGGCTGAGCTGAACTGCCAGGATCATCCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5616
hsIGH_2039_ D012_J002_I GHD3- 10_IGHJ2	GCCTTGCCAGCCCGCTCAGTTGGACTGGGATCATCCGATATTTTGAAGT GGTTATTATAACCACAGTGTACAGAGTCCATCAAAAACCCATGCCTG GAAGCTTCCCGCCACAGCCCTCCCCTATGGGGCCCTGCTGCCTCCTCAG GTCAGCCCCGGACATCCCAGGTTTCCCCAGGCCTGGGCGGTAGGTTTGG GGTGAGGTCTGTGTCAGTGTGGTATTACTATGGTTTCGGGGAGTTATTT TGGACTGGGATCATCGTCGACTGCTGGGGGCCCCCTGGACCCGACCCGC CCTGGAGACCGCAGCCACATCAGCCCCCAGCCCCACAGGCCCCCTACC AGCCGCAGGGTTTTGGCTGAGCTGATTGGACTGGGATCATCCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5617
hsIGH_2040_ D013_J002_I GHD3- 16_IGHJ2	GCCTTGCCAGCCCGCTCAGGTAGACACGGATCATCTGGACGCGGACAC TATCCACATAAGCGAGGGACAGACCCGAGTGTTCCTGCAGTAGACCTG AGAGCGCTGGGCCCACAGCCTCCCCTCGGTGCCCTGCTGCCTCCTCAG GTCAGCCCTGGACATCCCAGGTTTCCCCAGGCCAGATGGTAGGTTTGA AGTGAGGTCTGTGTCAGTGTGGTATTATGATTACGTTTGGGGGAGTTA TCGTTGTAGACACGGATCATCGTCGACTGCTGGGGGCCCCCTGGACCCG ACCCGCCCTGGAGACCGCAGCCACATCAGCCCCCAGCCCCACAGGCCC CCTACCAGCCGAGGGTTTTGGCTGAGCTGAGTAGACACGGATCATCC TGATGGCGCGAGGGAGGC	SEQ ID NO: 5618
hsIGH_2041_ D014_J002_I GHD3- 22_IGHJ2	GCCTTGCCAGCCCGCTCAGCACTGTACGGATCATCTGGGCATGGACAG TGTCACCTAAGCGAGGGACAGACCCGAGTGTCCCTGCAGTAGACCTG AGAGCGCTGGGCCCACAGCCTCCCCTCGGGGCCCTGCTGCCTCCTCAG GTCAGCCCTGGACATCCCAGGTTTCCCCAGGCCTGGCGGTAGGTTTGA AGTGAGGTCTGTGTCAGTGTGGTATTACTATGATAGTAGTGGTTATTC ACTGTACGGATCATCGTCGACTGCTGGGGGCCCCCTGGACCCGACCCGC CCTGGAGACCGCAGCCACATCAGCCCCCAGCCCCACAGGCCCCCTACC AGCCGCAGGGTTTTGGCTGAGCTGACACTGTACGGATCATCCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5619

Name	Sequence	SEQ ID NO
hsIGH_2042_ D015_J002_I GHD4- 04_IGHJ2	GCCTTGCCAGCCCGCTCAGGATGATCCGGATCATCCAAGGGTGAGTCA GACCCCTCCTGCCCTCGATGGCAGGCGGAGAAGATTAGAAAGGTCTGA GATCCCCAGGACGCAGCACCCTGTCAATGGGGGCCCCAGACGCCTGG ACCAGGGCCTGCGTGGGAAAGGCCTCTGGGCACACTCAGGGGCTTTTT GTGAAGGGTCCTCCTACTGTGTGACTACAGTAGATGATCCGGATCATC GTCGACTGCTGGGGGCCCCCTGGACCCGACCCGCCCTGGAGACCGCAGC CACATCAGCCCCCAGCCCCACAGGCCCCCTACCAGCCGCAGGGTTTTG GCTGAGCTGAGATGATCCGGATCATCCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5620
hsIGH_2043_ D016_J002_I GHD4- 11_IGHJ2	GCCTTGCCAGCCCGCTCAGCGCCAATAGGATCATCTGCCTCTCTCCCC AGTGGACACCCTCTTCCAGGACAGTCCTCAGTGGCATCACAGCGCCT GAGATCCCCAGGACGCAGCACCCTGTCAATAGGGGCCCCAAATGCCT GGACCAGGGCCTGCGTGGGAAAGGTCTCTGGCCACACTCGGGCTTTTT GTGAAGGGCCCTCCTGCTGTGTGACTACAGTACGCCAATAGGATCATC GTCGACTGCTGGGGGCCCCCTGGACCCGACCCGCCCTGGAGACCGCAGC CACATCAGCCCCCAGCCCCACAGGCCCCCTACCAGCCGCAGGGTTTTG GCTGAGCTGACGCCAATAGGATCATCCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5621
hsIGH_2044_ D017_J002_I GHD4- 17_IGHJ2	GCCTTGCCAGCCCGCTCAGTCAAGCCTGGATCATCGGAGGGTGAGTCA GACCCACCTGCCCTCGATGGCAGGCGGGGAAGATTAGAAAGGCCTGA GATCCCCAGGACGCAGCACCCTGTCAATGGGGGCCCCAGACGCCTGG ACCAGGGCCTGCGTGGGAAAGGCCGCTGGGCACACTCAGGGGCTTTTT GTGAAGGGCCCTCCTACTGTGTGACTACGGTGTCAAGCCTGGATCATC GTCGACTGCTGGGGGCCCCCTGGACCCGACCCGCCCTGGAGACCGCAGC CACATCAGCCCCCAGCCCCACAGGCCCCCTACCAGCCGCAGGGTTTTG GCTGAGCTGATCAAGCCTGGATCATCCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5622
hsIGH_2045_ D018_J002_I GHD4- 23_IGHJ2	GCCTTGCCAGCCCGCTCAGACGTGTGTGGATCATCGGAGGGTGAGTCA GACCCACCTGCCCTCAATGGCAGGCGGGGAAGATTAGAAAGGCCTGA GATCCCCAGGACGCAGCACCCTGTCAATGGGGGCCCCAGACGCCTGG ACCAGGGCCTGTGTGGGAAAGGCCTCTGGCCACACTCAGGGGCTTTTT GTGAAGGGCCCTCCTGCTGTGTGACTACGGTGGTAACGTGTGTGGATC ATCGTCGACTGCTGGGGGCCCCCTGGACCCGACCCGCCCTGGAGACCGC AGCCACATCAGCCCCCAGCCCCACAGGCCCCCTACCAGCCGCAGGGTT TTGGCTGAGCTGAACGTGTGTGGATCATCCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5623
hsIGH_2046_ D019_J002_I GHD5- 05_IGHJ2	GCCTTGCCAGCCCGCTCAGTCCGTCTAGGATCATCAGAGGCCTCTCCA GGGGGACACTGTGCATGTCTGGTCCCTGAGCAGCCCCCATGTCCCCA GTCCTGGGGGGCCCCCTGGCACAGCTGTCTGGACCCTCTCTATTCCCT GGGAAGCTCCTCCTGACAGCCCCGCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGTGAGACTGTGGTGGATACAGCTATGTCCGTCTAGGAT CATCGTCGACTGCTGGGGGCCCCCTGGACCCGACCCGCCCTGGAGACCG CAGCCACATCAGCCCCCAGCCCCACAGGCCCCCTACCAGCCGCAGGGT TTTGGCTGAGCTGATCCGTCTAGGATCATCCTGATGGCGCGAGGGAGG C	SEQ ID NO: 5624

Name	Sequence	SEQ ID NO
hsIGH_2047_ D020_J002_I GHD5- 12_IGHJ2	GCCTTGCCAGCCCGCTCAGAAGAGCTGGGATCATCGCAGAGGCCTCTC CAGGGAGACACTGTGCATGTCTGGTACCTAAGCAGCCCCCACGTCCC CAGTCCTGGGGGCCCCCTGGCTCAGCTGTCTGGACCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCTCCAGTTCCAGGTGTGGTTATT GTCAGGCGATGTCAGACTGTGGTGGATATAGTGGCTACGAAGAGCTGG GATCATCGTCGACTGCTGGGGGCCCCCTGGACCCGACCCGCCCTGGAGA CCGCAGCCACATCAGCCCCCAGCCCCACAGGCCCCCTACCAGCCGCAG GGTTTTGGCTGAGCTGAAAGAGCTGGGATCATCCTGATGGCGCGAGGG AGGC	SEQ ID NO: 5625
hsIGH_2048_ D021_J002_I GHD5- 18_IGHJ2	GCCTTGCCAGCCCGCTCAGTATCGCTCGGATCATCGCAGAGGCCTCTC CAGGGGGACACTGTGCATGTCTGGTCCCTGAGCAGCCCCCACGTCCC CAGTCCTGGGGGCCCCCTGGCACAGCTGTCTGGACCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGTGACACTGTGGTGGATACAGCTATGTATCGCTCGGAT CATCGTCGACTGCTGGGGGCCCCCTGGACCCGACCCGCCCTGGAGACCG CAGCCACATCAGCCCCCAGCCCCACAGGCCCCCTACCAGCCGCAGGGT TTTGGCTGAGCTGATATCGCTCGGATCATCCTGATGGCGCGAGGGAGG C	SEQ ID NO: 5626
hsIGH_2049_ D022_J002_I GHD5- 24_IGHJ2	GCCTTGCCAGCCCGCTCAGTCAGATGCGGATCATCGCAGAGGCCTCTC CAGGGGGACACAGTGCATGTCTGGTCCCTGAGCAGCCCCCAGGCTCTC TAGCACTGGGGGCCCCCTGGCACAGCTGTCTGGACCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGCCAGGCCGTGGTAGAGATGGCTACATCAGATGCGGAT CATCGTCGACTGCTGGGGGCCCCCTGGACCCGACCCGCCCTGGAGACCG CAGCCACATCAGCCCCCAGCCCCACAGGCCCCCTACCAGCCGCAGGGT TTTGGCTGAGCTGATCAGATGCGGATCATCCTGATGGCGCGAGGGAGG C	SEQ ID NO: 5627
hsIGH_2050_ D023_J002_I GHD6- 06_IGHJ2	GCCTTGCCAGCCCGCTCAGGTGTAGCAGGATCATCAGGCAGCTGACTC CTGACTTGACGCCTATTCCAGACACCAGACAGAGGGGCAGGCCCCC AGAACCAGGGATGAGGACGCCCCGTC AAGGCCAGAAAAGACCAAGTTG TGCTGAGCCCAGCAAGGGAAGGTCCCCAAACAAACCAGGAACGTTTCT GAAGGTGTCTGTGTACAGTGGAGTATAGCAGCTGTGTAGCAGGATCA TCGTCGACTGCTGGGGGCCCCCTGGACCCGACCCGCCCTGGAGACCGCA GCCACATCAGCCCCCAGCCCCACAGGCCCCCTACCAGCCGCAGGGTTT TGGCTGAGCTGAGTGTAGCAGGATCATCCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5628

Name	Sequence	SEQ ID NO
hsIGH_2051_ D024_J002_I GHD6- 13_IGHJ2	GCCTTGCCAGCCCGCTCAGTGGCAGTTGGATCATCAGGCAGCTGACCC CTGACTTGGACCCCTATTCCAGACACCAGACAGAGGCGCAGGCCCCC AGAACCAGGGTTGAGGGACGCCCCGTCAAAGCCAGACAAAACCAAGGG GTGTTGAGCCCAGCAAGGGAAGGCCCCCAAACAGACCAGGAGGTTTCT GAAGGTGTCTGTGTACAGTGGGGTATAGCAGCAGCTTGGCAGTTGGA TCATCGTCGACTGCTGGGGGCCCCCTGGACCCGACCCGCCCTGGAGACC GCAGCCACATCAGCCCCCAGCCCCACAGGCCCCCTACCAGCCGCAGGG TTTTGGCTGAGCTGATGGCAGTTGGATCATCCTGATGGCGCGAGGGAG GC	SEQ ID NO: 5629
hsIGH_2052_ D025_J002_I GHD6- 19_IGHJ2	GCCTTGCCAGCCCGCTCAGCAGTCCAAGGATCATCTGAGGTAGCTGGC CTCTGTCTCGGACCCCACTCCAGACACCAGACAGAGGGGCAGGCCCC CAAAACCAGGGTTGAGGGATGATCCGTCAAGGCAGACAAGACCAAGGG GCACTGACCCAGCAAGGGAAGGCTCCCAAACAGACGAGGAGGTTTCT GAAGCTGTCTGTATCACAGTGGGGTATAGCAGTGGCTCAGTCCAAGGA TCATCGTCGACTGCTGGGGGCCCCCTGGACCCGACCCGCCCTGGAGACC GCAGCCACATCAGCCCCCAGCCCCACAGGCCCCCTACCAGCCGCAGGG TTTTGGCTGAGCTGACAGTCCAAGGATCATCCTGATGGCGCGAGGGAG GC	SEQ ID NO: 5630
hsIGH_2053_ D026_J002_I GHD6- 25_IGHJ2	GCCTTGCCAGCCCGCTCAGTACGTACGGGATCATCCAGCTGGCCTCTG TCTCGGACCCCCATTCCAGACACCAGACAGAGGGACAGGCCCCCAGA ACCAGTGTTGAGGGACACCCCTGTCCAGGGCAGCCAAGTCCAAGAGGC GCGCTGAGCCCAGCAAGGGAAGGCCCCCAAACAAACCAGGAGGTTTCT GAAGCTGTCTGTGTACAGTCGGGTATAGCAGCGTACGTACGGGATCA TCGTCGACTGCTGGGGGCCCCCTGGACCCGACCCGCCCTGGAGACCGCA GCCACATCAGCCCCCAGCCCCACAGGCCCCCTACCAGCCGCAGGGTTT TGGCTGAGCTGATACGTACGGGATCATCCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5631
hsIGH_2054_ D027_J002_I GHD7- 27_IGHJ2	GCCTTGCCAGCCCGCTCAGAGTACCGAGGATCATCAGGGTTGAGGGCT GGGGTCTCCACGTGTTTTGGGGCTAACAGCGGAAGGGAGAGCACTGG CAAAGGTGCTGGGGGTCCCTGAACCCGACCCGCCCTGAGACCGCAGC CACATCAGCCCCCAGCCCCACAGGCCCCCTACCAGCCGCAGGGTTTTT GGCTGAGCTGAGAACCACTGTGCTAACTAGTACCGAGGATCATCGTCG ACTGCTGGGGGCCCCCTGGACCCGACCCGCCCTGGAGACCGCAGCCACA TCAGCCCCCAGCCCCACAGGCCCCCTACCAGCCGCAGGGTTTTGGCTG AGCTGAAGTACCGAGGATCATCCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5632

Name	Sequence	SEQ ID NO
hsIGH_2055_ D001_J003_I GHD1- 01_IGHJ3	GCCTTGCCAGCCCGCTCAGGACACTCTTATTGGCGGCCCCGGTCTCTG TGGGTGTTCGCTAACTGGGGCTCCCAGTGCTACCCCACTAAAG CGAGCCCCAGCCTCCAGAGCCCCGAAGGAGATGCCGCCACAAGCCC AGCCCCATCCAGGAGGCCAGAGCTCAGGGCGCCGGGCAGATTCT GAACAGCCCCGAGTCACGGTGGGTACAAC TGGAGACACTCTTATTGGC GGTCGACGGTACTTCGATCTCTGGGGCCGTGGCACCC TGGTCACTGTC TCCTCAGGTGAGTCCCAGTGCAGCCCCCTCCCAGTCTTCTCTGTCCAG GCACCAGGCCAGACACTCTTATTGGCGCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5633
hsIGH_2056_ D002_J003_I GHD1- 07_IGHJ3	GCCTTGCCAGCCCGCTCAGTTCGGAAC TATTGGCGGGCCTCGGTCTCT GTGGGTGTTCGCTAGCTGGGGCTCACAGTGCTACCCCACTAA ACGAGCCACAGCCTCAGAGCCCCCTGAAGGAGACCCCGCCACAAGCCC AGCCCCACCCAGGAGGCCAGAGCACAGGGCGCCCCGTCGGATTCT GAACAGCCCCGAGTCACAGTGGGTATAAC TGGATTTCGGAAC TATTGGC GGTCGACGGTACTTCGATCTCTGGGGCCGTGGCACCC TGGTCACTGTC TCCTCAGGTGAGTCCCAGTGCAGCCCCCTCCCAGTCTTCTCTGTCCAG GCACCAGGCCATTTCGGAAC TATTGGCGCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5634
hsIGH_2057_ D003_J003_I GHD1- 14_IGHJ3	GCCTTGCCAGCCCGCTCAGAAGTAACGTATTGGCGGGCCTCGGTCTCT GTGGGTGTTCGCTAGCTGGGGCTCACAGTGCTACCCCACTAA ATGAGCCACAGCCTCCGAGCCCCCGCAGAGACCCCGCCACAAGCCC AGCCCCACCCAGGAGGCCAGAGCTCAGGGCGCCCCGTCGGATTCC GAACAGCCCCGAGTCACAGCGGGTATAACCGGAAAGTAACGTATTGGC GGTCGACGGTACTTCGATCTCTGGGGCCGTGGCACCC TGGTCACTGTC TCCTCAGGTGAGTCCCAGTGCAGCCCCCTCCCAGTCTTCTCTGTCCAG GCACCAGGCCAAAGTAACGTATTGGCGCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5635
hsIGH_2058_ D004_J003_I GHD1- 20_IGHJ3	GCCTTGCCAGCCCGCTCAGGTCTCCTATATTGGCGGTCTCTGTGGGTG TTCCGCTAGCTGGGGCCCCAGTGCTACCCCACTAAAGCGAGCC CCAGCCTCCAGAGCCCCCTAAGCATTCCTCCCGCCAGCAGCCAGCCCC TGCCCCACCCAGGAGGCCAGAGCTCAGGGCGCCTGGTCCGATTCT GAACAGCCCCGAGTCACAGTGGGTATAAC TGGAGTCTCCTATATTGGC GGTCGACGGTACTTCGATCTCTGGGGCCGTGGCACCC TGGTCACTGTC TCCTCAGGTGAGTCCCAGTGCAGCCCCCTCCCAGTCTTCTCTGTCCAG GCACCAGGCCAGTCTCCTATATTGGCGCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5636
hsIGH_2059_ D005_J003_I GHD1- 26_IGHJ3	GCCTTGCCAGCCCGCTCAGAGAGTGTCTATTGGCGAGGCCTCAGGCTC TGTGGGTGCCGCTAGCTGGGGCTGCCAGTCC TACCCCACTAAAG TGAGCCACAGCCGCCAGAGCTCCACAGGAGACCCACCCAGCAGCCC AGCCCCTACCCAGGAGGCCAGAGCTCAGGGCGCCTGGGTGGATTCT GAACAGCCCCGAGTCACGGTGGGTATAGTGGGAGCTAGAGTGTCTATT GGCGGTGACGGTACTTCGATCTCTGGGGCCGTGGCACCC TGGTCACT GTCTCCTCAGGTGAGTCCCAGTGCAGCCCCCTCCCAGTCTTCTCTGTC CAGGCACCAGGCCAAGAGTGTCTATTGGCGCTGATGGCGCGAGGGAGG C	SEQ ID NO: 5637

Name	Sequence	SEQ ID NO
hsIGH_2060_ D006_J003_I GHD2- 02_IGHJ3	GCCTTGCCAGCCCGCTCAGGTTCCGAATATTGGCGAAAGGAGGAGCCC CCTGTACAGCACTGGGCTCAGAGTCCTCTCCCACACACCCTGAGTTTC AGACAAAAACCCCTGGAAATCATAGTATCAGCAGGAGAACTAGCCAG AGACAGCAAGAGGGGACTCAGTGACTCCCGCGGGGACAGGAGGATTTT GTGGGGGCTCGTGTCAGTGTGAGGATATTGTAGTAGTACCAGCTGCTG TTCCGAATATTGGCGGTCGACGGTACTTCGATCTCTGGGGCCGTGGCA CCCTGGTCACTGTCTCCTCAGGTGAGTCCCACTGCAGCCCCCTCCAG TCTTCTCTGTCCAGGCACCAGGCCAGTTCCGAATATTGGCGCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5638
hsIGH_2061_ D007_J003_I GHD2- 08_IGHJ3	GCCTTGCCAGCCCGCTCAGCGTTACTTTATTGGCGAAAGGAGGAGCCC CTTGTTACAGCACTGGGCTCAGAGTCCTCTCCAAGACACCAGAGTTTC AGACAAAAACCCCTGGAATGCACAGTCTCAGCAGGAGAGCCAGCCAG AGCCAGCAAGATGGGGCTCAGTGACACCCGCAGGGACAGGAGGATTTT GTGGGGGCTCGTGTCAGTGTGAGGATATTGTACTAATGGTGTATGCTC GTTACTTTATTGGCGGTCGACGGTACTTCGATCTCTGGGGCCGTGGCA CCCTGGTCACTGTCTCCTCAGGTGAGTCCCACTGCAGCCCCCTCCAG TCTTCTCTGTCCAGGCACCAGGCCACGTTACTTTATTGGCGCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5639
hsIGH_2062_ D008_J003_I GHD2- 15_IGHJ3	GCCTTGCCAGCCCGCTCAGTAGGAGACTATTGGCGAAAGGAGGAGCCC CCTATACAGCACTGGGCTCAGAGTCCTCTCTGAGACACCCTGAGTTTC AGACAACAACCCGCTGGAATGCACAGTCTCAGCAGGAGAAACAGACCAA AGCCAGCAAAAGGGACCTCGGTGACACCAGTAGGGACAGGAGGATTTT GTGGGGGCTCGTGTCAGTGTGAGGATATTGTAGTGGTGGTAGCTGCTT AGGAGACTATTGGCGGTCGACGGTACTTCGATCTCTGGGGCCGTGGCA CCCTGGTCACTGTCTCCTCAGGTGAGTCCCACTGCAGCCCCCTCCAG TCTTCTCTGTCCAGGCACCAGGCCATAGGAGACTATTGGCGCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5640
hsIGH_2063_ D009_J003_I GHD2- 21_IGHJ3	GCCTTGCCAGCCCGCTCAGGTGTCTACTATTGGCGAGCCCCCTGTACA GCACTGGGCTCAGAGTCCTCTCTGAGACAGGCTCAGTTTCAGACAACA ACCCGCTGGAATGCACAGTCTCAGCAGGAGAGCCAGGCCAGAGCCAGC AAGAGGAGACTCGGTGACACCAGTCTCCTGTAGGGACAGGAGGATTTT GTGGGGGTTCGTGTCACTGTGAGCATATTGTGGTGGTGAAGTGTGTGT CTACTATTGGCGGTCGACGGTACTTCGATCTCTGGGGCCGTGGCACCC TGGTCACTGTCTCCTCAGGTGAGTCCCACTGCAGCCCCCTCCAGTCT TCTCTGTCCAGGCACCAGGCCAGTGTCTACTATTGGCGCTGATGGCGC GAGGGAGGC	SEQ ID NO: 5641

Name	Sequence	SEQ ID NO
hsIGH_2064_ D010_J003_I GHD3- 03_IGHJ3	GCCTTGCCAGCCCGCTCAGTGCTACACTATTGGCGGTGGGCACGGACA CTGTCCACCTAAGCCAGGGGCAGACCCGAGTGTCCCCGAGTAGACCT GAGAGCGCTGGGCCCACAGCCTCCCCTCGGTGCCCTGCTACCTCCTCA GGTCAGCCCTGGACATCCCGGGTTTCCCCAGGCTGGCGGTAGGTTTGG GGTGAGGTCTGTGTCACTGTGGTATTACGATTTTTGGAGTGGTTATTT GCTACACTATTGGCGGTGACGGTACTTCGATCTCTGGGGCCGTGGCA CCCTGGTCACTGTCTCCTCAGGTGAGTCCCAGTGCAGCCCCCTCCAG TCTTCTCTGTCCAGGCACCAGGCCATGCTACACTATTGGCGCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5642
hsIGH_2065_ D011_J003_I GHD3- 09_IGHJ3	GCCTTGCCAGCCCGCTCAGAACTGCCATATTGGCGTGGGCACGGACAC TATCCACATAAGCGAGGGATAGACCCGAGTGTCCCCACAGCAGACCTG AGAGCGCTGGGCCCACAGCCTCCCCTCAGAGCCCTGCTGCCTCCTCCG GTCAGCCCTGGACATCCCAGGTTTCCCCAGGCTGCCGGTAGGTTTAG AATGAGGTCTGTGTCACTGTGGTATTACGATATTTTGACTGGTTATTA ACTGCCATATTGGCGGTGACGGTACTTCGATCTCTGGGGCCGTGGCA CCCTGGTCACTGTCTCCTCAGGTGAGTCCCAGTGCAGCCCCCTCCAG TCTTCTCTGTCCAGGCACCAGGCCAAACTGCCATATTGGCGCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5643
hsIGH_2066_ D012_J003_I GHD3- 10_IGHJ3	GCCTTGCCAGCCCGCTCAGTTGGACTGTATTGGCGCGATATTTTGA GGTTATTATAACCACAGTGTACAGAGTCCATCAAAAACCCATGCCTG GAAGCTTCCCGCCACAGCCCTCCCCTGCGGGCCCTGCTGCCTCCTCAG GTCAGCCCCGGACATCCCGGGTTTCCCCAGGCTGGCGGTAGGTTTGG GGTGAGGTCTGTGTCACTGTGGTATTACTATGGTTCGGGGAGTTATTT TGGACTGTATTGGCGGTGACGGTACTTCGATCTCTGGGGCCGTGGCA CCCTGGTCACTGTCTCCTCAGGTGAGTCCCAGTGCAGCCCCCTCCAG TCTTCTCTGTCCAGGCACCAGGCCATTGGACTGTATTGGCGCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5644
hsIGH_2067_ D013_J003_I GHD3- 16_IGHJ3	GCCTTGCCAGCCCGCTCAGGTAGACACTATTGGCGTGGACGCGGACAC TATCCACATAAGCGAGGGACAGACCCGAGTGTTCCTGCAGTAGACCTG AGAGCGCTGGGCCCACAGCCTCCCCTCGGTGCCCTGCTGCCTCCTCAG GTCAGCCCTGGACATCCCGGGTTTCCCCAGGCCAGATGGTAGGTTTGA AGTGAGGTCTGTGTCACTGTGGTATTATGATTACGTTTGGGGGAGTTA TCGTTGTAGACACTATTGGCGGTGACGGTACTTCGATCTCTGGGGCC GTGGCACCCCTGGTCACTGTCTCCTCAGGTGAGTCCCAGTGCAGCCCC TCCCAGTCTTCTCTGTCCAGGCACCAGGCCAGTAGACACTATTGGCGC TGATGGCGCGAGGGAGGC	SEQ ID NO: 5645

Name	Sequence	SEQ ID NO
hsIGH_2068_ D014_J003_I GHD3- 22_IGHJ3	GCCTTGCCAGCCCGCTCAGCACTGTACTATTGGCGTGGGCATGGACAG TGTCCACCTAAGCGAGGGACAGACCCGAGTGTCCCTGCAGTAGACCTG AGAGCGCTGGGCCCACAGCCTCCCCCTCGGGGCCCTGCTGCCTCCTCAG GTCAGCCCTGGACATCCCGGGTTTCCCCAGGCCTGGCGGTAGGTTTGA AGTGAGGTCTGTGTCACTGTGGTATTACTATGATAGTAGTGGTTATTC ACTGTACTATTGGCGGTGACGGTACTTCGATCTCTGGGGCCGTGGCA CCCTGGTCACTGTCTCCTCAGGTGAGTCCCAGTGCAGCCCCCTCCAG TCTTCTCTGTCCAGGCACCAGGCCACACTGTACTATTGGCGCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5646
hsIGH_2069_ D015_J003_I GHD4- 04_IGHJ3	GCCTTGCCAGCCCGCTCAGGATGATCCTATTGGCGCAAGGGTGAGTCA GACCTCCTGCCCTCGATGGCAGGCGGAGAAGATTAGAAAGGTCTGA GATCCCCAGGACGCAGCACCCTGTCAATGGGGGCCCCAGACGCCTGG ACCAGGGCCTGCGTGGGAAAGGCCTCTGGGCACACTCAGGGGCTTTTT GTGAAGGGTCTCTACTGTGTGACTACAGTAGATGATCCTATTGGCG GTCGACGGTACTTCGATCTCTGGGGCCGTGGCACCCCTGGTCACTGTCT CCTCAGGTGAGTCCCAGTGCAGCCCCCTCCCAGTCTTCTCTGTCCAGG CACCAGGCCAGATGATCCTATTGGCGCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5647
hsIGH_2070_ D016_J003_I GHD4- 11_IGHJ3	GCCTTGCCAGCCCGCTCAGCGCCAATATATTGGCGTGCCTCTCTCCCC AGTGGAACCCCTCTTCCAGGACAGTCCCTCAGTGGCATCACAGCGGCCT GAGATCCCCAGGACGCAGCACCCTGTCAATAGGGGCCCCAAATGCCT GGACCAGGGCCTGCGTGGGAAAGGTCTCTGGCCACACTCGGGCTTTTT GTGAAGGGCCCTCCTGCTGTGTGACTACAGTACGCCAATATATTGGCG GTCGACGGTACTTCGATCTCTGGGGCCGTGGCACCCCTGGTCACTGTCT CCTCAGGTGAGTCCCAGTGCAGCCCCCTCCCAGTCTTCTCTGTCCAGG CACCAGGCCACGCCAATATATTGGCGCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5648
hsIGH_2071_ D017_J003_I GHD4- 17_IGHJ3	GCCTTGCCAGCCCGCTCAGTCAAGCCTTATTGGCGGGAGGGTGAGTCA GACCCACCTGCCCTCGATGGCAGGCGGGGAAGATTAGAAAGGCCTGA GATCCCCAGGACGCAGCACCCTGTCAATGGGGGCCCCAGACGCCTGG ACCAGGGCCTGCGTGGGAAAGGCCGTGGGCACACTCAGGGGCTTTTT GTGAAGGGCCCTCCTACTGTGTGACTACGGTGTCAAGCCTTATTGGCG GTCGACGGTACTTCGATCTCTGGGGCCGTGGCACCCCTGGTCACTGTCT CCTCAGGTGAGTCCCAGTGCAGCCCCCTCCCAGTCTTCTCTGTCCAGG CACCAGGCCATCAAGCCTTATTGGCGCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5649
hsIGH_2072_ D018_J003_I GHD4- 23_IGHJ3	GCCTTGCCAGCCCGCTCAGACGTGTGTTATTGGCGGGAGGGTGAGTCA GACCCACCTGCCCTCAATGGCAGGCGGGGAAGATTAGAAAGGCCTGA GATCCCCAGGACGCAGCACCCTGTCAATGGGGGCCCCAGACGCCTGG ACCAGGGCCTGTGTGGGAAAGGCCTCTGGCCACACTCAGGGGCTTTTT GTGAAGGGCCCTCCTGCTGTGTGACTACGGTGGTAACGTGTGTTATTG GCGGTGACGGTACTTCGATCTCTGGGGCCGTGGCACCCCTGGTCACTG TCTCCTCAGGTGAGTCCCAGTGCAGCCCCCTCCCAGTCTTCTCTGTCC AGGCACCAGGCCAACGTGTGTTATTGGCGCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5650

Name	Sequence	SEQ ID NO
hsIGH_2073_ D019_J003_I GHD5- 05_IGHJ3	GCCTTGCCAGCCCGCTCAGTCCGTCTATATTGGCGAGAGGCCTCTCCA GGGGGACACTGTGCATGTCTGGTCCCTGAGCAGCCCCCATGTCCCCA GTCCTGGGGGGCCCCCTGGCACAGCTGTCTGGACCCTCTCTATTCCCT GGGAAGCTCCTCCTGACAGCCCCGCCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGTGCACTGTGGTGGATACAGCTATGTCCGTCTATATT GGCGGTCGACGGTACTTCGATCTCTGGGGCCGTGGCACCCCTGGTCACT GTCTCCTCAGGTGAGTCCCACTGCAGCCCCCTCCCAGTCTTCTCTGTC CAGGCACCAGGCCATCCGTCTATATTGGCGCTGATGGCGCGAGGGAGG C	SEQ ID NO: 5651
hsIGH_2074_ D020_J003_I GHD5- 12_IGHJ3	GCCTTGCCAGCCCGCTCAGAAGAGCTGTATTGGCGGCAGAGGCCTCTC CAGGGAGACACTGTGCATGTCTGGTACCTAAGCAGCCCCCACGTCCC CAGTCCCTGGGGGGCCCCCTGGCTCAGCTGTCTGGACCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCCTCCAGTTCCAGGTGTGGTTATT GTCAGGCGATGTGCACTGTGGTGGATATAGTGGCTACGAAGAGCTGT ATTGGCGGTCGACGGTACTTCGATCTCTGGGGCCGTGGCACCCCTGGTC ACTGTCTCCTCAGGTGAGTCCCACTGCAGCCCCCTCCCAGTCTTCTCT GTCCAGGCACCAGGCCAAAGAGCTGTATTGGCGCTGATGGCGCGAGGG AGGC	SEQ ID NO: 5652
hsIGH_2075_ D021_J003_I GHD5- 18_IGHJ3	GCCTTGCCAGCCCGCTCAGTATCGCTCTATTGGCGGCAGAGGCCTCTC CAGGGGGACACTGTGCATGTCTGGTCCCTGAGCAGCCCCCACGTCCC CAGTCCCTGGGGGGCCCCCTGGCACAGCTGTCTGGACCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGTGCACTGTGGTGGATACAGCTATGTATCGCTCTATT GGCGGTCGACGGTACTTCGATCTCTGGGGCCGTGGCACCCCTGGTCACT GTCTCCTCAGGTGAGTCCCACTGCAGCCCCCTCCCAGTCTTCTCTGTC CAGGCACCAGGCCATATCGCTCTATTGGCGCTGATGGCGCGAGGGAGG C	SEQ ID NO: 5653
hsIGH_2076_ D022_J003_I GHD5- 24_IGHJ3	GCCTTGCCAGCCCGCTCAGTCAGATGCTATTGGCGGCAGAGGCCTCTC CAGGGGGACACAGTGCATGTCTGGTCCCTGAGCAGCCCCCAGGCTCTC TAGCACTGGGGGGCCCCCTGGCACAGCTGTCTGGACCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGCCAGGCCGTGGTAGAGATGGCTACATCAGATGCTATT GGCGGTCGACGGTACTTCGATCTCTGGGGCCGTGGCACCCCTGGTCACT GTCTCCTCAGGTGAGTCCCACTGCAGCCCCCTCCCAGTCTTCTCTGTC CAGGCACCAGGCCATCAGATGCTATTGGCGCTGATGGCGCGAGGGAGG C	SEQ ID NO: 5654

Name	Sequence	SEQ ID NO
hsIGH_2077_ D023_J003_I GHD6- 06_IGHJ3	GCCTTGCCAGCCCGCTCAGGTGTAGCATATTGGCGAGGCAGCTGACTC CTGACTTGGACGCTTATTCCAGACACCAGACAGAGGGGCAGGCCCCC AGAACCAGGGATGAGGACGCCCCGTCAAGGCCAGAAAAGACCAAGTTG TGCTGAGCCCAGCAAGGGAAGGTCCCCAAACAAACCAGGAACGTTTCT GAAGGTGTCTGTGTACAGTGGAGTATAGCAGCTGTGTAGCATATTGG CGGTCGACGGTACTTTCGATCTCTGGGGCCGTGGCACCCCTGGTCACTGT CTCCTCAGGTGAGTCCCAGTGCAGCCCCCTCCCAGTCTTCTCTGTCCA GGCACCCAGGCCAGTGTAGCATATTGGCGCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5655
hsIGH_2078_ D024_J003_I GHD6- 13_IGHJ3	GCCTTGCCAGCCCGCTCAGTGGCAGTTTATTGGCGAGGCAGCTGACCC CTGACTTGGACCCCTTATTCCAGACACCAGACAGAGGCGCAGGCCCCC AGAACCAGGGTTGAGGGACGCCCCGTCAAAGCCAGACAAAACCAAGGG GTGTTGAGCCCAGCAAGGGAAGGCCCCCAAACAGACCAGGAGGTTTCT GAAGGTGTCTGTGTACAGTGGGGTATAGCAGCAGCTTGGCAGTTTAT TGGCGGTGACGGTACTTCGATCTCTGGGGCCGTGGCACCCCTGGTCAC TGTCTCCTCAGGTGAGTCCCAGTGCAGCCCCCTCCCAGTCTTCTCTGT CCAGGCACCAGGCCATGGCAGTTTATTGGCGCTGATGGCGCGAGGGAG GC	SEQ ID NO: 5656
hsIGH_2079_ D025_J003_I GHD6- 19_IGHJ3	GCCTTGCCAGCCCGCTCAGCAGTCCAATATTGGCGTGAGGTAGCTGGC CTCTGTCTCGGACCCCACTCCAGACACCAGACAGAGGGGCAGGCCCCC CAAACCCAGGGTTGAGGGATGATCCGTCAAGGCAGACAAGACCAAGGG GCACTGACCCAGCAAGGGAAGGCTCCCAAACAGACGAGGAGGTTTCT GAAGCTGTCTGTATCACAGTGGGGTATAGCAGTGGCTCAGTCCAATAT TGGCGGTGACGGTACTTCGATCTCTGGGGCCGTGGCACCCCTGGTCAC TGTCTCCTCAGGTGAGTCCCAGTGCAGCCCCCTCCCAGTCTTCTCTGT CCAGGCACCAGGCCACAGTCCAATATTGGCGCTGATGGCGCGAGGGAG GC	SEQ ID NO: 5657
hsIGH_2080_ D026_J003_I GHD6- 25_IGHJ3	GCCTTGCCAGCCCGCTCAGTACGTACGTATTGGCGCAGCTGGCCTCTG TCTCGGACCCCCATTCCAGACACCAGACAGAGGGACAGGCCCCCAGA ACCAGTGTGAGGGACACCCCTGTCCAGGGCAGCCAAGTCCAAGAGGC GCGCTGAGCCCAGCAAGGGAAGGCCCCAAACAAACCAGGAGGTTTCT GAAGCTGTCTGTGTACAGTGGGGTATAGCAGCGTACGTACGTATTGG CGGTCGACGGTACTTTCGATCTCTGGGGCCGTGGCACCCCTGGTCACTGT CTCCTCAGGTGAGTCCCAGTGCAGCCCCCTCCCAGTCTTCTCTGTCCA GGCACCCAGGCCATACGTACGTATTGGCGCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5658

Name	Sequence	SEQ ID NO
hsIGH_2081_ D027_J003_I GHD7- 27_IGHJ3	GCCTTGCCAGCCCGCTCAGAGTACCGATATTGGCGAGGGTTGAGGGCT GGGGTCTCCACGTGTTTTGGGGCTAACAGCGGAAGGGAGAGCACTGG CAAAGGTGCTGGGGGTCCCCTGAACCCGACCCGCCCTGAGACCGCAGC CACATCAGCCCCAGCCCCACAGGCCCCCTACCAGCCGAGGGTTTTT GGCTGAGCTGAGAACCACTGTGCTAACTAGTACCGATATTGGCGGTCG ACGGTACTTTCGATCTCTGGGGCCGTGGCACCTGGTCACTGTCTCCTC AGGTGAGTCCCACTGCAGCCCCCTCCCAGTCTTCTGTCCAGGCACC AGGCCAAGTACCGATATTGGCGCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5659
hsIGH_2082_ D001_J004_I GHD1- 01_IGHJ4	GCCTTGCCAGCCCGCTCAGGACACTCTAGGCTTGAGCCCCGGTCTCTG TGGGTGTTCCGCTAACTGGGGCTCCCAGTGCTCACCACAACTAAAG CGAGCCCCAGCCTCCAGAGCCCCCGAAGGAGATGCCGCCACAAGCCC AGCCCCCATCCAGGAGGCCCCAGAGCTCAGGGCGCCGGGGCAGATTCT GAACAGCCCCGAGTCACGGTGGGTACAACGGAGACACTCTAGGCTTG AGTCGACAAGTGCTTGGAGCACTGGGGCCAGGGCAGCCCGGCCACCGT CTCCCTGGGAACGTCACCCCTCCCTGCCTGGGTCTCAGCCCGGGGGTC TGTGTGGCTGGGACACTCTAGGCTTGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5660
hsIGH_2083_ D002_J004_I GHD1- 07_IGHJ4	GCCTTGCCAGCCCGCTCAGTTCGGAACAGGCTTGAGGCCTCGGTCTCT GTGGGTGTTCCGCTAGCTGGGGCTCACAGTGCTCACCACACCTAAA ACGAGCCACAGCCTCAGAGCCCCCTGAAGGAGACCCCGCCACAAGCCC AGCCCCACCCAGGAGGCCCCAGAGCACAGGGCGCCCCGTCGGATTCT GAACAGCCCCGAGTCACAGTGGGTATAACTGGATTTCGGAACAGGCTTG AGTCGACAAGTGCTTGGAGCACTGGGGCCAGGGCAGCCCGGCCACCGT CTCCCTGGGAACGTCACCCCTCCCTGCCTGGGTCTCAGCCCGGGGGTC TGTGTGGCTGGTTCGGAACAGGCTTGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5661
hsIGH_2084_ D003_J004_I GHD1- 14_IGHJ4	GCCTTGCCAGCCCGCTCAGAAGTAACGAGGCTTGAGGCCTCGGTCTCT GTGGGTGTTCCGCTAGCTGGGGCTCACAGTGCTCACCACACCTAAA ATGAGCCACAGCCTCCGGAGCCCCCGAGAGACCCCGCCACAAGCCC AGCCCCACCCAGGAGGCCCCAGAGCTCAGGGCGCCCCGTCGGATTCC GAACAGCCCCGAGTCACAGCGGGTATAACCGGAAAGTAACGAGGCTTG AGTCGACAAGTGCTTGGAGCACTGGGGCCAGGGCAGCCCGGCCACCGT CTCCCTGGGAACGTCACCCCTCCCTGCCTGGGTCTCAGCCCGGGGGTC TGTGTGGCTGGAAGTAACGAGGCTTGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5662
hsIGH_2085_ D004_J004_I GHD1- 20_IGHJ4	GCCTTGCCAGCCCGCTCAGGTCTCCTAAGGCTTGAGTCTCTGTGGGTG TTCCGCTAGCTGGGGCCCCCAGTGCTCACCACACCTAAAGCGAGCC CCAGCCTCCAGAGCCCCCTAAGCATTCCTCGCCAGCAGCCAGCCCC TGCCCCACCCAGGAGGCCCCAGAGCTCAGGGCGCCTGGTCGGATTCT GAACAGCCCCGAGTCACAGTGGGTATAACTGGAGTCTCCTAAGGCTTG AGTCGACAAGTGCTTGGAGCACTGGGGCCAGGGCAGCCCGGCCACCGT CTCCCTGGGAACGTCACCCCTCCCTGCCTGGGTCTCAGCCCGGGGGTC TGTGTGGCTGGGTCTCCTAAGGCTTGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5663

Name	Sequence	SEQ ID NO
hsIGH_2086_ D005_J004_I GHD1- 26_IGHJ4	GCCTTGCCAGCCCGCTCAGAGAGTGTGTCAGGCTTGAAGGCCTCAGGCTC TGTGGGTGCCGCTAGCTGGGGCTGCCAGTCCTCACCCACACCTAAGG TGAGCCACAGCCGCCAGAGCCTCCACAGGAGACCCACCCAGCAGCCC AGCCCCCTACCCAGGAGGCCCCAGAGCTCAGGGCGCCTGGGTGGATTCT GAACAGCCCCGAGTCACGGTGGGTATAGTGGGAGCTAGAGTGTGAGGC TTGAGTCGACAAGTGCTTGGAGCACTGGGGCCAGGGCAGCCCGGCCAC CGTCTCCCTGGGAACGTCACCCCTCCCTGCCTGGGTCTCAGCCCGGGG GTCTGTGTGGCTGGAGAGTGTGTCAGGCTTGACTGATGGCGCAGGGAGG C	SEQ ID NO: 5664
hsIGH_2087_ D006_J004_I GHD2- 02_IGHJ4	GCCTTGCCAGCCCGCTCAGGTTCCGAAAGGCTTGAAAAGGAGGAGCCC CCTGTACAGCACTGGGCTCAGAGTCCTCTCCACACACCCTGAGTTTC AGACAAAAACCCCTGGAAATCATAGTATCAGCAGGAGAACTAGCCAG AGACAGCAAGAGGGGACTCAGTGACTCCCGCGGGGACAGGAGGATTTT GTGGGGGCTCGTGTCACTGTGAGGATATTGTAGTAGTACCAGCTGCTG TTCCGAAAGGCTTGAGTCGACAAGTGCTTGGAGCACTGGGGCCAGGGC AGCCCGGCCACCGTCTCCCTGGGAACGTCACCCCTCCCTGCCTGGGTCT TCAGCCCGGGGTCTGTGTGGCTGGGTTCGAAAGGCTTGACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5665
hsIGH_2088_ D007_J004_I GHD2- 08_IGHJ4	GCCTTGCCAGCCCGCTCAGCGTTACTTAGGCTTGAAAAGGAGGAGCCC CTTGTTTCAGCACTGGGCTCAGAGTCCTCTCCAAGACACCAGAGTTTC AGACAAAAACCCCTGGAATGCACAGTCTCAGCAGGAGAGCCAGCCAG AGCCAGCAAGATGGGGCTCAGTGACACCCGAGGGACAGGAGGATTTT GTGGGGGCTCGTGTCACTGTGAGGATATTGTACTAATGGTGTATGCTC GTTACTTAGGCTTGAGTCGACAAGTGCTTGGAGCACTGGGGCCAGGGC AGCCCGGCCACCGTCTCCCTGGGAACGTCACCCCTCCCTGCCTGGGTCT TCAGCCCGGGGTCTGTGTGGCTGGCGTTACTTAGGCTTGACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5666
hsIGH_2089_ D008_J004_I GHD2- 15_IGHJ4	GCCTTGCCAGCCCGCTCAGTAGGAGACAGGCTTGAAAAGGAGGAGCCC CCTATACAGCACTGGGCTCAGAGTCCTCTCTGAGACACCCTGAGTTTC AGACAACAACCCGCTGGAATGCACAGTCTCAGCAGGAGAACAGACCAA AGCCAGCAAAAGGGACCTCGGTGACACCAGTAGGGACAGGAGGATTTT GTGGGGGCTCGTGTCACTGTGAGGATATTGTAGTGGTGGTAGCTGCTT AGGAGACAGGCTTGAGTCGACAAGTGCTTGGAGCACTGGGGCCAGGGC AGCCCGGCCACCGTCTCCCTGGGAACGTCACCCCTCCCTGCCTGGGTCT TCAGCCCGGGGTCTGTGTGGCTGGTAGGAGACAGGCTTGACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5667

Name	Sequence	SEQ ID NO
hsIGH_2090_ D009_J004_I GHD2- 21_IGHJ4	GCCTTGCCAGCCCGCTCAGGTGTCTACAGGCTTGAAGCCCCCTGTACA GCACTGGGCTCAGAGTCCTCTCTGAGACAGGCTCAGTTTCAGACAACA ACCCGCTGGAATGCACAGTCTCAGCAGGAGAGCCAGGCCAGAGCCAGC AAGAGGAGACTCGGTGACACCAGTCTCCTGTAGGGACAGGAGGATTTT GTGGGGGTTCGTGTCACTGTGAGCATATTGTGGTGGTGA CTGCTGTGT CTACAGGCTTGAGTCGACAAGTGCTTGGAGCACTGGGGCCAGGGCAGC CCGGCCACCGTCTCCCTGGGAACGTACCCCCCTCCCTGCCTGGGTCTCA GCCCCGGGGTCTGTGTGGCTGGGTGTCTACAGGCTTGACTGATGGCGC GAGGGAGGC	SEQ ID NO: 5668
hsIGH_2091_ D010_J004_I GHD3- 03_IGHJ4	GCCTTGCCAGCCCGCTCAGTGCTACACAGGCTTGAGTGGGCACGGACA CTGTCCACCTAAGCCAGGGGCAGACCCGAGTGTCCCCGCAGTAGACCT GAGAGCGCTGGGCCCACAGCCTCCCCTCGGTGCCCTGCTACCTCCTCA GGTCAGCCCTGGACATCCCGGGTTTCCCCAGGCTGGCGGTAGGTTTGG GGTGAGGTCTGTGTCACTGTGGTATTACGATTTTGGAGTGTTATTT GCTACACAGGCTTGAGTCGACAAGTGCTTGGAGCACTGGGGCCAGGGC AGCCCGGCCACCGTCTCCCTGGGAACGTACCCCCCTCCCTGCCTGGGTCT TCAGCCCGGGGTCTGTGTGGCTGGTGCTACACAGGCTTGACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5669
hsIGH_2092_ D011_J004_I GHD3- 09_IGHJ4	GCCTTGCCAGCCCGCTCAGAACTGCCAAGGCTTGATGGGCACGGACAC TATCCACATAAGCGAGGGATAGACCCGAGTGTCCCCACAGCAGACCTG AGAGCGCTGGGCCCACAGCCTCCCCCTCAGAGCCCTGCTGCCTCCTCCG GTCAGCCCTGGACATCCCAGGTTTCCCCAGGCTGCCGGTAGGTTTAG AATGAGGTCTGTGTCACTGTGGTATTACGATATTTTACTGGTTATTA ACTGCCAAGGCTTGAGTCGACAAGTGCTTGGAGCACTGGGGCCAGGGC AGCCCGGCCACCGTCTCCCTGGGAACGTACCCCCCTCCCTGCCTGGGTCT TCAGCCCGGGGTCTGTGTGGCTGGAAGTCCCAAGGCTTGACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5670
hsIGH_2093_ D012_J004_I GHD3- 10_IGHJ4	GCCTTGCCAGCCCGCTCAGTTGGACTGAGGCTTGACGATATTTTACT GGTTATTATAACCACAGTGTACAGAGTCCATCAAAAACCCATGCCTG GAAGCTTCCCGCCACAGCCCTCCCCATGGGGCCCTGCTGCCTCCTCAG GTCAGCCCCGGACATCCCGGGTTTCCCCAGGCTGGGCGGTAGGTTTGG GGTGAGGTCTGTGTCACTGTGGTATTACTATGGTTCGGGGAGTTATTT TGGACTGAGGCTTGAGTCGACAAGTGCTTGGAGCACTGGGGCCAGGGC AGCCCGGCCACCGTCTCCCTGGGAACGTACCCCCCTCCCTGCCTGGGTCT TCAGCCCGGGGTCTGTGTGGCTGGTTGACTGAGGCTTGACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5671

Name	Sequence	SEQ ID NO
hsIGH_2094_ D013_J004_I GHD3- 16_IGHJ4	GCCTTGCCAGCCCGCTCAGGTAGACACAGGCTTGATGGACGCGGACAC TATCCACATAAGCGAGGGACAGACCCGAGTGTTCCCTGCAGTAGACCTG AGAGCGCTGGGCCCCACAGCCTCCCCCTCGGTGCCCTGCTGCCTCCTCAG GTCAGCCCTGGACATCCCGGGTTTCCCCAGGCCAGATGGTAGGTTTGA AGTGAGGTCTGTGTCACTGTGGTATTATGATTACGTTTGGGGGAGTTA TCGTTGTAGACACAGGCTTGAGTCGACAAGTGCTTGGAGCACTGGGGC CAGGGCAGCCCGGCCACCGTCTCCCTGGGAACGTCACCCCTCCCTGCC TGGGTCTCAGCCCGGGGTCTGTGTGGCTGGGTAGACACAGGCTTGAC TGATGGCGCGAGGGAGGC	SEQ ID NO: 5672
hsIGH_2095_ D014_J004_I GHD3- 22_IGHJ4	GCCTTGCCAGCCCGCTCAGCACTGTACAGGCTTGATGGGCATGGACAG TGTCACCTAAGCGAGGGACAGACCCGAGTGTCCTGCAGTAGACCTG AGAGCGCTGGGCCCCACAGCCTCCCCCTCGGGGCCCTGCTGCCTCCTCAG GTCAGCCCTGGACATCCCGGGTTTCCCCAGGCCGCGGTAGGTTTGA AGTGAGGTCTGTGTCACTGTGGTATTACTATGATAGTAGTGTTATTC ACTGTACAGGCTTGAGTCGACAAGTGCTTGGAGCACTGGGGCCAGGGC AGCCCGGCCACCGTCTCCCTGGGAACGTCACCCCTCCCTGCCTGGGTCT TCAGCCCGGGGTCTGTGTGGCTGGCACTGTACAGGCTTGACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5673
hsIGH_2096_ D015_J004_I GHD4- 04_IGHJ4	GCCTTGCCAGCCCGCTCAGGATGATCCAGGCTTGACAAGGGTGAGTCA GACCTCCTGCCCTCGATGGCAGGCGGAGAAGATTCAGAAAGGTCTGA GATCCCCAGGACGACGACCACTGTCAATGGGGGCCCCAGACGCTGG ACCAGGGCCTGCGTGGGAAAGGCCTCTGGGCACACTCAGGGGCTTTTT GTGAAGGGTCCTCCTACTGTGTGACTACAGTAGATGATCCAGGCTTGA GTCGACAAGTGCTTGGAGCACTGGGGCCAGGGCAGCCCGGCCACCGTC TCCCTGGGAACGTCACCCCTCCCTGCCTGGGTCTCAGCCCGGGGTCT GTGTGGCTGGGATGATCCAGGCTTGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5674
hsIGH_2097_ D016_J004_I GHD4- 11_IGHJ4	GCCTTGCCAGCCCGCTCAGCGCCAATAAGGCTTGATGCCTCTCTCCCC AGTGGACACCCTCTTCCAGGACAGTCCTCAGTGGCATCACAGCGGCCT GAGATCCCCAGGACGACGACCGCTGTCAATAGGGGCCCCAAATGCCT GGACCAGGGCCTGCGTGGGAAAGGTCTCTGGCCACACTCGGGCTTTTT GTGAAGGGCCCTCCTGCTGTGTGACTACAGTACGCCAATAAGGCTTGA GTCGACAAGTGCTTGGAGCACTGGGGCCAGGGCAGCCCGGCCACCGTC TCCCTGGGAACGTCACCCCTCCCTGCCTGGGTCTCAGCCCGGGGTCT GTGTGGCTGGCGCCAATAAGGCTTGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5675

Name	Sequence	SEQ ID NO
hsIGH_2098_ D017_J004_I GHD4- 17_IGHJ4	GCCTTGCCAGCCCGCTCAGTCAAGCCTAGGCTTGAGGAGGGTGAGTCA GACCCACCTGCCCTCGATGGCAGGCGGGGAAGATTGAGAAAGGCCTGA GATCCCCAGGACGCAGCACCCTGTCAATGGGGGCCCCAGACGCCTGG ACCAGGGCCTGCGTGGGAAAGGCCGCTGGGCACACTCAGGGGCTTTTT GTGAAGGGCCCTCCTACTGTGTGACTACGGTGTCAAGCCTAGGCTTGA GTCGACAAGTGCTTGGAGCACTGGGGCCAGGGCAGCCCGGCCACCGTC TCCCTGGGAACGTCACCCCTCCCTGCCTGGGTCTCAGCCCGGGGTCT GTGTGGCTGGTCAAGCCTAGGCTTGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5676
hsIGH_2099_ D018_J004_I GHD4- 23_IGHJ4	GCCTTGCCAGCCCGCTCAGACGTGTGTAGGCTTGAGGAGGGTGAGTCA GACCCACCTGCCCTCAATGGCAGGCGGGGAAGATTGAGAAAGGCCTGA GATCCCCAGGACGCAGCACCCTGTCAATGGGGGCCCCAGACGCCTGG ACCAGGGCCTGTGTGGGAAAGGCCTCTGGCCACACTCAGGGGCTTTTT GTGAAGGGCCCTCCTGCTGTGTGACTACGGTGGTAACGTGTGTAGGCT TGAGTCGACAAGTGCTTGGAGCACTGGGGCCAGGGCAGCCCGGCCACC GTCTCCCTGGGAACGTCACCCCTCCCTGCCTGGGTCTCAGCCCGGGGG TCTGTGTGGCTGGACGTGTGTAGGCTTGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5677
hsIGH_2100_ D019_J004_I GHD5- 05_IGHJ4	GCCTTGCCAGCCCGCTCAGTCCGTCTAAGGCTTGAGAGGCCTCTCCA GGGGGACACTGTGCATGTCTGGTCCCTGAGCAGCCCCCATGTCCCCA GTCCTGGGGGGCCCCCTGGCACAGCTGTCTGGACCCTCTCTATTCCCT GGGAAGCTCCTCCTGACAGCCCCGCCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGTGAGCTGTGGTGGATACAGCTATGTCCGTCTAAGGC TTGAGTCGACAAGTGCTTGGAGCACTGGGGCCAGGGCAGCCCGGCCAC CGTCTCCCTGGGAACGTCACCCCTCCCTGCCTGGGTCTCAGCCCGGGG GTCTGTGTGGCTGGTCCGTCTAAGGCTTGACTGATGGCGCGAGGGAGG C	SEQ ID NO: 5678
hsIGH_2101_ D020_J004_I GHD5- 12_IGHJ4	GCCTTGCCAGCCCGCTCAGAAGAGCTGAGGCTTGAGCAGAGGCCTCTC CAGGGAGACACTGTGCATGTCTGGTACCTAAGCAGCCCCCACGTCCC CAGTCCTGGGGGGCCCCCTGGCTCAGCTGTCTGGACCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCCTCCAGTTCCAGGTGTGGTTATT GTCAGGCGATGTGAGCTGTGGTGGATATAGTGGCTACGAAGAGCTGA GGCTTGAGTCGACAAGTGCTTGGAGCACTGGGGCCAGGGCAGCCCGGC CACCGTCTCCCTGGGAACGTCACCCCTCCCTGCCTGGGTCTCAGCCCG GGGGTCTGTGTGGCTGGAAGAGCTGAGGCTTGACTGATGGCGCGAGGG AGGC	SEQ ID NO: 5679

Name	Sequence	SEQ ID NO
hsIGH_2102_ D021_J004_I GHD5- 18_IGHJ4	GCCTTGCCAGCCCGCTCAGTATCGCTCAGGCTTGAGCAGAGGCCTCTC CAGGGGGACACTGTGCATGTCTGGTCCCTGAGCAGCCCCCACGTCCC CAGTCCCTGGGGGCCCCCTGGCACAGCTGTCTGGACCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGTGAGACTGTGGTGGATACAGCTATGTATCGCTCAGGC TTGAGTCGACAAGTGCTTGGAGCACTGGGGCCAGGGCAGCCCGGCCAC CGTCTCCCTGGGAACGTCACCCCTCCCTGCCTGGGTCTCAGCCCGGGG GTCTGTGTGGCTGGTATCGCTCAGGCTTGACTGATGGCGCGAGGGAGG C	SEQ ID NO: 5680
hsIGH_2103_ D022_J004_I GHD5- 24_IGHJ4	GCCTTGCCAGCCCGCTCAGTCAGATGCAGGCTTGAGCAGAGGCCTCTC CAGGGGGACACAGTGCATGTCTGGTCCCTGAGCAGCCCCCAGGCTCTC TAGCACTGGGGGCCCCCTGGCACAGCTGTCTGGACCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGCCAGGCCGTGGTAGAGATGGCTACATCAGATGCAGGC TTGAGTCGACAAGTGCTTGGAGCACTGGGGCCAGGGCAGCCCGGCCAC CGTCTCCCTGGGAACGTCACCCCTCCCTGCCTGGGTCTCAGCCCGGGG GTCTGTGTGGCTGGTCAGATGCAGGCTTGACTGATGGCGCGAGGGAGG C	SEQ ID NO: 5681
hsIGH_2104_ D023_J004_I GHD6- 06_IGHJ4	GCCTTGCCAGCCCGCTCAGGTGTAGCAAGGCTTGAAGGCAGCTGACTC CTGACTTGAGCGCCTATTCCAGACACCAGACAGAGGGGCAGGCCCCC AGAACCAGGGATGAGGACGCCCCGTCAAGGCCAGAAAAGACCAAGTTG TGCTGAGCCCAGCAAGGGAAGGTCCCCAAACAAACCAGGAACGTTTCT GAAGGTGTCTGTGTACAGTGGAGTATAGCAGCTGTGTAGCAAGGCTT GAGTCGACAAGTGCTTGGAGCACTGGGGCCAGGGCAGCCCGGCCACCG TCTCCCTGGGAACGTCACCCCTCCCTGCCTGGGTCTCAGCCCGGGGT CTGTGTGGCTGGGTGTAGCAAGGCTTGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5682
hsIGH_2105_ D024_J004_I GHD6- 13_IGHJ4	GCCTTGCCAGCCCGCTCAGTGGCAGTTAGGCTTGAAGGCAGCTGACCC CTGACTTGAGCCCTATTCCAGACACCAGACAGAGGCGCAGGCCCCC AGAACCAGGGTTGAGGGACGCCCCGTCAAAGCCAGACAAAACCAAGGG GTGTTGAGCCCAGCAAGGGAAGGCCCCAAACAGACCAGGAGGTTTCT GAAGGTGTCTGTGTACAGTGGGGTATAGCAGCAGCTTGGCAGTTAGG CTTGAGTCGACAAGTGCTTGGAGCACTGGGGCCAGGGCAGCCCGGCCA CCGTCTCCCTGGGAACGTCACCCCTCCCTGCCTGGGTCTCAGCCCGGG GGTCTGTGTGGCTGGTGGCAGTTAGGCTTGACTGATGGCGCGAGGGAG GC	SEQ ID NO: 5683

Name	Sequence	SEQ ID NO
hsIGH_2106_ D025_J004_I GHD6- 19_IGHJ4	GCCTTGCCAGCCCGCTCAGCAGTCCAAAGGCTTGATGAGGTAGCTGGC CTCTGTCTCGGACCCCACTCCAGACACCAGACAGAGGGGCAGGCCCCC CAAAACCAGGGTTGAGGGATGATCCGTCAAGGCAGACAAGACCAAGGG GCACTGACCCAGCAAGGGAAGGCTCCCAAACAGACGAGGAGGTTTCT GAAGCTGTCTGTATCACAGTGGGGTATAGCAGTGGCTCAGTCCAAAGG CTTGAGTCGACAAGTGCTTGAGCACTGGGGCCAGGGCAGCCCGGCCA CCGTCTCCCTGGGAACGTCACCCCTCCCTGCCTGGGTCTCAGCCCGGG GGTCTGTGTGGCTGGCAGTCCAAAGGCTTGACTGATGGCGCGAGGGAG GC	SEQ ID NO: 5684
hsIGH_2107_ D026_J004_I GHD6- 25_IGHJ4	GCCTTGCCAGCCCGCTCAGTACGTACGAGGCTTGACAGCTGGCCTCTG TCTCGGACCCCAATTCCAGACACCAGACAGAGGGACAGGCCCCCAGA ACCAGTGTGAGGGACACCCCTGTCCAGGGCAGCCAAGTCCAAGAGGC GCGCTGAGCCCAGCAAGGGAAGGCCCCCAAACAAACCAGGAGGTTTCT GAAGCTGTCTGTGTACAGTCGGGTATAGCAGCGTACGTACGAGGCTT GAGTCGACAAGTGCTTGAGCACTGGGGCCAGGGCAGCCCGGCCACCG TCTCCCTGGGAACGTCACCCCTCCCTGCCTGGGTCTCAGCCCGGGGT CTGTGTGGCTGGTACGTACGAGGCTTGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5685
hsIGH_2108_ D027_J004_I GHD7- 27_IGHJ4	GCCTTGCCAGCCCGCTCAGAGTACCGAAGGCTTGAAGGGTTGAGGGCT GGGGTCTCCACGTGTTTTGGGGCTAACAGCGGAAGGGAGAGCACTGG CAAAGGTGCTGGGGGTCCCTGAACCCGACCCGCCCTGAGACCGCAGC CACATCAGCCCCAGCCCCACAGGCCCCCTACCAGCCGAGGGTTTTT GGCTGAGCTGAGAACCACTGTGCTAACTAGTACCGAAGGCTTGAGTCG ACAAGTGCTTGAGCACTGGGGCCAGGGCAGCCCGGCCACCGTCTCCC TGGGAACGTCACCCCTCCCTGCCTGGGTCTCAGCCCGGGGTCTGTGT GGCTGGAGTACCGAAGGCTTGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5686
hsIGH_2109_ D001_J005_I GHD1- 01_IGHJ5	GCCTTGCCAGCCCGCTCAGGACACTCTACACACGTGCCCCGGTCTCTG TGGGTGTTCCGCTAACTGGGGCTCCCACTGCTCACCACAACTAAAG CGAGCCCCAGCCTCCAGAGCCCCGAAGGAGATGCCGCCACAAGCCC AGCCCCCATCCAGGAGGCCCCAGAGCTCAGGGCGCCGGGGCAGATTCT GAACAGCCCCGAGTCACGGTGGGTACAACCTGGAGACACTCTACACAG TGTGACCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCT TCAGGTAAGATGGCTTTTCTTCTGCCTCCTTTCTCTGGGCCCAGCGTC CTCTGTCTGGGACACTCTACACACGTCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5687
hsIGH_2110_ D002_J005_I GHD1- 07_IGHJ5	GCCTTGCCAGCCCGCTCAGTTCCGAACACACACGTGGCCTCGGTCTCT GTGGGTGTTCCGCTAGCTGGGGCTCACAGTGCTCACCACACCTAAA ACGAGCCACAGCCTCAGAGCCCCGAAGGAGACCCCGCCACAAGCCC AGCCCCACCCAGGAGGCCCCAGAGCACAGGGCGCCCCGTCTGGATTCT GAACAGCCCCGAGTCACAGTGGGTATAACTGGATTGGAACACACAG TGTGACCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCT TCAGGTAAGATGGCTTTTCTTCTGCCTCCTTTCTCTGGGCCCAGCGTC CTCTGTCTGGTTCCGAACACACACGTCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5688

Name	Sequence	SEQ ID NO
hsIGH_2111_ D003_J005_I GHD1- 14_IGHJ5	GCCTTGCCAGCCCGCTCAGAAGTAACGACACACGTGGCCTCGGTCTCT GTGGGTGTTCCGCTAGCTGGGGCTCACAGTGCTCACCCACACCTAAA ATGAGCCACAGCCTCCGGAGCCCCCGCAGAGACCCCGCCCAAGCCC AGCCCCACCCAGGAGGCCCCAGAGCTCAGGGCGCCCGTCGGATTCC GAACAGCCCCGAGTCACAGCGGGTATAACCGGAAAGTAACGACACACG TGTCGACCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCT TCAGGTAAGATGGCTTTCTTCTGCCTCCTTTCTCTGGGCCCAGCGTC CTCTGTCTGGAAGTAACGACACACGTCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5689
hsIGH_2112_ D004_J005_I GHD1- 20_IGHJ5	GCCTTGCCAGCCCGCTCAGGTCTCCTAACACACGTGTCTCTGTGGGTG TTCCGCTAGCTGGGGCCCCCAGTGCTCACCCACACCTAAAGCGAGCC CCAGCTCCAGAGCCCCCTAAGCATTCCCCGCCAGCAGCCAGCCCC TGCCCCACCCAGGAGGCCCCAGAGCTCAGGGCGCCTGGTCGGATTCT GAACAGCCCCGAGTCACAGTGGGTATAACTGGAGTCTCCTAACACACG TGTCGACCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCT TCAGGTAAGATGGCTTTCTTCTGCCTCCTTTCTCTGGGCCCAGCGTC CTCTGTCTGGGTCTCCTAACACACGTCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5690
hsIGH_2113_ D005_J005_I GHD1- 26_IGHJ5	GCCTTGCCAGCCCGCTCAGAGAGTGTCACACACGTAGGCCTCAGGCTC TGTTGGGTGCCGCTAGCTGGGGCTGCCAGTCCTCACCCACACCTAAGG TGAGCCACAGCCGCCAGAGCCTCCACAGGAGACCCACCCAGCAGCCC AGCCCCTACCCAGGAGGCCCCAGAGCTCAGGGCGCCTGGGTGGATTCT GAACAGCCCCGAGTCACGGTGGGTATAGTGGGAGCTAGAGTGTCACAC ACGTGTGACCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTC TCTTCAGGTAAGATGGCTTTCTTCTGCCTCCTTTCTCTGGGCCCAGC GTCCTCTGTCTGGAGAGTGTCACACACGTCTGATGGCGCGAGGGAGG C	SEQ ID NO: 5691
hsIGH_2114_ D006_J005_I GHD2- 02_IGHJ5	GCCTTGCCAGCCCGCTCAGGTTCCGAAACACACGTAAAGGAGGAGCCC CCTGTACAGCACTGGGCTCAGAGTCCTCTCCACACACCCCTGAGTTTC AGACAAAACCCCTGGAAATCATAGTATCAGCAGGAGAACTAGCCAG AGACAGCAAGAGGGGACTCAGTGACTCCCGCGGGGACAGGAGGATTTT GTGGGGGCTCGTGTCAGTGAGGATATTGTAGTAGTACCAGCTGCTG TTCCGAAACACACGTGTGACCTTTTGATATCTGGGGCCAAGGGACAA TGGTCACCGTCTCTTCAGGTAAGATGGCTTTCTTCTGCCTCCTTTCT CTGGGCCCAGCGTCCTCTGTCTGGGTTCGAAACACACGTCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5692

Name	Sequence	SEQ ID NO
hsIGH_2115_ D007_J005_I GHD2- 08_IGHJ5	GCCTTGCCAGCCCGCTCAGCGTTACTTACACACGTAAAGGAGGAGCCC CTTGTTTCACTGAGTGGGCTCAGAGTCTCTCCAAGACACCCAGAGTTTC AGACAAAAACCCCTGGAATGCACAGTCTCAGCAGGAGAGCCAGCCAG AGCCAGCAAGATGGGGCTCAGTGACACCCGCAGGGACAGGAGGATTTT GTGGGGGCTCGTGTCACGTGTGAGGATATTGTACTAATGGTGTATGCTC GTTACTTACACACGTGTGACCTTTTGATATCTGGGGCCAAGGGACAA TGGTCACCGTCTCTTCAGGTAAGATGGCTTTCCTTCTGCCTCCTTTCT CTGGGCCCAGCGTCCTCTGTCTGGCGTTACTTACACACGTCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5693
hsIGH_2116_ D008_J005_I GHD2- 15_IGHJ5	GCCTTGCCAGCCCGCTCAGTAGGAGACACACACGTAAAGGAGGAGCCC CCTATACAGCACTGGGCTCAGAGTCTCTCTGAGACACCCTGAGTTTC AGACAACAACCCGCTGGAATGCACAGTCTCAGCAGGAGAACAGACCAA AGCCAGCAAAAGGGACCTCGGTGACACCACTAGGGACAGGAGGATTTT GTGGGGGCTCGTGTCACGTGTGAGGATATTGTAGTGGTGGTAGCTGCTT AGGAGACACACACGTGTGACCTTTTGATATCTGGGGCCAAGGGACAA TGGTCACCGTCTCTTCAGGTAAGATGGCTTTCCTTCTGCCTCCTTTCT CTGGGCCCAGCGTCCTCTGTCTGGTAGGAGACACACACGTCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5694
hsIGH_2117_ D009_J005_I GHD2- 21_IGHJ5	GCCTTGCCAGCCCGCTCAGGTGTCTACACACACGTAGCCCCCTGTACA GCACTGGGCTCAGAGTCTCTCTGAGACAGGCTCAGTTTCAGACAACA ACCCGCTGGAATGCACAGTCTCAGCAGGAGAGCCAGGCCAGAGCCAGC AAGAGGAGACTCGGTGACACCACTCTCCTGTAGGGACAGGAGGATTTT GTGGGGGTTCGTGTCACTGTGAGCATATTGTGGTGGTGAAGTGTGTGT CTACACACACGTGTGACCTTTTGATATCTGGGGCCAAGGGACAATGG TCACCGTCTCTTCAGGTAAGATGGCTTTCCTTCTGCCTCCTTTCTCTG GGCCAGCGTCCTCTGTCTGGGTGTCTACACACACGTCTGATGGCGC GAGGGAGGC	SEQ ID NO: 5695
hsIGH_2118_ D010_J005_I GHD3- 03_IGHJ5	GCCTTGCCAGCCCGCTCAGTGCTACACACACACGTGTGGGCACGGACA CTGTCCACCTAAGCCAGGGGCGAGCCCGAGTGTCCTCCGAGTAGACCT GAGAGCGCTGGGCCCACAGCCTCCCTCGGTGCCCTGCTACCTCCTCA GGTCAGCCCTGGACATCCCGGGTTTCCCCAGGCTGGCGGTAGGTTTGG GGTGAGGTCTGTGTCACTGTGGTATTACGATTTTGGAGTGGTTATTT GCTACACACACACGTGTGACCTTTTGATATCTGGGGCCAAGGGACAA TGGTCACCGTCTCTTCAGGTAAGATGGCTTTCCTTCTGCCTCCTTTCT CTGGGCCCAGCGTCCTCTGTCTGGTGCTACACACACACGTCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5696

Name	Sequence	SEQ ID NO
hsIGH_2119_ D011_J005_I GHD3- 09_IGHJ5	GCCTTGCCAGCCCGCTCAGAACTGCCAACACACGTTGGGCACGGACAC TATCCACATAAGCGAGGGATAGACCCGAGTGTCCCCACAGCAGACCTG AGAGCGCTGGGCCCCACAGCCTCCCCTCAGAGCCCTGCTGCCTCCTCCG GTCAGCCCTGGACATCCCAGGTTTCCCCAGGCCTGCCGGTAGGTTTAG AATGAGGTCTGTGTCACTGTGGTATTACGATATTTGACTGGTTATTA ACTGCCAACACACGTGTGACCTTTTGATATCTGGGGCCAAGGGACAA TGGTCACCGTCTCTTCAGGTAAGATGGCTTTCCTTCTGCCTCCTTTCT CTGGGCCCAGCGTCCTCTGTCTGGAAGTGGCAACACACGTCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5697
hsIGH_2120_ D012_J005_I GHD3- 10_IGHJ5	GCCTTGCCAGCCCGCTCAGTTGGACTGACACACGTCGATATTTGACT GGTTATTATAACCACAGTGTACAGAGTCCATCAAAAACCCATGCCTG GAAGCTTCCCGCCACAGCCCTCCCCTATGGGGCCCTGCTGCCTCCTCAG GTCAGCCCCGGACATCCCGGGTTTCCCCAGGCCTGGGCGGTAGGTTTGG GGTGAGGTCTGTGTCACTGTGGTATTACTATGGTTCGGGGAGTTATTT TGGACTGACACACGTGTGACCTTTTGATATCTGGGGCCAAGGGACAA TGGTCACCGTCTCTTCAGGTAAGATGGCTTTCCTTCTGCCTCCTTTCT CTGGGCCCAGCGTCCTCTGTCTGTTGGACTGACACACGTCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5698
hsIGH_2121_ D013_J005_I GHD3- 16_IGHJ5	GCCTTGCCAGCCCGCTCAGGTAGACACACACGTTGGACGCGGACAC TATCCACATAAGCGAGGGACAGACCCGAGTGTTCCTGCAGTAGACCTG AGAGCGCTGGGCCCCACAGCCTCCCCTCGGTGCCCTGCTGCCTCCTCAG GTCAGCCCTGGACATCCCGGGTTTCCCCAGGCCAGATGGTAGGTTTGA AGTGAGGTCTGTGTCACTGTGGTATTATGATTACGTTTGGGGGAGTTA TCGTTGTAGACACACACACGTGTGACCTTTTGATATCTGGGGCCAAG GGACAATGGTCACCGTCTCTTCAGGTAAGATGGCTTTCCTTCTGCCTC CTTTCTCTGGGCCCAGCGTCCTCTGTCTGCGGTAGACACACACACGTC TGATGGCGCGAGGGAGGC	SEQ ID NO: 5699
hsIGH_2122_ D014_J005_I GHD3- 22_IGHJ5	GCCTTGCCAGCCCGCTCAGCACTGTACACACACGTTGGGCATGGACAG TGTCCACCTAAGCGAGGGACAGACCCGAGTGTCCCTGCAGTAGACCTG AGAGCGCTGGGCCCCACAGCCTCCCCTCGGGGCCCTGCTGCCTCCTCAG GTCAGCCCTGGACATCCCGGGTTTCCCCAGGCCTGGCGGTAGGTTTGA AGTGAGGTCTGTGTCACTGTGGTATTACTATGATAGTAGTGTTATTC ACTGTACACACACGTGTGACCTTTTGATATCTGGGGCCAAGGGACAA TGGTCACCGTCTCTTCAGGTAAGATGGCTTTCCTTCTGCCTCCTTTCT CTGGGCCCAGCGTCCTCTGTCTGGCACTGTACACACACGTCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5700

Name	Sequence	SEQ ID NO
hsIGH_2123_ D015_J005_I GHD4- 04_IGHJ5	GCCTTGCCAGCCCGCTCAGGATGATCCACACACGTCAAGGGTGAGTCA GACCCCTCCTGCCCTCGATGGCAGGCGGAGAAGATTCAGAAAGGTCTGA GATCCCCAGGACGCAGCACCCTGTCAATGGGGGCCCCAGACGCCTGG ACCAGGGCCTGCGTGGGAAAGGCCTCTGGGCACACTCAGGGGCTTTTT GTGAAGGGTCCTCCTACTGTGTGACTACAGTAGATGATCCACACACGT GTCGACCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCTT CAGGTAAGATGGCTTTCTTCTGCCTCCTTTCTCTGGGCCCAGCGTCC TCTGTCCTGGGATGATCCACACACGTCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5701
hsIGH_2124_ D016_J005_I GHD4- 11_IGHJ5	GCCTTGCCAGCCCGCTCAGCGCCAATAACACACGTTCCTCTCTCCCC AGTGGACACCCTCTTCCAGGACAGTCCCTCAGTGGCATCACAGCGGCCCT GAGATCCCCAGGACGCAGCACCCTGTCAATAGGGGCCCCAAATGCCT GGACCAGGGCCTGCGTGGGAAAGGTCTCTGGCCACACTCGGGCTTTTT GTGAAGGGCCCTCCTGCTGTGTGACTACGTACGCCAATAACACACGT GTCGACCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCTT CAGGTAAGATGGCTTTCTTCTGCCTCCTTTCTCTGGGCCCAGCGTCC TCTGTCCTGGCGCCAATAACACACGTCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5702
hsIGH_2125_ D017_J005_I GHD4- 17_IGHJ5	GCCTTGCCAGCCCGCTCAGTCAAGCCTACACACGTGGAGGGTGAGTCA GACCCACCTGCCCTCGATGGCAGGCGGGGAAGATTCAGAAAGGCCTGA GATCCCCAGGACGCAGCACCCTGTCAATGGGGGCCCCAGACGCCTGG ACCAGGGCCTGCGTGGGAAAGGCCGCTGGGCACACTCAGGGGCTTTTT GTGAAGGGCCCTCCTACTGTGTGACTACGGTGTCAAGCCTACACACGT GTCGACCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCTT CAGGTAAGATGGCTTTCTTCTGCCTCCTTTCTCTGGGCCCAGCGTCC TCTGTCCTGGTCAAGCCTACACACGTCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5703
hsIGH_2126_ D018_J005_I GHD4- 23_IGHJ5	GCCTTGCCAGCCCGCTCAGACGTGTGTACACACGTGGAGGGTGAGTCA GACCCACCTGCCCTCAATGGCAGGCGGGGAAGATTCAGAAAGGCCTGA GATCCCCAGGACGCAGCACCCTGTCAATGGGGGCCCCAGACGCCTGG ACCAGGGCCTGTGTGGGAAAGGCCTCTGGCCACACTCAGGGGCTTTTT GTGAAGGGCCCTCCTGCTGTGTGACTACGGTGGTAACGTGTGTACACA CGTGTGACCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCT CTTCAGGTAAGATGGCTTTCTTCTGCCTCCTTTCTCTGGGCCCAGCG TCCTCTGTCTGGACGTGTGTACACACGTCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5704
hsIGH_2127_ D019_J005_I GHD5- 05_IGHJ5	GCCTTGCCAGCCCGCTCAGTCCGTCTAACACACGTAGAGGCCTCTCCA GGGGGACACTGTGCATGTCTGGTCCCTGAGCAGCCCCCATGTCCCCA GTCCTGGGGGGCCCCCTGGCACAGCTGTCTGGACCCTCTCTATTCCCT GGGAAGCTCCTCCTGACAGCCCCGCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGTGACACTGTGGTGGATACAGCTATGTCCGTCTAACAC ACGTGTGACCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTC TCTTCAGGTAAGATGGCTTTCTTCTGCCTCCTTTCTCTGGGCCCAGC GTCCTCTGTCTGGTCCGTCTAACACACGTCTGATGGCGCGAGGGAGG C	SEQ ID NO: 5705

Name	Sequence	SEQ ID NO
hsIGH_2128_ D020_J005_I GHD5- 12_IGHJ5	GCCTTGCCAGCCCGCTCAGAAGAGCTGACACACGTGCAGAGGCCTCTC CAGGGGAGACACTGTGCATGTCTGGTACCTAAGCAGCCCCCACGTCCC CAGTCCTGGGGGCCCCCTGGCTCAGCTGTCTGGACCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCTCCAGTTCCAGGTGTGGTTATT GTCAGGCGATGTCAGACTGTGGTGGATATAGTGGCTACGAAGAGCTGA CACACGTGTCGACCTTTTGATATCTGGGGCCAAGGGACAATGGTCACC GTCTCTTCAGGTAAGATGGCTTTCCTTCTGCCTCCTTTCTCTGGGCCC AGCGTCCTCTGTCTCTGGAAGAGCTGACACACGTCTGATGGCGCGAGGG AGGC	SEQ ID NO: 5706
hsIGH_2129_ D021_J005_I GHD5- 18_IGHJ5	GCCTTGCCAGCCCGCTCAGTATCGCTCACACACGTGCAGAGGCCTCTC CAGGGGGACACTGTGCATGTCTGGTCCCTGAGCAGCCCCCACGTCCC CAGTCCTGGGGGCCCCCTGGCACAGCTGTCTGGACCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGTGAGACTGTGGTGGATACAGCTATGTATCGCTCACAC ACGTGTCGACCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTC TCTTCAGGTAAGATGGCTTTCCTTCTGCCTCCTTTCTCTGGGCCCAGC GTCCTCTGTCTCTGGTATCGCTCACACACGTCTGATGGCGCGAGGGAGG C	SEQ ID NO: 5707
hsIGH_2130_ D022_J005_I GHD5- 24_IGHJ5	GCCTTGCCAGCCCGCTCAGTCAGATGCACACACGTGCAGAGGCCTCTC CAGGGGGACACAGTGCATGTCTGGTCCCTGAGCAGCCCCCAGGCTCTC TAGCACTGGGGGCCCCCTGGCACAGCTGTCTGGACCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGCCAGGCCGTGGTAGAGATGGCTACATCAGATGCACAC ACGTGTCGACCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTC TCTTCAGGTAAGATGGCTTTCCTTCTGCCTCCTTTCTCTGGGCCCAGC GTCCTCTGTCTCTGGTCAGATGCACACACGTCTGATGGCGCGAGGGAGG C	SEQ ID NO: 5708
hsIGH_2131_ D023_J005_I GHD6- 06_IGHJ5	GCCTTGCCAGCCCGCTCAGGTGTAGCAACACACGTAGGCAGCTGACTC CTGACTTGACGCCTATTCCAGACACCAGACAGAGGGGCAGGCCCCC AGAACCAGGGATGAGGACGCCCCGTCAAGGCCAGAAAAGACCAAGTTG TGCTGAGCCCAGCAAGGGAAGGTCCCCAAACAAACCAGGAACGTTTCT GAAGGTGTCTGTGTACAGTGGAGTATAGCAGCTGTGTAGCAACACAC GTGTGACCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTC TTCAGGTAAGATGGCTTTCCTTCTGCCTCCTTTCTCTGGGCCCAGCGT CCTCTGTCTCTGGGTGTAGCAACACACGTCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5709

Name	Sequence	SEQ ID NO
hsIGH_2132_ D024_J005_I GHD6- 13_IGHJ5	GCCTTGCCAGCCCGCTCAGTGGCAGTTACACACGTAGGCAGCTGACCC CTGACTTGGACCCCTATTCCAGACACCAGACAGAGGCGCAGGCCCCC AGAACCAGGGTTGAGGGACGCCCCGTCAAAGCCAGACAAAACCAAGGG GTGTTGAGCCCAGCAAGGGAAGGCCCCCAAACAGACCAGGAGGTTTCT GAAGGTGTCTGTGTACAGTGGGGTATAGCAGCAGCTTGGCAGTTACA CACGTGTCGACCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGT CTCTTCAGGTAAGATGGCTTTCCTTCTGCCTCCTTCTCTGGGCCCAG CGTCCTCTGTCTGGTGGCAGTTACACACGTCTGATGGCGCGAGGGAG GC	SEQ ID NO: 5710
hsIGH_2133_ D025_J005_I GHD6- 19_IGHJ5	GCCTTGCCAGCCCGCTCAGCAGTCCAAACACACGTTGAGGTAGCTGGC CTCTGTCTCGGACCCCACTCCAGACACCAGACAGAGGGGCAGGCCCC CAAAACCAGGGTTGAGGGATGATCCGTCAAGGCAGACAAGACCAAGGG GCACTGACCCAGCAAGGGAAGGCTCCCAAACAGACGAGGAGGTTTCT GAAGCTGTCTGTATCACAGTGGGGTATAGCAGTGGCTCAGTCCAAACA CACGTGTCGACCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGT CTCTTCAGGTAAGATGGCTTTCCTTCTGCCTCCTTCTCTGGGCCCAG CGTCCTCTGTCTGGCAGTCCAAACACACGTCTGATGGCGCGAGGGAG GC	SEQ ID NO: 5711
hsIGH_2134_ D026_J005_I GHD6- 25_IGHJ5	GCCTTGCCAGCCCGCTCAGTACGTACGACACACGTACGCTGGCCTCTG TCTCGGACCCCCATTCCAGACACCAGACAGAGGGACAGGCCCCCAGA ACCAGTGTTGAGGGACACCCCTGTCCAGGGCAGCCAAGTCCAAGAGGC GCGCTGAGCCCAGCAAGGGAAGGCCCCCAAACAAACCAGGAGGTTTCT GAAGCTGTCTGTGTACAGTCGGGTATAGCAGCGTACGTACGACACAC GTGTGACCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTC TTCAGGTAAGATGGCTTTCCTTCTGCCTCCTTCTCTGGGCCCAGCGT CCTCTGTCTGGTACGTACGACACACGTCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5712
hsIGH_2135_ D027_J005_I GHD7- 27_IGHJ5	GCCTTGCCAGCCCGCTCAGAGTACCGAACACACGTAGGGTTGAGGGCT GGGGTCTCCACGTGTTTTGGGGCTAACAGCGGAAGGGAGAGCACTGG CAAAGGTGCTGGGGGTCCCTTGAACCCGACCCGCCCTGAGACCGCAGC CACATCAGCCCCAGCCCCACAGGCCCCCTACCAGCCGCAGGGTTTTT GGCTGAGCTGAGAACCACTGTGCTAACTAGTACCGAACACACGTGTCTG ACCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCAGG TAAGATGGCTTTCCTTCTGCCTCCTTCTCTGGGCCCAGCGTCCTCTG TCCTGGAGTACCGAACACACGTCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5713

Name	Sequence	SEQ ID NO
hsIGH_2136_ D001_J006_I GHD1- 01_IGHJ6	GCCTTGCCAGCCCGCTCAGGACACTCTTAGACGGAGCCCCGGTCTCTG TGGGTGTTCCGCTAACTGGGGCTCCCAGTGCTCACCACAACTAAAG CGAGCCCCAGCCTCCAGAGCCCCGAAGGAGATGCCGCCACAAGCCC AGCCCCCATCCAGGAGGCCCCAGAGCTCAGGGCGCCGGGGCAGATTCT GAACAGCCCCGAGTCACGGTGGGTACAACCTGGAGACACTCTTAGACGG AGTCGACAGTTGGACTTCCCAGGCCGACAGTGGTCTGGCTTCTGAGGG GTCAGGCCAGAATGTGGGGTACGTGGGAGGCCAGCAGAGGGTTCCATG AGAAGGGCAGGGACACTCTTAGACGGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5714
hsIGH_2137_ D002_J006_I GHD1- 07_IGHJ6	GCCTTGCCAGCCCGCTCAGTTCGGAAC TAGACGGAGGCCTCGGTCTCT GTGGGTGTTCCGCTAGCTGGGGCTCACAGTGCTCACCACACCTAAA ACGAGCCACAGCCTCAGAGCCCCCTGAAGGAGACCCCGCCACAAGCCC AGCCCCACCCAGGAGGCCCCAGAGCACAGGGCGCCCCGTCGGATTCT GAACAGCCCCGAGTCACAGTGGGTATAACTGGATTTCGGAAC TAGACGG AGTCGACAGTTGGACTTCCCAGGCCGACAGTGGTCTGGCTTCTGAGGG GTCAGGCCAGAATGTGGGGTACGTGGGAGGCCAGCAGAGGGTTCCATG AGAAGGGCAGGTTTCGGAAC TAGACGGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5715
hsIGH_2138_ D003_J006_I GHD1- 14_IGHJ6	GCCTTGCCAGCCCGCTCAGAAGTAACGTAGACGGAGGCCTCGGTCTCT GTGGGTGTTCCGCTAGCTGGGGCTCACAGTGCTCACCACACCTAAA ATGAGCCACAGCCTCCGGAGCCCCCGCAGAGACCCCGCCACAAGCCC AGCCCCACCCAGGAGGCCCCAGAGCTCAGGGCGCCCCGTCGGATTCC GAACAGCCCCGAGTCACAGCGGGTATAACCGAAAGTAACGTAGACGG AGTCGACAGTTGGACTTCCCAGGCCGACAGTGGTCTGGCTTCTGAGGG GTCAGGCCAGAATGTGGGGTACGTGGGAGGCCAGCAGAGGGTTCCATG AGAAGGGCAGGAAGTAACGTAGACGGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5716
hsIGH_2139_ D004_J006_I GHD1- 20_IGHJ6	GCCTTGCCAGCCCGCTCAGGTCTCCTATAGACGGAGTCTCTGTGGGTG TTCCGCTAGCTGGGGCCCCCAGTGCTCACCACACCTAAAGCGAGCC CCAGCCTCCAGAGCCCCCTAAGCATTCCTCCCGCCAGCAGCCAGCCCC TGCCCCACCCAGGAGGCCCCAGAGCTCAGGGCGCCTGGTTCGGATTCT GAACAGCCCCGAGTCACAGTGGGTATAACTGGAGTCTCCTATAGACGG AGTCGACAGTTGGACTTCCCAGGCCGACAGTGGTCTGGCTTCTGAGGG GTCAGGCCAGAATGTGGGGTACGTGGGAGGCCAGCAGAGGGTTCCATG AGAAGGGCAGGGTCTCCTATAGACGGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5717
hsIGH_2140_ D005_J006_I GHD1- 26_IGHJ6	GCCTTGCCAGCCCGCTCAGAGAGTGCTAGACGGAAGGCCTCAGGCTC TGTGGGTGCCGCTAGCTGGGGCTGCCAGTCTCACCACACCTAAGG TGAGCCACAGCCGCCAGAGCTCCACAGGAGACCCACCCAGCAGCCC AGCCCCTACCCAGGAGGCCCCAGAGCTCAGGGCGCCTGGGTGGATTCT GAACAGCCCCGAGTCACGGTGGGTATAGTGGGAGCTAGAGTGTCTAGA CGGAGTCGACAGTTGGACTTCCCAGGCCGACAGTGGTCTGGCTTCTGA GGGGTCAGGCCAGAATGTGGGGTACGTGGGAGGCCAGCAGAGGGTTCC ATGAGAAGGGCAGGAGAGTGTCTAGACGGACTGATGGCGCGAGGGAGG C	SEQ ID NO: 5718

Name	Sequence	SEQ ID NO
hsIGH_2141_ D006_J006_I GHD2- 02_IGHJ6	GCCTTGCCAGCCCGCTCAGGTTCCGAATAGACGGAAAAGGAGGAGCCC CCTGTACAGCACTGGGCTCAGAGTCCTCTCCACACACCCTGAGTTTC AGACAAAAACCCCTGGAAATCATAGTATCAGCAGGAGAACTAGCCAG AGACAGCAAGAGGGGACTCAGTGACTCCCGCGGGACAGGAGGATTTT GTGGGGGCTCGTGTCAGTGTGAGGATATTGTAGTAGTACCAGCTGCTG TTCCGAATAGACGGAGTCGACAGTTGGACTTCCCAGGCCGACAGTGGT CTGGCTTCTGAGGGGTCAGGCCAGAATGTGGGGTACGTGGGAGGCCAG CAGAGGGTTCCATGAGAAGGGCAGGGTTCCGAATAGACGGACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5719
hsIGH_2142_ D007_J006_I GHD2- 08_IGHJ6	GCCTTGCCAGCCCGCTCAGCGTTACTTTAGACGGAAAAGGAGGAGCCC CTTGTTTCAGCACTGGGCTCAGAGTCCTCTCCAAGACACCAGAGTTTC AGACAAAAACCCCTGGAAATGCACAGTCTCAGCAGGAGAGCCAGCCAG AGCCAGCAAGATGGGGCTCAGTGACACCCGACAGGACAGGAGGATTTT GTGGGGGCTCGTGTCAGTGTGAGGATATTGTACTAATGGTGTATGCTC GTTACTTTAGACGGAGTCGACAGTTGGACTTCCCAGGCCGACAGTGGT CTGGCTTCTGAGGGGTCAGGCCAGAATGTGGGGTACGTGGGAGGCCAG CAGAGGGTTCCATGAGAAGGGCAGGCGTTACTTTAGACGGACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5720
hsIGH_2143_ D008_J006_I GHD2- 15_IGHJ6	GCCTTGCCAGCCCGCTCAGTAGGAGACTAGACGGAAAAGGAGGAGCCC CCTATACAGCACTGGGCTCAGAGTCCTCTCTGAGACACCCTGAGTTTC AGACAACAACCCGCTGGAAATGCACAGTCTCAGCAGGAGAACAGACCAA AGCCAGCAAAAGGGACCTCGGTGACACCAGTAGGGACAGGAGGATTTT GTGGGGGCTCGTGTCAGTGTGAGGATATTGTAGTGGTGGTAGCTGCTT AGGAGACTAGACGGAGTCGACAGTTGGACTTCCCAGGCCGACAGTGGT CTGGCTTCTGAGGGGTCAGGCCAGAATGTGGGGTACGTGGGAGGCCAG CAGAGGGTTCCATGAGAAGGGCAGGTAGGAGACTAGACGGACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5721
hsIGH_2144_ D009_J006_I GHD2- 21_IGHJ6	GCCTTGCCAGCCCGCTCAGGTGTCTACTAGACGGAAGCCCCCTGTACA GCACTGGGCTCAGAGTCCTCTCTGAGACAGGCTCAGTTTCAGACAACA ACCCGCTGGAATGCACAGTCTCAGCAGGAGAGCCAGGCCAGAGCCAGC AAGAGGAGACTCGGTGACACCAGTCTCCTGTAGGGACAGGAGGATTTT GTGGGGGTTCTGTGTCAGTGTGAGCATATTGTGGTGGTGAAGTGTGTG CTACTAGACGGAGTCGACAGTTGGACTTCCCAGGCCGACAGTGGTCTG GCTTCTGAGGGGTCAGGCCAGAATGTGGGGTACGTGGGAGGCCAGCAG AGGGTTCCATGAGAAGGGCAGGGTGTCTACTAGACGGACTGATGGCGC GAGGGAGGC	SEQ ID NO: 5722

Name	Sequence	SEQ ID NO
hsIGH_2145_ D010_J006_I GHD3- 03_IGHJ6	GCCTTGCCAGCCCGCTCAGTGCTACACTAGACGGAGTGGGCACGGACA CTGTCCACCTAAGCCAGGGGCAGACCCGAGTGTCCTCCGACGTAGACCT GAGAGCGCTGGGCCCCACAGCCTCCCCTCGGTGCCCTGCTACCTCCTCA GGTCAGCCCTGGACATCCCGGGTTTCCCCAGGCTGGCGGTAGGTTTGG GGTGAGGTCTGTGTCACTGTGGTATTACGATTTTGGAGTGTTATTT GCTACACTAGACGGAGTCGACAGTTGGACTTCCCAGGCCGACAGTGGT CTGGCTTCTGAGGGGTGAGGCCAGAATGTGGGGTACGTGGGAGGCCAG CAGAGGGTTCCATGAGAAGGGCAGGTGCTACACTAGACGGACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5723
hsIGH_2146_ D011_J006_I GHD3- 09_IGHJ6	GCCTTGCCAGCCCGCTCAGAACTGCCATAGACGGATGGGCACGGACAC TATCCACATAAGCGAGGGATAGACCCGAGTGTCCTCCACAGCAGACCTG AGAGCGCTGGGCCCCACAGCCTCCCCTCAGAGCCCTGCTGCCTCCTCCG GTCAGCCCTGGACATCCCAGGTTTCCCCAGGCCCTGCCGGTAGGTTTAG AATGAGGTCTGTGTCACTGTGGTATTACGATATTTGACTGGTTATTA ACTGCCATAGACGGAGTCGACAGTTGGACTTCCCAGGCCGACAGTGGT CTGGCTTCTGAGGGGTGAGGCCAGAATGTGGGGTACGTGGGAGGCCAG CAGAGGGTTCCATGAGAAGGGCAGGAACTGCCATAGACGGACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5724
hsIGH_2147_ D012_J006_I GHD3- 10_IGHJ6	GCCTTGCCAGCCCGCTCAGTTGGACTGTAGACGGACGATATTTTGGACT GGTTATTATAACCACAGTGTACAGAGTCCATCAAAAACCCATGCCTG GAAGCTTCCCGCCACAGCCCTCCCCATGGGGCCCTGCTGCCTCCTCAG GTCAGCCCCGGACATCCCGGGTTTCCCCAGGCTGGGCGGTAGGTTTGG GGTGAGGTCTGTGTCACTGTGGTATTACTATGGTTCCGGGAGTTATTT TGGACTGTAGACGGAGTCGACAGTTGGACTTCCCAGGCCGACAGTGGT CTGGCTTCTGAGGGGTGAGGCCAGAATGTGGGGTACGTGGGAGGCCAG CAGAGGGTTCCATGAGAAGGGCAGGTTGGACTGTAGACGGACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5725
hsIGH_2148_ D013_J006_I GHD3- 16_IGHJ6	GCCTTGCCAGCCCGCTCAGGTAGACACTAGACGGATGGACGCGGACAC TATCCACATAAGCGAGGGACAGACCCGAGTGTTCTCCTGCAGTAGACCTG AGAGCGCTGGGCCCCACAGCCTCCCCTCGGTGCCCTGCTGCCTCCTCAG GTCAGCCCTGGACATCCCGGGTTTCCCCAGGCCAGATGGTAGGTTTGA AGTGAGGTCTGTGTCACTGTGGTATTATGATTACGTTTGGGGAGTTA TCGTTGTAGACACTAGACGGAGTCGACAGTTGGACTTCCCAGGCCGAC AGTGGTCTGGCTTCTGAGGGGTGAGGCCAGAATGTGGGGTACGTGGGA GGCCAGCAGAGGGTTCCATGAGAAGGGCAGGGTAGACACTAGACGGAC TGATGGCGCGAGGGAGGC	SEQ ID NO: 5726

Name	Sequence	SEQ ID NO
hsIGH_2149_ D014_J006_I GHD3- 22_IGHJ6	GCCTTGCCAGCCCGCTCAGCACTGTACTAGACGGATGGGCATGGACAG TGTCCACCTAAGCGAGGGACAGACCCGAGTGTCCCTGCAGTAGACCTG AGAGCGCTGGGCCCACAGCCTCCCCCTCGGGGCCCTGCTGCCTCCTCAG GTCAGCCCTGGACATCCCCGGGTTTCCCCAGGCCTGGCGGTAGGTTTGA AGTGAGGTCTGTGTCACCTGTGGTATTACTATGATAGTAGTGTTATTC ACTGTACTAGACGGAGTCGACAGTTGGACTTCCCAGGCCGACAGTGGT CTGGCTTCTGAGGGGTCAGGCCAGAATGTGGGGTACGTGGGAGGCCAG CAGAGGGTTCCATGAGAAGGGCAGGCACTGTACTAGACGGACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5727
hsIGH_2150_ D015_J006_I GHD4- 04_IGHJ6	GCCTTGCCAGCCCGCTCAGGATGATCCTAGACGGACAAGGGTGAGTCA GACCTTCTGCCCTCGATGGCAGGCGGAGAAGATTAGAAAGGTCTGA GATCCCCAGGACGCAGCACCCTGTCAATGGGGGCCCCAGACGCCTGG ACCAGGGCCTGCGTGGGAAAGGCCTCTGGGCACACTCAGGGGCTTTTT GTGAAGGGTCCCTCTACTGTGTGACTACAGTAGATGATCCTAGACGGA GTCGACAGTTGGACTTCCCAGGCCGACAGTGGTCTGGCTTCTGAGGGG TCAGGCCAGAATGTGGGGTACGTGGGAGGCCAGCAGAGGGTTCCATGA GAAGGGCAGGGATGATCCTAGACGGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5728
hsIGH_2151_ D016_J006_I GHD4- 11_IGHJ6	GCCTTGCCAGCCCGCTCAGCGCCAATATAGACGGATGCCTCTCTCCCC AGTGGACACCCTCTTCCAGGACAGTCTCAGTGGCATCACAGCGGCCT GAGATCCCCAGGACGCAGCACCCTGTCAATAGGGGCCCCAAATGCCT GGACCAGGGCCTGCGTGGGAAAGGTCTCTGGCCACACTCGGGCTTTTT GTGAAGGGCCCTCCTGCTGTGTGACTACAGTACGCCAATATAGACGGA GTCGACAGTTGGACTTCCCAGGCCGACAGTGGTCTGGCTTCTGAGGGG TCAGGCCAGAATGTGGGGTACGTGGGAGGCCAGCAGAGGGTTCCATGA GAAGGGCAGGCGCCAATATAGACGGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5729
hsIGH_2152_ D017_J006_I GHD4- 17_IGHJ6	GCCTTGCCAGCCCGCTCAGTCAAGCCTTAGACGGAGGAGGGTGAGTCA GACCCACCTGCCCTCGATGGCAGGCGGGGAAGATTAGAAAGGCCTGA GATCCCCAGGACGCAGCACCCTGTCAATGGGGGCCCCAGACGCCTGG ACCAGGGCCTGCGTGGGAAAGGCCGCTGGGCACACTCAGGGGCTTTTT GTGAAGGGCCCTCCTACTGTGTGACTACGGTGTCAAGCCTTAGACGGA GTCGACAGTTGGACTTCCCAGGCCGACAGTGGTCTGGCTTCTGAGGGG TCAGGCCAGAATGTGGGGTACGTGGGAGGCCAGCAGAGGGTTCCATGA GAAGGGCAGGTCAAGCCTTAGACGGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5730
hsIGH_2153_ D018_J006_I GHD4- 23_IGHJ6	GCCTTGCCAGCCCGCTCAGACGTGTGTTAGACGGAGGAGGGTGAGTCA GACCCACCTGCCCTCAATGGCAGGCGGGGAAGATTAGAAAGGCCTGA GATCCCCAGGACGCAGCACCCTGTCAATGGGGGCCCCAGACGCCTGG ACCAGGGCCTGTGTGGGAAAGGCCTCTGGCCACACTCAGGGGCTTTTT GTGAAGGGCCCTCCTGCTGTGTGACTACGGTGGTAACGTGTGTTAGAC GGAGTCGACAGTTGGACTTCCCAGGCCGACAGTGGTCTGGCTTCTGAG GGGTCAGGCCAGAATGTGGGGTACGTGGGAGGCCAGCAGAGGGTTCCA TGAGAAGGGCAGGACGTGTGTTAGACGGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5731

Name	Sequence	SEQ ID NO
hsIGH_2154_ D019_J006_I GHD5- 05_IGHJ6	GCCTTGCCAGCCCGCTCAGTCCGTCTATAGACGGAAGAGGCCTCTCCA GGGGGACACTGTGCATGTCTGGTCCCTGAGCAGCCCCCATGTCCCCA GTCCTGGGGGGCCCCCTGGCACAGCTGTCTGGACCCTCTCTATTCCCT GGGAAGCTCCTCCTGACAGCCCCGCCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGTGAGACTGTGGTGGATACAGCTATGTCCGTCTATAGA CGGAGTCGACAGTTGGACTTCCCAGGCCGACAGTGGTCTGGCTTCTGA GGGGTCAGGCCAGAATGTGGGGTACGTGGGAGGCCAGCAGAGGGTTCC ATGAGAAGGGCAGGTCCGTCTATAGACGGACTGATGGCGCGAGGGAGG C	SEQ ID NO: 5732
hsIGH_2155_ D020_J006_I GHD5- 12_IGHJ6	GCCTTGCCAGCCCGCTCAGAAGAGCTGTAGACGGAGCAGAGGCCTCTC CAGGGAGACACTGTGCATGTCTGGTACCTAAGCAGCCCCCACGTCCC CAGTCTGGGGGGCCCCCTGGCTCAGCTGTCTGGACCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCCTCCAGTTCCAGGTGTGGTTATT GTCAGGCGATGTGAGACTGTGGTGGATATAGTGGCTACGAAGAGCTGT AGACGGAGTCGACAGTTGGACTTCCCAGGCCGACAGTGGTCTGGCTTC TGAGGGGTGAGGCCAGAATGTGGGGTACGTGGGAGGCCAGCAGAGGGT TCCATGAGAAGGGCAGGAAGAGCTGTAGACGGACTGATGGCGCGAGGG AGGC	SEQ ID NO: 5733
hsIGH_2156_ D021_J006_I GHD5- 18_IGHJ6	GCCTTGCCAGCCCGCTCAGTATCGCTCTAGACGGAGCAGAGGCCTCTC CAGGGGGACACTGTGCATGTCTGGTCCCTGAGCAGCCCCCACGTCCC CAGTCTGGGGGGCCCCCTGGCACAGCTGTCTGGACCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGTGAGACTGTGGTGGATACAGCTATGTATCGCTCTAGA CGGAGTCGACAGTTGGACTTCCCAGGCCGACAGTGGTCTGGCTTCTGA GGGGTCAGGCCAGAATGTGGGGTACGTGGGAGGCCAGCAGAGGGTTCC ATGAGAAGGGCAGGTATCGCTCTAGACGGACTGATGGCGCGAGGGAGG C	SEQ ID NO: 5734
hsIGH_2157_ D022_J006_I GHD5- 24_IGHJ6	GCCTTGCCAGCCCGCTCAGTCAGATGCTAGACGGAGCAGAGGCCTCTC CAGGGGGACACAGTGCATGTCTGGTCCCTGAGCAGCCCCCAGGCTCTC TAGCACTGGGGGGCCCCCTGGCACAGCTGTCTGGACCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGCCAGGCCGTGGTAGAGATGGCTACATCAGATGCTAGA CGGAGTCGACAGTTGGACTTCCCAGGCCGACAGTGGTCTGGCTTCTGA GGGGTCAGGCCAGAATGTGGGGTACGTGGGAGGCCAGCAGAGGGTTCC ATGAGAAGGGCAGGTGAGATGCTAGACGGACTGATGGCGCGAGGGAGG C	SEQ ID NO: 5735

Name	Sequence	SEQ ID NO
hsIGH_2158_ D023_J006_I GHD6- 06_IGHJ6	GCCTTGCCAGCCCGCTCAGGTGTAGCATAGACGGAAGGCAGCTGACTC CTGACTTGGACGCCTATTCCAGACACCAGACAGAGGGGCAGGCCCCC AGAACCAGGGATGAGGACGCCCCGTCAAGGCCAGAAAAGACCAAGTTG TGCTGAGCCCAGCAAGGGAAGGTCCCCAAACAAACCAGGAACGTTTCT GAAGGTGTCTGTGTACAGTGGAGTATAGCAGCTGTGTAGCATAGACG GAGTCGACAGTTGGACTTCCCAGGCCGACAGTGGTCTGGCTTCTGAGG GGTCAGGCCAGAATGTGGGGTACGTGGGAGGCCAGCAGAGGGTTCCAT GAGAAGGGCAGGGTGTAGCATAGACGGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5736
hsIGH_2159_ D024_J006_I GHD6- 13_IGHJ6	GCCTTGCCAGCCCGCTCAGTGGCAGTTTAGACGGAAGGCAGCTGACCC CTGACTTGGACCCCTATTCCAGACACCAGACAGAGGCGCAGGCCCCC AGAACCAGGGTTGAGGGACGCCCCGTCAAAGCCAGACAAAACCAAGGG GTGTTGAGCCCAGCAAGGGAAGGCCCCCAAACAGACCAGGAGGTTTCT GAAGGTGTCTGTGTACAGTGGGGTATAGCAGCAGCTTGGCAGTTTAG ACGGAGTCGACAGTTGGACTTCCCAGGCCGACAGTGGTCTGGCTTCTG AGGGGTCAGGCCAGAATGTGGGGTACGTGGGAGGCCAGCAGAGGGTTC CATGAGAAGGGCAGGTGGCAGTTTAGACGGACTGATGGCGCGAGGGAG GC	SEQ ID NO: 5737
hsIGH_2160_ D025_J006_I GHD6- 19_IGHJ6	GCCTTGCCAGCCCGCTCAGCAGTCCAATAGACGGATGAGGTAGCTGGC CTCTGTCTCGGACCCCACTCCAGACACCAGACAGAGGGGCAGGCCCC CAAAACCAGGGTTGAGGGATGATCCGTCAAGGCAGACAAGACCAAGGG GCACTGACCCAGCAAGGGAAGGCTCCCAACAGACGAGGAGGTTTCT GAAGCTGTCTGTATCACAGTGGGGTATAGCAGTGGCTCAGTCCAATAG ACGGAGTCGACAGTTGGACTTCCCAGGCCGACAGTGGTCTGGCTTCTG AGGGGTCAGGCCAGAATGTGGGGTACGTGGGAGGCCAGCAGAGGGTTC CATGAGAAGGGCAGGCAGTCCAATAGACGGACTGATGGCGCGAGGGAG GC	SEQ ID NO: 5738
hsIGH_2161_ D026_J006_I GHD6- 25_IGHJ6	GCCTTGCCAGCCCGCTCAGTACGTACGTAGACGGACAGCTGGCCTCTG TCTCGGACCCCAATTCCAGACACCAGACAGAGGGACAGGCCCCCAGA ACCAGTGTGAGGGACACCCCTGTCCAGGGCAGCCAAGTCCAAGAGGC GCGCTGAGCCCAGCAAGGGAAGGCCCCAAACAAACCAGGAGGTTTCT GAAGCTGTCTGTGTACAGTCGGGTATAGCAGCGTACGTACGTAGACG GAGTCGACAGTTGGACTTCCCAGGCCGACAGTGGTCTGGCTTCTGAGG GGTCAGGCCAGAATGTGGGGTACGTGGGAGGCCAGCAGAGGGTTCCAT GAGAAGGGCAGGTACGTACGTAGACGGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5739

Name	Sequence	SEQ ID NO
hsIGH_2162_ D027_J006_I GHD7- 27_IGHJ6	GCCTTGCCAGCCCGCTCAGAGTACCGATAGACGGAAGGGTTGAGGGCT GGGGTCTCCACGTGTTTTGGGGCTAACAGCGGAAGGGAGAGCACTGG CAAAGGTGCTGGGGGTCCCCCTGAACCCGACCCGCCCTGAGACCGCAGC CACATCAGCCCCCAGCCCCACAGGCCCCCTACCAGCCGCAGGGTTTTT GGCTGAGCTGAGAACCCTGTGCTAACTAGTACCGATAGACGGAGTCG ACAGTTGGA CT TCCAGGCCGACAGTGGTCTGGCTTCTGAGGGGTCAG GCCAGAATGTGGGGTACGTGGGAGGCCAGCAGAGGGTTCCATGAGAAG GGCAGGAGTACCGATAGACGGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5740
hsIGH_2163_ D001_J007_I GHD1- 01_IGHJp1	GCCTTGCCAGCCCGCTCAGGACACTCTCAGCTCTTGCCCCGGTCTCTG TGGGTGTTCCGCTAACTGGGGCTCCAGTGCTCACCCCACTAAAG CGAGCCCCAGCCTCCAGAGCCCCCGAAGGAGATGCCGCCCAAGCCC AGCCCCCATCCAGGAGGCCCCAGAGCTCAGGGCGCCGGGGCAGATTCT GAACAGCCCCGAGTCACGGTGGGTACAACCTGGAGACACTCTCAGCTCT TGTCGACTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTC AGGTGAGTCCTCACAACCTCTCTCCTGCTTTAACTCTGAAGGGTTTTG CTGCATTTCTGGACACTCTCAGCTCTTCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5741
hsIGH_2164_ D002_J007_I GHD1- 07_IGHJp1	GCCTTGCCAGCCCGCTCAGTTCGGAACCAGCTCTTGGCCTCGGTCTCT GTGGGTGTTCCGCTAGCTGGGGCTCACAGTGCTCACCCACACCTAAA ACGAGCCACAGCCTCAGAGCCCCCTGAAGGAGACCCCGCCACAAGCCC AGCCCCCACCAGGAGGCCCCAGAGCACAGGGCGCCCCGTCGGATTCT GAACAGCCCCGAGTCACAGTGGGTATAACTGGATTTCGGAACCAGCTCT TGTCGACTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTC AGGTGAGTCCTCACAACCTCTCTCCTGCTTTAACTCTGAAGGGTTTTG CTGCATTTCTGTTTCGGAACCAGCTCTTCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5742
hsIGH_2165_ D003_J007_I GHD1- 14_IGHJp1	GCCTTGCCAGCCCGCTCAGAAGTAACGCAGCTCTTGGCCTCGGTCTCT GTGGGTGTTCCGCTAGCTGGGGCTCACAGTGCTCACCCACACCTAAA ATGAGCCACAGCCTCCGGAGCCCCCGCAGAGACCCCGCCACAAGCCC AGCCCCCACCAGGAGGCCCCAGAGCTCAGGGCGCCCCGTCGGATTCC GAACAGCCCCGAGTCACAGCGGGTATAACCGGAAAGTAACGCAGCTCT TGTCGACTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTC AGGTGAGTCCTCACAACCTCTCTCCTGCTTTAACTCTGAAGGGTTTTG CTGCATTTCTGAAGTAACGCAGCTCTTCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5743
hsIGH_2166_ D004_J007_I GHD1- 20_IGHJp1	GCCTTGCCAGCCCGCTCAGGTCTCTACAGCTCTTGTCTCTGTGGGTG TTCCGCTAGCTGGGGCCCCCAGTGCTCACCCACACCTAAAGCGAGCC CCAGCCTCCAGAGCCCCCTAAGCATCCCCGCCAGCAGCCAGCCCC TGCCCCCACCAGGAGGCCCCAGAGCTCAGGGCGCCTGGTCGGATTCT GAACAGCCCCGAGTCACAGTGGGTATAACTGGAGTCTCCTACAGCTCT TGTCGACTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTC AGGTGAGTCCTCACAACCTCTCTCCTGCTTTAACTCTGAAGGGTTTTG CTGCATTTCTGGTCTCCTACAGCTCTTCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5744

Name	Sequence	SEQ ID NO
hsIGH_2167_ D005_J007_I GHD1- 26_IGHJp1	GCCTTGCCAGCCCGCTCAGAGAGTGTCCAGCTCTTAGGCCTCAGGCTC TGTGGGTGCCGCTAGCTGGGGCTGCCAGTCCTCACCACACCTAAGG TGAGCCACAGCCGCCAGAGCCTCCACAGGAGACCCACCCAGCAGCCC AGCCCCTACCCAGGAGGCCCCAGAGCTCAGGGCGCCTGGGTGGATTCT GAACAGCCCCGAGTCACGGTGGGTATAGTGGGAGCTAGAGTGTCCAGC TCTTGTCGACTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTC CTCAGGTGAGTCCTCACAACCTCTCTCCTGCTTTAACTCTGAAGGGTT TTGCTGCATTTCTGAGAGTGTCCAGCTCTTCTGATGGCGCGAGGGAGG C	SEQ ID NO: 5745
hsIGH_2168_ D006_J007_I GHD2- 02_IGHJp1	GCCTTGCCAGCCCGCTCAGGTTCCGAACAGCTCTTAAAGGAGGAGCCC CCTGTACAGCACTGGGCTCAGAGTCCTCTCCACACACCCTGAGTTTC AGACAAAAACCCCTGGAAATCATAGTATCAGCAGGAGAACTAGCCAG AGACAGCAAGAGGGGACTCAGTGACTCCCGCGGGGACAGGAGGATTTT GTGGGGGCTCGTGTCACTGTGAGGATATTGTAGTAGTACCAGCTGCTG TTCCGAACAGCTCTTGTGCACTTTGACTACTGGGGCCAGGGAACCCCTG GTCACCGTCTCCTCAGGTGAGTCCTCACAACCTCTCTCCTGCTTTAAC TCTGAAGGGTTTTGCTGCATTTCTGGTTCCGAACAGCTCTTCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5746
hsIGH_2169_ D007_J007_I GHD2- 08_IGHJp1	GCCTTGCCAGCCCGCTCAGCGTTACTTCAGCTCTTAAAGGAGGAGCCC CTTGTTACAGCACTGGGCTCAGAGTCCTCTCCAAGACACCCAGAGTTTC AGACAAAAACCCCTGGAATGCACAGTCTCAGCAGGAGAGCCAGCCAG AGCCAGCAAGATGGGGCTCAGTGACACCCGCAGGGACAGGAGGATTTT GTGGGGGCTCGTGTCACTGTGAGGATATTGTACTAATGGTGTATGCTC GTTACTTCAGCTCTTGTGCACTTTGACTACTGGGGCCAGGGAACCCCTG GTCACCGTCTCCTCAGGTGAGTCCTCACAACCTCTCTCCTGCTTTAAC TCTGAAGGGTTTTGCTGCATTTCTGCGTTACTTCAGCTCTTCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5747
hsIGH_2170_ D008_J007_I GHD2- 15_IGHJp1	GCCTTGCCAGCCCGCTCAGTAGGAGACCAGCTCTTAAAGGAGGAGCCC CCTATACAGCACTGGGCTCAGAGTCCTCTCTGAGACACCCTGAGTTTC AGACAACAACCCGCTGGAATGCACAGTCTCAGCAGGAGAACAGACCAA AGCCAGCAAAAGGGACCTCGGTGACACCAGTAGGGACAGGAGGATTTT GTGGGGGCTCGTGTCACTGTGAGGATATTGTAGTGGTGGTAGCTGCTT AGGAGACCAGCTCTTGTGCACTTTGACTACTGGGGCCAGGGAACCCCTG GTCACCGTCTCCTCAGGTGAGTCCTCACAACCTCTCTCCTGCTTTAAC TCTGAAGGGTTTTGCTGCATTTCTGTAGGAGACCAGCTCTTCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5748

Name	Sequence	SEQ ID NO
hsIGH_2171_ D009_J007_I GHD2- 21_IGHJp1	GCCTTGCCAGCCCGCTCAGGTGTCTACCAGCTCTTAGCCCCCTGTACA GCACTGGGCTCAGAGTCTCTCTGAGACAGGCTCAGTTTCAGACAACA ACCCGCTGGAATGCACAGTCTCAGCAGGAGAGCCAGGCCAGAGCCAGC AAGAGGAGACTCGGTGACACCAGTCTCCTGTAGGGACAGGAGGATTTT GTGGGGGTTTCGTGTCACTGTGAGCATATTGTGGTGGTGA CTGCTGTGT CTACCAGTCTTGTGCGACTTTGACTACTGGGGCCAGGGAACCCCTGGTC ACCGTCTCCTCAGGTGAGTCCTCACAACCTCTCTCCTGCTTTAACTCT GAAGGGTTTTGCTGCATTTCTGGTGTCTACCAGCTCTTCTGATGGCGC GAGGGAGGC	SEQ ID NO: 5749
hsIGH_2172_ D010_J007_I GHD3- 03_IGHJp1	GCCTTGCCAGCCCGCTCAGTGCTACACCAGCTCTTGTGGGCACGGACA CTGTCCACCTAAGCCAGGGGCAGACCCGAGTGTCCTCCGACAGTAGACCT GAGAGCGCTGGGCCCCACAGCCTCCCCTCGGTGCCCTGCTACCTCCTCA GGTCAGCCCTGGACATCCCGGGTTTCCCCAGGCTGGCGGTAGGTTTGG GGTGAGGTCTGTGTCACTGTGGTATTACGATTTTGGAGTGGTTATTT GCTACACCAGCTCTTGTGCGACTTTGACTACTGGGGCCAGGGAACCCCTG GTCACCGTCTCCTCAGGTGAGTCCTCACAACCTCTCTCCTGCTTTAAC TCTGAAGGGTTTTGCTGCATTTCTGTGCTACACCAGCTCTTCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5750
hsIGH_2173_ D011_J007_I GHD3- 09_IGHJp1	GCCTTGCCAGCCCGCTCAGAACTGCCACAGCTCTTTGGGCACGGACAC TATCCACATAAGCGAGGGATAGACCCGAGTGTCCTCCACAGCAGACCTG AGAGCGCTGGGCCCCACAGCCTCCCCTCAGAGCCCTGCTGCCTCCTCCG GTCAGCCCTGGACATCCCAGGTTTCCCCAGGCTGCCGGTAGGTTTAG AATGAGGTCTGTGTCACTGTGGTATTACGATATTTTACTGAGTTATTA ACTGCCACAGCTCTTGTGCGACTTTGACTACTGGGGCCAGGGAACCCCTG GTCACCGTCTCCTCAGGTGAGTCCTCACAACCTCTCTCCTGCTTTAAC TCTGAAGGGTTTTGCTGCATTTCTGAAGTCCACAGCTCTTCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5751
hsIGH_2174_ D012_J007_I GHD3- 10_IGHJp1	GCCTTGCCAGCCCGCTCAGTTGGACTGCAGCTCTTCGATATTTTGA CT GGTTATTATAACCACAGTGTACAGAGTCCATCAAAAACCCATGCCTG GAAGCTTCCCGCCACAGCCCTCCCCATGGGGCCCTGCTGCCTCCTCAG GTCAGCCCCGGACATCCCGGGTTTCCCCAGGCTGGGCGGTAGGTTTGG GGTGAGGTCTGTGTCACTGTGGTATTACTATGGTTCGGGGAGTTATTT TGGACTGCAGCTCTTGTGCGACTTTGACTACTGGGGCCAGGGAACCCCTG GTCACCGTCTCCTCAGGTGAGTCCTCACAACCTCTCTCCTGCTTTAAC TCTGAAGGGTTTTGCTGCATTTCTGTTGGACTGCAGCTCTTCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5752

Name	Sequence	SEQ ID NO
hsIGH_2175_ D013_J007_I GHD3- 16_IGHJp1	GCCTTGCCAGCCCGCTCAGGTAGACACCAGCTCTTTGGACGCGGACAC TATCCACATAAGCGAGGGACAGACCCGAGTGTTCCCTGCAGTAGACCTG AGAGCGCTGGGCCCCACAGCCTCCCCTCGGTGCCCTGCTGCCTCCTCAG GTCAGCCCTGGACATCCCGGGTTTCCCCAGGCCAGATGGTAGGTTTGA AGTGAGGTCTGTGTCACTGTGGTATTATGATTACGTTTGGGGGAGTTA TCGTTGTAGACACCAGCTCTTGTGCACTTTGACTACTGGGGCCAGGGA ACCCGTGGTCACCGTCTCCTCAGGTGAGTCCTCACAACCTCTCTCCTGC TTTAACTCTGAAGGGTTTTGCTGCATTTCTGGTAGACACCAGCTCTTC TGATGGCGCGAGGGAGGC	SEQ ID NO: 5753
hsIGH_2176_ D014_J007_I GHD3- 22_IGHJp1	GCCTTGCCAGCCCGCTCAGCACTGTACCAGCTCTTTGGGCATGGACAG TGTCACCTAAGCGAGGGACAGACCCGAGTGTCCTGCAGTAGACCTG AGAGCGCTGGGCCCCACAGCCTCCCCTCGGGGCCCTGCTGCCTCCTCAG GTCAGCCCTGGACATCCCGGGTTTCCCCAGGCCTGGCGGTAGGTTTGA AGTGAGGTCTGTGTCACTGTGGTATTACTATGATAGTAGTGTTATTC ACTGTACCAGCTCTTGTGCACTTTGACTACTGGGGCCAGGGAACCTG GTCACCGTCTCCTCAGGTGAGTCCTCACAACCTCTCTCTGCTTTAAC TCTGAAGGGTTTTGCTGCATTTCTGCACTGTACCAGCTCTTCTGATGG CGCGAGGGAGGC	SEQ ID NO: 5754
hsIGH_2177_ D015_J007_I GHD4- 04_IGHJp1	GCCTTGCCAGCCCGCTCAGGATGATCCCAGCTCTTCAAGGGTGAGTCA GACCTCCTGCCCTCGATGGCAGGCGGAGAAGATTAGAAAGGTCTGA GATCCCCAGGACGACGACCCTGTCAATGGGGGCCCCAGACGCTGG ACCAGGGCCTGCGTGGGAAAGGCCTCTGGGCACACTCAGGGGCTTTTT GTGAAGGGTCTCCTACTGTGTGACTACAGTAGATGATCCCAGCTCTT GTCGACTTTGACTACTGGGGCCAGGGAACCTGGTCACCGTCTCCTCA GGTGAGTCCTCACAACCTCTCTCCTGCTTTAACTCTGAAGGGTTTTGC TGCATTTCTGGATGATCCCAGCTCTTCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5755
hsIGH_2178_ D016_J007_I GHD4- 11_IGHJp1	GCCTTGCCAGCCCGCTCAGCGCCAATACAGCTCTTTGCCTCTCTCCCC AGTGGACACCCTCTTCCAGGACAGTCCTCAGTGGCATCACAGCGGCCT GAGATCCCCAGGACGACGACCCTGTCAATAGGGGCCCCAAATGCCT GGACCAGGGCCTGCGTGGGAAAGGTCTCTGGCCACACTCGGGCTTTTT GTGAAGGGCCCTCCTGCTGTGTGACTACAGTACGCCAATACAGCTCTT GTCGACTTTGACTACTGGGGCCAGGGAACCTGGTCACCGTCTCCTCA GGTGAGTCCTCACAACCTCTCTCCTGCTTTAACTCTGAAGGGTTTTGC TGCATTTCTGCGCCAATACAGCTCTTCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5756

Name	Sequence	SEQ ID NO
hsIGH_2179_ D017_J007_I GHD4- 17_IGHJp1	GCCTTGCCAGCCCGCTCAGTCAAGCCTCAGCTCTTGAGGGTGAGTCA GACCCACCTGCCCTCGATGGCAGGCGGGGAAGATTAGAAAGGCCTGA GATCCCCAGGACGCAGCACCACCTGTCAATGGGGGCCCCAGACGCCTGG ACCAGGGCCTGCGTGGGAAAGGCCGCTGGGCACACTCAGGGGCTTTTT GTGAAGGGCCCTCCTACTGTGTGACTACGGTGTCAAGCCTCAGCTCTT GTCGACTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA GGTGAGTCCTCACAACCTCTCTCCTGCTTTAACTCTGAAGGGTTTTGC TGCATTTCTGTCAAGCCTCAGCTCTTCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5757
hsIGH_2180_ D018_J007_I GHD4- 23_IGHJp1	GCCTTGCCAGCCCGCTCAGACGTGTGTGACGCTCTTGAGGGTGAGTCA GACCCACCTGCCCTCAATGGCAGGCGGGGAAGATTAGAAAGGCCTGA GATCCCCAGGACGCAGCACCACCTGTCAATGGGGGCCCCAGACGCCTGG ACCAGGGCCTGTGTGGGAAAGGCCCTCTGGCCACACTCAGGGGCTTTTT GTGAAGGGCCCTCCTGCTGTGTGACTACGGTGGTAACGTGTGTGACGT CTTGTCGACTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCC TCAGGTGAGTCCTCACAACCTCTCTCCTGCTTTAACTCTGAAGGGTTT TGCTGCATTTCTGACGTGTGTGACGCTCTTCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5758
hsIGH_2181_ D019_J007_I GHD5- 05_IGHJp1	GCCTTGCCAGCCCGCTCAGTCCGTCTACAGCTCTTAGAGGCCTCTCCA GGGGGACACTGTGCATGTCTGGTCCCTGAGCAGCCCCCATGTCCCCA GTCCTGGGGGGCCCCCTGGCACAGCTGTCTGGACCCCTCTCTATTCCCT GGGAAGCTCCTCCTGACAGCCCCGCCCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGTGACACTGTGGTGGATACAGCTATGTCCGTCTACAGC TCTTGTCGACTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTC CTCAGGTGAGTCCTCACAACCTCTCTCCTGCTTTAACTCTGAAGGGTT TTGCTGCATTTCTGTCCGTCTACAGCTCTTCTGATGGCGCGAGGGAGG C	SEQ ID NO: 5759
hsIGH_2182_ D020_J007_I GHD5- 12_IGHJp1	GCCTTGCCAGCCCGCTCAGAAGAGCTGCAGCTCTTGACAGAGGCCTCTC CAGGGAGACACTGTGCATGTCTGGTACCTAAGCAGCCCCCACGTCCC CAGTCCCTGGGGGGCCCCCTGGCTCAGCTGTCTGGACCCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCCCTCCAGTTCCAGGTGTGGTTATT GTCAGGCGATGTGACACTGTGGTGGATATAGTGGCTACGAAGAGCTGC AGCTCTTGTCGACTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGT CTCCTCAGGTGAGTCCTCACAACCTCTCTCCTGCTTTAACTCTGAAGG GTTTTGCTGCATTTCTGAAGAGCTGCAGCTCTTCTGATGGCGCGAGGG AGGC	SEQ ID NO: 5760

Name	Sequence	SEQ ID NO
hsIGH_2183_ D021_J007_I GHD5- 18_IGHJp1	GCCTTGCCAGCCCGCTCAGTATCGCTCCAGCTCTTGCAGAGGCCTCTC CAGGGGGACACTGTGCATGTCTGGTCCCTGAGCAGCCCCCACGTCCC CAGTCCTGGGGGCCCTGGCACAGCTGTCTGGACCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGTGAGCTGTGGTGGATACAGCTATGTATCGCTCCAGC TCTTGTCGACTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTC CTCAGGTGAGTCCTCACAACCTCTCTCCTGCTTTAACTCTGAAGGGTT TTGCTGCATTTCTGTATCGCTCCAGCTCTTCTGATGGCGCGAGGGAGG C	SEQ ID NO: 5761
hsIGH_2184_ D022_J007_I GHD5- 24_IGHJp1	GCCTTGCCAGCCCGCTCAGTCAGATGCCAGCTCTTGCAGAGGCCTCTC CAGGGGGACACAGTGCATGTCTGGTCCCTGAGCAGCCCCCAGGCTCTC TAGCACTGGGGGCCCTGGCACAGCTGTCTGGACCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGCCAGGCCGCTGGTAGAGATGGCTACATCAGATGCCAGC TCTTGTCGACTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTC CTCAGGTGAGTCCTCACAACCTCTCTCCTGCTTTAACTCTGAAGGGTT TTGCTGCATTTCTGTGATGCCAGCTCTTCTGATGGCGCGAGGGAGG C	SEQ ID NO: 5762
hsIGH_2185_ D023_J007_I GHD6- 06_IGHJp1	GCCTTGCCAGCCCGCTCAGGTGTAGCACAGCTCTTAGGCAGCTGACTC CTGACTTGACGCCTATTCCAGACACCAGACAGAGGGGCAGGCCCCC AGAACCAGGGATGAGGACGCCCCGTCAAGGCCAGAAAAGACCAAGTTG TGCTGAGCCCAGCAAGGGAAGGTCCCCAAACAAACCAGGAACGTTTCT GAAGGTGTCTGTGTACAGTGGAGTATAGCAGCTGTGTAGCACAGCTC TTGTCGACTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCT CAGGTGAGTCCTCACAACCTCTCTCCTGCTTTAACTCTGAAGGGTTTT GCTGCATTTCTGGTGTAGCACAGCTCTTCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5763
hsIGH_2186_ D024_J007_I GHD6- 13_IGHJp1	GCCTTGCCAGCCCGCTCAGTGGCAGTTCAGCTCTTAGGCAGCTGACCC CTGACTTGACCCCTATTCCAGACACCAGACAGAGGCGCAGGCCCCC AGAACCAGGGTTGAGGGACGCCCCGTCAAAGCCAGACAAAACCAAGGG GTGTTGAGCCCAGCAAGGGAAGGCCCCCAAACAGACCAGGAGGTTTCT GAAGGTGTCTGTGTACAGTGGGGTATAGCAGCAGCTTGGCAGTTCAG CTCTTGTCGACTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCAGGTGAGTCCTCACAACCTCTCTCCTGCTTTAACTCTGAAGGGT TTTGCTGCATTTCTGTGGCAGTTCAGCTCTTCTGATGGCGCGAGGGAG GC	SEQ ID NO: 5764

Name	Sequence	SEQ ID NO
hsIGH_2187_ D025_J007_I GHD6- 19_IGHJp1	GCCTTGCCAGCCCGCTCAGCAGTCCAACAGCTCTTTGAGGTAGCTGGC CTCTGTCTCGGACCCCCACTCCAGACACCAGACAGAGGGGCAGGCCCCC CAAAACCAGGGTTGAGGGATGATCCGTCAAGGCAGACAAGACCAAGGG GCACTGACCCCAGCAAGGGAAGGCTCCCAAACAGACGAGGAGGTTTCT GAAGCTGTCTGTATCACAGTGGGGTATAGCAGTGGCTCAGTCCAACAG CTCTTGTCGACTTTGACTACTGGGGCCAGGGAACCTGGTCACCGTCT CCTCAGGTGAGTCCTCACAACCTCTCTCCTGCTTTAACTCTGAAGGGT TTTGCTGCATTTCTGCAGTCCAACAGCTCTTCTGATGGCGCGAGGGAG GC	SEQ ID NO: 5765
hsIGH_2188_ D026_J007_I GHD6- 25_IGHJp1	GCCTTGCCAGCCCGCTCAGTACGTACGCAGCTCTTCAGCTGGCCTCTG TCTCGGACCCCCATTCCAGACACCAGACAGAGGGACAGGCCCCCAGA ACCAGTGTGAGGGACACCCCTGTCCAGGGCAGCCAAGTCCAAGAGGC GCGCTGAGCCCAGCAAGGGAAGGCCCCCAAACAAACCAGGAGGTTTCT GAAGCTGTCTGTGTACAGTCGGGTATAGCAGCGTACGTACGCAGCTC TTGTGCACTTTGACTACTGGGGCCAGGGAACCTGGTCACCGTCTCCT CAGGTGAGTCCTCACAACCTCTCTCCTGCTTTAACTCTGAAGGGTTTT GCTGCATTTCTGTACGTACGCAGCTCTTCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5766
hsIGH_2189_ D027_J007_I GHD7- 27_IGHJp1	GCCTTGCCAGCCCGCTCAGAGTACCGACAGCTCTTAGGGTTGAGGGCT GGGGTCTCCACGTGTTTTGGGGCTAACAGCGGAAGGGAGAGCACTGG CAAAGGTGCTGGGGGTCCCTGAACCCGACCCGCCCTGAGACCGCAGC CACATCAGCCCCAGCCCCACAGGCCCCCTACCAGCCGAGGGTTTTT GGCTGAGCTGAGAACCACTGTGCTAACTAGTACCGACAGCTCTTGTCG ACTTTGACTACTGGGGCCAGGGAACCTGGTCACCGTCTCCTCAGGTG AGTCCTCACAACCTCTCTCCTGCTTTAACTCTGAAGGGTTTTGCTGCA TTTCTGAGTACCGACAGCTCTTCTGATGGCGCGAGGGAGGC	SEQ ID NO: 5767
hsIGH_2190_ D001_J008_I GHD1- 01_IGHJp2	GCCTTGCCAGCCCGCTCAGGACACTCTGAGCGATAGCCCCGGTCTCTG TGGGTGTTCCGCTAACTGGGGCTCCCAGTGCTCACCACAACTAAAG CGAGCCCCAGCCTCCAGAGCCCCGAAGGAGATGCCGCCACAAAGCCC AGCCCCCATCCAGGAGGCCCCAGAGCTCAGGGCGCCGGGGCAGATTCT GAACAGCCCCGAGTCACGGTGGGTACAACCTGGAGACACTCTGAGCGAT AGTCGACTGGTTCGACCCCTGGGGCCAGGGAACCTGGTCACCGTCTC CTCAGGTGAGTCCTCACCACCCCTCTCTGAGTCCACTTAGGGAGACT CAGCTTGCCAGGACACTCTGAGCGATACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5768
hsIGH_2191_ D002_J008_I GHD1- 07_IGHJp2	GCCTTGCCAGCCCGCTCAGTTCGGAACGAGCGATAGGCCTCGGTCTCT GTGGGTGTTCCGCTAGCTGGGGCTCACAGTGCTCACCACACCTAAA ACGAGCCACAGCCTCAGAGCCCCGAAGGAGACCCCGCCACAAGCCC AGCCCCACCCAGGAGGCCCCAGAGCACAGGGCGCCCCGTCGGATTCT GAACAGCCCCGAGTCACAGTGGGTATAACTGGATTTCGGAACGAGCGAT AGTCGACTGGTTCGACCCCTGGGGCCAGGGAACCTGGTCACCGTCTC CTCAGGTGAGTCCTCACCACCCCTCTCTGAGTCCACTTAGGGAGACT CAGCTTGCCAGTTCGGAACGAGCGATACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5769

Name	Sequence	SEQ ID NO
hsIGH_2192_ D003_J008_I GHD1- 14_IGHJp2	GCCTTGCCAGCCCGCTCAGAAGTAACGGAGCGATAGGCCTCGGTCTCT GTGGGTGTTCCGCTAGCTGGGGCTCACAGTGCTCACCCACACCTAAA ATGAGCCACAGCCTCCGGAGCCCCCGCAGAGACCCCGCCACAAGCCC AGCCCCACCCAGGAGGCCCCAGAGCTCAGGGCGCCCCGTCGGATTCC GAACAGCCCCGAGTCACAGCGGGTATAACCGGAAAGTAACGGAGCGAT AGTCGACTGGTTCGACCCCTGGGGCCAGGGAACCCCTGGTCACCGTCTC CTCAGGTGAGTCCTCACCACCCCTCTCTGAGTCCACTTAGGGAGACT CAGCTTGCCAGAAGTAACGGAGCGATACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5770
hsIGH_2193_ D004_J008_I GHD1- 20_IGHJp2	GCCTTGCCAGCCCGCTCAGGTCTCCTAGAGCGATAGTCTCTGTGGGTG TTCCGCTAGCTGGGGCCCCCAGTGCTCACCCACACCTAAAGCGAGCC CCAGCCTCCAGAGCCCCCTAAGCATTCCTCCGCCCAGCAGCCAGCCCC TGCCCCCACCAGGAGGCCCCAGAGCTCAGGGCGCCTGGTCGGATTCT GAACAGCCCCGAGTCACAGTGGGTATAACTGGAGTCTCCTAGAGCGAT AGTCGACTGGTTCGACCCCTGGGGCCAGGGAACCCCTGGTCACCGTCTC CTCAGGTGAGTCCTCACCACCCCTCTCTGAGTCCACTTAGGGAGACT CAGCTTGCCAGGTCTCCTAGAGCGATACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5771
hsIGH_2194_ D005_J008_I GHD1- 26_IGHJp2	GCCTTGCCAGCCCGCTCAGAGAGTGTCGAGCGATAAGGCCTCAGGCTC TGTGGGTGCCGCTAGCTGGGGTGCCAGTCCTCACCCACACCTAAGG TGAGCCACAGCCGCCAGAGCCTCCACAGGAGACCCACCCAGCAGCCC AGCCCCTACCCAGGAGGCCCCAGAGCTCAGGGCGCCTGGGTGGATTCT GAACAGCCCCGAGTCACGGTGGGTATAGTGGGAGCTAGAGTGTCGAGC GATAGTCGACTGGTTCGACCCCTGGGGCCAGGGAACCCCTGGTCACCGT CTCCTCAGGTGAGTCCTCACCACCCCTCTCTGAGTCCACTTAGGGAG ACTCAGCTTGCCAGAGAGTGTCGAGCGATACTGATGGCGCGAGGGAGG C	SEQ ID NO: 5772
hsIGH_2195_ D006_J008_I GHD2- 02_IGHJp2	GCCTTGCCAGCCCGCTCAGGTTCGAAGAGCGATAAAAGGAGGAGCCC CCTGTACAGCACTGGGCTCAGAGTCCTCTCCACACACCCCTGAGTTTC AGACAAAAACCCCTGGAAATCATAGTATCAGCAGGAGAACTAGCCAG AGACAGCAAGAGGGGACTCAGTGACTCCCGCGGGGACAGGAGGATTTT GTGGGGGCTCGTGTCAGTGTGAGGATATTGTAGTAGTACCAGCTGCTG TTCCGAAGAGCGATAGTCGACTGGTTCGACCCCTGGGGCCAGGGAACC CTGGTCACCGTCTCCTCAGGTGAGTCCTCACCACCCCTCTCTGAGTC CACTTAGGGAGACTCAGCTTGCCAGGTTCGAAGAGCGATACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5773

Name	Sequence	SEQ ID NO
hsIGH_2196_ D007_J008_I GHD2- 08_IGHJp2	GCCTTGCCAGCCCGCTCAGCGTTACTTGAGCGATAAAAGGAGGAGCCC CTTGTTCAGCACTGGGCTCAGAGTCCTCTCCAAGACACCCAGAGTTTC AGACAAAACCCCTGGAATGCACAGTCTCAGCAGGAGAGCCAGCCAG AGCCAGCAAGATGGGGCTCAGTGACACCCGACGGGACAGGAGGATTTT GTGGGGGCTCGTGTCAGTGTGAGGATATTGTACTAATGGTGTATGCTC GTTACTTGAGCGATAGTCGACTGGTTCGACCCCTGGGGCCAGGGAACC CTGGTCACCGTCTCCTCAGGTGAGTCCTCACCACCCCTCTCTGAGTC CACTTAGGGAGACTCAGCTTGCCAGCGTTACTTGAGCGATACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5774
hsIGH_2197_ D008_J008_I GHD2- 15_IGHJp2	GCCTTGCCAGCCCGCTCAGTAGGAGACGAGCGATAAAAGGAGGAGCCC CCTATACAGCACTGGGCTCAGAGTCCTCTCTGAGACACCCAGAGTTTC AGACAACAACCCGCTGGAATGCACAGTCTCAGCAGGAGAACAGACCAA AGCCAGCAAAAGGGACCTCGGTGACACCACTAGGGACAGGAGGATTTT GTGGGGGCTCGTGTCAGTGTGAGGATATTGTAGTGGTGGTAGCTGCTT AGGAGACGAGCGATAGTCGACTGGTTCGACCCCTGGGGCCAGGGAACC CTGGTCACCGTCTCCTCAGGTGAGTCCTCACCACCCCTCTCTGAGTC CACTTAGGGAGACTCAGCTTGCCAGTAGGAGACGAGCGATACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5775
hsIGH_2198_ D009_J008_I GHD2- 21_IGHJp2	GCCTTGCCAGCCCGCTCAGGTGTCTACGAGCGATAAGCCCCCTGTACA GCACTGGGCTCAGAGTCCTCTCTGAGACAGGCTCAGTTTCAGACAACA ACCCGCTGGAATGCACAGTCTCAGCAGGAGAGCCAGGCCAGAGCCAGC AAGAGGAGACTCGGTGACACCACTCTCCTGTAGGGACAGGAGGATTTT GTGGGGGTTCGTGTCACTGTGAGCATATTGTGGTGGTGAAGTGTGTGT CTACGAGCGATAGTCGACTGGTTCGACCCCTGGGGCCAGGGAACCCTG GTCACCGTCTCCTCAGGTGAGTCCTCACCACCCCTCTCTGAGTCCAC TTAGGGAGACTCAGCTTGCCAGGTGTCTACGAGCGATACTGATGGCGC GAGGGAGGC	SEQ ID NO: 5776
hsIGH_2199_ D010_J008_I GHD3- 03_IGHJp2	GCCTTGCCAGCCCGCTCAGTGCTACACGAGCGATAGTGGGCACGGACA CTGTCCACCTAAGCCAGGGGCAGACCCGAGTGTCCTCCGAGTAGACCT GAGAGCGCTGGGCCCACAGCCTCCCTCGGTGCCCTGCTACCTCCTCA GGTCAGCCCTGGACATCCCGGGTTTCCCCAGGCTGGCGGTAGGTTTGG GGTGAGGTCTGTGTCACTGTGGTATTACGATTTTGGAGTGGTTATTT GCTACACGAGCGATAGTCGACTGGTTCGACCCCTGGGGCCAGGGAACC CTGGTCACCGTCTCCTCAGGTGAGTCCTCACCACCCCTCTCTGAGTC CACTTAGGGAGACTCAGCTTGCCAGTGCTACACGAGCGATACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5777

Name	Sequence	SEQ ID NO
hsIGH_2200_ D011_J008_I GHD3- 09_IGHJp2	GCCTTGCCAGCCCGCTCAGAACTGCCAGAGCGATATGGGCACGGACAC TATCCACATAAGCGAGGGATAGACCCGAGTGTCACACAGCAGACCTG AGAGCGCTGGGCCCCACAGCCTCCCCTCAGAGCCCTGCTGCCTCCTCCG GTCAGCCCTGGACATCCCAGGTTTCCCCAGGCCTGCCGGTAGGTTTAG AATGAGGTCTGTGTCACTGTGGTATTACGATATTTGACTGGTTATTA ACTGCCAGAGCGATAGTCGACTGGTTCGACCCCTGGGGCCAGGGAACC CTGGTCACCGTCTCCTCAGGTGAGTCCTCACCACCCCTCTCTGAGTC CACTTAGGGAGACTCAGCTTGCCAGAACTGCCAGAGCGATACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5778
hsIGH_2201_ D012_J008_I GHD3- 10_IGHJp2	GCCTTGCCAGCCCGCTCAGTTGGACTGGAGCGATACGATATTTGACT GGTTATTATAACCACAGTGTCACAGAGTCCATCAAAAACCCATGCCTG GAAGCTTCCCCGCCACAGCCCTCCCCATGGGGCCCTGCTGCCTCCTCAG GTCAGCCCCGGACATCCCGGGTTTCCCCAGGCCTGGGCGGTAGGTTTGG GGTGAGGTCTGTGTCACTGTGGTATTACTATGGTTCGGGGAGTTATTT TGGACTGGAGCGATAGTCGACTGGTTCGACCCCTGGGGCCAGGGAACC CTGGTCACCGTCTCCTCAGGTGAGTCCTCACCACCCCTCTCTGAGTC CACTTAGGGAGACTCAGCTTGCCAGTTGGACTGGAGCGATACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5779
hsIGH_2202_ D013_J008_I GHD3- 16_IGHJp2	GCCTTGCCAGCCCGCTCAGGTAGACACGAGCGATATGGACGCGGACAC TATCCACATAAGCGAGGGACAGACCCGAGTGTTCTTCAGTAGACCTG AGAGCGCTGGGCCCCACAGCCTCCCCTCGGTGCCCTGCTGCCTCCTCAG GTCAGCCCTGGACATCCCGGGTTTCCCCAGGCCAGATGGTAGGTTTGA AGTGAGGTCTGTGTCACTGTGGTATTATGATTACGTTTGGGGGAGTTA TCGTTGTAGACACGAGCGATAGTCGACTGGTTCGACCCCTGGGGCCAG GGAACCCTGGTCACCGTCTCCTCAGGTGAGTCCTCACCACCCCTCTC TGAGTCCACTTAGGGAGACTCAGCTTGCCAGGTAGACACGAGCGATAC TGATGGCGCGAGGGAGGC	SEQ ID NO: 5780
hsIGH_2203_ D014_J008_I GHD3- 22_IGHJp2	GCCTTGCCAGCCCGCTCAGCACTGTACGAGCGATATGGGCATGGACAG TGTCCACCTAAGCGAGGGACAGACCCGAGTGTCCTTCAGTAGACCTG AGAGCGCTGGGCCCCACAGCCTCCCCTCGGGGCCCTGCTGCCTCCTCAG GTCAGCCCTGGACATCCCGGGTTTCCCCAGGCCTGGGCGGTAGGTTTGA AGTGAGGTCTGTGTCACTGTGGTATTACTATGATAGTAGTGTTATTC ACTGTACGAGCGATAGTCGACTGGTTCGACCCCTGGGGCCAGGGAACC CTGGTCACCGTCTCCTCAGGTGAGTCCTCACCACCCCTCTCTGAGTC CACTTAGGGAGACTCAGCTTGCCAGCACTGTACGAGCGATACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5781

Name	Sequence	SEQ ID NO
hsIGH_2204_ D015_J008_I GHD4- 04_IGHJp2	GCCTTGCCAGCCCGCTCAGGATGATCCGAGCGATACAAGGGTGAGTCA GACCCCTCCTGCCCTCGATGGCAGGCGGAGAAGATTAGAAAAGGTCTGA GATCCCCAGGACGCAGCACCCTGTCAATGGGGGCCCCAGACGCCTGG ACCAGGGCCTGCGTGGGAAAGGCCTCTGGGCACACTCAGGGGCTTTTT GTGAAGGGTCCTCCTACTGTGTGACTACAGTAGATGATCCGAGCGATA GTCGACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCC TCAGGTGAGTCCTCACCACCCCTCTCTGAGTCCACTTAGGGAGACTC AGCTTGCCAGGATGATCCGAGCGATACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5782
hsIGH_2205_ D016_J008_I GHD4- 11_IGHJp2	GCCTTGCCAGCCCGCTCAGCGCCAATAGAGCGATATGCCTCTCTCCCC AGTGGACACCCTCTTCCAGGACAGTCCTCAGTGGCATCACAGCGGCCT GAGATCCCCAGGACGCAGCACCCTGTCAATAGGGGCCCCAAATGCCT GGACCAGGGCCTGCGTGGGAAAGGTCTCTGGCCACACTCGGGCTTTTT GTGAAGGGCCCTCCTGCTGTGTGACTACAGTACGCCAATAGAGCGATA GTCGACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCC TCAGGTGAGTCCTCACCACCCCTCTCTGAGTCCACTTAGGGAGACTC AGCTTGCCAGCGCCAATAGAGCGATACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5783
hsIGH_2206_ D017_J008_I GHD4- 17_IGHJp2	GCCTTGCCAGCCCGCTCAGTCAAGCCTGAGCGATAGGAGGGTGAGTCA GACCCACCTGCCCTCGATGGCAGGCGGGGAAGATTAGAAAAGGCCTGA GATCCCCAGGACGCAGCACCCTGTCAATGGGGGCCCCAGACGCCTGG ACCAGGGCCTGCGTGGGAAAGGCCGCTGGGCACACTCAGGGGCTTTTT GTGAAGGGCCCTCCTACTGTGTGACTACGGTGTCAAGCCTGAGCGATA GTCGACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCC TCAGGTGAGTCCTCACCACCCCTCTCTGAGTCCACTTAGGGAGACTC AGCTTGCCAGTCAAGCCTGAGCGATACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5784
hsIGH_2207_ D018_J008_I GHD4- 23_IGHJp2	GCCTTGCCAGCCCGCTCAGACGTGTGTGAGCGATAGGAGGGTGAGTCA GACCCACCTGCCCTCAATGGCAGGCGGGGAAGATTAGAAAAGGCCTGA GATCCCCAGGACGCAGCACCCTGTCAATGGGGGCCCCAGACGCCTGG ACCAGGGCCTGTGTGGGAAAGGCCTCTGGCCACACTCAGGGGCTTTTT GTGAAGGGCCCTCCTGCTGTGTGACTACGGTGGTAACGTGTGTGAGCG ATAGTCGACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTC TCCTCAGGTGAGTCCTCACCACCCCTCTCTGAGTCCACTTAGGGAGA CTCAGCTTGCCAGACGTGTGTGAGCGATACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5785
hsIGH_2208_ D019_J008_I GHD5- 05_IGHJp2	GCCTTGCCAGCCCGCTCAGTCCGTCTAGAGCGATAAGAGGCCTCTCCA GGGGGACACTGTGCATGTCTGGTCCCTGAGCAGCCCCCATGTCCCA GTCTGGGGGGCCCCCTGGCACAGCTGTCTGGACCCTCTCTATTCCCT GGGAAGCTCCTCCTGACAGCCCCGCCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGTGAGACTGTGGTGGATACAGCTATGTCCGTCTAGAGC GATAGTCGACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGT CTCCTCAGGTGAGTCCTCACCACCCCTCTCTGAGTCCACTTAGGGAG ACTCAGCTTGCCAGTCCGTCTAGAGCGATACTGATGGCGCGAGGGAGG C	SEQ ID NO: 5786

Name	Sequence	SEQ ID NO
hsIGH_2209_ D020_J008_I GHD5- 12_IGHJp2	GCCTTGCCAGCCCGCTCAGAAGAGCTGGAGCGATAGCAGAGGCCTCTC CAGGGAGACACTGTGCATGTCTGGTACCTAAGCAGCCCCCACGTCCC CAGTCCTGGGGGCCCCCTGGCTCAGCTGTCTGGACCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCCTCCAGTTCCAGGTGTGGTTATT GTCAGGCGATGTCAGACTGTGGTGGATATAGTGGCTACGAAGAGCTGG AGCGATAGTCGACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCAC CGTCTCCTCAGGTGAGTCCTCACCACCCCTCTCTGAGTCCACTTAGG GAGACTCAGCTTGCCAGAAGAGCTGGAGCGATACTGATGGCGCGAGGG AGGC	SEQ ID NO: 5787
hsIGH_2210_ D021_J008_I GHD5- 18_IGHJp2	GCCTTGCCAGCCCGCTCAGTATCGCTCGAGCGATAGCAGAGGCCTCTC CAGGGGGACACTGTGCATGTCTGGTCCCTGAGCAGCCCCCACGTCCC CAGTCCTGGGGGCCCCCTGGCACAGCTGTCTGGACCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGTGACTGTGGTGGATACAGCTATGTATCGCTCGAGC GATAGTCGACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGT CTCCTCAGGTGAGTCCTCACCACCCCTCTCTGAGTCCACTTAGGGAG ACTCAGCTTGCCAGTATCGCTCGAGCGATACTGATGGCGCGAGGGAGG C	SEQ ID NO: 5788
hsIGH_2211_ D022_J008_I GHD5- 24_IGHJp2	GCCTTGCCAGCCCGCTCAGTCAGATGCGAGCGATAGCAGAGGCCTCTC CAGGGGGACACAGTGCATGTCTGGTCCCTGAGCAGCCCCCAGGCTCTC TAGCACTGGGGGCCCCCTGGCACAGCTGTCTGGACCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGCCAGGCCGTGGTAGAGATGGCTACATCAGATGCGAGC GATAGTCGACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGT CTCCTCAGGTGAGTCCTCACCACCCCTCTCTGAGTCCACTTAGGGAG ACTCAGCTTGCCAGTCAGATGCGAGCGATACTGATGGCGCGAGGGAGG C	SEQ ID NO: 5789
hsIGH_2212_ D023_J008_I GHD6- 06_IGHJp2	GCCTTGCCAGCCCGCTCAGGTGTAGCAGAGCGATAAGGCAGCTGACTC CTGACTTGGACGCCTATTCAGACACCAGACAGAGGGGCAGGCCCCC AGAACCAGGGATGAGGACGCCCCGTCAAGGCCAGAAAAGACCAAGTTG TGCTGAGCCCAGCAAGGGAAGGTCCCCAAACAAACCAGGAACGTTTCT GAAGGTGTCTGTGTACAGTGGAGTATAGCAGCTGTGTAGCAGAGCGA TAGTCGACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCAGGTGAGTCCTCACCACCCCTCTCTGAGTCCACTTAGGGAGAC TCAGCTTGCCAGGTGTAGCAGAGCGATACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5790

Name	Sequence	SEQ ID NO
hsIGH_2213_ D024_J008_I GHD6- 13_IGHJp2	GCCTTGCCAGCCCGCTCAGTGGCAGTTGAGCGATAAGGCAGCTGACCC CTGACTTGGACCCCTATTCCAGACACCAGACAGAGGCGCAGGCCCCC AGAACCAGGGTTGAGGGACGCCCCGTCAAAGCCAGACAAAACCAAGGG GTGTTGAGCCAGCAAGGGAAGGCCCCCAAACAGACCAGGAGGTTTCT GAAGGTGTCTGTGTACAGTGGGGTATAGCAGCAGCTTGGCAGTTGAG CGATAGTCGACTGGTTCGACCCCTGGGGCCAGGGAACCTTGGTCACCG TCTCCTCAGGTGAGTCCTCACCACCCCTCTCTGAGTCCACTTAGGGA GACTCAGCTTGCCAGTGGCAGTTGAGCGATACTGATGGCGCGAGGGAG GC	SEQ ID NO: 5791
hsIGH_2214_ D025_J008_I GHD6- 19_IGHJp2	GCCTTGCCAGCCCGCTCAGCAGTCCAAGAGCGATATGAGGTAGCTGGC CTCTGTCTCGGACCCCACTCCAGACACCAGACAGAGGGCGAGGCCCC CAAAACCAGGGTTGAGGGATGATCCGTCAAGGCAGACAAGACCAAGGG GCACTGACCCAGCAAGGGAAGGCTCCCAAACAGACGAGGAGGTTTCT GAAGCTGTCTGTATCACAGTGGGGTATAGCAGTGGCTCAGTCCAAGAG CGATAGTCGACTGGTTCGACCCCTGGGGCCAGGGAACCTTGGTCACCG TCTCCTCAGGTGAGTCCTCACCACCCCTCTCTGAGTCCACTTAGGGA GACTCAGCTTGCCAGCAGTCCAAGAGCGATACTGATGGCGCGAGGGAG GC	SEQ ID NO: 5792
hsIGH_2215_ D026_J008_I GHD6- 25_IGHJp2	GCCTTGCCAGCCCGCTCAGTACGTACGGAGCGATAACAGCTGGCCTCTG TCTCGGACCCCCATTCCAGACACCAGACAGAGGGACAGGCCCCCAGA ACCAGTGTTGAGGGACACCCCTGTCCAGGGCAGCCAAGTCCAAGAGGC GCGCTGAGCCAGCAAGGGAAGGCCCCCAAACAAACCAGGAGGTTTCT GAAGCTGTCTGTGTACAGTCGGGTATAGCAGCGTACGTACGGAGCGA TAGTCGACTGGTTCGACCCCTGGGGCCAGGGAACCTTGGTCACCGTCT CCTCAGGTGAGTCCTCACCACCCCTCTCTGAGTCCACTTAGGGAGAC TCAGCTTGCCAGTACGTACGGAGCGATACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5793
hsIGH_2216_ D027_J008_I GHD7- 27_IGHJp2	GCCTTGCCAGCCCGCTCAGAGTACCGAGAGCGATAAGGGTTGAGGGCT GGGGTCTCCACGTGTTTTGGGGCTAACAGCGGAAGGGAGAGCACTGG CAAAGGTGCTGGGGGTCCCTGAACCCGACCCGCCCTGAGACCGCAGC CACATCAGCCCCAGCCCCACAGGCCCCCTACCAGCCGCAGGGTTTTT GGCTGAGCTGAGAACCCTGTGCTAACTAGTACCGAGAGCGATAGTCG ACTGGTTTCGACCCCTGGGGCCAGGGAACCTTGGTCACCGTCTCCTCAG GTGAGTCCTCACCACCCCTCTCTGAGTCCACTTAGGGAGACTCAGCT TGCCAGAGTACCGAGAGCGATACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5794

Name	Sequence	SEQ ID NO
hsIGH_2217_ D001_J009_I GHD1- 01_IGHJp3	GCCTTGCCAGCCCGCTCAGGACACTCTGCATCTGAGCCCGGTCTCTG TGGGTGTTCCGCTAACTGGGGCTCCCAGTGCTCACCACAACTAAAG CGAGCCCCAGCCTCCAGAGCCCCCGAAGGAGATGCCGCCACAAGCCC AGCCCCCATCCAGGAGGCCCGAGAGCTCAGGGCGCCGGGGCAGATTCT GAACAGCCCCGAGTCACGGTGGGTACAAC TGGAGACACTCTGCATCTG AGTCGACTACTACTACTACTACATGGACGTCTGGGGCAAAGGGACCAC GGTCACCGTCTCCTCAGGTAAGAATGGCCACTCTAGGGCCTTTGTTTT CTGCTACTGCCGACACTCTGCATCTGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5795
hsIGH_2218_ D002_J009_I GHD1- 07_IGHJp3	GCCTTGCCAGCCCGCTCAGTTCCGGAACGCATCTGAGGCCTCGGTCTCT GTGGGTGTTCCGCTAGCTGGGGCTCACAGTGCTCACCACACCTAAA ACGAGCCACAGCCTCAGAGCCCCCTGAAGGAGACCCCGCCACAAGCCC AGCCCCACCCAGGAGGCCCGAGAGCACAGGGCGCCCCGTCGGATTCT GAACAGCCCCGAGTCACAGTGGGTATAAC TGGATTCCGGAACGCATCTG AGTCGACTACTACTACTACTACATGGACGTCTGGGGCAAAGGGACCAC GGTCACCGTCTCCTCAGGTAAGAATGGCCACTCTAGGGCCTTTGTTTT CTGCTACTGCCTTCGGAACGCATCTGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5796
hsIGH_2219_ D003_J009_I GHD1- 14_IGHJp3	GCCTTGCCAGCCCGCTCAGAAGTAACGGCATCTGAGGCCTCGGTCTCT GTGGGTGTTCCGCTAGCTGGGGCTCACAGTGCTCACCACACCTAAA ATGAGCCACAGCCTCCGGAGCCCCCGCAGAGACCCCGCCACAAGCCC AGCCCCACCCAGGAGGCCCGAGAGCTCAGGGCGCCCCGTCGGATTCC GAACAGCCCCGAGTCACAGCGGGTATAACCGGAAAGTAACGGCATCTG AGTCGACTACTACTACTACTACATGGACGTCTGGGGCAAAGGGACCAC GGTCACCGTCTCCTCAGGTAAGAATGGCCACTCTAGGGCCTTTGTTTT CTGCTACTGCCAAGTAACGGCATCTGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5797
hsIGH_2220_ D004_J009_I GHD1- 20_IGHJp3	GCCTTGCCAGCCCGCTCAGGTCTCCTAGCATCTGAGTCTCTGTGGGTG TTCCGCTAGCTGGGGCCCCCAGTGCTCACCACACCTAAAGCGAGCC CCAGCCTCCAGAGCCCCCTAAGCATTCCTCCGCCAGCAGCCAGCCCC TGCCCCACCCAGGAGGCCCGAGAGCTCAGGGCGCCTGGTCGGATTCT GAACAGCCCCGAGTCACAGTGGGTATAAC TGGAGTCTCCTAGCATCTG AGTCGACTACTACTACTACTACATGGACGTCTGGGGCAAAGGGACCAC GGTCACCGTCTCCTCAGGTAAGAATGGCCACTCTAGGGCCTTTGTTTT CTGCTACTGCCGTCTCCTAGCATCTGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5798
hsIGH_2221_ D005_J009_I GHD1- 26_IGHJp3	GCCTTGCCAGCCCGCTCAGAGAGTGTCGCATCTGAAGGCCTCAGGCTC TGTGGGTGCCGCTAGCTGGGGCTGCCAGTCTCACCACACCTAAGG TGAGCCACAGCCGCCAGAGCCTCCACAGGAGACCCACCCAGCAGCCC AGCCCCACCCAGGAGGCCCGAGAGCTCAGGGCGCCTGGGTGGATTCT GAACAGCCCCGAGTCACGGTGGGTATAGTGGGAGCTAGAGTGTGCAT CTGAGTCGACTACTACTACTACTACATGGACGTCTGGGGCAAAGGGAC CACGGTCACCGTCTCCTCAGGTAAGAATGGCCACTCTAGGGCCTTTGT TTTCTGCTACTGCCAGAGTGTCGCATCTGACTGATGGCGCGAGGGAGG C	SEQ ID NO: 5799

Name	Sequence	SEQ ID NO
hsIGH_2222_ D006_J009_I GHD2- 02_IGHJp3	GCCTTGCCAGCCCGCTCAGGTTCCGAAGCATCTGAAAAGGAGGAGCCC CCTGTACAGCACTGGGCTCAGAGTCCTCTCCACACACCCTGAGTTTC AGACAAAAACCCCTGGAAATCATAGTATCAGCAGGAGAACTAGCCAG AGACAGCAAGAGGGGACTCAGTGACTCCCGCGGGGACAGGAGGATTTT GTGGGGGCTCGTGTCAGTGTGAGGATATTGTAGTAGTACCAGCTGCTG TTCCGAAGCATCTGAGTCGACTACTACTACTACTACATGGACGTCTGG GGCAAAGGGACACGGTCACCGTCTCCTCAGGTAAGAATGGCCACTCT AGGGCCTTTGTTTTCTGCTACTGCCGTTCCGAAGCATCTGACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5800
hsIGH_2223_ D007_J009_I GHD2- 08_IGHJp3	GCCTTGCCAGCCCGCTCAGCGTTACTTGCATCTGAAAAGGAGGAGCCC CTTGTTACAGCACTGGGCTCAGAGTCCTCTCCAAGACACCCAGAGTTTC AGACAAAAACCCCTGGAATGCACAGTCTCAGCAGGAGAGCCAGCCAG AGCCAGCAAGATGGGGCTCAGTGACACCCGACGGGACAGGAGGATTTT GTGGGGGCTCGTGTCAGTGTGAGGATATTGTACTAATGGTGTATGCTC GTTACTTGCATCTGAGTCGACTACTACTACTACTACATGGACGTCTGG GGCAAAGGGACACGGTCACCGTCTCCTCAGGTAAGAATGGCCACTCT AGGGCCTTTGTTTTCTGCTACTGCCCGTTACTTGCATCTGACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5801
hsIGH_2224_ D008_J009_I GHD2- 15_IGHJp3	GCCTTGCCAGCCCGCTCAGTAGGAGACGCATCTGAAAAGGAGGAGCCC CCTATACAGCACTGGGCTCAGAGTCCTCTCTGAGACACCCTGAGTTTC AGACAACAACCCGCTGGAATGCACAGTCTCAGCAGGAGAACAGACCAA AGCCAGCAAAAGGGACCTCGGTGACACCAGTAGGGACAGGAGGATTTT GTGGGGGCTCGTGTCAGTGTGAGGATATTGTAGTGGTGGTAGCTGCTT AGGAGACGCATCTGAGTCGACTACTACTACTACTACATGGACGTCTGG GGCAAAGGGACACGGTCACCGTCTCCTCAGGTAAGAATGGCCACTCT AGGGCCTTTGTTTTCTGCTACTGCCTAGGAGACGCATCTGACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5802
hsIGH_2225_ D009_J009_I GHD2- 21_IGHJp3	GCCTTGCCAGCCCGCTCAGGTGTCTACGCATCTGAAGCCCCCTGTACA GCACTGGGCTCAGAGTCCTCTCTGAGACAGGCTCAGTTTCAGACAACA ACCCGCTGGAATGCACAGTCTCAGCAGGAGAGCCAGGCCAGAGCCAGC AAGAGGAGACTCGGTGACACCAGTCTCCTGTAGGGACAGGAGGATTTT GTGGGGGTTCGTGTCACTGTGAGCATATTGTGGTGGTGAAGTGTGTGT CTACGCATCTGAGTCGACTACTACTACTACTACTACATGGACGTCTGGGGC AAAGGGACACGGTCACCGTCTCCTCAGGTAAGAATGGCCACTCTAGG GCCTTTGTTTTCTGCTACTGCCGTGTCTACGCATCTGACTGATGGCGC GAGGGAGGC	SEQ ID NO: 5803

Name	Sequence	SEQ ID NO
hsIGH_2226_ D010_J009_I GHD3- 03_IGHJp3	GCCTTGCCAGCCCGCTCAGTGCTACACGCATCTGAGTGGGCACGGACA CTGTCCACCTAAGCCAGGGGCAGACCCGAGTGTCCCCGAGTAGACCT GAGAGCGCTGGGCCCACAGCCTCCCCTCGGTGCCCTGCTACCTCCTCA GGTCAGCCCTGGACATCCCGGGTTTCCCCAGGCTGGCGGTAGGTTTGG GGTGAGGTCTGTGTCACTGTGGTATTACGATTTTGGAGTGGTTATTT GCTACACGCATCTGAGTCGACTACTACTACTACTACATGGACGTCTGG GGCAAAGGGACCACGGTCACCGTCTCCTCAGGTAAGAATGGCCACTCT AGGGCCTTTGTTTTCTGCTACTGCCTGCTACACGCATCTGACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5804
hsIGH_2227_ D011_J009_I GHD3- 09_IGHJp3	GCCTTGCCAGCCCGCTCAGAACTGCCAGCATCTGATGGGCACGGACAC TATCCACATAAGCGAGGGATAGACCCGAGTGTCCCCACAGCAGACCTG AGAGCGCTGGGCCCACAGCCTCCCCTCAGAGCCCTGCTGCCTCCTCCG GTCAGCCCTGGACATCCCAGGTTTCCCCAGGCTGCCGGTAGGTTTAG AATGAGGTCTGTGTCACTGTGGTATTACGATATTTGACTGGTTATTA ACTGCCAGCATCTGAGTCGACTACTACTACTACTACATGGACGTCTGG GGCAAAGGGACCACGGTCACCGTCTCCTCAGGTAAGAATGGCCACTCT AGGGCCTTTGTTTTCTGCTACTGCCAACTGCCAGCATCTGACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5805
hsIGH_2228_ D012_J009_I GHD3- 10_IGHJp3	GCCTTGCCAGCCCGCTCAGTTGGACTGGCATCTGACGATATTTTACT GGTTATTATAACCACAGTGTACAGAGTCCATCAAAAACCCATGCCTG GAAGCTTCCCGCCACAGCCCTCCCCTGCGGGCCCTGCTGCCTCCTCAG GTCAGCCCCGACATCCCGGGTTTCCCCAGGCTGGGCGGTAGGTTTGG GGTGAGGTCTGTGTCACTGTGGTATTACTATGGTTCGGGGAGTTATTT TGGACTGGCATCTGAGTCGACTACTACTACTACTACATGGACGTCTGG GGCAAAGGGACCACGGTCACCGTCTCCTCAGGTAAGAATGGCCACTCT AGGGCCTTTGTTTTCTGCTACTGCCTTGGACTGGCATCTGACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5806
hsIGH_2229_ D013_J009_I GHD3- 16_IGHJp3	GCCTTGCCAGCCCGCTCAGGTAGACACGCATCTGATGGACGCGGACAC TATCCACATAAGCGAGGGACAGACCCGAGTGTTCCTGCAGTAGACCTG AGAGCGCTGGGCCCACAGCCTCCCCTCGGTGCCCTGCTGCCTCCTCAG GTCAGCCCTGGACATCCCGGGTTTCCCCAGGCCAGATGGTAGGTTTGA AGTGAGGTCTGTGTCACTGTGGTATTATGATTACGTTTGGGGAGTTA TCGTTGTAGACACGCATCTGAGTCGACTACTACTACTACTACATGGAC GTCTGGGGCAAAGGGACCACGGTCACCGTCTCCTCAGGTAAGAATGGC CACTCTAGGGCCTTTGTTTTCTGCTACTGCCGTAGACACGCATCTGAC TGATGGCGCGAGGGAGGC	SEQ ID NO: 5807

Name	Sequence	SEQ ID NO
hsIGH_2230_ D014_J009_I GHD3- 22_IGHJp3	GCCTTGCCAGCCCGCTCAGCACTGTACGCATCTGATGGGCATGGACAG TGTCCACCTAAGCGAGGGACAGACCCGAGTGTCCCTGCAGTAGACCTG AGAGCGCTGGGCCCCACAGCCTCCCCTCGGGGCCCTGCTGCCTCCTCAG GTCAGCCCTGGACATCCCGGGTTTCCCCAGGCCTGGCGGTAGGTTTGA AGTGAGGTCTGTGTCACTGTGGTATTACTATGATAGTAGTGTTATTTC ACTGTACGCATCTGAGTCGACTACTACTACTACTACATGGACGTCTGG GGCAAAGGGACCACGGTCACCGTCTCCTCAGGTAAGAATGGCCACTCT AGGGCCTTTGTTTTCTGCTACTGCCCACTGTACGCATCTGACTGATGG CGCGAGGGAGGC	SEQ ID NO: 5808
hsIGH_2231_ D015_J009_I GHD4- 04_IGHJp3	GCCTTGCCAGCCCGCTCAGGATGATCCGCATCTGACAAGGGTGAGTCA GACCCCTCCTGCCCTCGATGGCAGGCGGAGAAGATTCAGAAAGGTCTGA GATCCCCAGGACGCAGCACCCTGTCAATGGGGGCCCCAGACGCCTGG ACCAGGGCCTGCGTGGGAAAGGCCTCTGGGCACACTCAGGGGCTTTTT GTGAAGGGTCTCCTACTGTGTGACTACAGTAGATGATCCGCATCTGA GTCGACTACTACTACTACTACATGGACGTCTGGGGCAAAGGGACCACG GTCACCGTCTCCTCAGGTAAGAATGGCCACTCTAGGGCCTTTGTTTTTC TGCTACTGCCGATGATCCGCATCTGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5809
hsIGH_2232_ D016_J009_I GHD4- 11_IGHJp3	GCCTTGCCAGCCCGCTCAGCGCCAATAGCATCTGATGCCTCTCTCCCC AGTGGACACCCTCTTCCAGGACAGTCCTCAGTGGCATCACAGCGGCCT GAGATCCCCAGGACGCAGCACCCTGTCAATAGGGGCCCCAAATGCCT GGACCAGGGCCTGCGTGGGAAAGGTCTCTGGCCACACTCGGGCTTTTT GTGAAGGGCCCTCCTGCTGTGTGACTACAGTACGCCAATAGCATCTGA GTCGACTACTACTACTACTACATGGACGTCTGGGGCAAAGGGACCACG GTCACCGTCTCCTCAGGTAAGAATGGCCACTCTAGGGCCTTTGTTTTTC TGCTACTGCCCCGCCAATAGCATCTGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5810
hsIGH_2233_ D017_J009_I GHD4- 17_IGHJp3	GCCTTGCCAGCCCGCTCAGTCAAGCCTGCATCTGAGGAGGGTGAGTCA GACCCACCTGCCCTCGATGGCAGGCGGGGAAGATTCAGAAAGGCCTGA GATCCCCAGGACGCAGCACCCTGTCAATGGGGGCCCCAGACGCCTGG ACCAGGGCCTGCGTGGGAAAGGCCCTCTGGGCACACTCAGGGGCTTTTT GTGAAGGGCCCTCCTACTGTGTGACTACGGTGTCAAGCCTGCATCTGA GTCGACTACTACTACTACTACATGGACGTCTGGGGCAAAGGGACCACG GTCACCGTCTCCTCAGGTAAGAATGGCCACTCTAGGGCCTTTGTTTTTC TGCTACTGCCTCAAGCCTGCATCTGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5811
hsIGH_2234_ D018_J009_I GHD4- 23_IGHJp3	GCCTTGCCAGCCCGCTCAGACGTGTGTGCATCTGAGGAGGGTGAGTCA GACCCACCTGCCCTCAATGGCAGGCGGGGAAGATTCAGAAAGGCCTGA GATCCCCAGGACGCAGCACCCTGTCAATGGGGGCCCCAGACGCCTGG ACCAGGGCCTGTGTGGGAAAGGCCTCTGGCCACACTCAGGGGCTTTTT GTGAAGGGCCCTCCTGCTGTGTGACTACGGTGGTAACGTGTGTGCATC TGAGTCGACTACTACTACTACTACATGGACGTCTGGGGCAAAGGGACC ACGGTCACCGTCTCCTCAGGTAAGAATGGCCACTCTAGGGCCTTTGTTT TTCTGCTACTGCCACGTGTGTGCATCTGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5812

Name	Sequence	SEQ ID NO
hsIGH_2235_ D019_J009_I GHD5- 05_IGHJp3	GCCTTGCCAGCCCGCTCAGTCCGTCTAGCATCTGAAGAGGCCTCTCCA GGGGGACACTGTGCATGTCTGGTCCCTGAGCAGCCCCCATGTCCCCA GTCCTGGGGGGCCCCCTGGCACAGCTGTCTGGACCCTCTCTATTCCCT GGGAAGCTCCTCCTGACAGCCCCGCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGTGAGACTGTGGTGGATACAGCTATGTCCGTCTAGCAT CTGAGTCGACTACTACTACTACTACATGGACGTCTGGGGCAAAGGGAC CACGGTCACCGTCTCCTCAGGTAAGAATGGCCACTCTAGGGCCTTTGT TTTCTGCTACTGCCTCCGTCTAGCATCTGACTGATGGCGCGAGGGAGG C	SEQ ID NO: 5813
hsIGH_2236_ D020_J009_I GHD5- 12_IGHJp3	GCCTTGCCAGCCCGCTCAGAAGAGCTGGCATCTGAGCAGAGGCCTCTC CAGGGAGACACTGTGCATGTCTGGTACCTAAGCAGCCCCCACGTCCC CAGTCTGGGGGGCCCCCTGGCTCAGCTGTCTGGACCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCTCCAGTTCCAGGTGTGGTTATT GTCAGGCGATGTGAGACTGTGGTGGATATAGTGGCTACGAAGAGCTGG CATCTGAGTCGACTACTACTACTACTACATGGACGTCTGGGGCAAAGG GACCACGGTCACCGTCTCCTCAGGTAAGAATGGCCACTCTAGGGCCTT TGTTTTCTGCTACTGCCAAGAGCTGGCATCTGACTGATGGCGCGAGGG AGGC	SEQ ID NO: 5814
hsIGH_2237_ D021_J009_I GHD5- 18_IGHJp3	GCCTTGCCAGCCCGCTCAGTATCGCTCGCATCTGAGCAGAGGCCTCTC CAGGGGGACACTGTGCATGTCTGGTCCCTGAGCAGCCCCCACGTCCC CAGTCTGGGGGGCCCCCTGGCACAGCTGTCTGGACCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGTGAGACTGTGGTGGATACAGCTATGTATCGCTCGCAT CTGAGTCGACTACTACTACTACTACATGGACGTCTGGGGCAAAGGGAC CACGGTCACCGTCTCCTCAGGTAAGAATGGCCACTCTAGGGCCTTTGT TTTCTGCTACTGCCTATCGCTCGCATCTGACTGATGGCGCGAGGGAGG C	SEQ ID NO: 5815
hsIGH_2238_ D022_J009_I GHD5- 24_IGHJp3	GCCTTGCCAGCCCGCTCAGTCAGATGCGCATCTGAGCAGAGGCCTCTC CAGGGGGACACAGTGCATGTCTGGTCCCTGAGCAGCCCCCAGGCTCTC TAGCACTGGGGGGCCCCCTGGCACAGCTGTCTGGACCCTCCCTGTTCCCT GGGAAGCTCCTCCTGACAGCCCCGCTCCAGTTCCAGGTGTGGTTATT GTCAGGGGGTGCCAGGCCGTGGTAGAGATGGCTACATCAGATGCGCAT CTGAGTCGACTACTACTACTACTACATGGACGTCTGGGGCAAAGGGAC CACGGTCACCGTCTCCTCAGGTAAGAATGGCCACTCTAGGGCCTTTGT TTTCTGCTACTGCCTCAGATGCGCATCTGACTGATGGCGCGAGGGAGG C	SEQ ID NO: 5816

Name	Sequence	SEQ ID NO
hsIGH_2239_ D023_J009_I GHD6- 06_IGHJp3	GCCTTGCCAGCCCGCTCAGGTGTAGCAGCATCTGAAGGCAGCTGACTC CTGACTTGGACGCCTATTCCAGACACCAGACAGAGGGGCAGGCCCCC AGAACCAGGGATGAGGACGCCCCGTCAAGGCCAGAAAAGACCAAGTTG TGCTGAGCCCAGCAAGGGAAGGTCCCCAAACAAACCAGGAACGTTTCT GAAGGTGTCTGTGTACAGTGGAGTATAGCAGCTGTGTAGCAGCATCT GAGTCGACTACTACTACTACTACATGGACGTCTGGGGCAAAGGGACCA CGGTCACCGTCTCCTCAGGTAAGAATGGCCACTCTAGGGCCTTTGTTT TCTGCTACTGCCGTGTAGCAGCATCTGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5817
hsIGH_2240_ D024_J009_I GHD6- 13_IGHJp3	GCCTTGCCAGCCCGCTCAGTGGCAGTTGCATCTGAAGGCAGCTGACCC CTGACTTGGACCCCTATTCCAGACACCAGACAGAGGCGCAGGCCCCC AGAACCAGGGTTGAGGGACGCCCCGTCAAAGCCAGACAAAACCAAGGG GTGTTGAGCCCAGCAAGGGAAGGCCCCCAAACAGACCAGGAGGTTTCT GAAGGTGTCTGTGTACAGTGGGGTATAGCAGCAGCTTGGCAGTTGCA TCTGAGTCGACTACTACTACTACTACATGGACGTCTGGGGCAAAGGGA CCACGGTCACCGTCTCCTCAGGTAAGAATGGCCACTCTAGGGCCTTTG TTTTCTGCTACTGCCTGGCAGTTGCATCTGACTGATGGCGCGAGGGAG GC	SEQ ID NO: 5818
hsIGH_2241_ D025_J009_I GHD6- 19_IGHJp3	GCCTTGCCAGCCCGCTCAGCAGTCCAAGCATCTGATGAGGTAGCTGGC CTCTGTCTCGGACCCCACTCCAGACACCAGACAGAGGGGCAGGCCCCC CAAACACAGGGTTGAGGGATGATCCGTCAAGGCAGACAAGACCAAGGG GCACTGACCCAGCAAGGGAAGGCTCCCAAACAGACGAGGAGGTTTCT GAAGCTGTCTGTATCACAGTGGGGTATAGCAGTGGCTCAGTCCAAGCA TCTGAGTCGACTACTACTACTACTACATGGACGTCTGGGGCAAAGGGA CCACGGTCACCGTCTCCTCAGGTAAGAATGGCCACTCTAGGGCCTTTG TTTTCTGCTACTGCCCAGTCCAAGCATCTGACTGATGGCGCGAGGGAG GC	SEQ ID NO: 5819
hsIGH_2242_ D026_J009_I GHD6- 25_IGHJp3	GCCTTGCCAGCCCGCTCAGTACGTACGGCATCTGACAGCTGGCCTCTG TCTCGGACCCCAATTCCAGACACCAGACAGAGGGACAGGCCCCCAGA ACCAGTGTTGAGGGACACCCCTGTCCAGGGCAGCCAAGTCCAAGAGGC GCGCTGAGCCCAGCAAGGGAAGGCCCCAAACAAACCAGGAGGTTTCT GAAGCTGTCTGTGTACAGTCGGGTATAGCAGCGTACGTACGGCATCT GAGTCGACTACTACTACTACTACATGGACGTCTGGGGCAAAGGGACCA CGGTCACCGTCTCCTCAGGTAAGAATGGCCACTCTAGGGCCTTTGTTT TCTGCTACTGCCTACGTACGGCATCTGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5820

Name	Sequence	SEQ ID NO
hsIGH_2243_ D027_J009_I GHD7- 27_IGHJp3	GCCTTGCCAGCCCGCTCAGAGTACCGAGCATCTGAAGGGTTGAGGGCT GGGGTCTCCACGTGTTTTGGGGCTAACAGCGGAAGGGAGAGCACTGG CAAAGGTGCTGGGGGTCCCCTGAACCCGACCCGCCCTGAGACCGCAGC CACATCAGCCCCCAGCCCCACAGGCCCCCTACCAGCCGCAGGGTTTTT GGCTGAGCTGAGAACCACTGTGCTAACTAGTACCGAGCATCTGAGTCG ACTACTACTACTACTACATGGACGTCTGGGGCAAAGGGACCACGGTCA CCGTCTCCTCAGGTAAGAATGGCCACTCTAGGGCCTTTGTTTTCTGCT ACTGCCAGTACCGAGCATCTGACTGATGGCGCGAGGGAGGC	SEQ ID NO: 5821

Bias Control Sequences for hs-IGL

Name	Sequence	SEQ ID NO
hsIGL_0001 _V001_J001 _IGLV01- 36_IGLJ1_F	GCCTTGCCAGCCCGCTCAGTAGGAGACGACACTCTGGTCCTGGGCCCAG TCTGTGCTGACTCAGCCACCCTCGGTGTCTGAAGCCCCCAGGCAGAGGG TCACCATCTCCTGTTCTGGAAGCAGCTCCAACATCGGAAATAATGCTGT AAACTGGTACCAGCAGCTCCCAGGAAAGGCTCCCAAACCTCCTCATCTAT TATGATGATCTGCTGCCCTCAGGGGTCTCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGA TGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGATGATAGGA GACGACACTCTGTGCGACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTTAGGAGACGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5822
hsIGL_0002 _V002_J001 _IGLV01- 40_IGLJ1_F	GCCTTGCCAGCCCGCTCAGGTGTCTACGACACTCTCCTGGGCCCAGTCT GTCGTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCA CCATCTCCTGCACTGGGAGCAGCTCCAACATCGGGGCAGGTTATGATGT ACACTGGTACCAGCAGCTTCCAGGAACAGCCCCAACTCCTCATCTAT GGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGA TGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGATGAGTGTCT TACGACACTCTGTGCGACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTGTGTCTACGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5823
hsIGL_0003 _V003_J001 _IGLV01- 44_IGLJ1_F	GCCTTGCCAGCCCGCTCAGGTACAGTGGACACTCTGGTCCTGGGCCCAG TCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGG TCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGAAGTAATACTGT AAACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAACCTCCTCATCTAT AGTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGA TGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGATGAGTACA GTGGACACTCTGTGCGACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTGTACAGTGGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5824
hsIGL_0004 _V004_J001 _IGLV01- 47_IGLJ1_F	GCCTTGCCAGCCCGCTCAGGGATCATCGACACTCTGGTCCTGGGCCCAG TCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGG TCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGAAGTAATTATGT ATACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAACCTCCTCATCTAT AGTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGGTCCGAGGA	SEQ ID NO: 5825

Name	Sequence	SEQ ID NO
	TGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGATGAGGATC ATCGACACTCTGTGACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCTCTGCTGTCCC TGGAAAATCTGTTTCTCTGGATCATCGACACTCTCTGATGGCGCGAGG GAGGC	
hsIGL_0005 _V005_J001 _IGLV01- 50- ORF_IGLJ1_ F	GCCTTGCCAGCCCGCTCAGTATTGGCGGACACTCTCCTGGGCCCAGTCT GTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCA CCATCTCCTGCACTGGGAGCAGCTCCAACATTGGGGCGGGTTATGTTGT ACATTGGTACCAGCAGCTTCCAGGAACAGCCCCAACTCCTCATCTAT GGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCAATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGACTCCAGTCTGAGGA TGAGGCTGATTATTACTGCAAAGCATGGGATAACAGCCTGATGATATTG GCGGACACTCTGTGACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTTATTGGCGGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5826
hsIGL_0006 _V006_J001 _IGLV01- 51_IGLJ1_F	GCCTTGCCAGCCCGCTCAGAGGCTTGAGACACTCTGGTCTGGGCCCAG TCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAGG TCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAATTATGT ATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCAACTCCTCATTTAT GACAATAATAAGCGACCCTCAGGGATTCTTGACCGATTCTCTGGCTCCA AGTCTGGCACGTCAGCCACCCTGGGCATCACCGACTCCAGACTGGGGA CGAGGCCGATTATTACTGCGGAACATGGGATAGCAGCCTGATGAAGGCT TGAGACACTCTGTGACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTAGGCTTGAGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5827
hsIGL_0007 _V007_J001 _IGLV02- 08_IGLJ1_F	GCCTTGCCAGCCCGCTCAGACACACGTGACACTCTGTCTGGGCCCAGT CTGCCCTGACTCAGCCTCCCTCCGCGTCCAGGTCTCCTGGACAGTCAGT CACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATAACTAT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCAACTCATGATTT ATGAGGTCAGTAAGCGGCCCTCAGGGGTCCCTGATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGGCTCCAGGCTGAG GATGAGGCTGATTATTACTGCAGCTCATATGCAGGCAGCAATGAACACA CGTGACACTCTGTGACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTACACACGTGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5828
hsIGL_0008 _V008_J001 _IGLV02-	GCCTTGCCAGCCCGCTCAGTAGACGGAGACACTCTATCCTGGGCTCAGT CTGCCCTGACTCAGCCTCGCTCAGTGTCCGGGTCTCCTGGACAGTCAGT CACCATCTCCTGCACTGGAACCAGCAGTGATGTTGGTGGTTATAACTAT	SEQ ID NO: 5829

Name	Sequence	SEQ ID NO
11_IGLJ1_F	GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCAACTCATGATTT ATGATGTCAGTAAGCGGCCCTCAGGGGTCCCTGATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAG GATGAGGCTGATTATTACTGCTGCTCATATGCAGGCAGCTATGATAGAC GGAGACACTCTGTCGACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCCAGCCTGTCTCACCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTTAGACGGAGACACTCTCTGATGGCGCGAGG GAGGC	
hsIGL_0009 _V009_J001 _IGLV02- 14_IGLJ1_F	GCCTTGCCAGCCCGCTCAGCAGCTCTTGACACTCTGTCCTGGGCCAGT CTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGAT CACCATCTCCTGCACTGGAACCAGCAGTGATGTTGGGAGTTATAACCTT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCAACTCATGATTT ATGAGGGCAGTAAGCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAG GACGAGGCTGATTATTACTGCAGCTCATATAACAAGCAGCAGTGACAGCT CTTGACACTCTGTCGACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCCAGCCTGTCTCACCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTCAGCTCTTGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5830
hsIGL_0010 _V010_J001 _IGLV02- 18_IGLJ1_F	GCCTTGCCAGCCCGCTCAGGAGCGATAGACACTCTATCCTGGGCTCAGT CTGCCCTGACTCAGCCTCCCTCCGTGTCCGGGTCTCCTGGACAGTCAGT CACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTAGTTATAACCGT GTCTCCTGGTACCAGCAGCCCCCAGGCACAGCCCCAACTCATGATTT ATGAGGTCAAGTAAATCGGCCCTCAGGGGTCCCTGATCGCTTCTCTGGGTC CAAGTCTGGCAACACGGCCTCCCTGACCACCTCTGGGCTCCAGGCTGAG GACGAGGCTGATTATTACTGCAGCTCATATAACAAGCAGCAGTGAGAGCG ATAGACACTCTGTCGACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCCAGCCTGTCTCACCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTGAGCGATAGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5831
hsIGL_0011 _V011_J001 _IGLV02- 23_IGLJ1_F	GCCTTGCCAGCCCGCTCAGGCATCTGAGACACTCTGTCCTGGGCCAGT CTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGAT CACCATCTCCTGCACTGGAACCAGCAGTGATGTTGGGAGTTATAACCTT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCAACTCATGATTT ATGAGGGCAGTAAGCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACAATCTCTGGGCTCCAGGCTGAG GACGAGGCTGATTATTACTGCTGCTCATATGCAGGTAGTAGTGAGCATC TGAGACACTCTGTCGACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCCAGCCTGTCTCACCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTGCATCTGAGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5832

Name	Sequence	SEQ ID NO
hsIGL_0012 _V012_J001 _IGLV02- 33- ORF_IGLJ1_ F	GCCTTGCCAGCCCGCTCAGTGCTACACGACACTCTGTCCTGGGCCCAGT CTGCCCTGACTCAGCCTCCTTTTGTGTCCGGGGCTCCTGGACAGTCGGT CACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGGGATTATGATCAT GTCTTCTGGTACCAAAAGCGTCTCAGCACTACCTCCAGACTCCTGATTT ACAATGTCAATACTCGGCCCTCAGGGATCTCTGACCTCTTCTCAGGCTC CAAGTCTGGCAACATGGCTTCCCTGACCATCTCTGGGCTCAAGTCCGAG GTTGAGGCTAATTATCACTGCAGCTTATATTCAAGTAGTTATGATGCTA CACGACACTCTGTCGACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTTGCTACACGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5833
hsIGL_0013 _V013_J001 _IGLV03- 01_IGLJ1_F	GCCTTGCCAGCCCGCTCAGAACTGCCAGACACTCTCTCTCCTGTAGGAT CCGTGGCCTCCTATGAGCTGACTCAGCCACCCTCAGTGTCGGTGTCCTCC AGGACAGACAGCCAGCATCACCTGCTCTGGAGATAAATTGGGGGATAAA TATGCTTGCTGGTATCAGCAGAAGCCAGGCCAGTCCCCTGTGCTGGTCA TCTATCAAGATAGCAAGCGGCCCTCAGGGATCCCCTGAGCGATTCTCTGG CTCCAACCTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCT ATGGATGAGGCTGACTATTACTGTCAGGCGTGGGACAGCAGTGAAACTG CCAGACACTCTGTCGACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTAACTGCCAGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5834
hsIGL_0014 _V014_J001 _IGLV03- 09- FP_IGLJ1_F	GCCTTGCCAGCCCGCTCAGTTGGACTGGACACTCTTTTCTTGCAAGTT CTGTGGCCTCCTATGAGCTGACTCAGCCACTCTCAGTGTCAGTGGCCCT GGGACAGGCGGCCAGGATTACCTGTGGGGGAAACAACCTTGGATATAAA AATGTGCACTGGTACCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTCA TCTATAGGGATAACAACCGGCCCTCTGGGATCCCCTGAGCGATTCTCTGG CTCCAACCTCGGGGAACACGGCCACCCTGACCATCAGCAGAGCCCAAGCC GGGGATGAGGCTGACTATTACTGTCAGGTGTGGGACAGCAGTGATTGGA CTGGACACTCTGTCGACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTTTGGACTGGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5835
hsIGL_0015 _V015_J001 _IGLV03- 10_IGLJ1_F	GCCTTGCCAGCCCGCTCAGGTAGACACGACACTTTTGCACTCTCTGAG GCCTCCTATGAGCTGACACAGCCACCCTCGGTGTGAGTGTCCTCCAGGAC AAACGGCCAGGATCACCTGCTCTGGAGATGCATTGCCAAAAAATATGC TTATTGGTACCAGCAGAAGTCAGGCCAGGCCCTGTGCTGGTCATCTAT GAGGACAGCAAACGACCCTCCGGGATCCCTGAGAGATTCTCTGGCTCCA GCTCAGGGACAATGGCCACCTTGACTATCAGTGGGGCCCAGGTGGAGGA TGAAGCTGACTACTACTGTTACTCAACAGACAGCAGTGGTATGAGTAGA CACGACACTCTGTCGACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA	SEQ ID NO: 5836

Name	Sequence	SEQ ID NO
	GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTGTAGACACGACACTCTCTGATGGCGCGAGG GAGGC	
hsIGL_0016 _V016_J001 _IGLV03- 12_IGLJ1_F	GCCTTGCCAGCCCGCTCAGCACTGTACGACACTCTTTGCAGGCTCTGCG ACCTCCTATGAGCTGACTCAGCCACACTCAGTGTGAGTGGCCACAGCAC AGATGGCCAGGATCACCTGTGGGGGAAACAACATTGGAAGTAAAGCTGT GCACTGGTACCAGCAAAAGCCAGGCCAGGACCCTGTGCTGGTCATCTAT AGCGATAGCAACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA ACCCAGGGAACACCGCCACCCTAACCATCAGCAGGATCGAGGCTGGGGA TGAGGCTGACTATTACTGTGTCAGGTGTGGGACAGTAGTAGTGTGACACTG TACGACACTCTGTGCACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTCACTGTACGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5837
hsIGL_0017 _V017_J001 _IGLV03- 16_IGLJ1_F	GCCTTGCCAGCCCGCTCAGGATGATCCGACACTCTTTGCAGGCTCTGAG GCCTCCTATGAGCTGACACAGCCACCCTCGGTGTGAGTGTCCCTAGGAC AGATGGCCAGGATCACCTGCTCTGGAGAAGCATTGCCAAAAAATATGC TTATTGGTACCAGCAGAAGCCAGGCCAGTTCCCTGTGCTGGTGATATAT AAAGACAGCGAGAGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA GCTCAGGGACAATAGTCACATTGACCATCAGTGGAGTCCAGGCAGAAGA CGAGGCTGACTATTACTGTCTATCAGCAGACAGCAGTGGTATGAGATGA TCCGACACTCTGTGCACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTGATGATCCGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5838
hsIGL_0018 _V018_J001 _IGLV03- 19_IGLJ1_F	GCCTTGCCAGCCCGCTCAGCGCCAATAGACACTCTTTGCAGGTTCTGTG GTTTCTTCTGAGCTGACTCAGGACCCTGCTGTGTCTGTGGCCTTGGGAC AGACAGTCAGGATCACATGCCAAGGAGACAGCCTCAGAAGCTATTATGC AAGCTGGTACCAGCAGAAGCCAGGACAGGCCCTGTACTTGTCTATCTAT GGTAAAAACAACCGGCCCTCAGGGATCCCAGACCGATTCTCTGGCTCCA GCTCAGGAAACACAGCTTCCTTGACCATCACTGGGGCTCAGGCGGAAGA TGAGGCTGACTATTACTGTAAGTCCCGGGACAGCAGTGGTATGACGCCA ATAGACACTCTGTGCACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTCGCCAATAGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5839
hsIGL_0019 _V019_J001 _IGLV03- 21_IGLJ1_F	GCCTTGCCAGCCCGCTCAGTCAAGCCTGACACTCTTTGCAGGCTCTGTG ACCTCCTATGTGCTGACTCAGCCACCCTCAGTGTGAGTGGCCCCAGGAA AGACGGCCAGGATTACCTGTGGGGGAAACAACATTGGAAGTAAAAGTGT GCACTGGTACCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTCATCTAT TATGATAGCGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA	SEQ ID NO: 5840

Name	Sequence	SEQ ID NO
	ACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAAGCCGGGGA TGAGGCCGACTATTACTGTGTCAGGTGTGGGACAGTAGTAGTGTGATCAAG CCTGACACTCTGTGCGACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCCCTGTGCTGTCCC TGGAAAATCTGTTTTCTCTTCAAGCCTGACACTCTCTGATGGCGCGAGG GAGGC	
hsIGL_0020 _V020_J001 _IGLV03- 22- FP_IGLJ1_F	GCCTTGCCAGCCCGCTCAGACGTGTGTGACACTCTCCTCTCTGCAGGC TCTGTTGCCCTCCTATGAGCTGACACAGCTACCCTCGGTGTCAGTGTCCC CAGGACAGAAAGCCAGGATCACCTGCTCTGGAGATGTACTGGGGAAAAA TTATGCTGACTGGTACCAGCAGAAGCCAGGCCAGGCCCTGAGTTGGTG ATATACGAAGATAGTGAGCGGTACCCTGGAATCCCTGAACGATTCTCTG GGTCCACCTCAGGGAACACGACCACCCTGACCATCAGCAGGGTCCTGAC CGAAGACGAGGCTGACTATTACTGTTTGTCTGGGAATGAGGTGAACGTG TGTGACACTCTGTGCGACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCCCTGTGCTGTCCC TGGAAAATCTGTTTTCTCTACGTGTGTGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5841
hsIGL_0021 _V021_J001 _IGLV03- 25_IGLJ1_F	GCCTTGCCAGCCCGCTCAGTCCGTCTAGACACTCTTTGCAGGCTCTGAG GCCTCCTATGAGCTGACACAGCCACCCTCGGTGTCAGTGTCCCAGGAC AGACGGCCAGGATCACCTGCTCTGGAGATGCATTGCCAAAGCAATATGC TTATTGGTACCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTGATATAT AAAGACAGTGAGAGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA GCTCAGGGACAACAGTCACGTTGACCATCAGTGGAGTCCAGGCAGAAGA TGAGGCTGACTATTACTGTCAATCAGCAGACAGCAGTGGTATGATCCGT CTAGACACTCTGTGCGACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCCCTGTGCTGTCCC TGGAAAATCTGTTTTCTCTTCCGTCTAGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5842
hsIGL_0022 _V022_J001 _IGLV03- 27_IGLJ1_F	GCCTTGCCAGCCCGCTCAGAAGAGCTGGACACTCTCTTTTCTTGACGTC TCTGTGGCCTCCTATGAGCTGACACAGCCATCCTCAGTGTGAGTGTCTC CGGGACAGACAGCCAGGATCACCTGCTCAGGAGATGTACTGGCAAAAAA ATATGCTCGGTGGTTCCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTG ATTTATAAAGACAGTGAGCGGCCCTCAGGGATCCCTGAGCGATTCTCCG GCTCCAGCTCAGGGACCACAGTCACCTTGACCATCAGCGGGGCCAGGT TGAGGATGAGGCTGACTATTACTGTTACTCTGCGGCTGACATGAAAGAG CTGGACACTCTGTGCGACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCCCTGTGCTGTCCC TGGAAAATCTGTTTTCTCTAAGAGCTGGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5843
hsIGL_0023 _V023_J001	GCCTTGCCAGCCCGCTCAGTATCGCTCGACACTCTTGCTGACTCAGCCC CCGTCTGCATCTGCCTTGCTGGGAGCCTCGATCAAGCTCACCTGCACCC	SEQ ID NO: 5844

Name	Sequence	SEQ ID NO
_IGLV04- 03_IGLJ1_F	TAAGCAGTGAGCACAGCACCTACACCATCGAATGGTATCAACAGAGACC AGGGAGGTCCCCCAGTATATAATGAAGGTTAAGAGTGATGGCAGCCAC AGCAAGGGGGACGGGATCCCCGATCGCTTCATGGGCTCCAGTTCTGGGG CTGACCGCTACCTCACCTTCTCCAACCTCCAGTCTGACGATGAGGCTGA GTATCACTGTGGAGAGAGCCACACGATTGATGGCCAAGTCGTGATATCG CTCGACACTCTGTCGACTCTTCGGAACCTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCCCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTTATCGCTCGACACTCTCTGATGGCGCGAGG GAGGC	
hsIGL_0024 _V024_J001 _IGLV04- 60_IGLJ1_F	GCCTTGCCAGCCCGCTCAGTCAGATGCGACACTCTCTCTCTCCAGCCT GTGCTGACTCAATCATCCTCTGCCTCTGCTTCCCTGGGATCCTCGGTCA AGCTCACCTGCACTCTGAGCAGTGGGCACAGTAGCTACATCATCGCATG GCATCAGCAGCAGCCAGGGAAGGCCCTCGGTACTTGATGAAGCTTGAA GGTAGTGGGAAGCTACAACAAGGGGAGCGGAGTTCCTGATCGCTTCTCAG GCTCCAGCTCTGGGGCTGACCGCTACCTCACCATCTCCAACCTCCAGTT TGAGGATGAGGCTGATTATTACTGTGAGACCTGGGACAGTATGATCAGA TGCGACACTCTGTCGACTCTTCGGAACCTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCCCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTTCAGATGCGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5845
hsIGL_0025 _V025_J001 _IGLV04- 69_IGLJ1_F	GCCTTGCCAGCCCGCTCAGGTGTAGCAGACACTCTCTCTCTCCAGCTT GTGCTGACTCAATCGCCCTCTGCCTCTGCCTCCCTGGGAGCCTCGGTCA AGCTCACCTGCACTCTGAGCAGTGGGCACAGCAGCTACGCCATCGCATG GCATCAGCAGCAGCCAGAGAAGGGCCCTCGGTACTTGATGAAGCTTAAC AGTGATGGCAGCCACAGCAAGGGGGACGGGATCCCTGATCGCTTCTCAG GCTCCAGCTCTGGGGCTGAGCGCTACCTCACCATCTCCAGCCTCCAGTC TGAGGATGAGGCTGACTATTACTGTGAGACCTGGGGCACTGTGAGTGTA GCAGACACTCTGTCGACTCTTCGGAACCTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCCCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTGTGTAGCAGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5846
hsIGL_0026 _V026_J001 _IGLV05- 37_IGLJ1_F	GCCTTGCCAGCCCGCTCAGTGGCAGTTGACACTCTTGTGCTGACTCAGC CACCTTCCTCCTCCGCATCTCCTGGAGAATCCGCCAGACTCACCTGCAC CTTGCCAGTGACATCAATGTTGGTAGCTACAACATATACTGGTACCAG CAGAAGCCAGGGAGCCCTCCAGGTATCTCCTGTACTACTACTCAGACT CAGATAAGGGCCAGGGCTCTGGAGTCCCCAGCCGCTTCTCTGGATCCAA AGATGCTTCAGCCAATACAGGGATTTTACTCATCTCCGGGCTCCAGTCT GAGGATGAGGCTGACTATTACTGTATGATTGGCCAAGCAATGATGGCA GTTGACACTCTGTCGACTCTTCGGAACCTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCCCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTTGGCAGTTGACACTCTCTGATGGCGCGAGG	SEQ ID NO: 5847

Name	Sequence	SEQ ID NO
	GAGGC	
hsIGL_0027 _V027_J001 _IGLV05- 39_IGLJ1_F	GCCTTGCCAGCCCGCTCAGCAGTCCAAGACACTCTTGTGCTGACTCAGC CAACCTCCCTCTCAGCATCTCCTGGAGCATCAGCCAGATTCACCTGCAC CTTGCGCAGCGGCATCAATGTTGGTACCTACAGGATATACTGGTACCAG CAGAATCCAGGGAGTCTTCCCCGGTATCTCCTGAGGTACAAATCAGACT CAGATAAGCAGCAGGGCTCTGGAGTCCCCAGCCGCTTCTCTGGATCCAA AGATGCTTCAACCAATGCAGGCCCTTTTACTCATCTCTGGGCTCCAGTCT GAAGATGAGGCTGACTATTACTGTGCCATTTGGTACAGCAGTGACAGTC CAAGACACTCTGTGACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCCCTGTCTGTCCC TGGAAAATCTGTTTTCTCTCAGTCCAAGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5848
hsIGL_0028 _V028_J001 _IGLV05- 45_IGLJ1_F	GCCTTGCCAGCCCGCTCAGTACGTACGGACACTCTTGTGCTGACTCAGC CGTCTTCCCTCTCTGCATCTCCTGGAGCATCAGCCAGTCTCACCTGCAC CTTGCGCAGTGGCATCAATGTTGGTACCTACAGGATATACTGGTACCAG CAGAAGCCAGGGAGTCTTCCCCAGTATCTCCTGAGGTACAAATCAGACT CAGATAAGCAGCAGGGCTCTGGAGTCCCCAGCCGCTTCTCTGGATCCAA AGATGCTTCGGCCAATGCAGGGATTTTACTCATCTCTGGGCTCCAGTCT GAGGATGAGGCTGACTATTACTGTATGATTTGGCACAGCAGTGATACGT ACGGACACTCTGTGACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCCCTGTCTGTCCC TGGAAAATCTGTTTTCTCTTACGTACGGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5849
hsIGL_0029 _V029_J001 _IGLV05- 52_IGLJ1_F	GCCTTGCCAGCCCGCTCAGAGTACCGAGACACTCTTGACTCAGCCATCT TCCCATTCTGCATCTTCTGGAGCATCAGTCAGACTCACCTGCATGCTGA GCAGTGGCTTCAGTGTGGGGACTTCTGGATAAGGTGGTACCAACAAAA GCCAGGGAACCCCTCCCCGGTATCTCCTGTACTACCACTCAGACTCCAAT AAGGGCCAAGGCTCTGGAGTTCAGCCGCTTCTCTGGATCCAACGATG CATCAGCCAATGCAGGGATTCTGCGTATCTCTGGGCTCCAGCCTGAGGA TGAGGCTGACTATTACTGTGGTACATGGCACAGCAACTCTATGAAGTAC CGAGACACTCTGTGACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCCCTGTCTGTCCC TGGAAAATCTGTTTTCTCTAGTACCGAGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5850
hsIGL_0030 _V030_J001 _IGLV07- 43_IGLJ1_F	GCCTTGCCAGCCCGCTCAGATCCATGGGACACTCTAGGGTCCAATTCTC AGACTGTGGTGACTCAGGAGCCCTCACTGACTGTGTCCCCAGGAGGGAC AGTCACTCTCACCTGTGCTTCCAGCACTGGAGCAGTCACCACTGGTTAC TATCCAAACTGGTTCCAGCAGAAACCTGGACAAGCACCCAGGGCACTGA TTATAGTACAAGCAACAAACACTCCTGGACCCCTGCCCCGGTTCTCAGG CTCCCTCCTTGGGGGGCAAAGCTGCCCTGACACTGTCAGGTGTGCAGCCT GAGGACGAGGCTGAGTATTACTGCCTGCTCTACTATGGTGGTGAATCCA	SEQ ID NO: 5851

Name	Sequence	SEQ ID NO
	TGGGACACTCTGTGCTGACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCCAGCCTGTCTCACCCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTATCCATGGGACACTCTCTGATGGCGCGAGG GAGGC	
hsIGL_0031 _V031_J001 _IGLV07- 46- FP_IGLJ1_F	GCCTTGCCAGCCCGCTCAGGTAGCAGTGACACTCTAGGGTCCAATTCCC AGGCTGTGGTGACTCAGGAGCCCTCACTGACTGTGTCCCAGGAGGGAC AGTCACTCTCACCTGTGGCTCCAGCACTGGAGCTGTCACCAGTGGTCAT TATCCCTACTGGTTCCAGCAGAAGCCTGGCCAAGCCCCCAGGACACTGA TTTATGATACAAGCAACAAACACTCCTGGACACCTGCCCGGTTCTCAGG CTCCCTCCTTGGGGGCAAAGCTGCCCTGACCCCTTTTGGGTGCGCAGCCT GAGGATGAGGCTGAGTATTACTGCTTGCTCTCCTATAGTGGTGAGTAGC AGTGACACTCTGTGCTGACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCCAGCCTGTCTCACCCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTGTAGCAGTGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5852
hsIGL_0032 _V032_J001 _IGLV08- 61_IGLJ1_F	GCCTTGCCAGCCCGCTCAGATCTTCGTGACACTCTGAGTGGATTCTCAG ACTGTGGTGACCCAGGAGCCATCGTTTCTCAGTGTCCCCTGGAGGGACAG TCACACTCACTTGTGGCTTGAGCTCTGGCTCAGTCTCTACTAGTTACTA CCCCAGCTGGTACCAGCAGACCCAGGCCAGGCTCCACGCACGCTCATC TACAGCACAAACACTCGCTCTTCTGGGGTCCCTGATTGCTTCTCTGGCT CCATCCTTGGGAACAAAGCTGCCCTCACCATCACGGGGGGCCAGGCAGA TGATGAATCTGATTATTACTGTGTGCTGTATATGGGTAGTGTGAATCTT CGTGACACTCTGTGCTGACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCCAGCCTGTCTCACCCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTATCTTCGTGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5853
hsIGL_0033 _V033_J001 _IGLV09- 49_IGLJ1_F	GCCTTGCCAGCCCGCTCAGTCCACAGTGACACTCTTGACTCAGCCACCT TCTGCATCAGCCTCCCTGGGAGCCTCGGTCACTCACCTGCACCCTGA GCAGCGGCTACAGTAATTATAAAGTGGACTGGTACCAGCAGAGACCAGG GAAGGGCCCCCGGTTTGTGATGCGAGTGGGCACTGGTGGGATTGTGGGA TCCAAGGGGGATGGCATCCCTGATCGCTTCTCAGTCTTGGGCTCAGGCC TGAATCGGTACCTGACCATCAAGAACATCCAGGAAGAAGATGAGAGTGA CTACCACTGTGGGGCAGACCATGGCAGTGGGAGCAACTTCGTGATCCAC AGTGACACTCTGTGCTGACTCTTCGGAAGTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCCAGCCTGTCTCACCCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTTCCACAGTGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5854
hsIGL_0034 _V034_J001 _IGLV10- 54-	GCCTTGCCAGCCCGCTCAGATGACACCGACACTCTTGTCAGTGGTCCAG GCAGGGCTGACTCAGCCACCCTCGGTCTCCAAGGGCTTGAGACAGACCG CCACACTCACCTGCACTGGGAACAGCAACAATGTTGGCAACCAAGGAGC AGCTTGCCCTGAGCAGCACCAGGGCCACCCTCCCAAACCTCCTATCTAC	SEQ ID NO: 5855

Name	Sequence	SEQ ID NO
FP_IGLJ1_F	AGGAATAACAACCGGCCCTCAGGGATCTCAGAGAGATTATCTGCATCCA GGTCAGGAAACACAGCCTCCCTGACCATTACTGGACTCCAGCCTGAGGA CGAGGCTGACTATTACTGCTCAGCATGGGACAGCAGCCTCATGAATGAC ACCGACACTCTGTCGACTCTTCGGAACCTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCCCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTATGACACCGACACTCTCTGATGGCGCGAGG GAGGC	
hsIGL_0035 _V035_J001 _IGLV11- 55- ORF_IGLJ1_F	GCCTTGCCAGCCCGCTCAGCTTCACGAGACACTCTCGTGCTGACTCAGC CGCCCTCTCTGTCTGCATCCCCGGGAGCAACAGCCAGACTCCCTGCAC CCTGAGCAGTGACCTCAGTGTGGTGGTAAAAACATGTTCTGGTACCAG CAGAAGCCAGGGAGCTCTCCAGGTTATTCTGTATCACTACTCAGACT CAGACAAGCAGCTGGGACCTGGGGTCCCCAGTCGAGTCTCTGGCTCCAA GGAGACCTCAAGTAACACAGCGTTTTTGCTCATCTCTGGGCTCCAGCCT GAGGACGAGGCCGATTATTACTGCCAGGTGTACGAAAGTAGTGACTTCA CGAGACACTCTGTCGACTCTTCGGAACCTGGGACCAAGGTCACCGTCCTA GGTAAGTGGCTCTCAACCTTTCCAGCCTGTCTCACCCCTCTGCTGTCCC TGGAAAATCTGTTTTCTCTCTTCACGAGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5856
hsIGL_0036 _V001_J002 _IGLV01- 36_IGLJ2_F	GCCTTGCCAGCCCGCTCAGTAGGAGACTTCGGAACGGTCTGGGCCAG TCTGTGCTGACTCAGCCACCCTCGGTGTCTGAAGCCCCAGGCAGAGGG TCACCATCTCCTGTTCTGGAAGCAGCTCCAACATCGGAAATAATGCTGT AAACTGGTACCAGCAGCTCCCAGGAAAGGCTCCCAAACCTCCTCATCTAT TATGATGATCTGCTGCCCTCAGGGGTCTCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGA TGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGATGATAGGA GACTTCGGAACGTCGACTATTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTTGTTTCTGTTAGGAGACTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5857
hsIGL_0037 _V002_J002 _IGLV01- 40_IGLJ2_F	GCCTTGCCAGCCCGCTCAGGTGTCTACTTCGGAACCCTGGGCCAGTCT GTCGTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCA CCATCTCCTGCACTGGGAGCAGCTCCAACATCGGGCAGGTTATGATGT ACACTGGTACCAGCAGCTTCCAGGAACAGCCCCAAACTCCTCATCTAT GGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGA TGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGATGAGTGTC TACTTCGGAACGTCGACTATTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTTGTTTCTGTGTGTCTACTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5858
hsIGL_0038	GCCTTGCCAGCCCGCTCAGGTACAGTGTTCGGAACGGTCTGGGCCAG	SEQ ID NO:

Name	Sequence	SEQ ID NO
_V003_J002 _IGLV01- 44_IGLJ2_F	TCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGG TCACCATCTCTTGTCTGGAAGCAGCTCCAACATCGGAAGTAATACTGT AAACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAACCTCCTCATCTAT AGTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGA TGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGATGAGTACA GTGTTCCGAACGTCGACTATTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTGTACAGTGTTTCGGAACCTGATGGCGCGAGG GAGGC	5859
hsIGL_0039 _V004_J002 _IGLV01- 47_IGLJ2_F	GCCTTGCCAGCCCGCTCAGGGATCATCTTCGGAACGGTCCTGGGCCCAG TCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGG TCACCATCTCTTGTCTGGAAGCAGCTCCAACATCGGAAGTAATTATGT ATACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAACCTCCTCATCTAT AGTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGGTCCGAGGA TGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGATGAGGATC ATCTTCGGAACGTCGACTATTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTGGATCATCTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5860
hsIGL_0040 _V005_J002 _IGLV01- 50- ORF_IGLJ2_ F	GCCTTGCCAGCCCGCTCAGTATTGGCGTTCGGAACCCTGGGCCCAGTCT GTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCA CCATCTCCTGCACTGGGAGCAGCTCCAACATTGGGGCGGGTTATGTTGT ACATTGGTACCAGCAGCTTCCAGGAACAGCCCCCAAACCTCCTCATCTAT GGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCAATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGACTCCAGTCTGAGGA TGAGGCTGATTATTACTGCAAAGCATGGGATAACAGCCTGATGATATTG GCGTTCGGAACGTCGACTATTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTTATTGGCGTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5861
hsIGL_0041 _V006_J002 _IGLV01- 51_IGLJ2_F	GCCTTGCCAGCCCGCTCAGAGGCTTGATTTCGGAACGGTCCTGGGCCCAG TCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAGG TCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAATTATGT ATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCAAACCTCCTCATTTAT GACAATAATAAGCGACCCCTCAGGGATTCTTGACCGATTCTCTGGCTCCA AGTCTGGCACGTGAGCCACCCTGGGCATCACCAGGACTCCAGACTGGGGA CGAGGCCGATTATTACTGCGGAACATGGGATAGCAGCCTGATGAAGGCT TGATTTCGGAACGTCGACTATTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC	SEQ ID NO: 5862

Name	Sequence	SEQ ID NO
	TGTTTTTGTGTTTCTGTAGGCTTGATTTCGGAACCTGATGGCGCGAGG GAGGC	
hsIGL_0042 _V007_J002 _IGLV02- 08_IGLJ2_F	GCCTTGCCAGCCCGCTCAGACACACGTTTCGGAACGTCCTGGGCCCAGT CTGCCCTGACTCAGCCTCCCTCCGCGTCCAGGTCTCCTGGACAGTCAGT CACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATAACTAT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCCAAACATCATGATTT ATGAGGTCAGTAAGCGGCCCTCAGGGGTCCCTGATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGGCTCCAGGCTGAG GATGAGGCTGATTATTACTGCAGCTCATATGCAGGCAGCAATGAACACA CGTTTCGGAACGTCGACTATTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTACACACGTTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5863
hsIGL_0043 _V008_J002 _IGLV02- 11_IGLJ2_F	GCCTTGCCAGCCCGCTCAGTAGACGGATTTCGGAACATCCTGGGCTCAGT CTGCCCTGACTCAGCCTCGCTCAGTGTCCGGGTCTCCTGGACAGTCAGT CACCATCTCCTGCACTGGAACCAGCAGTGATGTTGGTGGTTATAACTAT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCCAAACATCATGATTT ATGATGTCAGTAAGCGGCCCTCAGGGGTCCCTGATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAG GATGAGGCTGATTATTACTGCTGCTCATATGCAGGCAGCTATGATAGAC GGATTTCGGAACGTCGACTATTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTTAGACGGATTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5864
hsIGL_0044 _V009_J002 _IGLV02- 14_IGLJ2_F	GCCTTGCCAGCCCGCTCAGCAGCTCTTTTCGGAACGTCCTGGGCCCAGT CTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGAT CACCATCTCCTGCACTGGAACCAGCAGTGATGTTGGGAGTTATAACCTT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCCAAACATCATGATTT ATGAGGGCAGTAAGCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAG GACGAGGCTGATTATTACTGCAGCTCATATACAAGCAGCAGTGACAGCT CTTTTCGGAACGTCGACTATTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTTCAGCTCTTTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5865
hsIGL_0045 _V010_J002 _IGLV02- 18_IGLJ2_F	GCCTTGCCAGCCCGCTCAGGAGCGATATTCGGAACATCCTGGGCTCAGT CTGCCCTGACTCAGCCTCCCTCCGTGTCCGGGTCTCCTGGACAGTCAGT CACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTAGTTATAACCGT GTCTCCTGGTACCAGCAGCCCCCAGGCACAGCCCCCAAACATCATGATTT ATGAGGTCAGTAATCGGCCCTCAGGGGTCCCTGATCGCTTCTCTGGGTC CAAGTCTGGCAACACGGCCTCCCTGACCACCTCTGGGCTCCAGGCTGAG	SEQ ID NO: 5866

Name	Sequence	SEQ ID NO
	GACGAGGCTGATTATTACTGCAGCTCATATACAAGCAGCAGTGAGAGCG ATATTCGGAACGTCGACTATTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCTCTCCTTCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGGTTTCTGTGAGCGATATTCGGAACCTGATGGCGCGAGG GAGGC	
hsIGL_0046 _V011_J002 _IGLV02- 23_IGLJ2_F	GCCTTGCCAGCCCGCTCAGGCATCTGATTCGGAACGTCCTGGGCCCAGT CTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGAT CACCATCTCCTGCACTGGAACCAGCAGTGATGTTGGGAGTTATAACCTT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCAACTCATGATTT ATGAGGGCAGTAAGCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACAATCTCTGGGCTCCAGGCTGAG GACGAGGCTGATTATTACTGCTGCTCATATGCAGGTAGTAGTGAGCATC TGATTCGGAACGTCGACTATTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCTCTCCTTCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGGTTTCTGTGCATCTGATTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5867
hsIGL_0047 _V012_J002 _IGLV02- 33- ORF_IGLJ2_ F	GCCTTGCCAGCCCGCTCAGTGCTACACTTCGGAACGTCCTGGGCCCAGT CTGCCCTGACTCAGCCTCCTTTTGTGTCCGGGGCTCCTGGACAGTCGGT CACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGGGATTATGATCAT GTCTTCTGGTACCAAAAGCGTCTCAGCACTACCTCCAGACTCCTGATTT ACAATGTCAATACTCGGCCCTCAGGGATCTCTGACCTCTTCTCAGGCTC CAAGTCTGGCAACATGGCTTCCCTGACCATCTCTGGGCTCAAGTCCGAG GTTGAGGCTAATTATCACTGCAGCTTATATTCAAGTAGTTATGATGCTA CACTTCGGAACGTCGACTATTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCTCTCCTTCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGGTTTCTGTTGCTACACTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5868
hsIGL_0048 _V013_J002 _IGLV03- 01_IGLJ2_F	GCCTTGCCAGCCCGCTCAGAACTGCCATTTCGGAACCTCTCCTGTAGGAT CCGTGGCCTCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCC AGGACAGACAGCCAGCATCACCTGCTCTGGAGATAAATTGGGGGATAAA TATGCTTGCTGGTATCAGCAGAAGCCAGGCCAGTCCCCGTGTGCTGGTCA TCTATCAAGATAGCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGG CTCCAACCTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCT ATGGATGAGGCTGACTATTACTGTGTCAGGCGTGGGACAGCAGTGAACTG CCATTTCGGAACGTCGACTATTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCTCTCCTTCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGGTTTCTGTAACTGCCATTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5869
hsIGL_0049 _V014_J002 _IGLV03-	GCCTTGCCAGCCCGCTCAGTTGGACTGTTTCGGAACCTTTTCTTGAGGTT CTGTGGCCTCCTATGAGCTGACTCAGCCACTCTCAGTGTGAGTGGCCCT GGGACAGGCGGCCAGGATTACCTGTGGGGGAAACAACCTTGGATATAAA	SEQ ID NO: 5870

Name	Sequence	SEQ ID NO
09- FP_IGLJ2_F	AATGTGCACTGGTACCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTCA TCTATAGGGATAACAACCGGCCCTCTGGGATCCCTGAGCGATTCTCTGG CTCCAACCTCGGGGAACACGGCCACCCTGACCATCAGCAGAGCCCAAGCC GGGGATGAGGCTGACTATTACTGTCTAGGTGTGGGACAGCAGTGATTGGA CTGTTTCGGAACGTCGACTATTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTGTTTCTGTTTGGACTGTTTCGGAACCTGATGGCGCGAGG GAGGC	
hsIGL_0050 _V015_J002 _IGLV03- 10_IGLJ2_F	GCCTTGCCAGCCCGCTCAGGTAGACACTTCGGAACCTGCAGTCTCTGAG GCCTCCTATGAGCTGACACAGCCACCCTCGGTGTCTAGTGTCCCCAGGAC AAACGGCCAGGATCACCTGCTCTGGAGATGCATTGCCAAAAAATATGC TTATTGGTACCAGCAGAAGTCAGGCCAGGCCCTGTGCTGGTCATCTAT GAGGACAGCAAACGACCCTCCGGGATCCCTGAGAGATTCTCTGGCTCCA GCTCAGGGACAATGGCCACCTTGACTATCAGTGGGGCCAGGTGGAGGA TGAAGCTGACTACTACTGTTACTCAACAGACAGCAGTGGTATGAGTAGA CACTTCGGAACGTCGACTATTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTGTTTCTGTGTAGACACTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5871
hsIGL_0051 _V016_J002 _IGLV03- 12_IGLJ2_F	GCCTTGCCAGCCCGCTCAGCACTGTACTTCGGAACCTGCAGGCTCTGCG ACCTCCTATGAGCTGACTCAGCCACACTCAGTGTCTAGTGGCCACAGCAC AGATGGCCAGGATCACCTGTGGGGGAAACAACATTGGAAGTAAAGCTGT GCACTGGTACCAGCAAAAGCCAGGCCAGGACCCTGTGCTGGTCATCTAT AGCGATAGCAACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA ACCCAGGGAACACCGCCACCCTAACCATCAGCAGGATCGAGGCTGGGGA TGAGGCTGACTATTACTGTCTAGGTGTGGGACAGTAGTAGTGTGACACTG TACTTCGGAACGTCGACTATTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTGTTTCTGTCACTGTACTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5872
hsIGL_0052 _V017_J002 _IGLV03- 16_IGLJ2_F	GCCTTGCCAGCCCGCTCAGGATGATCCTTCGGAACCTGCAGGCTCTGAG GCCTCCTATGAGCTGACACAGCCACCCTCGGTGTCTAGTGTCCCTAGGAC AGATGGCCAGGATCACCTGCTCTGGAGAAGCATTGCCAAAAAATATGC TTATTGGTACCAGCAGAAGCCAGGCCAGTTCCCTGTGCTGGTGATATAT AAAGACAGCGAGAGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA GCTCAGGGACAATAGTCACATTGACCATCAGTGGAGTCCAGGCAGAAGA CGAGGCTGACTATTACTGTCTATCAGCAGACAGCAGTGGTATGAGATGA TCCTTCGGAACGTCGACTATTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTGTTTCTGTGATGATCCTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5873

Name	Sequence	SEQ ID NO
hsIGL_0053 _V018_J002 _IGLV03- 19_IGLJ2_F	GCCTTGCCAGCCCGCTCAGCGCCAATATTCGGAACCTGCAGGTTCTGTG GTTTCTTCTGAGCTGACTCAGGACCCTGCTGTGTCTGTGGCCTTGGGAC AGACAGTCAGGATCACATGCCAAGGAGACAGCCTCAGAAGCTATTATGC AAGCTGGTACCAGCAGAAGCCAGGACAGGCCCTGTACTTGTCTATCTAT GGTAAAAACAACCGGCCCTCAGGGATCCCAGACCGATTCTCTGGCTCCA GCTCAGGAAACACAGCTTCCTTGACCATCACTGGGGCTCAGGCGGAAGA TGAGGCTGACTATTACTGTAACCTCCCGGGACAGCAGTGGTATGACGCCA ATATTCGGAACGTCGACTATTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCTCTCCTTCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTGCGCCAATATTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5874
hsIGL_0054 _V019_J002 _IGLV03- 21_IGLJ2_F	GCCTTGCCAGCCCGCTCAGTCAAGCCTTTCGGAACCTGCAGGCTCTGTG ACCTCCTATGTGCTGACTCAGCCACCCTCAGTGTGAGTGGCCCCAGGAA AGACGGCCAGGATTACCTGTGGGGGAAACAACATTGGAAGTAAAAGTGT GCACTGGTACCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTCATCTAT TATGATAGCGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA ACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAAGCCGGGGA TGAGGCCGACTATTACTGTGAGGTGTGGGACAGTAGTAGTGTGATCAAG CCTTTCGGAACGTCGACTATTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCTCTCCTTCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTTCAAGCCTTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5875
hsIGL_0055 _V020_J002 _IGLV03- 22- FP_IGLJ2_F	GCCTTGCCAGCCCGCTCAGACGTGTGTTTCGGAACCCTCTCTTGAGGC TCTGTTGCCTCCTATGAGCTGACACAGCTACCCTCGGTGTGAGTGTCCC CAGGACAGAAAGCCAGGATCACCTGCTCTGGAGATGTACTGGGGAAAAA TTATGCTGACTGGTACCAGCAGAAGCCAGGCCAGGCCCTGAGTTGGTG ATATACGAAGATAGTGAGCGGTACCCTGGAATCCCTGAACGATTCTCTG GGTCCACCTCAGGGAACACGACCACCCTGACCATCAGCAGGGTCCTGAC CGAAGACGAGGCTGACTATTACTGTTTGTCTGGGAATGAGGTGAACGTG TGTTTCGGAACGTCGACTATTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCTCTCCTTCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTACGTGTGTTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5876
hsIGL_0056 _V021_J002 _IGLV03- 25_IGLJ2_F	GCCTTGCCAGCCCGCTCAGTCCGTCTATTCGGAACCTGCAGGCTCTGAG GCCTCCTATGAGCTGACACAGCCACCCTCGGTGTGAGTGTCCCCAGGAC AGACGGCCAGGATCACCTGCTCTGGAGATGCATTGCCAAAGCAATATGC TTATTGGTACCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTGATATAT AAAGACAGTGAGAGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA GCTCAGGGACAACAGTCACGTTGACCATCAGTGGAGTCCAGGCAGAAGA TGAGGCTGACTATTACTGTCAATCAGCAGACAGCAGTGGTATGATCCGT CTATTCGGAACGTCGACTATTCGGCGGAGGGACCAAGCTGACCGTCCTA	SEQ ID NO: 5877

Name	Sequence	SEQ ID NO
	GCTCCAGCTCTGGGGCTGAGCGCTACCTCACCATCTCCAGCCTCCAGTC TGAGGATGAGGCTGACTATTACTGTCTAGACCTGGGGCACTGTGAGTGTA GCATTCGGAACGTCGACTATTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTGTTTCTGTGTGTAGCATTTCGGAACCTGATGGCGCGAGG GAGGC	
hsIGL_0061 _V026_J002 _IGLV05- 37_IGLJ2_F	GCCTTGCCAGCCCGCTCAGTGGCAGTTTTTCGGAACCTGTGCTGACTCAGC CACCTTCCTCCTCCGCATCTCCTGGAGAATCCGCCAGACTCACCTGCAC CTTGCCAGTGACATCAATGTTGGTAGCTACAACATATACTGGTACCAG CAGAAGCCAGGGAGCCCTCCCAGGTATCTCCTGTACTACTACTCAGACT CAGATAAGGGCCAGGGCTCTGGAGTCCCCAGCCGCTTCTCTGGATCCAA AGATGCTTCAGCCAATACAGGGATTTTACTCATCTCCGGGCTCCAGTCT GAGGATGAGGCTGACTATTACTGTATGATTGGCCAAGCAATGATGGCA GTTTTTCGGAACGTCGACTATTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTGTTTCTGTTGGCAGTTTTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5882
hsIGL_0062 _V027_J002 _IGLV05- 39_IGLJ2_F	GCCTTGCCAGCCCGCTCAGCAGTCCAATTCGGAACCTGTGCTGACTCAGC CAACCTCCCTCTCAGCATCTCCTGGAGCATCAGCCAGATTCACCTGCAC CTTGCGCAGCGGCATCAATGTTGGTACCTACAGGATATACTGGTACCAG CAGAAATCCAGGGAGTCTTCCCCGGTATCTCCTGAGGTACAAATCAGACT CAGATAAGCAGCAGGGCTCTGGAGTCCCCAGCCGCTTCTCTGGATCCAA AGATGCTTCAACCAATGCAGGCCTTTTACTCATCTCTGGGCTCCAGTCT GAAGATGAGGCTGACTATTACTGTGCCATTTGGTACAGCAGTGACAGTC CAATTCGGAACGTCGACTATTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTGTTTCTGTCTAGTCCAATTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5883
hsIGL_0063 _V028_J002 _IGLV05- 45_IGLJ2_F	GCCTTGCCAGCCCGCTCAGTACGTACGTTTCGGAACCTGTGCTGACTCAGC CGTCTTCCCTCTCTGCATCTCCTGGAGCATCAGCCAGTCTCACCTGCAC CTTGCGCAGTGGCATCAATGTTGGTACCTACAGGATATACTGGTACCAG CAGAAGCCAGGGAGTCTTCCCCAGTATCTCCTGAGGTACAAATCAGACT CAGATAAGCAGCAGGGCTCTGGAGTCCCCAGCCGCTTCTCTGGATCCAA AGATGCTTCGCCAATGCAGGGATTTTACTCATCTCTGGGCTCCAGTCT GAGGATGAGGCTGACTATTACTGTATGATTGGCACAGCAGTGATACGT ACGTTTCGGAACGTCGACTATTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTGTTTCTGTTACGTACGTTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5884
hsIGL_0064 _V029_J002	GCCTTGCCAGCCCGCTCAGAGTACCGATTTCGGAACCTGACTCAGCCATCT TCCCATTCTGCATCTTCTGGAGCATCAGTCAGACTCACCTGCATGCTGA	SEQ ID NO: 5885

Name	Sequence	SEQ ID NO
_IGLV05- 52_IGLJ2_F	GCAGTGGCTTCAGTGTTGGGGACTTCTGGATAAGGTGGTACCAACAAAA GCCAGGGAACCCTCCCCGGTATCTCCTGTACTACCACTCAGACTCCAAT AAGGGCCAAGGCTCTGGAGTTCCAGCCGCTTCTCTGGATCCAACGATG CATCAGCCAATGCAGGGATTCTGCGTATCTCTGGGCTCCAGCCTGAGGA TGAGGCTGACTATTACTGTGGTACATGGCACAGCAACTCTATGAAGTAC CGATTCCGAACGTCGACTATTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTAGTACCGATTCCGAACCTGATGGCGCGAGG GAGGC	
hsIGL_0065 _V030_J002 _IGLV07- 43_IGLJ2_F	GCCTTGCCAGCCCGCTCAGATCCATGGTTCGGAACAGGGTCCAATTCTC AGACTGTGGTGACTCAGGAGCCCTCACTGACTGTGTCCCCAGGAGGGAC AGTCACTCTCACCTGTGCTTCCAGCACTGGAGCAGTCACCAGTGGTTAC TATCCAAACTGGTTCCAGCAGAAACCTGGACAAGCACCCAGGGCACTGA TTTATAGTACAAGCAACAAACACTCCTGGACCCCTGCCCGGTTCTCAGG CTCCCTCCTTGGGGGCAAAGCTGCCCTGACACTGTCAGGTGTGCAGCCT GAGGACGAGGCTGAGTATTACTGCCTGCTCTACTATGGTGGTGAATCCA TG GTTCGGAACGTCGACTATTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTATCCATGGTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5886
hsIGL_0066 _V031_J002 _IGLV07- 46- FP_IGLJ2_F	GCCTTGCCAGCCCGCTCAGGTAGCAGTTTCGGAACAGGGTCCAATTCCC AGGCTGTGGTGACTCAGGAGCCCTCACTGACTGTGTCCCCAGGAGGGAC AGTCACTCTCACCTGTGGCTCCAGCACTGGAGCTGTCACCAGTGGTCAT TATCCCTACTGGTTCCAGCAGAAGCCTGGCCAAGCCCCCAGGACACTGA TTTATGATACAAGCAACAAACACTCCTGGACACCTGCCCGGTTCTCAGG CTCCCTCCTTGGGGGCAAAGCTGCCCTGACCCTTTTGGGTGCGCAGCCT GAGGATGAGGCTGAGTATTACTGCTTGCTCTCCTATAGTGGTGAGTAGC AGTTTCGGAACGTCGACTATTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTGTAGCAGTTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5887
hsIGL_0067 _V032_J002 _IGLV08- 61_IGLJ2_F	GCCTTGCCAGCCCGCTCAGATCTTCGTTTCGGAACGAGTGGATTCTCAG ACTGTGGTGACCCAGGAGCCATCGTTCTCAGTGTCCCCCTGGAGGGACAG TCACACTCACTTGTGGCTTGAGCTCTGGCTCAGTCTCTACTAGTTACTA CCCCAGCTGGTACCAGCAGACCCAGGCCAGGCTCCACGCACGCTCATC TACAGCACAAACACTCGCTCTTCTGGGGTCCCTGATTGCTTCTCTGGCT CCATCCTTGGGAACAAAGCTGCCCTCACCATCACGGGGGCCAGGCAGA TGATGAATCTGATTATTACTGTGTGCTGTATATGGGTAGTGTGAATCTT CGTTTCGGAACGTCGACTATTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTATCTTCGTTTCGGAACCTGATGGCGCGAGG	SEQ ID NO: 5888

Name	Sequence	SEQ ID NO
	GAGGC	
hsIGL_0068 _V033_J002 _IGLV09- 49_IGLJ2_F	GCCTTGCCAGCCCGCTCAGTCCACAGTTTCGGAACCTGACTCAGCCACCT TCTGCATCAGCCTCCCTGGGAGCCTCGGTACACTCACCTGCACCCTGA GCAGCGGCTACAGTAATTATAAAGTGGACTGGTACCAGCAGAGACCAGG GAAGGGCCCCCGGTTTGTGATGCGAGTGGGCACCTGGTGGGATTGTGGGA TCCAAGGGGGATGGCATCCCTGATCGCTTCTCAGTCTTGGGCTCAGGCC TGAATCGGTACCTGACCATCAAGAACATCCAGGAAGAAGATGAGAGTGA CTACCACCTGTGGGGCAGACCATGGCAGTGGGAGCAACTTCGTGATCCAC AGTTTCGGAACGTCGACTATTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTGTTTCTGTTCCACAGTTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5889
hsIGL_0069 _V034_J002 _IGLV10- 54- FP_IGLJ2_F	GCCTTGCCAGCCCGCTCAGATGACACCTTCGGAACCTGTGAGTGGTCCAG GCAGGGCTGACTCAGCCACCCTCGGTCTCCAAGGGCTTGAGACAGACCG CCACACTCACCTGCAGTGGGAACAGCAACAATGTTGGCAACCAAGGAGC AGCTTGGCCTGAGCAGCACCAGGGCCACCCTCCCAAACCTCCTATCCTAC AGGAATAACAACCGGCCCTCAGGGATCTCAGAGAGATTATCTGCATCCA GGTCAGGAACACAGCCTCCCTGACCATTACTGGACTCCAGCCTGAGGA CGAGGCTGACTATTACTGCTCAGCATGGGACAGCAGCCTCATGAATGAC ACCTTCGGAACGTCGACTATTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTGTTTCTGTATGACACCTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5890
hsIGL_0070 _V035_J002 _IGLV11- 55- ORF_IGLJ2_ F	GCCTTGCCAGCCCGCTCAGCTTCACGATTCGGAACCGTGCTGACTCAGC CGCCCTCTCTGTCTGCATCCCCGGGAGCAACAGCCAGACTCCCCCTGCAC CCTGAGCAGTGACCTCAGTGTGGTGGTAAAAACATGTTCTGGTACCAG CAGAAGCCAGGAGCTCTCCCAGGTTATTCTGTATCACTACTCAGACT CAGACAAGCAGCTGGGACCTGGGGTCCCCAGTCGAGTCTCTGGCTCCAA GGAGACCTCAAGTAACACAGCGTTTTTGTCTATCTCTGGGCTCCAGCCT GAGGACGAGGCCGATTATTACTGCCAGGTGTACGAAAGTAGTGACTTCA CGATTTCGGAACGTCGACTATTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTGTTTCTGTCTTCACGATTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5891
hsIGL_0071 _V001_J003 _IGLV01- 36_IGLJ3_F	GCCTTGCCAGCCCGCTCAGTAGGAGACAAGTAACGGGTCTGGGCCCAG TCTGTGCTGACTCAGCCACCCTCGGTGTCTGAAGCCCCCAGGCAGAGGG TCACCATCTCCTGTTCTGGAAGCAGCTCCAACATCGGAAATAATGCTGT AAACTGGTACCAGCAGCTCCCAGGAAAGGCTCCCAAACCTCATCTAT TATGATGATCTGCTGCCCTCAGGGGTCTCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGA TGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGATGATAGGA	SEQ ID NO: 5892

Name	Sequence	SEQ ID NO
	GACAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTGTCTGTAGGAGACAAGTAACGCTGATGGCGCGAGG GAGGC	
hsIGL_0072 _V002_J003 _IGLV01- 40_IGLJ3_F	GCCTTGCCAGCCCGCTCAGGTGTCTACAAGTAACGCCTGGGCCAGTCT GTCGTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCA CCATCTCCTGCACTGGGAGCAGCTCCAACATCGGGGCAGGTTATGATGT ACACTGGTACCAGCAGCTTCCAGGAACAGCCCCAACTCCTCATCTAT GGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGA TGAGGCTGATTATTACTGCCAGTCTATGACAGCAGCCTGATGAGTGTCT TACAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTGTCTGTGTGTCTACAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5893
hsIGL_0073 _V003_J003 _IGLV01- 44_IGLJ3_F	GCCTTGCCAGCCCGCTCAGGTACAGTGAAGTAACGGGTCTGGGCCAG TCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCGGGCAGAGGG TCACCATCTCTTGTCTGGAAGCAGCTCCAACATCGGAAGTAATACTGT AAACTGGTACCAGCAGCTCCCAGGAACGGCCCCAACTCCTCATCTAT AGTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGA TGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGATGAGTACA GTGAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTGTCTGTGTACAGTGAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5894
hsIGL_0074 _V004_J003 _IGLV01- 47_IGLJ3_F	GCCTTGCCAGCCCGCTCAGGGATCATCAAGTAACGGGTCTGGGCCAG TCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCGGGCAGAGGG TCACCATCTCTTGTCTGGAAGCAGCTCCAACATCGGAAGTAATTATGT ATACTGGTACCAGCAGCTCCCAGGAACGGCCCCAACTCCTCATCTAT AGTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGGTCCGAGGA TGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGATGAGGATC ATCAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTGTCTGTGGATCATCAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5895
hsIGL_0075 _V005_J003 _IGLV01- 50-	GCCTTGCCAGCCCGCTCAGTATTGGCGAAGTAACGCCTGGGCCAGTCT GTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCA CCATCTCCTGCACTGGGAGCAGCTCCAACATTGGGGCGGGTTATGTTGT ACATTGGTACCAGCAGCTTCCAGGAACAGCCCCAACTCCTCATCTAT	SEQ ID NO: 5896

Name	Sequence	SEQ ID NO
ORF_IGLJ3_F	GGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCAATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGACTCCAGTCTGAGGA TGAGGCTGATTATTACTGCAAAGCATGGGATAACAGCCTGATGATATTG GCGAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTTGTTTCTGTTATTGGCGAAGTAACGCTGATGGCGCGAGG GAGGC	
hsIGL_0076_V006_J003_IGLV01-51_IGLJ3_F	GCCTTGCCAGCCCGCTCAGAGGCTTGAAAGTAACGGGTCTGGGCCAG TCTGTGTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAGG TCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAATTATGT ATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCAACTCCTCATTTAT GACAATAATAAGCGACCCTCAGGGATTCTTGACCGATTCTCTGGCTCCA AGTCTGGCACGTCAGCCACCCTGGGCATCACC GGACTCCAGACTGGGGA CGAGGCCGATTATTACTGCGGAACATGGGATAGCAGCCTGATGAAGGCT TGAAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTTGTTTCTGTAGGCTTGAAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5897
hsIGL_0077_V007_J003_IGLV02-08_IGLJ3_F	GCCTTGCCAGCCCGCTCAGACACACGTAAGTAACGGTCCTGGGCCAGT CTGCCCTGACTCAGCCTCCCTCCGCGTCCAGGTCTCCTGGACAGTCAGT CACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATAACTAT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCAACTCATGATTT ATGAGGTCAGTAAGCGGCCCTCAGGGGTCCCTGATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGGCTCCAGGCTGAG GATGAGGCTGATTATTACTGCAGCTCATATGCAGGCAGCAATGAACACA CGTAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTTGTTTCTGTACACACGTAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5898
hsIGL_0078_V008_J003_IGLV02-11_IGLJ3_F	GCCTTGCCAGCCCGCTCAGTAGACGGAAGTAACGATCCTGGGCTCAGT CTGCCCTGACTCAGCCTCGCTCAGTGTCCGGGTCTCCTGGACAGTCAGT CACCATCTCCTGCACTGGAACCAGCAGTGATGTTGGTGGTTATAACTAT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCAACTCATGATTT ATGATGTCAGTAAGCGGCCCTCAGGGGTCCCTGATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAG GATGAGGCTGATTATTACTGCTGCTCATATGCAGGCAGCTATGATAGAC GGAAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTTGTTTCTGTAGACGGAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5899
hsIGL_0079	GCCTTGCCAGCCCGCTCAGCAGCTCTTAAGTAACGGTCCTGGGCCAGT	SEQ ID NO:

Name	Sequence	SEQ ID NO
_V009_J003 _IGLV02- 14_IGLJ3_F	CTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGAT CACCATCTCCTGCACTGGAACCAGCAGTGATGTTGGGAGTTATAACCTT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCAACTCATGATTT ATGAGGGCAGTAAGCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAG GACGAGGCTGATTATTACTGCAGCTCATATACAAGCAGCAGTGACAGCT CTTAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTGTCAGCTCTTAAGTAACGCTGATGGCGCGAGG GAGGC	5900
hsIGL_0080 _V010_J003 _IGLV02- 18_IGLJ3_F	GCCTTGCCAGCCCGCTCAGGAGCGATAAAGTAACGATCCTGGGCTCAGT CTGCCCTGACTCAGCCTCCCTCCGTGTCCGGGTCTCCTGGACAGTCAGT CACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTAGTTATAACCGT GTCTCCTGGTACCAGCAGCCCCCAGGCACAGCCCCAACTCATGATTT ATGAGGTCAAGTAATCGGCCCTCAGGGGTCCCTGATCGCTTCTCTGGGTC CAAGTCTGGCAACACGGCCTCCCTGACCACCTCTGGGCTCCAGGCTGAG GACGAGGCTGATTATTACTGCAGCTCATATACAAGCAGCAGTGAGAGCG ATAAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTGAGCGATAAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5901
hsIGL_0081 _V011_J003 _IGLV02- 23_IGLJ3_F	GCCTTGCCAGCCCGCTCAGGCATCTGAAAGTAACGGTCCTGGGCCCAGT CTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGAT CACCATCTCCTGCACTGGAACCAGCAGTGATGTTGGGAGTTATAACCTT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCAACTCATGATTT ATGAGGGCAGTAAGCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACAATCTCTGGGCTCCAGGCTGAG GACGAGGCTGATTATTACTGCTGCTCATATGCAGGTAGTAGTGAGCATC TGAAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTGCATCTGAAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5902
hsIGL_0082 _V012_J003 _IGLV02- 33- ORF_IGLJ3_F	GCCTTGCCAGCCCGCTCAGTGCTACACAAGTAACGGTCCTGGGCCCAGT CTGCCCTGACTCAGCCTCCTTTTGTGTCCGGGGCTCCTGGACAGTCGGT CACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGGGATTATGATCAT GTCTTCTGGTACCAAAAGCGTCTCAGCACTACCTCCAGACTCCTGATTT ACAATGTCAATACTCGGCCTTCAGGGATCTCTGACCTCTTCTCAGGCTC CAAGTCTGGCAACATGGCTTCCCTGACCATCTCTGGGCTCAAGTCCGAG GTTGAGGCTAATTATCACTGCAGCTTATATTCAAGTAGTTATGATGCTA CACAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC	SEQ ID NO: 5903

Name	Sequence	SEQ ID NO
	TGTTTTTGTGTTTCTGTTGCTACACAAGTAACGCTGATGGCGCGAGG GAGGC	
hsIGL_0083 _V013_J003 _IGLV03- 01_IGLJ3_F	GCCTTGCCAGCCCGCTCAGAACTGCCAAAGTAACGCTCTCCTGTAGGAT CCGTGGCCTCCTATGAGCTGACTCAGCCACCCTCAGTGTCGTGTCCTCC AGGACAGACAGCCAGCATCACCTGCTCTGGAGATAAATTGGGGGATAAA TATGCTTGCTGGTATCAGCAGAAGCCAGGCCAGTCCCCGTGTGCTGGTCA TCTATCAAGATAGCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGG CTCCAACCTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCT ATGGATGAGGCTGACTATTACTGTCAGGCGTGGGACAGCAGTGAAACTG CCAAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTAAGTACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5904
hsIGL_0084 _V014_J003 _IGLV03- 09- FP_IGLJ3_F	GCCTTGCCAGCCCGCTCAGTTGGACTGAAGTAACGTTTTCTTGCAGGTT CTGTGGCCTCCTATGAGCTGACTCAGCCACTCTCAGTGTCAGTGGCCCT GGGACAGGCGGCCAGGATTACCTGTGGGGGAAACAACCTTGGATATAAA AATGTGCACTGGTACCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTCA TCTATAGGGATAACAACCGGCCCTCTGGGATCCCTGAGCGATTCTCTGG CTCCAACCTCGGGGAACACGGCCACCCTGACCATCAGCAGAGCCCAAGCC GGGGATGAGGCTGACTATTACTGTCAGGTGTGGGACAGCAGTGATTGGA CTGAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTTTGGACTGAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5905
hsIGL_0085 _V015_J003 _IGLV03- 10_IGLJ3_F	GCCTTGCCAGCCCGCTCAGGTAGACACAAGTAACGTTGCAGTCTCTGAG GCCTCCTATGAGCTGACACAGCCACCCTCGGTGTGAGTGTCCTCCAGGAC AAACGGCCAGGATCACCTGCTCTGGAGATGCATTGCCAAAAAATATGC TTATTGGTACCAGCAGAAGTCAGGCCAGGCCCTGTGCTGGTCATCTAT GAGGACAGCAAACGACCCTCCGGGATCCCTGAGAGATTCTCTGGCTCCA GCTCAGGGACAATGGCCACCTTGACTATCAGTGGGGCCAGGTGGAGGA TGAAGCTGACTACTACTGTTACTCAACAGACAGCAGTGGTATGAGTAGA CACAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTGTAGACACAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5906
hsIGL_0086 _V016_J003 _IGLV03- 12_IGLJ3_F	GCCTTGCCAGCCCGCTCAGCACTGTACAAGTAACGTTGCAGGCTCTGCG ACCTCCTATGAGCTGACTCAGCCACACTCAGTGTCAGTGGCCACAGCAC AGATGGCCAGGATCACCTGTGGGGGAAACAACATTGGAAGTAAAGCTGT GCACTGGTACCAGCAAAAGCCAGGCCAGGACCCTGTGCTGGTCATCTAT AGCGATAGCAACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA ACCCAGGGAACACCGCCACCCTAACCATCAGCAGGATCGAGGCTGGGGA	SEQ ID NO: 5907

Name	Sequence	SEQ ID NO
	TGAGGCTGACTATTACTGTCAGGTGTGGGACAGTAGTAGTGTGACACTG TACAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTCACTGTACAAGTAACGCTGATGGCGCGAGG GAGGC	
hsIGL_0087 _V017_J003 _IGLV03- 16_IGLJ3_F	GCCTTGCCAGCCCGCTCAGGATGATCCAAGTAACGTTGCAGGCTCTGAG GCCTCCTATGAGCTGACACAGCCACCCTCGGTGTCAAGTGTCCCTAGGAC AGATGGCCAGGATCACCTGCTCTGGAGAAGCATTGCCAAAAAATATGC TTATTGGTACCAGCAGAAGCCAGGCCAGTTCCCTGTGCTGGTGATATAT AAAGACAGCGAGAGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA GCTCAGGGACAATAGTCACATTGACCATCAGTGGAGTCCAGGCAGAAGA CGAGGCTGACTATTACTGTCTATCAGCAGACAGCAGTGGTATGAGATGA TCCAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTGATGATCCAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5908
hsIGL_0088 _V018_J003 _IGLV03- 19_IGLJ3_F	GCCTTGCCAGCCCGCTCAGCGCCAATAAAGTAACGTTGCAGGTTCTGTG GTTTCTTCTGAGCTGACTCAGGACCCTGCTGTGTCTGTGGCCTTGGGAC AGACAGTCAGGATCACATGCCAAGGAGACAGCCTCAGAAGCTATTATGC AAGCTGGTACCAGCAGAAGCCAGGACAGGCCCTGTACTTGTCTATCTAT GGTAAAAACAACCGGCCCTCAGGGATCCCAGACCGATTCTCTGGCTCCA GCTCAGGAAACACAGCTTCCCTTGACCATCACTGGGGCTCAGGCGGAAGA TGAGGCTGACTATTACTGTAACCTCCCGGGACAGCAGTGGTATGACGCCA ATAAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTGCGCCAATAAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5909
hsIGL_0089 _V019_J003 _IGLV03- 21_IGLJ3_F	GCCTTGCCAGCCCGCTCAGTCAAGCCTAAGTAACGTTGCAGGCTCTGTG ACCTCCTATGTGCTGACTCAGCCACCCTCAGTGTCAAGTGGCCCCAGGAA AGACGGCCAGGATTACCTGTGGGGGAAACAACATTGGAAGTAAAAGTGT GCACTGGTACCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTCATCTAT TATGATAGCGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA ACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAAGCCGGGGA TGAGGCCGACTATTACTGTCAAGTGTGGGACAGTAGTAGTGTGATCAAG CCTAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTTCAAGCCTAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5910
hsIGL_0090 _V020_J003 _IGLV03-	GCCTTGCCAGCCCGCTCAGACGTGTGTAAGTAACGCCTCTCTTGACGGC TCTGTTGCCTCCTATGAGCTGACACAGCTACCCTCGGTGTCAAGTGTCCC CAGGACAGAAAGCCAGGATCACCTGCTCTGGAGATGTACTGGGGAAAAA	SEQ ID NO: 5911

Name	Sequence	SEQ ID NO
22- FP_IGLJ3_F	TTATGCTGACTGGTACCAGCAGAAGCCAGGCCAGGCCCTGAGTTGGTG ATATACGAAGATAGTGAGCGGTACCCTGGAATCCCTGAACGATTCTCTG GGTCCACCTCAGGGAACACGACCACCCTGACCATCAGCAGGGTCCTGAC CGAAGACGAGGCTGACTATTACTGTTTGTCTGGGAATGAGGTGAACGTG TGTAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTGTGTTCTGTACGTGTGTAAGTAACGCTGATGGCGCGAGG GAGGC	
hsIGL_0091 _V021_J003 _IGLV03- 25_IGLJ3_F	GCCTTGCCAGCCCGCTCAGTCCGTCTAAAGTAACGTTGCAGGCTCTGAG GCCTCCTATGAGCTGACACAGCCACCCTCGGTGTCACTGTCCCCAGGAC AGACGGCCAGGATCACCTGCTCTGGAGATGCATTGCCAAAGCAATATGC TTATTGGTACCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTGATATAT AAAGACAGTGAGAGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA GCTCAGGACAACAGTCACGTTGACCATCAGTGGAGTCCAGGCAGAAGA TGAGGCTGACTATTACTGTCAATCAGCAGACAGCAGTGGTATGATCCGT CTAAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTGTGTTCTGTTCCGTCTAAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5912
hsIGL_0092 _V022_J003 _IGLV03- 27_IGLJ3_F	GCCTTGCCAGCCCGCTCAGAAGAGCTGAAGTAACGCTTTTCTTGAGTC TCTGTGGCCTCCTATGAGCTGACACAGCCATCCTCAGTGTCACTGTCTC CGGGACAGACAGCCAGGATCACCTGCTCAGGAGATGTACTGGCAAAAAA ATATGCTCGGTGGTTCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTG ATTTATAAAGACAGTGAGCGGCCCTCAGGGATCCCTGAGCGATTCTCCG GCTCCAGCTCAGGGACCACAGTCACCTTGACCATCAGCGGGGGCCAGGT TGAGGATGAGGCTGACTATTACTGTTACTCTGCGGCTGACATGAAAGAG CTGAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTGTGTTCTGTAAGAGCTGAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5913
hsIGL_0093 _V023_J003 _IGLV04- 03_IGLJ3_F	GCCTTGCCAGCCCGCTCAGTATCGCTCAAGTAACGTGCTGACTCAGCCC CCGTCTGCATCTGCCTTGCTGGGAGCCTCGATCAAGCTCACCTGCACCC TAAGCAGTGAGCACAGCACCTACACCATCGAATGGTATCAACAGAGACC AGGGAGGTCCCCCAGTATATAATGAAGGTTAAGAGTGATGGCAGCCAC AGCAAGGGGGACGGGATCCCCGATCGCTTCATGGGCTCCAGTTCTGGGG CTGACCGCTACCTCACCTTCTCCAACCTCCAGTCTGACGATGAGGCTGA GTATCACTGTGGAGAGAGCCACACGATTGATGGCCAAGTCGTGATATCG CTCAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTGTGTTCTGTTATCGCTCAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5914

Name	Sequence	SEQ ID NO
hsIGL_0094 _V024_J003 _IGLV04- 60_IGLJ3_F	GCCTTGCCAGCCCGCTCAGTCAGATGCAAGTAACGCTCTCTCCCAGCCT GTGCTGACTCAATCATCCTCTGCCTCTGCTTCCCTGGGATCCTCGGTCA AGCTCACCTGCACTCTGAGCAGTGGGCACAGTAGCTACATCATCGCATG GCATCAGCAGCAGCCAGGGAAGGCCCTCGGTACTTGATGAAGCTTGAA GGTAGTGGAAGCTACAACAAGGGGAGCGGAGTTCCTGATCGCTTCTCAG GCTCCAGCTCTGGGGCTGACCGCTACCTCACCATCTCCAACCTCCAGTT TGAGGATGAGGCTGATTATTACTGTGAGACCTGGGACAGTATGATCAGA TGCAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTTCAGATGCAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5915
hsIGL_0095 _V025_J003 _IGLV04- 69_IGLJ3_F	GCCTTGCCAGCCCGCTCAGGTGTAGCAAAGTAACGCTCTCTCCCAGCTT GTGCTGACTCAATCGCCCTCTGCCTCTGCCTCCCTGGGAGCCTCGGTCA AGCTCACCTGCACTCTGAGCAGTGGGCACAGCAGCTACGCCATCGCATG GCATCAGCAGCAGCCAGAGAAGGGCCCTCGGTACTTGATGAAGCTTAAC AGTGATGGCAGCCACAGCAAGGGGGACGGGATCCCTGATCGCTTCTCAG GCTCCAGCTCTGGGGCTGAGCGCTACCTCACCATCTCCAGCCTCCAGTC TGAGGATGAGGCTGACTATTACTGTGAGACCTGGGGCACTGTGAGTGTA GCAAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTGTGTAGCAAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5916
hsIGL_0096 _V026_J003 _IGLV05- 37_IGLJ3_F	GCCTTGCCAGCCCGCTCAGTGGCAGTTAAGTAACGTGTGCTGACTCAGC CACCTTCCTCCTCCGCATCTCCTGGAGAATCCGCCAGACTCACCTGCAC CTTGCCCACTGACATCAATGTTGGTAGCTACAACATATACTGGTACCAG CAGAAGCCAGGGAGCCCTCCCAGGTATCTCCTGTACTACTACTCAGACT CAGATAAGGGCCAGGGCTCTGGAGTCCCCAGCCGCTTCTCTGGATCCAA AGATGCTTCAGCCAATACAGGGATTTTACTCATCTCCGGGCTCCAGTCT GAGGATGAGGCTGACTATTACTGTATGATTTGGCCAAGCAATGATGGCA GTTAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTGTCAGTTAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5917
hsIGL_0097 _V027_J003 _IGLV05- 39_IGLJ3_F	GCCTTGCCAGCCCGCTCAGCAGTCCAAAAGTAACGTGTGCTGACTCAGC CAACCTCCCTCTCAGCATCTCCTGGAGCATCAGCCAGATTCACCTGCAC CTTGCGCAGCGGCATCAATGTTGGTACCTACAGGATATACTGGTACCAG CAGAAATCCAGGGAGTCTTCCCCGGTATCTCCTGAGGTACAAATCAGACT CAGATAAGCAGCAGGGCTCTGGAGTCCCCAGCCGCTTCTCTGGATCCAA AGATGCTTCAACCAATGCAGGCCTTTTACTCATCTCTGGGCTCCAGTCT GAAGATGAGGCTGACTATTACTGTGCCATTTGGTACAGCAGTGACAGTC CAAAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA	SEQ ID NO: 5918

Name	Sequence	SEQ ID NO
	GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTCTAGTCCAAAAGTAACGCTGATGGCGCGAGG GAGGC	
hsIGL_0098 _V028_J003 _IGLV05- 45_IGLJ3_F	GCCTTGCCAGCCCGCTCAGTACGTACGAAGTAACGTGTGCTGACTCAGC CGTCTTCCCTCTCTGCATCTCCTGGAGCATCAGCCAGTCTCACCTGCAC CTTGCGCAGTGGCATCAATGTTGGTACCTACAGGATATACTGGTACCAG CAGAAGCCAGGGAGTCCCTCCCCAGTATCTCCTGAGGTACAAATCAGACT CAGATAAGCAGCAGGGCTCTGGAGTCCCCAGCCGCTTCTCTGGATCCAA AGATGCTTCGGCCAATGCAGGGATTTTACTCATCTCTGGGCTCCAGTCT GAGGATGAGGCTGACTATTACTGTATGATTTGGCACAGCAGTGATACGT ACGAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTGTACGTACGAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5919
hsIGL_0099 _V029_J003 _IGLV05- 52_IGLJ3_F	GCCTTGCCAGCCCGCTCAGAGTACCGAAAGTAACGTGACTCAGCCATCT TCCCATTCTGCATCTTCTGGAGCATCAGTCAGACTCACCTGCATGCTGA GCAGTGGCTTCAGTGTGTTGGGGACTTCTGGATAAGGTGGTACCAACAAAA GCCAGGGAACCCCTCCCCGGTATCTCCTGTACTACCACTCAGACTCCAAT AAGGGCCAAGGCTCTGGAGTTCAGCCGCTTCTCTGGATCCAACGATG CATCAGCCAATGCAGGGATTCTGCGTATCTCTGGGCTCCAGCCTGAGGA TGAGGCTGACTATTACTGTGGTACATGGCACAGCAACTCTATGAAGTAC CGAAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTAGTACCGAAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5920
hsIGL_0100 _V030_J003 _IGLV07- 43_IGLJ3_F	GCCTTGCCAGCCCGCTCAGATCCATGGAAGTAACGAGGGTCCAATTCTC AGACTGTGGTGACTCAGGAGCCCTCACTGACTGTGTCCCCAGGAGGGAC AGTCACTCTCACCTGTGCTTCCAGCACTGGAGCAGTCACCAGTGGTTAC TATCCAAACTGGTTCCAGCAGAAACCTGGACAAGCACCCAGGGCACTGA TTTATAGTACAAGCAACAAACACTCCTGGACCCCTGCCCGGTTCTCAGG CTCCCTCCTTGGGGGGCAAAGCTGCCCTGACACTGTCAGGTGTGCAGCCT GAGGACGAGGCTGAGTATTACTGCCTGCTCTACTATGGTGGTGAATCCA TGGAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTATCCATGGAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5921
hsIGL_0101 _V031_J003 _IGLV07- 46- FP_IGLJ3_F	GCCTTGCCAGCCCGCTCAGGTAGCAGTAAGTAACGAGGGTCCAATTCCT AGGCTGTGGTGACTCAGGAGCCCTCACTGACTGTGTCCCCAGGAGGGAC AGTCACTCTCACCTGTGGCTCCAGCACTGGAGCTGTCACCAGTGGTCAT TATCCCTACTGGTTCCAGCAGAAAGCTGGCCAAGCCCCAGGACACTGA TTTATGATACAAGCAACAAACACTCCTGGACACCTGCCCGGTTCTCAGG	SEQ ID NO: 5922

Name	Sequence	SEQ ID NO
	CTCCCTCCTTGGGGGCAAAGCTGCCCTGACCCTTTTGGGTGCGCAGCCT GAGGATGAGGCTGAGTATTACTGCTTGCTCTCCTATAGTGGTGAGTAGC AGTAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTGTAGCAGTAAGTAACGCTGATGGCGCGAGG GAGGC	
hsIGL_0102 _V032_J003 _IGLV08- 61_IGLJ3_F	GCCTTGCCAGCCCGCTCAGATCTTCGTAAGTAACGGAGTGGATTCTCAG ACTGTGGTGACCCAGGAGCCATCGTTCTCAGTGTCCTTGGAGGGACAG TCACACTCACTTGTGGCTTGAGCTCTGGCTCAGTCTCTACTAGTTACTA CCCCAGCTGGTACCAGCAGACCCAGGCCAGGCTCCACGCACGCTCATC TACAGCACAAACACTCGCTCTTCTGGGGTCCCTGATTGCTTCTCTGGCT CCATCCTTGGGAACAAAGCTGCCCTCACCATCACGGGGGCCAGGCAGA TGATGAATCTGATTATTACTGTGTGCTGTATATGGGTAGTGTGAATCTT CGTAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTATCTTCGTAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5923
hsIGL_0103 _V033_J003 _IGLV09- 49_IGLJ3_F	GCCTTGCCAGCCCGCTCAGTCCACAGTAAGTAACGTGACTCAGCCACCT TCTGCATCAGCCTCCCTGGGAGCCTCGGTCACACTCACCTGCACCCTGA GCAGCGGCTACAGTAATTATAAAGTGGACTGGTACCAGCAGAGACCAGG GAAGGGCCCCCGTTGTGATGCGAGTGGGCACTGGTGGGATTGTGGGA TCCAAGGGGGATGGCATCCCTGATCGCTTCTCAGTCTTGGGCTCAGGCC TGAATCGGTACCTGACCATCAAGAACATCCAGGAAGAAGATGAGAGTGA CTACCACTGTGGGGCAGACCATGGCAGTGGGAGCAACTTCGTGATCCAC AGTAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTTCACAGTAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5924
hsIGL_0104 _V034_J003 _IGLV10- 54- FP_IGLJ3_F	GCCTTGCCAGCCCGCTCAGATGACACCAAGTAACGTGTGAGTGGTCCAG GCAGGGCTGACTCAGCCACCCTCGGTCTCCAAGGGCTTGAGACAGACCG CCACACTCACCTGCAGTGGGAACAGCAACAATGTTGGCAACCAAGGAGC AGCTTGGCCTGAGCAGCACCAGGGCCACCCTCCCAAACCTCCTATCCTAC AGGAATAACAACCGGCCCTCAGGGATCTCAGAGAGATTATCTGCATCCA GGTCAGGAAACACAGCCTCCCTGACCATTACTGGACTCCAGCCTGAGGA CGAGGCTGACTATTACTGCTCAGCATGGGACAGCAGCCTCATGAATGAC ACCAAGTAACGGTCGACTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTATGACACCAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5925
hsIGL_0105 _V035_J003	GCCTTGCCAGCCCGCTCAGCTTACGAAAGTAACGCGTGCTGACTCAGC CGCCCTCTCTGTCTGCATCCCCGGGAGCAACAGCCAGACTCCCTGCAC	SEQ ID NO: 5926

Name	Sequence	SEQ ID NO
_IGLV11-55-ORF_IGLJ3_F	CCTGAGCAGTGACCTCAGTGTGGTGGTAAAAACATGTTCTGGTACCAG CAGAAGCCAGGGAGCTCTCCAGGTTATTCCTGTATCACTACTCAGACT CAGACAAGCAGCTGGGACCTGGGGTCCCCAGTCGAGTCTCTGGCTCCAA GGAGACCTCAAGTAACACAGCGTTTTTGTCTATCTCTGGGCTCCAGCCT GAGGACGAGGCCGATTATTACTGCCAGGTGTACGAAAGTAGTGACTTCA CGAAAGTAACGGTCGACTGTTCTGGCGGAGGGACCAAGCTGACCGTCCTA GGTGAGTCTCTTCTCCCTCTCCTTCCCCGCTCTTGGGACAATTTCTGC TGTTTTTGTGTTTCTGTCTTCACGAAAGTAACGCTGATGGCGCGAGG GAGGC	
hsIGL_0106_V001_J004_IGLV01-36_IGLJ4_P	GCCTTGCCAGCCCGCTCAGTAGGAGACGTCTCCTAGGTCCTGGGCCCAG TCTGTGCTGACTCAGCCACCCTCGGTGTCTGAAGCCCCCAGGCAGAGGG TCACCATCTCCTGTTCTGGAAGCAGCTCCAACATCGGAAATAATGCTGT AAACTGGTACCAGCAGCTCCCAGGAAAGGCTCCCAAACCTCCTCATCTAT TATGATGATCTGCTGCCCTCAGGGGTCTCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGA TGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGATGATAGGA GACGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGTAGGAGACGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5927
hsIGL_0107_V002_J004_IGLV01-40_IGLJ4_P	GCCTTGCCAGCCCGCTCAGGTGTCTACGTCTCCTACCTGGGCCCAGTCT GTCGTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCA CCATCTCCTGCACTGGGAGCAGCTCCAACATCGGGGCAGGTTATGATGT ACACTGGTACCAGCAGCTTCCAGGAACAGCCCCCAAACCTCCTCATCTAT GGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGA TGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGATGAGTGTC TACGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGGTGTCTACGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5928
hsIGL_0108_V003_J004_IGLV01-44_IGLJ4_P	GCCTTGCCAGCCCGCTCAGGTACAGTGGTCTCCTAGGTCCTGGGCCCAG TCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGG TCACCATCTCTTGTCTGGAAGCAGCTCCAACATCGGAAGTAATACTGT AAACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAACCTCCTCATCTAT AGTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGA TGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGATGAGTACA GTGGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGGTACAGTGGTCTCCTACTGATGGCGCGAGG	SEQ ID NO: 5929

Name	Sequence	SEQ ID NO
	GAGGC	
hsIGL_0109 _V004_J004 _IGLV01- 47_IGLJ4_P	GCCTTGCCAGCCCGCTCAGGGATCATCGTCTCCTAGGTCCCTGGGCCCAG TCTGTGCTGACTCAGCCACCCCTCAGCGTCTGGGACCCCCGGGCAGAGGG TCACCATCTCTTGTCTGGAAGCAGCTCCAACATCGGAAGTAATTATGT ATACTGGTACCAGCAGCTCCCAGGAACGGCCCCAACTCCTCATCTAT AGTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGGTCCGAGGA TGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGATGAGGATC ATCGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTCGATCTTTGGGATCATCGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5930
hsIGL_0110 _V005_J004 _IGLV01- 50- ORF_IGLJ4_P	GCCTTGCCAGCCCGCTCAGTATTGGCGGTCTCCTACCTGGGCCCAGTCT GTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCA CCATCTCCTGCACTGGGAGCAGCTCCAACATTGGGGCGGGTTATGTTGT ACATTGGTACCAGCAGCTTCCAGGAACAGCCCCAACTCCTCATCTAT GGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCAATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGACTCCAGTCTGAGGA TGAGGCTGATTATTACTGCAAAGCATGGGATAACAGCCTGATGATATTG GCGGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTCGATCTTTGTATTGGCGGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5931
hsIGL_0111 _V006_J004 _IGLV01- 51_IGLJ4_P	GCCTTGCCAGCCCGCTCAGAGGCTTGAGTCTCCTAGGTCCCTGGGCCCAG TCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAGG TCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAATTATGT ATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCAACTCCTCATTTAT GACAATAATAAGCGACCCTCAGGGATTCTTGACCGATTCTCTGGCTCCA AGTCTGGCACGTCAGCCACCCTGGGCATCACCGGACTCCAGACTGGGGA CGAGGCCGATTATTACTGCGGAACATGGGATAGCAGCCTGATGAAGGCT TGAGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTCGATCTTTGAGGCTTGAGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5932
hsIGL_0112 _V007_J004 _IGLV02- 08_IGLJ4_P	GCCTTGCCAGCCCGCTCAGACACACGTGTCTCCTAGTCCTGGGCCCAGT CTGCCCTGACTCAGCCTCCCTCCGCGTCCAGGTCTCCTGGACAGTCAGT CACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATAACTAT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCCAAACATCATGATTT ATGAGGTCAGTAAGCGGCCCTCAGGGGTCCCTGATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGGCTCCAGGCTGAG GATGAGGCTGATTATTACTGCAGCTCATATGCAGGCAGCAATGAACACA	SEQ ID NO: 5933

Name	Sequence	SEQ ID NO
	CGTGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGACACACGTGTCTCCTACTGATGGCGCGAGG GAGGC	
hsIGL_0113 _V008_J004 _IGLV02- 11_IGLJ4_P	GCCTTGCCAGCCCGCTCAGTAGACGGAGTCTCCTAATCCTGGGCTCAGT CTGCCCTGACTCAGCCTCGCTCAGTGTCCGGGTCTCCTGGACAGTCAGT CACCATCTCCTGCACTGGAACACAGCAGTGATGTTGGTGGTTATAACTAT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCAACTCATGATTT ATGATGTCAGTAAGCGGCCCTCAGGGGTCCCTGATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAG GATGAGGCTGATTATTACTGTCTCATATGCAGGCAGCTATGATAGAC GGAGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGTAGACGGAGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5934
hsIGL_0114 _V009_J004 _IGLV02- 14_IGLJ4_P	GCCTTGCCAGCCCGCTCAGCAGCTCTTGTCTCCTAGTCCTGGGCCAGT CTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGAT CACCATCTCCTGCACTGGAACACAGCAGTGATGTTGGGAGTTATAACCTT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCAACTCATGATTT ATGAGGGCAGTAAGCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAG GACGAGGCTGATTATTACTGCAGCTCATATACAAGCAGCAGTGACAGCT CTTGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGCAGCTCTTGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5935
hsIGL_0115 _V010_J004 _IGLV02- 18_IGLJ4_P	GCCTTGCCAGCCCGCTCAGGAGCGATAGTCTCCTAATCCTGGGCTCAGT CTGCCCTGACTCAGCCTCCCTCCGTGTCCGGGTCTCCTGGACAGTCAGT CACCATCTCCTGCACTGGAACACAGCAGTGACGTTGGTAGTTATAACCGT GTCTCCTGGTACCAGCAGCCCCAGGCACAGCCCCAACTCATGATTT ATGAGGTCAGTAATCGGCCCTCAGGGGTCCCTGATCGCTTCTCTGGGTC CAAGTCTGGCAACACGGCCTCCCTGACCACCTCTGGGCTCCAGGCTGAG GACGAGGCTGATTATTACTGCAGCTCATATACAAGCAGCAGTGAGAGCG ATAGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGGAGCGATAGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5936
hsIGL_0116 _V011_J004 _IGLV02- 23_IGLJ4_P	GCCTTGCCAGCCCGCTCAGGCATCTGAGTCTCCTAGTCCTGGGCCAGT CTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGAT CACCATCTCCTGCACTGGAACACAGCAGTGATGTTGGGAGTTATAACCTT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCAACTCATGATTT	SEQ ID NO: 5937

Name	Sequence	SEQ ID NO
	ATGAGGGCAGTAAGCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCCTCCCTGACAATCTCTGGGCTCCAGGCTGAG GACGAGGCTGATTATTACTGCTGCTCATATGCAGGTAGTAGTGAGCATC TGAGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTGATCTTTGGCATCTGAGTCTCCTACTGATGGCGCGAGG GAGGC	
hsIGL_0117 _V012_J004 _IGLV02- 33- ORF_IGLJ4_ P	GCCTTGCCAGCCCGCTCAGTGCTACACGTCTCCTAGTCCTGGGCCCAGT CTGCCCTGACTCAGCCTCCTTTTGTGTCCGGGGCTCCTGGACAGTCGGT CACCATCTCCTGCACTGGAACAGCAGTGACGTTGGGGATTATGATCAT GTCTTCTGGTACCAAAAGCGTCTCAGCACTACCTCCAGACTCCTGATTT ACAATGTCAATACTCGGCCCTTCAGGGATCTCTGACCTCTTCTCAGGCTC CAAGTCTGGCAACATGGCTTCCCTGACCATCTCTGGGCTCAAGTCCGAG GTTGAGGCTAATTATCACTGCAGCTTATATTCAAGTAGTTATGATGCTA CACGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTGATCTTTGTGCTACACGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5938
hsIGL_0118 _V013_J004 _IGLV03- 01_IGLJ4_P	GCCTTGCCAGCCCGCTCAGAACTGCCAGTCTCCTACTCTCCTGTAGGAT CCGTGGCCTCCTATGAGCTGACTCAGCCACCCCTCAGTGTCCTGTCCCC AGGACAGACAGCCAGCATCACCTGCTCTGGAGATAAAATGGGGGATAAA TATGCTTGCTGGTATCAGCAGAAGCCAGGCCAGTCCCTGTGCTGGTCA TCTATCAAGATAGCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGG CTCCAACCTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCT ATGGATGAGGCTGACTATTACTGTGAGGCGTGGGACAGCAGTGAACTG CCAGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTGATCTTTGAACTGCCAGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5939
hsIGL_0119 _V014_J004 _IGLV03- 09- FP_IGLJ4_P	GCCTTGCCAGCCCGCTCAGTTGGACTGGTCTCCTATTTTCTTGACGGTT CTGTGGCCTCCTATGAGCTGACTCAGCCACTCTCAGTGTCAGTGGCCCT GGGACAGGCGGCCAGGATTACCTGTGGGGGAAACAACCTTGATATAAA AATGTGCACTGGTACCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTCA TCTATAGGGATAACAACCGGCCCTCTGGGATCCCTGAGCGATTCTCTGG CTCCAACCTCGGGGAACACGGCCACCCTGACCATCAGCAGAGCCCCAAGCC GGGGATGAGGCTGACTATTACTGTGAGGTGTGGGACAGCAGTGATTGGA CTGGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTGATCTTTGTTGGACTGGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5940
hsIGL_0120	GCCTTGCCAGCCCGCTCAGGTAGACACGTCTCCTATTGCAGTCTCTGAG	SEQ ID NO:

Name	Sequence	SEQ ID NO
_V015_J004 _IGLV03- 10_IGLJ4_P	GCCTCCTATGAGCTGACACAGCCACCCTCGGTGTCAGTGTCCCCAGGAC AAACGGCCAGGATCACCTGCTCTGGAGATGCATTGCCAAAAAATATGC TTATTGGTACCAGCAGAAGTCAGGCCAGGCCCTGTGCTGGTCATCTAT GAGGACAGCAAACGACCCTCCGGGATCCCTGAGAGATTCTCTGGCTCCA GCTCAGGGACAATGGCCACCTTGACTATCAGTGGGGCCCAGGTGGAGGA TGAAGCTGACTACTACTGTTACTCAACAGACAGCAGTGGTATGAGTAGA CACGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGGTAGACACGTCTCCTACTGATGGCGCGAGG GAGGC	5941
hsIGL_0121 _V016_J004 _IGLV03- 12_IGLJ4_P	GCCTTGCCAGCCCGCTCAGCACTGTACGTCTCCTATTGCAGGCTCTGCG ACCTCCTATGAGCTGACTCAGCCACACTCAGTGTGAGTGGCCACAGCAC AGATGGCCAGGATCACCTGTGGGGGAAACAACATTGGAAGTAAAGCTGT GCACTGGTACCAGCAAAAGCCAGGCCAGGACCCTGTGCTGGTCATCTAT AGCGATAGCAACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA ACCCAGGGAACACCGCCACCCTAACCATCAGCAGGATCGAGGCTGGGGA TGAGGCTGACTATTACTGTGAGGTGTGGGACAGTAGTAGTGTGACACTG TACGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGCACTGTACGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5942
hsIGL_0122 _V017_J004 _IGLV03- 16_IGLJ4_P	GCCTTGCCAGCCCGCTCAGGATGATCCGTCTCCTATTGCAGGCTCTGAG GCCTCCTATGAGCTGACACAGCCACCCTCGGTGTCAGTGTCCCTAGGAC AGATGGCCAGGATCACCTGCTCTGGAGAAGCATTGCCAAAAAATATGC TTATTGGTACCAGCAGAAGCCAGGCCAGTTCCCTGTGCTGGTGATATAT AAAGACAGCGAGAGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA GCTCAGGGACAATAGTCACATTGACCATCAGTGGAGTCCAGGCAGAAGA CGAGGCTGACTATTACTGTCTATCAGCAGACAGCAGTGGTATGAGATGA TCCGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGGATGATCCGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5943
hsIGL_0123 _V018_J004 _IGLV03- 19_IGLJ4_P	GCCTTGCCAGCCCGCTCAGCGCCAATAGTCTCCTATTGCAGGTTCTGTG GTTTCTTCTGAGCTGACTCAGGACCCTGCTGTGTCTGTGGCCTTGGGAC AGACAGTCAGGATCACATGCCAAGGAGACAGCCTCAGAAGCTATTATGC AAGCTGGTACCAGCAGAAGCCAGGACAGGCCCTGTACTTGTCTATCTAT GGTAAAAACAACCGGCCCTCAGGGATCCCAGACCGATTCTCTGGCTCCA GCTCAGGAAACACAGCTTCCTTGACCATCACTGGGGCTCAGGCGGAAGA TGAGGCTGACTATTACTGTAACCTCCCGGGACAGCAGTGGTATGACGCCA ATAGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT	SEQ ID NO: 5944

Name	Sequence	SEQ ID NO
	ATTCTGATTTTCGATCTTTGCGCCAATAGTCTCCTACTGATGGCGCGAGG GAGGC	
hsIGL_0124 _V019_J004 _IGLV03- 21_IGLJ4_P	GCCTTGCCAGCCCGCTCAGTCAAGCCTGTCTCCTATTGCAGGCTCTGTG ACCTCCTATGTGCTGACTCAGCCACCCTCAGTGTGAGTGGCCCCAGGAA AGACGGCCAGGATTACCTGTGGGGGAAACAACATTGGAAGTAAAAGTGT GCACTGGTACCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTCATCTAT TATGATAGCGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA ACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAAGCCGGGGA TGAGGCCGACTATTACTGTGCTAGGTGTGGGACAGTAGTAGTGTGATCAAG CCTGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGTCAAGCCTGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5945
hsIGL_0125 _V020_J004 _IGLV03- 22- FP_IGLJ4_P	GCCTTGCCAGCCCGCTCAGACGTGTGTGTCTCCTACCTCTCTGCAGGC TCTGTTGCCCTCCTATGAGCTGACACAGCTACCCTCGGTGTGAGTGTCCC CAGGACAGAAAGCCAGGATCACCTGCTCTGGAGATGTACTGGGGAAAAA TTATGCTGACTGGTACCAGCAGAAGCCAGGCCAGGCCCTGAGTTGGTG ATATACGAAGATAGTGAGCGGTACCCTGGAATCCCTGAACGATTCTCTG GGTCCACCTCAGGGAACACGACCACCCTGACCATCAGCAGGGTCCTGAC CGAAGACGAGGCTGACTATTACTGTTTGTCTGGGAATGAGGTGAACGTG TGTGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGACGTGTGTGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5946
hsIGL_0126 _V021_J004 _IGLV03- 25_IGLJ4_P	GCCTTGCCAGCCCGCTCAGTCCGTCTAGTCTCCTATTGCAGGCTCTGAG GCCTCCTATGAGCTGACACAGCCACCCTCGGTGTGAGTGTCCCCAGGAC AGACGGCCAGGATCACCTGCTCTGGAGATGCATTGCCAAAGCAATATGC TTATTGGTACCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTGATATAT AAAGACAGTGAGAGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA GCTCAGGGACAACAGTCACGTTGACCATCAGTGGAGTCCAGGCAGAAGA TGAGGCTGACTATTACTGTCAATCAGCAGACAGCAGTGGTATGATCCGT CTAGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGTCCGTCTAGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5947
hsIGL_0127 _V022_J004 _IGLV03- 27_IGLJ4_P	GCCTTGCCAGCCCGCTCAGAAGAGCTGGTCTCCTACTTTTCTTGAGTC TCTGTGGCCTCCTATGAGCTGACACAGCCATCCTCAGTGTGAGTGTCTC CGGGACAGACAGCCAGGATCACCTGCTCAGGAGATGTACTGGCAAAAAA ATATGCTCGGTGGTTCCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTG ATTTATAAAGACAGTGAGCGGCCCTCAGGGATCCCTGAGCGATTCTCCG GCTCCAGCTCAGGGACCACAGTCACCTTGACCATCAGCGGGGCCAGGT	SEQ ID NO: 5948

Name	Sequence	SEQ ID NO
	TGAGGATGAGGCTGACTATTACTGTTACTCTGCGGCTGACATGAAAGAG CTGGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGAAGAGCTGGTCTCCTACTGATGGCGCGAGG GAGGC	
hsIGL_0128 _V023_J004 _IGLV04- 03_IGLJ4_P	GCCTTGCCAGCCCGCTCAGTATCGCTCGTCTCCTATGCTGACTCAGCCC CCGTCTGCATCTGCCTTGCTGGGAGCCTCGATCAAGCTCACCTGCACCC TAAGCAGTGAGCACAGCACCTACACCATCGAATGGTATCAACAGAGACC AGGGAGGTCCCCCAGTATATAATGAAGGTTAAGAGTGATGGCAGCCAC AGCAAGGGGGACGGGATCCCCGATCGCTTCATGGGCTCCAGTTCTGGGG CTGACCGCTACCTCACCTTCTCCAACCTCCAGTCTGACGATGAGGCTGA GTATCACTGTGGAGAGAGCCACACGATTGATGGCCAAGTCGTGATATCG CTCGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGTATCGCTCGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5949
hsIGL_0129 _V024_J004 _IGLV04- 60_IGLJ4_P	GCCTTGCCAGCCCGCTCAGTCAGATGCGTCTCCTACTCTCTCCAGCCT GTGCTGACTCAATCATCCTCTGCCTCTGCTTCCCTGGGATCCTCGGTCA AGCTCACCTGCACTCTGAGCAGTGGGCACAGTAGCTACATCATCGCATG GCATCAGCAGCAGCCAGGGAAGGCCCTCGGTACTTGATGAAGCTTGAA GGTAGTGGAAGCTACAACAAGGGGAGCGGAGTTCCTGATCGCTTCTCAG GCTCCAGCTCTGGGGCTGACCGCTACCTCACCATCTCCAACCTCCAGTT TGAGGATGAGGCTGATTATTACTGTGAGACCTGGGACAGTATGATCAGA TGCGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGTGATGCGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5950
hsIGL_0130 _V025_J004 _IGLV04- 69_IGLJ4_P	GCCTTGCCAGCCCGCTCAGGTGTAGCAGTCTCCTACTCTCTCCAGCTT GTGCTGACTCAATCGCCCTCTGCCTCTGCCTCCCTGGGAGCCTCGGTCA AGCTCACCTGCACTCTGAGCAGTGGGCACAGCAGCTACGCCATCGCATG GCATCAGCAGCAGCCAGAGAAGGGCCCTCGGTACTTGATGAAGCTTAAC AGTGATGGCAGCCACAGCAAGGGGGACGGGATCCCTGATCGCTTCTCAG GCTCCAGCTCTGGGGCTGAGCGCTACCTCACCATCTCCAGCCTCCAGTC TGAGGATGAGGCTGACTATTACTGTGAGACCTGGGGCACTGTGAGTGTA GCAGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGGTGTAGCAGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5951
hsIGL_0131 _V026_J004 _IGLV05-	GCCTTGCCAGCCCGCTCAGTGGCAGTTGTCTCCTATGTGCTGACTCAGC CACCTTCCTCCTCCGCATCTCCTGGAGAATCCGCCAGACTCACCTGCAC CTTGCCAGTGACATCAATGTTGGTAGCTACAACATATACTGGTACCAG	SEQ ID NO: 5952

Name	Sequence	SEQ ID NO
37_IGLJ4_P	CAGAAGCCAGGGAGCCCTCCCAGGTATCTCCTGTACTACTACTCAGACT CAGATAAGGGCCAGGGCTCTGGAGTCCCCAGCCGCTTCTCTGGATCCAA AGATGCTTCAGCCAATACAGGGATTTTACTCATCTCCGGGCTCCAGTCT GAGGATGAGGCTGACTATTACTGTATGATTTGGCCAAGCAATGATGGCA GTTGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGTGGCAGTTGTCTCCTACTGATGGCGCGAGG GAGGC	
hsIGL_0132 _V027_J004 _IGLV05- 39_IGLJ4_P	GCCTTGCCAGCCCGCTCAGCAGTCCAAGTCTCCTATGTGCTGACTCAGC CAACCTCCCTCTCAGCATCTCCTGGAGCATCAGCCAGATTACCTGCAC CTTGCGCAGCGGCATCAATGTTGGTACCTACAGGATATACTGGTACCAG CAGAATCCAGGGAGTCTTCCCCGGTATCTCCTGAGGTACAAATCAGACT CAGATAAGCAGCAGGGCTCTGGAGTCCCCAGCCGCTTCTCTGGATCCAA AGATGCTTCAACCAATGCAGGCCTTTTACTCATCTCTGGGCTCCAGTCT GAAGATGAGGCTGACTATTACTGTGCCATTTGGTACAGCAGTGACAGTC CAAGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGCAGTCCAAGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5953
hsIGL_0133 _V028_J004 _IGLV05- 45_IGLJ4_P	GCCTTGCCAGCCCGCTCAGTACGTACGGTCTCCTATGTGCTGACTCAGC CGTCTTCCCTCTCTGCATCTCCTGGAGCATCAGCCAGTCTCACCTGCAC CTTGCGCAGTGGCATCAATGTTGGTACCTACAGGATATACTGGTACCAG CAGAAGCCAGGGAGTCTTCCCCAGTATCTCCTGAGGTACAAATCAGACT CAGATAAGCAGCAGGGCTCTGGAGTCCCCAGCCGCTTCTCTGGATCCAA AGATGCTTCGGCCAATGCAGGGATTTTACTCATCTCTGGGCTCCAGTCT GAGGATGAGGCTGACTATTACTGTATGATTTGGCACAGCAGTGATACGT ACGGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGTACGTACGGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5954
hsIGL_0134 _V029_J004 _IGLV05- 52_IGLJ4_P	GCCTTGCCAGCCCGCTCAGAGTACCGAGTCTCCTATGACTCAGCCATCT TCCCATTCTGCATCTTCTGGAGCATCAGTCAGACTCACCTGCATGCTGA GCAGTGGCTTCAGTGTTGGGGACTTCTGGATAAGGTGGTACCAACAAAA GCCAGGGAACCTCCCCGGTATCTCCTGTACTACCACTCAGACTCCAAT AAGGGCCAAGGCTCTGGAGTTCCAGCCGCTTCTCTGGATCCAACGATG CATCAGCCAATGCAGGGATTCTGCGTATCTCTGGGCTCCAGCCTGAGGA TGAGGCTGACTATTACTGTGGTACATGGCACAGCAACTCTATGAAGTAC CGAGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGAGTACCGAGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5955

Name	Sequence	SEQ ID NO
hsIGL_0135 _V030_J004 _IGLV07- 43_IGLJ4_P	GCCTTGCCAGCCCGCTCAGATCCATGGGTCTCCTAAGGGTCCAATTCTC AGACTGTGGTGACTCAGGAGCCCTCACTGACTGTGTCCCCAGGAGGGAC AGTCACTCTCACCTGTGCTTCCAGCACTGGAGCAGTCACCACTGGTTAC TATCCAACTGGTTCCAGCAGAAACCTGGACAAGCACCCAGGGCACTGA TTTATAGTACAAGCAACAAACACTCCTGGACCCCTGCCCGGTTCTCAGG CTCCCTCCTTGGGGGCAAAGCTGCCCTGACACTGTCAGGTGTGCAGCCT GAGGACGAGGCTGAGTATTACTGCCTGCTCTACTATGGTGGTGAATCCA TGGGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGATCCATGGGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5956
hsIGL_0136 _V031_J004 _IGLV07- 46- FP_IGLJ4_P	GCCTTGCCAGCCCGCTCAGGTAGCAGTGTCTCCTAAGGGTCCAATTCCC AGGCTGTGGTGACTCAGGAGCCCTCACTGACTGTGTCCCCAGGAGGGAC AGTCACTCTCACCTGTGGCTCCAGCACTGGAGCTGTCACCACTGGTCAT TATCCCTACTGGTTCCAGCAGAAGCCTGGCCAAGCCCCCAGGACACTGA TTTATGATACAAGCAACAAACACTCCTGGACACCTGCCCGGTTCTCAGG CTCCCTCCTTGGGGGCAAAGCTGCCCTGACCTTTTGGGTGCGCAGCCT GAGGATGAGGCTGAGTATTACTGCTTGCTCTCCTATAGTGGTGAGTAGC AGTGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGGTAGCAGTGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5957
hsIGL_0137 _V032_J004 _IGLV08- 61_IGLJ4_P	GCCTTGCCAGCCCGCTCAGATCTTCGTGTCTCCTAGAGTGGATTCTCAG ACTGTGGTGACCCAGGAGCCATCGTTCTCAGTGTCCCCTGGAGGGACAG TCACACTCACTTGTGGCTTGAGCTCTGGCTCAGTCTCTACTAGTTACTA CCCCAGCTGGTACCAGCAGACCCAGGCCAGGCTCCACGCACGCTCATC TACAGCACAAACACTCGCTCTTCTGGGGTCCCTGATTGCTTCTCTGGCT CCATCCTTGGGAACAAAGCTGCCCTCACCATCACGGGGGCCAGGCAGA TGATGAATCTGATTATTACTGTGTGCTGTATATGGGTAGTGTGAATCTT CGTGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGATCTTCGTGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5958
hsIGL_0138 _V033_J004 _IGLV09- 49_IGLJ4_P	GCCTTGCCAGCCCGCTCAGTCCACAGTGTCTCCTATGACTCAGCCACCT TCTGCATCAGCCTCCCTGGGAGCCTCGGTCACACTCACCTGCACCCTGA GCAGCGGCTACAGTAATTATAAAGTGGACTGGTACCAGCAGAGACCAGG GAAGGGCCCCCGGTTTGTGATGCGAGTGGGCACTGGTGGGATTGTGGGA TCCAAGGGGGATGGCATCCCTGATCGCTTCTCAGTCTTGGGCTCAGGCC TGAATCGGTACCTGACCATCAAGAACATCCAGGAAGAAGATGAGAGTGA CTACCACTGTGGGGCAGACCATGGCAGTGGGAGCAACTTCGTGATCCAC AGTGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA	SEQ ID NO: 5959

Name	Sequence	SEQ ID NO
	GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGTCCACAGTGTCTCCTACTGATGGCGCGAGG GAGGC	
hsIGL_0139 _V034_J004 _IGLV10- 54- FP_IGLJ4_P	GCCTTGCCAGCCCGCTCAGATGACACCGTCTCCTATGTCAGTGGTCCAG GCAGGGCTGACTCAGCCACCCCTCGGTCTCCAAGGGCTTGAGACAGACCG CCACACTCACCTGCACTGGGAACAGCAACAATGTTGGCAACCAAGGAGC AGCTTGGCCTGAGCAGCACCAGGGCCACCCTCCCAAACCTCCTATCCTAC AGGAATAACAACCGGCCCTCAGGGATCTCAGAGAGATTATCTGCATCCA GGTCAGGAAACACAGCCTCCCTGACCATTACTGGACTCCAGCCTGAGGA CGAGGCTGACTATTACTGCTCAGCATGGGACAGCAGCCTCATGAATGAC ACCGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGATGACACCGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5960
hsIGL_0140 _V035_J004 _IGLV11- 55- ORF_IGLJ4_P	GCCTTGCCAGCCCGCTCAGCTTCACGAGTCTCCTACGTGCTGACTCAGC CGCCCTCTCTGTCTGCATCCCCGGGAGCAACAGCCAGACTCCCCTGCAC CCTGAGCAGTGACCTCAGTGTGGTGGTAAAAACATGTTCTGGTACCAG CAGAAGCCAGGGAGCTCTCCAGGTTATTCCTGTATCACTACTCAGACT CAGACAAGCAGCTGGGACCTGGGGTCCCCAGTCGAGTCTCTGGCTCCAA GGAGACCTCAAGTAACACAGCGTTTTTTGCTCATCTCTGGGCTCCAGCCT GAGGACGAGGCCGATTATTACTGCCAGGTGTACGAAAGTAGTGACTTCA CGAGTCTCCTAGTCGACTATTTGGTGGAGGAACCCAGCTGATCATTTTA GATGAGTCTCTTCTTCCCTTTCTTTCCCTGCCAAGTTGGTGACAATTTT ATTCTGATTTTCGATCTTTGCTTCACGAGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 5961
hsIGL_0141 _V001_J005 _IGLV01- 36_IGLJ5_P	GCCTTGCCAGCCCGCTCAGTAGGAGACAGAGTGTTCGGTCTGGGCCAG TCTGTGCTGACTCAGCCACCCCTCGGTGTCTGAAGCCCCCAGGCAGAGGG TCACCATCTCCTGTTCTGGAAGCAGCTCCAACATCGGAAATAATGCTGT AAACTGGTACCAGCAGCTCCCAGGAAAGGCTCCCAAACCTCCTCATCTAT TATGATGATCTGCTGCCCTCAGGGGTCTCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGA TGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGATGATAGGA GACAGAGTGTGTCGACTGTTTGGTGGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTCTAGGAGACAGAGTGTCCCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5962
hsIGL_0142 _V002_J005 _IGLV01- 40_IGLJ5_P	GCCTTGCCAGCCCGCTCAGGTGTCTACAGAGTGTCCCTGGGCCAGTCT GTCGTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCA CCATCTCCTGCACTGGGAGCAGCTCCAACATCGGGGCAGGTTATGATGT ACACTGGTACCAGCAGCTTCCAGGAACAGCCCCCAAACCTCCTCATCTAT GGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA	SEQ ID NO: 5963

Name	Sequence	SEQ ID NO
	AGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGA TGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGATGAGTGTC TACAGAGTGTCGTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCGTGTCTACAGAGTGTCCTGATGGCGCGAGG GAGGC	
hsIGL_0143 _V003_J005 _IGLV01- 44_IGLJ5_P	GCCTTGCCAGCCCGCTCAGGTACAGTGAGAGTGTCGGTCCTGGGCCAG TCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGG TCACCATCTCTTGTCTGGAAGCAGCTCCAACATCGGAAGTAATACTGT AAACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAACCTCATCTAT AGTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGA TGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGATGAGTACA GTGAGAGTGTCGTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCGTACAGTGAGAGTGTCCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5964
hsIGL_0144 _V004_J005 _IGLV01- 47_IGLJ5_P	GCCTTGCCAGCCCGCTCAGGGATCATCAGAGTGTCGGTCCTGGGCCAG TCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGG TCACCATCTCTTGTCTGGAAGCAGCTCCAACATCGGAAGTAATTATGT ATACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAACCTCATCTAT AGTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGGTCCGAGGA TGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGATGAGGATC ATCAGAGTGTCGTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCGGATCATCAGAGTGTCCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5965
hsIGL_0145 _V005_J005 _IGLV01- 50- ORF_IGLJ5_P	GCCTTGCCAGCCCGCTCAGTATTGGCGAGAGTGTCCTGGGCCAGTCT GTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCA CCATCTCCTGCACTGGGAGCAGCTCCAACATTGGGGCGGGTTATGTTGT ACATTGGTACCAGCAGCTTCCAGGAACAGCCCCCAAACCTCATCTAT GGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCAATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGACTCCAGTCTGAGGA TGAGGCTGATTATTACTGCAAAGCATGGGATAACAGCCTGATGATATTG GCGAGAGTGTCGTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCATTGGCGAGAGTGTCCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5966
hsIGL_0146 _V006_J005	GCCTTGCCAGCCCGCTCAGAGGCTTGAAGAGTGTCGGTCCTGGGCCAG TCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAGG	SEQ ID NO: 5967

Name	Sequence	SEQ ID NO
_IGLV01- 51_IGLJ5_P	TCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAATTATGT ATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCAACTCCTCATTTAT GACAATAATAAGCGACCCCTCAGGGATTCTTGACCGATTCTCTGGCTCCA AGTCTGGCACGTCAGCCACCCTGGGCATCACCGGACTCCAGACTGGGGA CGAGGCCGATTATTACTGCGGAACATGGGATAGCAGCCTGATGAAGGCT TGAAGAGTGTCTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTTCAGGCTTGAAGAGTGTCTGATGGCGCGAGG GAGGC	
hsIGL_0147 _V007_J005 _IGLV02- 08_IGLJ5_P	GCCTTGCCAGCCCGCTCAGACACACGTAGAGTGTCTGCTGGGCCAGT CTGCCCTGACTCAGCCTCCCTCCGCGTCCAGGTCTCCTGGACAGTCAGT CACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATAACTAT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCCAAACATCATGATTT ATGAGGTCAGTAAGCGGCCCTCAGGGGTCCCTGATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGGCTCCAGGCTGAG GATGAGGCTGATTATTACTGCAGCTCATATGCAGGCAGCAATGAACACA CGTAGAGTGTCTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTTCACACACGTAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5968
hsIGL_0148 _V008_J005 _IGLV02- 11_IGLJ5_P	GCCTTGCCAGCCCGCTCAGTAGACGGAAGAGTGTCTCCTGGGCTCAGT CTGCCCTGACTCAGCCTCGCTCAGTGTCCGGGTCTCCTGGACAGTCAGT CACCATCTCCTGCACTGGAACCAGCAGTGATGTTGGTGGTTATAACTAT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCCAAACATCATGATTT ATGATGTCAGTAAGCGGCCCTCAGGGGTCCCTGATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAG GATGAGGCTGATTATTACTGCTGCTCATATGCAGGCAGCTATGATAGAC GGAAGAGTGTCTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCTAGACGGAAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5969
hsIGL_0149 _V009_J005 _IGLV02- 14_IGLJ5_P	GCCTTGCCAGCCCGCTCAGCAGCTCTTAGAGTGTCTGCTGGGCCAGT CTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGAT CACCATCTCCTGCACTGGAACCAGCAGTGATGTTGGGAGTTATAACCTT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCCAAACATCATGATTT ATGAGGGCAGTAAGCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAG GACGAGGCTGATTATTACTGCAGCTCATATACAAGCAGCAGTGACAGCT CTTAGAGTGTCTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCCAGCTCTTAGAGTGTCTGATGGCGCGAGG	SEQ ID NO: 5970

Name	Sequence	SEQ ID NO
	GAGGC	
hsIGL_0150 _V010_J005 _IGLV02- 18_IGLJ5_P	GCCTTGCCAGCCCGCTCAGGAGCGATAAGAGTGTATCCTGGGCTCAGT CTGCCCTGACTCAGCCTCCCTCCGTGTCCGGGTCTCCTGGACAGTCAGT CACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTAGTTATAACCGT GTCTCCTGGTACCAGCAGCCCCCAGGCACAGCCCCAACTCATGATTT ATGAGGTCAGTAATCGGCCCTCAGGGGTCCCTGATCGCTTCTCTGGGTC CAAGTCTGGCAACACGGCCTCCCTGACCACCTCTGGGCTCCAGGCTGAG GACGAGGCTGATTATTACTGCAGCTCATATACAAGCAGCAGTGAGAGCG ATAAGAGTGTGTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCGAGCGATAAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5971
hsIGL_0151 _V011_J005 _IGLV02- 23_IGLJ5_P	GCCTTGCCAGCCCGCTCAGGCATCTGAAGAGTGTCTCCTGGGCCCAGT CTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGAT CACCATCTCCTGCACTGGAACCAGCAGTGATGTTGGGAGTTATAACCTT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCAACTCATGATTT ATGAGGGCAGTAAGCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACAATCTCTGGGCTCCAGGCTGAG GACGAGGCTGATTATTACTGCTGCTCATATGCAGGTAGTAGTGAGCATC TGAAGAGTGTGTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCGCATCTGAAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5972
hsIGL_0152 _V012_J005 _IGLV02- 33- ORF_IGLJ5_P	GCCTTGCCAGCCCGCTCAGTGCTACACAGAGTGTCTCCTGGGCCCAGT CTGCCCTGACTCAGCCTCCTTTTGTGTCCGGGGCTCCTGGACAGTCGGT CACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGGGATTATGATCAT GTCTTCTGGTACCAAAAGCGTCTCAGCACTACCTCCAGACTCCTGATTT ACAATGTCAATACTCGGCCTTCAGGGATCTCTGACCTCTTCTCAGGCTC CAAGTCTGGCAACATGGCTTCCCTGACCATCTCTGGGCTCAAGTCCGAG GTTGAGGCTAATTATCACTGCAGCTTATATTCAAGTAGTTATGATGCTA CACAGAGTGTGTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCGCTACACAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5973
hsIGL_0153 _V013_J005 _IGLV03- 01_IGLJ5_P	GCCTTGCCAGCCCGCTCAGAACTGCCAAGAGTGTCTCCTGATAGGAT CCGTGGCCTCCTATGAGCTGACTCAGCCACCCTCAGTGTCCTGTCCCC AGGACAGACAGCCAGCATCACCTGCTCTGGAGATAAATTGGGGGATAAA TATGCTTGCTGGTATCAGCAGAAGCCAGGCCAGTCCCCGTGCTGGTCA TCTATCAAGATAGCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGG CTCCAACCTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCT ATGGATGAGGCTGACTATTACTGTCAGGCGTGGGACAGCAGTGAACTG	SEQ ID NO: 5974

Name	Sequence	SEQ ID NO
	CCAAGAGTGTCTGTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCAACTGCCAAGAGTGTCTGATGGCGCGAGG GAGGC	
hsIGL_0154 _V014_J005 _IGLV03- 09- FP_IGLJ5_P	GCCTTGCCAGCCCGCTCAGTTGGACTGAGAGTGTCTTTTCTTGCAAGTT CTGTGGCCCTCCTATGAGCTGACTCAGCCACTCTCAGTGTCACTGGCCCT GGGACAGGCGGCCAGGATTACCTGTGGGGGAAACAACCTTGGATATAAA AATGTGCACTGGTACCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTCA TCTATAGGGATAACAACCGGCCCTCTGGGATCCCTGAGCGATTCTCTGG CTCCAACCTCGGGGAACACGGCCACCCTGACCATCAGCAGAGCCCAAGCC GGGGATGAGGCTGACTATTACTGTCAAGTGTGGGACAGCAGTGATTGGA CTGAGAGTGTCTGTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCCTGGACTGAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5975
hsIGL_0155 _V015_J005 _IGLV03- 10_IGLJ5_P	GCCTTGCCAGCCCGCTCAGGTAGACACAGAGTGTCTTGCACTCTCTGAG GCCTCCTATGAGCTGACACAGCCACCCTCGGTGTCACTGTCCCCAGGAC AAACGGCCAGGATCACCTGCTCTGGAGATGCATTGCCAAAAAATATGC TTATTGGTACCAGCAGAAGTCAGGCCAGGCCCTGTGCTGGTCATCTAT GAGGACAGCAAACGACCCTCCGGGATCCCTGAGAGATTCTCTGGCTCCA GCTCAGGGACAATGGCCACCTTGACTATCAGTGGGGCCCAGGTGGAGGA TGAAGCTGACTACTACTGTTACTCAACAGACAGCAGTGGTATGAGTAGA CACAGAGTGTCTGTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCGTAGACACAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5976
hsIGL_0156 _V016_J005 _IGLV03- 12_IGLJ5_P	GCCTTGCCAGCCCGCTCAGCACTGTACAGAGTGTCTTGCAAGCTCTGCG ACCTCCTATGAGCTGACTCAGCCACACTCAGTGTCACTGGCCACAGCAC AGATGGCCAGGATCACCTGTGGGGGAAACAACATTGGAAGTAAAGCTGT GCACTGGTACCAGCAAAGCCAGGCCAGGACCCTGTGCTGGTCATCTAT AGCGATAGCAACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA ACCCAGGGAACACCGCCACCCTAACCATCAGCAGGATCGAGGCTGGGGA TGAGGCTGACTATTACTGTCAAGTGTGGGACAGTAGTAGTGTGACACTG TACAGAGTGTCTGTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCCTACTGTACAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5977
hsIGL_0157 _V017_J005 _IGLV03- 16_IGLJ5_P	GCCTTGCCAGCCCGCTCAGGATGATCCAGAGTGTCTTGCAAGCTCTGAG GCCTCCTATGAGCTGACACAGCCACCCTCGGTGTCACTGTCCCTAGGAC AGATGGCCAGGATCACCTGCTCTGGAGAAGCATTGCCAAAAAATATGC TTATTGGTACCAGCAGAAGCCAGGCCAGTTCCTGTGCTGGTGATATAT	SEQ ID NO: 5978

Name	Sequence	SEQ ID NO
	AAAGACAGCGAGAGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA GCTCAGGGACAATAGTCACATTGACCATCAGTGGAGTCCAGGCAGAAGA CGAGGCTGACTATTACTGTCTATCAGCAGACAGCAGTGGTATGAGATGA TCCAGAGTGTCTGTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCGATGATCCAGAGTGTCTGATGGCGCGAGG GAGGC	
hsIGL_0158 _V018_J005 _IGLV03- 19_IGLJ5_P	GCCTTGCCAGCCCGCTCAGCGCCAATAAGAGTGTCTTGACGGTTCTGTG GTTTCTTCTGAGCTGACTCAGGACCCTGCTGTGTCTGTGGCCTTGGGAC AGACAGTCAGGATCACATGCCAAGGAGACAGCCTCAGAAGCTATTATGC AAGCTGGTACCAGCAGAAGCCAGGACAGGCCCTGTACTTGTCTATCTAT GGTAAAAACAACCGGCCCTCAGGGATCCCAGACCGATTCTCTGGCTCCA GCTCAGGAAACACAGCTTCCTTGACCATCACTGGGGCTCAGGCGGAAGA TGAGGCTGACTATTACTGTAACCTCCCGGGACAGCAGTGGTATGACGCCA ATAAGAGTGTCTGTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCGCCAATAAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5979
hsIGL_0159 _V019_J005 _IGLV03- 21_IGLJ5_P	GCCTTGCCAGCCCGCTCAGTCAAGCCTAGAGTGTCTTGACGGCTCTGTG ACCTCCTATGTGCTGACTCAGCCACCCTCAGTGTGAGTGGCCCCAGGAA AGACGGCCAGGATTACCTGTGGGGGAAACAACATTGGAAGTAAAAGTGT GCACTGGTACCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTCATCTAT TATGATAGCGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA ACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAAGCCGGGGA TGAGGCCGACTATTACTGTGAGGTGTGGGACAGTAGTAGTGTGATCAAG CCTAGAGTGTCTGTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTCTCAAGCCTAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5980
hsIGL_0160 _V020_J005 _IGLV03- 22- FP_IGLJ5_P	GCCTTGCCAGCCCGCTCAGACGTGTGTAGAGTGTCCCTCTCTTGACGGC TCTGTTGCCTCCTATGAGCTGACACAGCTACCCTCGGTGTCAGTGTCCC CAGGACAGAAAGCCAGGATCACCTGCTCTGGAGATGTACTGGGGAAAAA TTATGCTGACTGGTACCAGCAGAAGCCAGGCCAGGCCCTGAGTTGGTG ATATACGAAGATAGTGAGCGGTACCCTGGAATCCCTGAACGATTCTCTG GGTCCACCTCAGGGAACACGACCACCCTGACCATCAGCAGGGTCCTGAC CGAAGACGAGGCTGACTATTACTGTTTGTCTGGGAATGAGGTGAACGTG TGTAAGTGTCTGTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCACGTGTGTAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5981
hsIGL_0161	GCCTTGCCAGCCCGCTCAGTCCGTCTAAGAGTGTCTTGACGGCTCTGAG	SEQ ID NO:

Name	Sequence	SEQ ID NO
_V021_J005 _IGLV03- 25_IGLJ5_P	GCCTCCTATGAGCTGACACAGCCACCTCGGTGTCAGTGTCCCCAGGAC AGACGGCCAGGATCACCTGCTCTGGAGATGCATTGCCAAAGCAATATGC TTATTGGTACCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTGATATAT AAAGACAGTGAGAGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA GCTCAGGGACAACAGTCACGTTGACCATCAGTGGAGTCCAGGCAGAAGA TGAGGCTGACTATTACTGTCAATCAGCAGACAGCAGTGGTATGATCCGT CTAAGAGTGTCGTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTCTCCGTCTAAGAGTGTCTGATGGCGCGAGG GAGGC	5982
hsIGL_0162 _V022_J005 _IGLV03- 27_IGLJ5_P	GCCTTGCCAGCCCGCTCAGAAGAGCTGAGAGTGTCTTTTCTTGCAGTC TCTGTGGCCTCCTATGAGCTGACACAGCCATCCTCAGTGTGAGTGTCTC CGGGACAGACAGCCAGGATCACCTGCTCAGGAGATGTACTGGCAAAAAA ATATGCTCGGTGGTTCCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTG ATTTATAAAGACAGTGAGCGGCCCTCAGGGATCCCTGAGCGATTCTCCG GCTCCAGCTCAGGGACCACAGTCACCTTGACCATCAGCGGGGCCAGGT TGAGGATGAGGCTGACTATTACTGTTACTCTGCGGTGACATGAAAGAG CTGAGAGTGTGTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCAGAGCTGAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5983
hsIGL_0163 _V023_J005 _IGLV04- 03_IGLJ5_P	GCCTTGCCAGCCCGCTCAGTATCGCTCAGAGTGTCTGCTGACTCAGCCC CCGTCTGCATCTGCCTTGCTGGGAGCCTCGATCAAGCTCACCTGCACCC TAAGCAGTGAGCACAGCACCTACACCATCGAATGGTATCAACAGAGACC AGGGAGGTCCCCCAGTATATAATGAAGGTTAAGAGTGATGGCAGCCAC AGCAAGGGGGACGGGATCCCCGATCGCTTCATGGGCTCCAGTTCTGGGG CTGACCGCTACCTCACCTTCTCCAACCTCCAGTCTGACGATGAGGCTGA GTATCACTGTGGAGAGAGCCACACGATTGATGGCCAAGTCGTGATATCG CTCAGAGTGTGTCGTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCATCGCTCAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5984
hsIGL_0164 _V024_J005 _IGLV04- 60_IGLJ5_P	GCCTTGCCAGCCCGCTCAGTCAGATGCAGAGTGTCTCTCTCCAGCCT GTGCTGACTCAATCATCCTCTGCCTCTGCTTCCCTGGGATCCTCGGTCA AGCTCACCTGCACTCTGAGCAGTGGGCACAGTAGCTACATCATCGCATG GCATCAGCAGCAGCCAGGGAAGGCCCTCGGTACTTGATGAAGCTTGAA GGTAGTGGAAGCTACAACAAGGGGAGCGGAGTTCTGATCGCTTCTCAG GCTCCAGCTCTGGGGCTGACCGCTACCTCACCATCTCCAACCTCCAGTT TGAGGATGAGGCTGATTATTACTGTGAGACCTGGGACAGTATGATCAGA TGCAGAGTGTGTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA	SEQ ID NO: 5985

Name	Sequence	SEQ ID NO
	TTTTCTGCTGCTTTTGTTCAGATGCAGAGTGTCTGATGGCGCGAGG GAGGC	
hsIGL_0165 _V025_J005 _IGLV04- 69_IGLJ5_P	GCCTTGCCAGCCCGCTCAGGTGTAGCAAGAGTGTCTCTCTCCAGCTT GTGCTGACTCAATCGCCCTCTGCCTCTGCCTCCCTGGGAGCCTCGGTCA AGCTCACCTGCACTCTGAGCAGTGGGCACAGCAGCTACGCCATCGCATG GCATCAGCAGCAGCCAGAGAAGGGCCCTCGGTACTTGATGAAGCTTAAC AGTGATGGCAGCCACAGCAAGGGGGACGGGATCCCTGATCGCTTCTCAG GCTCCAGCTCTGGGGCTGAGCGCTACCTCACCATCTCCAGCCTCCAGTC TGAGGATGAGGCTGACTATTACTGTCAGACCTGGGGCACTGTGAGTGTA GCAAGAGTGTCTGCTGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCGTGTAGCAAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5986
hsIGL_0166 _V026_J005 _IGLV05- 37_IGLJ5_P	GCCTTGCCAGCCCGCTCAGTGGCAGTTAGAGTGTCTGTGCTGACTCAGC CACCTTCCTCCTCCGCATCTCCTGGAGAATCCGCCAGACTCACCTGCAC CTTGCCAGTGACATCAATGTTGGTAGCTACAACATATACTGGTACCAG CAGAAGCCAGGGAGCCCTCCCAGGTATCTCCTGTACTACTACTCAGACT CAGATAAGGGCCAGGGCTCTGGAGTCCCCAGCCGCTTCTCTGGATCCAA AGATGCTTCAGCCAATACAGGGATTTTACTCATCTCCGGGCTCCAGTCT GAGGATGAGGCTGACTATTACTGTATGATTTGGCCAAGCAATGATGGCA GTTAGAGTGTCTGCTGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCGTGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5987
hsIGL_0167 _V027_J005 _IGLV05- 39_IGLJ5_P	GCCTTGCCAGCCCGCTCAGCAGTCCAAAGAGTGTCTGTGCTGACTCAGC CAACCTCCCTCTCAGCATCTCCTGGAGCATCAGCCAGATTCACCTGCAC CTTGCGCAGCGGCATCAATGTTGGTACCTACAGGATATACTGGTACCAG CAGAATCCAGGGAGTCTTCCCCGGTATCTCCTGAGGTACAAATCAGACT CAGATAAGCAGCAGGGCTCTGGAGTCCCCAGCCGCTTCTCTGGATCCAA AGATGCTTCAACCAATGCAGGCCTTTTACTCATCTCTGGGCTCCAGTCT GAAGATGAGGCTGACTATTACTGTGCCATTTGGTACAGCAGTGACAGTC CAAAGAGTGTCTGCTGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCAGTCCAAAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5988
hsIGL_0168 _V028_J005 _IGLV05- 45_IGLJ5_P	GCCTTGCCAGCCCGCTCAGTACGTACGAGAGTGTCTGTGCTGACTCAGC CGTCTTCCCTCTCTGCATCTCCTGGAGCATCAGCCAGTCTCACCTGCAC CTTGCGCAGTGGCATCAATGTTGGTACCTACAGGATATACTGGTACCAG CAGAAGCCAGGGAGTCTTCCCCAGTATCTCCTGAGGTACAAATCAGACT CAGATAAGCAGCAGGGCTCTGGAGTCCCCAGCCGCTTCTCTGGATCCAA AGATGCTTCGGCCAATGCAGGGATTTTACTCATCTCTGGGCTCCAGTCT	SEQ ID NO: 5989

Name	Sequence	SEQ ID NO
	GAGGATGAGGCTGACTATTACTGTATGATTTGGCACAGCAGTGATACGT ACGAGAGTGTGTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTCTACGTACGAGAGTGTCTGATGGCGCGAGG GAGGC	
hsIGL_0169 _V029_J005 _IGLV05- 52_IGLJ5_P	GCCTTGCCAGCCCGCTCAGAGTACCGAAGAGTGTCTGACTCAGCCATCT TCCCATTCTGCATCTTCTGGAGCATCAGTCAGACTCACCTGCATGCTGA GCAGTGGCTTCAGTGTGGGGACTTCTGGATAAGGTGGTACCAACAAAA GCCAGGGAACCCTCCCCGGTATCTCCTGTACTACCACTCAGACTCCAAT AAGGGCCAAGGCTCTGGAGTTCAGCCGCTTCTCTGGATCCAACGATG CATCAGCCAATGCAGGGATTCTGCGTATCTCTGGGCTCCAGCCTGAGGA TGAGGCTGACTATTACTGTGGTACATGGCACAGCAACTCTATGAAGTAC CGAAGAGTGTGTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCAGTACCGAAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5990
hsIGL_0170 _V030_J005 _IGLV07- 43_IGLJ5_P	GCCTTGCCAGCCCGCTCAGATCCATGGAGAGTGTGAGGGTCCAATTCTC AGACTGTGGTGACTCAGGAGCCCTCACTGACTGTGTCCCCAGGAGGGAC AGTCACTCTCACCTGTGCTTCCAGCACTGGAGCAGTCACCAGTGGTTAC TATCCAAACTGGTTCCAGCAGAAACCTGGACAAGCACCAGGGCACTGA TTTATAGTACAAGCAACAAACACTCCTGGACCCCTGCCCGGTTCTCAGG CTCCCTCCTTGGGGGGCAAAGCTGCCCTGACACTGTGAGGTGTGCAGCCT GAGGACGAGGCTGAGTATTACTGCCTGCTCTACTATGGTGGTGAATCCA TGGAGAGTGTGTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCATCCATGGAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5991
hsIGL_0171 _V031_J005 _IGLV07- 46- FP_IGLJ5_P	GCCTTGCCAGCCCGCTCAGGTAGCAGTAGAGTGTGAGGGTCCAATTCCC AGGCTGTGGTGACTCAGGAGCCCTCACTGACTGTGTCCCCAGGAGGGAC AGTCACTCTCACCTGTGGCTCCAGCACTGGAGCTGTCAACAGTGGTCAT TATCCCTACTGGTTCCAGCAGAAGCCTGGCCAAGCCCCAGGACACTGA TTTATGATACAAGCAACAAACACTCCTGGACACCTGCCCGGTTCTCAGG CTCCCTCCTTGGGGGGCAAAGCTGCCCTGACCCTTTGGGTGCGCAGCCT GAGGATGAGGCTGAGTATTACTGCTTGTCTCTCTATAGTGGTGAGTAGC AGTAGAGTGTGTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCGTAGCAGTAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5992
hsIGL_0172 _V032_J005 _IGLV08-	GCCTTGCCAGCCCGCTCAGATCTTCGTAGAGTGTGAGTGGATTCTCAG ACTGTGGTGACCCAGGAGCCATCGTTCTCAGTGTCCCTGGAGGGACAG TCACACTCACTTGTGGCTTGAGCTCTGGCTCAGTCTCTACTAGTTACTA	SEQ ID NO: 5993

Name	Sequence	SEQ ID NO
61_IGLJ5_P	CCCCAGCTGGTACCAGCAGACCCAGGCCAGGCTCCACGCACGTCATC TACAGCACAAACACTCGCTCTTCTGGGGTCCCTGATTGCTTCTCTGGCT CCATCCTTGGGAACAAAGCTGCCCTCACCATCACGGGGGCCAGGCAGA TGATGAATCTGATTATTACTGTGTGCTGTATATGGGTAGTGTGAATCTT CGTAGAGTGTCTGCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCATCTTCGTAGAGTGTCTGATGGCGCGAGG GAGGC	
hsIGL_0173 _V033_J005 _IGLV09- 49_IGLJ5_P	GCCTTGCCAGCCCGCTCAGTCCACAGTAGAGTGTCTGACTCAGCCACCT TCTGCATCAGCCTCCCTGGGAGCCTCGGTACACTCACCTGCACCCTGA GCAGCGGCTACAGTAATTATAAAGTGGACTGGTACCAGCAGAGACCAGG GAAGGGCCCCCGGTTTGTGATGCGAGTGGGCACCTGGTGGGATTGTGGGA TCCAAGGGGGATGGCATCCCTGATCGCTTCTCAGTCTTGGGCTCAGGCC TGAATCGGTACCTGACCATCAAGAACATCCAGGAAGAAGATGAGAGTGA CTACCACTGTGGGGCAGACCATGGCAGTGGGAGCAACTTCGTGATCCAC AGTAGAGTGTCTGCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCACAGTAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5994
hsIGL_0174 _V034_J005 _IGLV10- 54- FP_IGLJ5_P	GCCTTGCCAGCCCGCTCAGATGACACCAGAGTGTCTGTGAGTGGTCCAG GCAGGGCTGACTCAGCCACCCTCGGTCTCCAAGGGCTTGAGACAGACCG CCACACTCACCTGCACTGGGAACAGCAACAATGTTGGCAACCAAGGAGC AGCTTGGCCTGAGCAGCACCAGGGCCACCCTCCCAAACCTCCTATCCTAC AGGAATAACAACCGGCCCTCAGGGATCTCAGAGAGATTATCTGCATCCA GGTCAGGAAACACAGCCTCCCTGACCATTACTGGACTCCAGCCTGAGGA CGAGGCTGACTATTACTGCTCAGCATGGGACAGCAGCCTCATGAATGAC ACCAGAGTGTCTGTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCATGACACCAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5995
hsIGL_0175 _V035_J005 _IGLV11- 55- ORF_IGLJ5_P	GCCTTGCCAGCCCGCTCAGCTTCACGAAGAGTGTCCGTGCTGACTCAGC CGCCCTCTCTGTCTGCATCCCCGGGAGCAACAGCCAGACTCCCCTGCAC CCTGAGCAGTGACCTCAGTGTGGTGGTAAAAACATGTTCTGGTACCAG CAGAAGCCAGGGAGCTCTCCAGGTTATTCCTGTATCACTACTCAGACT CAGACAAGCAGCTGGGACCTGGGGTCCCCAGTCGAGTCTCTGGCTCCAA GGAGACCTCAAGTAACACAGCGTTTTTGCTCATCTCTGGGCTCCAGCCT GAGGACGAGGCCGATTATTACTGCCAGGTGTACGAAAGTAGTGACTTCA CGAAGAGTGTCTGTCGACTGTTTGGTGAGGGGACGGAGCTGACCGTCCTA GATGAGTCTTTTCCCCCTCCTTCCCTGGTCTCCCCAAGGTACTGGGAAA TTTTCTGCTGCTTTTGTTCCTTCACGAAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5996

Name	Sequence	SEQ ID NO
hsIGL_0176 _V001_J006 _IGLV01- 36_IGLJ6_F	GCCTTGCCAGCCCGCTCAGTAGGAGACGTTCCGAAGGTCCTGGGCCCAG TCTGTGCTGACTCAGCCACCCTCGGTGTCTGAAGCCCCCAGGCAGAGGG TCACCATCTCCTGTTCTGGAAGCAGCTCCAACATCGGAAATAATGCTGT AAACTGGTACCAGCAGCTCCCAGGAAAGGCTCCCAAACCTCCTCATCTAT TATGATGATCTGCTGCCCTCAGGGGTCTCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGA TGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGATGATAGGA GACGTTCCGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCTTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCTTTCTGTAGGAGACGTTCCGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5997
hsIGL_0177 _V002_J006 _IGLV01- 40_IGLJ6_F	GCCTTGCCAGCCCGCTCAGGTGTCTACGTTCCGAACCTGGGCCCAGTCT GTCGTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCA CCATCTCCTGCACTGGGAGCAGCTCCAACATCGGGGCAGGTTATGATGT ACACTGGTACCAGCAGCTTCCAGGAACAGCCCCCAAACCTCCTCATCTAT GGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGA TGAGGCTGATTATTACTGCCAGTCTATGACAGCAGCCTGATGAGTGTCT TACGTTCCGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCTTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCTTTCTGTGTGTCTACGTTCCGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5998
hsIGL_0178 _V003_J006 _IGLV01- 44_IGLJ6_F	GCCTTGCCAGCCCGCTCAGGTACAGTGGTTCCGAAGGTCCTGGGCCCAG TCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGG TCACCATCTCTTGTCTGGAAGCAGCTCCAACATCGGAAGTAATACTGT AAACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAACCTCCTCATCTAT AGTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGA TGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGATGAGTACA GTGGTTCGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCTTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCTTTCTGTGTACAGTGGTTCCGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 5999
hsIGL_0179 _V004_J006 _IGLV01- 47_IGLJ6_F	GCCTTGCCAGCCCGCTCAGGGATCATCGTTCCGAAGGTCCTGGGCCCAG TCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGG TCACCATCTCTTGTCTGGAAGCAGCTCCAACATCGGAAGTAATTATGT ATACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAACCTCCTCATCTAT AGTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGGTCCGAGGA TGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGATGAGGATC ATCGTTCGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTC	SEQ ID NO: 6000

Name	Sequence	SEQ ID NO
	GGTGAGTCCCCTTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCCTTTCTGTGGATCATCGTTCCGAACGATGGCGCGAGG GAGGC	
hsIGL_0180 _V005_J006 _IGLV01- 50- ORF_IGLJ6_ F	GCCTTGCCAGCCCGCTCAGTATTGGCGGTTCCGAACCTGGGCCCAGTCT GTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCA CCATCTCCTGCACTGGGAGCAGCTCCAACATTGGGGCGGGTTATGTTGT ACATTGGTACCAGCAGCTTCCAGGAACAGCCCCAACTCCTCATCTAT GGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCAATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGACTCCAGTCTGAGGA TGAGGCTGATTATTACTGCAAAGCATGGGATAACAGCCTGATGATATTG GCGGTTCCGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCTTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCCTTTCTGTATTATTGGCGGTTCCGAACGATGGCGCGAGG GAGGC	SEQ ID NO: 6001
hsIGL_0181 _V006_J006 _IGLV01- 51_IGLJ6_F	GCCTTGCCAGCCCGCTCAGAGGCTTGAGTTCCGAAGTCTGGGCCCAG TCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAGG TCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAATTATGT ATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCAACTCCTCATTAT GACAATAATAAGCGACCCTCAGGGATTCTTGACCGATTCTCTGGCTCCA AGTCTGGCACGTCAGCCACCCTGGGCATCACCGACTCCAGACTGGGGA CGAGGCCGATTATTACTGCGGAACATGGGATAGCAGCCTGATGAAGGCT TGAGTTCCGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCTTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCCTTTCTGTAGGCTTGAGTTCCGAACGATGGCGCGAGG GAGGC	SEQ ID NO: 6002
hsIGL_0182 _V007_J006 _IGLV02- 08_IGLJ6_F	GCCTTGCCAGCCCGCTCAGACACACGTGTTCCGAAGTCTGGGCCCAGT CTGCCCTGACTCAGCCTCCCTCCGCGTCCAGGTCTCCTGGACAGTCAGT CACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATAACTAT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCAACTCATGATTT ATGAGGTCAGTAAGCGGCCCTCAGGGGTCCCTGATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGGCTCCAGGCTGAG GATGAGGCTGATTATTACTGCAGCTCATATGCAGGCAGCAATGAACACA CGTGTTCGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCTTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCCTTTCTGTACACACGTGTTCCGAACGATGGCGCGAGG GAGGC	SEQ ID NO: 6003
hsIGL_0183 _V008_J006 _IGLV02- 11_IGLJ6_F	GCCTTGCCAGCCCGCTCAGTAGACGGAGTTCCGAAATCCTGGGCTCAGT CTGCCCTGACTCAGCCTCGCTCAGTGTCCGGGTCTCCTGGACAGTCAGT CACCATCTCCTGCACTGGAACCAGCAGTGATGTTGGTGGTTATAACTAT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCAACTCATGATTT ATGATGTCAGTAAGCGGCCCTCAGGGGTCCCTGATCGCTTCTCTGGCTC	SEQ ID NO: 6004

Name	Sequence	SEQ ID NO
	CAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAG GATGAGGCTGATTATTACTGCTGCTCATATGCAGGCAGCTATGATAGAC GGAGTTCCGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCCTTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCCTTTTCTGTTAGACGGAGTTCCGAAGTATGGCGCGAGG GAGGC	
hsIGL_0184 _V009_J006 _IGLV02- 14_IGLJ6_F	GCCTTGCCAGCCCCTCAGCAGCTCTTGTTCGAAGTCCTGGGCCCAGT CTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGAT CACCATCTCCTGCACTGGAACCAGCAGTGATGTTGGGAGTTATAACCTT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCAACTCATGATTT ATGAGGGCAGTAAGCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAG GACGAGGCTGATTATTACTGCAGCTCATATACAAGCAGCAGTGACAGCT CTTGTTCGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCCTTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCCTTTTCTGTGAGCTCTTGTTCGAAGTATGGCGCGAGG GAGGC	SEQ ID NO: 6005
hsIGL_0185 _V010_J006 _IGLV02- 18_IGLJ6_F	GCCTTGCCAGCCCCTCAGGAGCGATAGTTCCGAAATCCTGGGCTCAGT CTGCCCTGACTCAGCCTCCCTCCGTGTCCGGGTCTCCTGGACAGTCAGT CACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTAGTTATAACCGT GTCTCCTGGTACCAGCAGCCCCCAGGCACAGCCCCCAAACCTCATGATTT ATGAGGTCAGTAATCGGCCCTCAGGGGTCCCTGATCGCTTCTCTGGGTC CAAGTCTGGCAACACGGCCTCCCTGACCACCTCTGGGCTCCAGGCTGAG GACGAGGCTGATTATTACTGCAGCTCATATACAAGCAGCAGTGAGAGCG ATAGTTCCGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCCTTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCCTTTTCTGTGAGCGATAGTTCCGAAGTATGGCGCGAGG GAGGC	SEQ ID NO: 6006
hsIGL_0186 _V011_J006 _IGLV02- 23_IGLJ6_F	GCCTTGCCAGCCCCTCAGGCATCTGAGTTCCGAAGTCCTGGGCCCAGT CTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGAT CACCATCTCCTGCACTGGAACCAGCAGTGATGTTGGGAGTTATAACCTT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCAACTCATGATTT ATGAGGGCAGTAAGCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACAATCTCTGGGCTCCAGGCTGAG GACGAGGCTGATTATTACTGCTGCTCATATGCAGGTAGTAGTGAGCATC TGAGTTCCGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCCTTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCCTTTTCTGTGCATCTGAGTTCCGAAGTATGGCGCGAGG GAGGC	SEQ ID NO: 6007
hsIGL_0187 _V012_J006	GCCTTGCCAGCCCCTCAGTGCTACACGTTCCGAAGTCCTGGGCCCAGT CTGCCCTGACTCAGCCTCCTTTTGTGTCCGGGGCTCCTGGACAGTCGGT	SEQ ID NO: 6008

Name	Sequence	SEQ ID NO
_IGLV02-33-ORF_IGLJ6_F	CACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGGGATTATGATCATGTCTTCTGGTACCAAAAAGCGTCTCAGCACTACCTCCAGACTCCTGATTTACAATGTCAATACTCGGCCCTTCAGGGATCTCTGACCTCTTCTCAGGCTCCAAGTCTGGCAACATGGCTTCCCTGACCATCTCTGGGCTCAAGTCCGAGGTTGAGGCTAATTATCACTGCAGCTTATATTCAAGTAGTTATGATGCTACACGTTCCGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTCAGGTGAGTCCCCCTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAGACTTTTCTGTCCTTTCTGTTGCTACACGTTCCGAAGTATGGCGCGAGGGAGGC	
hsIGL_0188_V013_J006_IGLV03-01_IGLJ6_F	GCCTTGCCAGCCCGCTCAGAACTGCCAGTTCCGAAGTCTCCTGTAGGATCCGTGGCCTCCTATGAGCTGACTCAGCCACCCTCAGTGTCCTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAAATTGGGGGATAAAATATGCTTGCTGGTATCAGCAGAAGCCAGGCCAGTCCCCGTGCTGGTCACTATCAAGATAGCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAAGTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGACAGCAGTGAACTGCCAGTCCGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTCAGGTGAGTCCCCCTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAGACTTTTCTGTCCTTTCTGTAACTGCCAGTCCGAAGTATGGCGCGAGGGAGGC	SEQ ID NO: 6009
hsIGL_0189_V014_J006_IGLV03-09-FP_IGLJ6_F	GCCTTGCCAGCCCGCTCAGTTGGACTGGTTCCGAATTTTCTTGCAGGTTCTGTGGCCTCCTATGAGCTGACTCAGCCACTCTCAGTGTCAGTGGCCCTGGGACAGGCGGCCAGGATTACCTGTGGGGGAAACAACCTTGGATATAAAATGTGCACTGGTACCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTCACTATAGGGATAACAACCGGCCCTCTGGGATCCCTGAGCGATTCTCTGGCTCCAAGTCTGGGGAACACGGCCACCCTGACCATCAGCAGAGCCCAAGCCGGGGATGAGGCTGACTATTACTGTCAGGTGTGGGACAGCAGTGATTGGACTGGTTCCGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTCAGGTGAGTCCCCCTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAGACTTTTCTGTCCTTTCTGTTTGGACTGGTTCCGAAGTATGGCGCGAGGGAGGC	SEQ ID NO: 6010
hsIGL_0190_V015_J006_IGLV03-10_IGLJ6_F	GCCTTGCCAGCCCGCTCAGGTAGACACGTTCCGAATTGCAGTCTCTGAGGCCTCCTATGAGCTGACACAGCCACCCTCGGTGTCAGTGTCCTCCAGGACAAACGGCCAGGATCACCTGCTCTGGAGATGCATTGCCAAAAAATATGCTTATTGGTACCAGCAGAAGTCAGGCCAGGCCCTGTGCTGGTCATCTATGAGGACAGCAAACGACCCTCCGGGATCCCTGAGAGATTCTCTGGCTCCAGCTCAGGGACAATGGCCACCTTGACTATCAGTGGGGCCAGGTGGAGGATGAAGCTGACTACTACTGTTACTCAACAGACAGCAGTGGTATGAGTAGACACGTTCCGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTCAGGTGAGTCCCCCTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAGACTTTTCTGTCCTTTCTGTGTAGACACGTTCCGAAGTATGGCGCGAGGGAGGC	SEQ ID NO: 6011

Name	Sequence	SEQ ID NO
	GAGGC	
hsIGL_0191 _V016_J006 _IGLV03- 12_IGLJ6_F	GCCTTGCCAGCCCGCTCAGCACTGTACGTTCCGAATTGCAGGCTCTGCG ACCTCCTATGAGCTGACTCAGCCACACTCAGTGTGAGTGGCCACAGCAC AGATGGCCAGGATCACCTGTGGGGGAAACAACATTGGAAGTAAAGCTGT GCACTGGTACCAGCAAAAGCCAGGCCAGGACCCTGTGCTGGTCATCTAT AGCGATAGCAACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA ACCCAGGGAACACCGCCACCCTAACCATCAGCAGGATCGAGGCTGGGGA TGAGGCTGACTATTACTGTGAGGTGTGGGACAGTAGTAGTGTGACACTG TACGTTCCGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCCTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCCTTTCTGTCACTGTACGTTCCGAAGTATGGCGCGAGG GAGGC	SEQ ID NO: 6012
hsIGL_0192 _V017_J006 _IGLV03- 16_IGLJ6_F	GCCTTGCCAGCCCGCTCAGGATGATCCGTTCCGAATTGCAGGCTCTGAG GCCTCCTATGAGCTGACACAGCCACCCTCGGTGTGAGTGTCCCTAGGAC AGATGGCCAGGATCACCTGCTCTGGAGAAGCATTGCCAAAAAATATGC TTATTGGTACCAGCAGAAGCCAGGCCAGTTCCCTGTGCTGGTGATATAT AAAGACAGCGAGAGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA GCTCAGGGACAATAGTCACATTGACCATCAGTGGAGTCCAGGCAGAAGA CGAGGCTGACTATTACTGTCTATCAGCAGACAGCAGTGGTATGAGATGA TCCGTTCCGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCCTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCCTTTCTGTGATGATCCGTTCCGAAGTATGGCGCGAGG GAGGC	SEQ ID NO: 6013
hsIGL_0193 _V018_J006 _IGLV03- 19_IGLJ6_F	GCCTTGCCAGCCCGCTCAGCGCCAATAGTTCCGAATTGCAGGTTCTGTG GTTTCTTCTGAGCTGACTCAGGACCCTGCTGTGTCTGTGGCCTTGGGAC AGACAGTCAGGATCACATGCCAAGGAGACAGCCTCAGAAGCTATTATGC AAGCTGGTACCAGCAGAAGCCAGGACAGGCCCTGTACTTGTATCTAT GGTAAAAACAACCGGCCCTCAGGGATCCCAGACCGATTCTCTGGCTCCA GCTCAGGAAACACAGCTTCCTTGACCATCACTGGGGCTCAGGCGGAAGA TGAGGCTGACTATTACTGTAACCTCCCGGACAGCAGTGGTATGACGCCA ATAGTTCCGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCCTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCCTTTCTGTGCGCCAATAGTTCCGAAGTATGGCGCGAGG GAGGC	SEQ ID NO: 6014
hsIGL_0194 _V019_J006 _IGLV03- 21_IGLJ6_F	GCCTTGCCAGCCCGCTCAGTCAAGCCTGTTCCGAATTGCAGGCTCTGTG ACCTCCTATGTGCTGACTCAGCCACCCTCAGTGTGAGTGGCCCCAGGAA AGACGGCCAGGATTACCTGTGGGGGAAACAACATTGGAAGTAAAAGTGT GCACTGGTACCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTCATCTAT TATGATAGCGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA ACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAAGCCGGGGA TGAGGCCGACTATTACTGTGAGGTGTGGGACAGTAGTAGTGTGATCAAG	SEQ ID NO: 6015

Name	Sequence	SEQ ID NO
	CCTGTTCCGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCCTTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCCTTTTCTGTTCAAGCCTGTTCCGAAGTATGGCGCGAGG GAGGC	
hsIGL_0195 _V020_J006 _IGLV03- 22- FP_IGLJ6_F	GCCTTGCCAGCCCGCTCAGACGTGTGTGTTCCGAACCTCTCTTGCAGGC TCTGTTGCCCTCCTATGAGCTGACACAGCTACCCTCGGTGTCAGTGTCCC CAGGACAGAAAGCCAGGATCACCTGCTCTGGAGATGTACTGGGGAAAAA TTATGCTGACTGGTACCAGCAGAAGCCAGGCCAGGCCCTGAGTTGGTG ATATACGAAGATAGTGAGCGGTACCCTGGAATCCCTGAACGATTCTCTG GGTCCACCTCAGGGAACACGACCACCCTGACCATCAGCAGGGTCCTGAC CGAAGACGAGGCTGACTATTACTGTTTGTCTGGGAATGAGGTGAACGTG TGTGTTCCGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCCTTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCCTTTTCTGTACGTGTGTGTTCCGAAGTATGGCGCGAGG GAGGC	SEQ ID NO: 6016
hsIGL_0196 _V021_J006 _IGLV03- 25_IGLJ6_F	GCCTTGCCAGCCCGCTCAGTCCGTCTAGTTCCGAATTGCAGGCTCTGAG GCCTCCTATGAGCTGACACAGCCACCCTCGGTGTCAGTGTCCCCAGGAC AGACGGCCAGGATCACCTGCTCTGGAGATGCATTGCCAAAGCAATATGC TTATTGGTACCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTGATATAT AAAGACAGTGAGAGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA GCTCAGGGACAACAGTCACGTTGACCATCAGTGGAGTCCAGGCAGAAGA TGAGGCTGACTATTACTGTCAATCAGCAGACAGCAGTGGTATGATCCGT CTAGTTCCGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCCTTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCCTTTTCTGTTCCGTCTAGTTCCGAAGTATGGCGCGAGG GAGGC	SEQ ID NO: 6017
hsIGL_0197 _V022_J006 _IGLV03- 27_IGLJ6_F	GCCTTGCCAGCCCGCTCAGAAGAGCTGGTTCCGAACCTTTTCTTGCAGTC TCTGTGGCCTCCTATGAGCTGACACAGCCATCCTCAGTGTCAGTGTCTC CGGGACAGACAGCCAGGATCACCTGCTCAGGAGATGTACTGGCAAAAAA ATATGCTCGGTGGTTCCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTG ATTTATAAAGACAGTGAGCGGCCCTCAGGGATCCCTGAGCGATTCTCCG GCTCCAGCTCAGGGACCACAGTCACCTTGACCATCAGCGGGGCCAGGT TGAGGATGAGGCTGACTATTACTGTTACTCTGCGGCTGACATGAAAGAG CTGGTTCCGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCCTTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCCTTTTCTGTAAGAGCTGGTTCCGAAGTATGGCGCGAGG GAGGC	SEQ ID NO: 6018
hsIGL_0198 _V023_J006 _IGLV04- 03_IGLJ6_F	GCCTTGCCAGCCCGCTCAGTATCGCTCGTTCCGAATGCTGACTCAGCCC CCGTCTGCATCTGCCTTGCTGGGAGCCTCGATCAAGCTCACCTGCACCC TAAGCAGTGAGCACAGCACCTACACCATCGAATGGTATCAACAGAGACC AGGGAGGTCCCCCAGTATATAATGAAGGTTAAGAGTGATGGCAGCCAC	SEQ ID NO: 6019

Name	Sequence	SEQ ID NO
	AGCAAGGGGGACGGGATCCCCGATCGCTTCATGGGCTCCAGTTCTGGGG CTGACCGCTACCTCACCTTCTCCAACCTCCAGTCTGACGATGAGGCTGA GTATCACTGTGGAGAGAGCCACACGATTGATGGCCAAGTCGTGATATCG CTCGTTCCGAAGTCGACTGTTCCGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCTTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCCTTTCTGTTATCGCTCGTTCCGAAGTATGGCGCGAGG GAGGC	
hsIGL_0199 _V024_J006 _IGLV04- 60_IGLJ6_F	GCCTTGCCAGCCCGCTCAGTCAGATGCGTTCCGAAGTCTCTCCCAGCCT GTGCTGACTCAATCATCCTCTGCCTCTGCTTCCCTGGGATCCTCGGTCA AGCTCACCTGCACTCTGAGCAGTGGGCACAGTAGCTACATCATCGCATG GCATCAGCAGCAGCCAGGGAAGGCCCTCGGTACTTGATGAAGCTTGAA GGTAGTGGAAGCTACAACAAGGGGAGCGGAGTTCCTGATCGCTTCTCAG GCTCCAGCTCTGGGGCTGACCGCTACCTACCATCTCCAACCTCCAGTT TGAGGATGAGGCTGATTATTACTGTGAGACCTGGGACAGTATGATCAGA TGCGTTCCGAAGTCGACTGTTCCGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCTTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCCTTTCTGTTTCTGATGCGTTCCGAAGTATGGCGCGAGG GAGGC	SEQ ID NO: 6020
hsIGL_0200 _V025_J006 _IGLV04- 69_IGLJ6_F	GCCTTGCCAGCCCGCTCAGGTGTAGCAGTTCCGAAGTCTCTCCCAGCTT GTGCTGACTCAATCGCCCTCTGCCTCTGCCTCCCTGGGAGCCTCGGTCA AGCTCACCTGCACTCTGAGCAGTGGGCACAGCAGCTACGCCATCGCATG GCATCAGCAGCAGCCAGAGAAGGGCCCTCGGTACTTGATGAAGCTTAAC AGTGATGGCAGCCACAGCAAGGGGGACGGGATCCCTGATCGCTTCTCAG GCTCCAGCTCTGGGGCTGAGCGCTACCTACCATCTCCAGCCTCCAGTC TGAGGATGAGGCTGACTATTACTGTGAGACCTGGGGCACTGTGAGTGTA GCAGTTCCGAAGTCGACTGTTCCGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCTTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCCTTTCTGTGTGTAGCAGTTCCGAAGTATGGCGCGAGG GAGGC	SEQ ID NO: 6021
hsIGL_0201 _V026_J006 _IGLV05- 37_IGLJ6_F	GCCTTGCCAGCCCGCTCAGTGGCAGTTGTTCCGAATGTGCTGACTCAGC CACCTTCCTCCTCCGCATCTCCTGGAGAATCCGCCAGACTCACCTGCAC CTTGCCAGTGACATCAATGTTGGTAGCTACAACATATACTGGTACCAG CAGAAGCCAGGGAGCCCTCCCAGGTATCTCCTGTACTACTACTCAGACT CAGATAAGGGCCAGGGCTCTGGAGTCCCCAGCCGCTTCTCTGGATCCAA AGATGCTTCAGCCAATACAGGGATTTTACTCATCTCCGGGCTCCAGTCT GAGGATGAGGCTGACTATTACTGTATGATTTGGCCAAGCAATGATGGCA GTTGTTCCGAAGTCGACTGTTCCGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCTTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCCTTTCTGTTGGCAGTTGTTCCGAAGTATGGCGCGAGG GAGGC	SEQ ID NO: 6022
hsIGL_0202	GCCTTGCCAGCCCGCTCAGCAGTCCAAGTTCCGAATGTGCTGACTCAGC	SEQ ID NO:

Name	Sequence	SEQ ID NO
_V027_J006 _IGLV05- 39_IGLJ6_F	CAACCTCCCTCTCAGCATCTCCTGGAGCATCAGCCAGATTACCTGCAC CTTGCGCAGCGGCATCAATGTTGGTACCTACAGGATATACTGGTACCAG CAGAATCCAGGGAGTCTTCCCCGGTATCTCCTGAGGTACAAATCAGACT CAGATAAGCAGCAGGGCTCTGGAGTCCCCAGCCGCTTCTCTGGATCCAA AGATGCTTCAACCAATGCAGGCCTTTTACTCATCTCTGGGCTCCAGTCT GAAGATGAGGCTGACTATTACTGTGCCATTTGGTACAGCAGTGACAGTC CAAGTTCCGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCTTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCCTTTCTGTGTCAGTCCAAGTTCCGAAGTATGGCGCGAGG GAGGC	6023
hsIGL_0203 _V028_J006 _IGLV05- 45_IGLJ6_F	GCCTTGCCAGCCCGCTCAGTACGTACGGTTCCGAATGTGCTGACTCAGC CGTCTTCCCTCTCTGCATCTCCTGGAGCATCAGCCAGTCTCACCTGCAC CTTGCGCAGTGGCATCAATGTTGGTACCTACAGGATATACTGGTACCAG CAGAAGCCAGGGAGTCTTCCCCAGTATCTCCTGAGGTACAAATCAGACT CAGATAAGCAGCAGGGCTCTGGAGTCCCCAGCCGCTTCTCTGGATCCAA AGATGCTTCGGCCAATGCAGGGATTTTACTCATCTCTGGGCTCCAGTCT GAGGATGAGGCTGACTATTACTGTATGATTTGGCACAGCAGTGATACGT ACGGTTCCGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCTTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCCTTTCTGTGTACGTACGGTTCCGAAGTATGGCGCGAGG GAGGC	SEQ ID NO: 6024
hsIGL_0204 _V029_J006 _IGLV05- 52_IGLJ6_F	GCCTTGCCAGCCCGCTCAGAGTACCGAGTTCCGAATGACTCAGCCATCT TCCCATTTCTGCATCTTCTGGAGCATCAGTCAGACTCACCTGCATGCTGA GCAGTGGCTTCAGTGTTGGGGACTTCTGGATAAGGTGGTACCAACAAAA GCCAGGGAACCCTCCCCGGTATCTCCTGTACTACCACTCAGACTCCAAT AAGGGCCAAGGCTCTGGAGTTCCAGCCGCTTCTCTGGATCCAACGATG CATCAGCCAATGCAGGGATTCTGCGTATCTCTGGGCTCCAGCCTGAGGA TGAGGCTGACTATTACTGTGGTACATGGCACAGCAACTCTATGAAGTAC CGAGTTCCGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCTTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCCTTTCTGTAGTACCGAGTTCCGAAGTATGGCGCGAGG GAGGC	SEQ ID NO: 6025
hsIGL_0205 _V030_J006 _IGLV07- 43_IGLJ6_F	GCCTTGCCAGCCCGCTCAGATCCATGGGTTCCGAAAGGGTCCAATTCTC AGACTGTGGTGACTCAGGAGCCCTCACTGACTGTGTCCCAGGAGGGAC AGTCACTCTCACCTGTGCTTCCAGCACTGGAGCAGTCACCAGTGGTTAC TATCCAAACTGGTTCCAGCAGAAACCTGGACAAGCACCCAGGGCACTGA TTTATAGTACAAGCAACAAACACTCCTGGACCCCTGCCGGTTCTCAGG CTCCCTCCTTGGGGGCAAAGCTGCCCTGACACTGTGTCAGGTGTGCAGCCT GAGGACGAGGCTGAGTATTACTGCCTGCTCTACTATGGTGGTGAATCCA TGGGTTCCGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCTTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG	SEQ ID NO: 6026

Name	Sequence	SEQ ID NO
	ACTTTTCTGTCTTTCTGTATCCATGGGTTCCGAAGTATGGCGCGAGG GAGGC	
hsIGL_0206 _V031_J006 _IGLV07- 46- FP_IGLJ6_F	GCCTTGCCAGCCCGCTCAGGTAGCAGTGTTCGAAAGGGTCCAATTCCC AGGCTGTGGTGACTCAGGAGCCCTCACTGACTGTGTCCCCAGGAGGGAC AGTCACTCTCACCTGTGGCTCCAGCACTGGAGCTGTCACCAGTGGTCAT TATCCCTACTGGTTCCAGCAGAAGCCTGGCCAAGCCCCCAGGACACTGA TTTATGATACAAGCAACAAACACTCCTGGACACCTGCCCGGTTCTCAGG CTCCCTCCTTGGGGGCAAAGCTGCCCTGACCTTTTGGGTGCGCAGCCT GAGGATGAGGCTGAGTATTACTGCTTGCTCTCCTATAGTGGTGAGTAGC AGTGTTCGGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCTTTCTGTGTAGCAGTGTTCGAAGTATGGCGCGAGG GAGGC	SEQ ID NO: 6027
hsIGL_0207 _V032_J006 _IGLV08- 61_IGLJ6_F	GCCTTGCCAGCCCGCTCAGATCTTCGTGTTCCGAAGAGTGGATTCTCAG ACTGTGGTGACCCAGGAGCCATCGTTCTCAGTGTCCCCTGGAGGGACAG TCACACTCACTTGTGGCTTGAGCTCTGGCTCAGTCTCTACTAGTTACTA CCCCAGCTGGTACCAGCAGACCCAGGCCAGGCTCCACGCACGCTCATC TACAGCACAAACACTCGCTCTTCTGGGGTCCCTGATTGCTTCTCTGGCT CCATCCTTGGGAACAAAGCTGCCCTCACCATCACGGGGGCCAGGCAGA TGATGAATCTGATTATTACTGTGTGCTGTATATGGGTAGTGTGAATCTT CGTGTTCGGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCTTTCTGTATCTTCGTGTTCCGAAGTATGGCGCGAGG GAGGC	SEQ ID NO: 6028
hsIGL_0208 _V033_J006 _IGLV09- 49_IGLJ6_F	GCCTTGCCAGCCCGCTCAGTCCACAGTGTTCGAATGACTCAGCCACCT TCTGCATCAGCCTCCCTGGGAGCCTCGGTACACTCACCTGCACCCTGA GCAGCGGTACAGTAATTATAAAGTGGACTGGTACCAGCAGAGACCAGG GAAGGGCCCCCGGTTTGTGATGCGAGTGGGCACTGGTGGGATTGTGGGA TCCAAGGGGGATGGCATCCCTGATCGCTTCTCAGTCTTGGGCTCAGGCC TGAATCGGTACCTGACCATCAAGAACATCCAGGAAGAAGATGAGAGTGA CTACCACTGTGGGGCAGACCATGGCAGTGGGAGCAACTTCGTGATCCAC AGTGTTCGGAAGTCGACTGTTTCGGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCTTTCTGTTCACAGTGTTCGAAGTATGGCGCGAGG GAGGC	SEQ ID NO: 6029
hsIGL_0209 _V034_J006 _IGLV10- 54- FP_IGLJ6_F	GCCTTGCCAGCCCGCTCAGATGACACCGTTCCGAATGTCAGTGGTCCAG GCAGGGCTGACTCAGCCACCCTCGGTCTCCAAGGGCTTGAGACAGACCG CCACACTCACCTGCACTGGGAACAGCAACAATGTTGGCAACCAAGGAGC AGCTTGGCCTGAGCAGCACCAGGGCCACCCTCCCAAACCTCCTATCCTAC AGGAATAACAACCGGCCCTCAGGGATCTCAGAGAGATTATCTGCATCCA GGTCAGGAAACACAGCCTCCCTGACCATTACTGGACTCCAGCCTGAGGA	SEQ ID NO: 6030

Name	Sequence	SEQ ID NO
	CGAGGCTGACTATTACTGCTCAGCATGGGACAGCAGCCTCATGAATGAC ACCGTTCCGAAGTCGACTGTTCCGGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCCTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCCCTTTCTGTATGACACCGTTCCGAAGTATGGCGCGAGG GAGGC	
hsIGL_0210 _V035_J006 _IGLV11- 55- ORF_IGLJ6_ F	GCCTTGCCAGCCCGCTCAGCTTACGAGTTCCGAACGTGCTGACTCAGC CGCCCTCTCTGTCTGCATCCCCGGGAGCAACAGCCAGACTCCCTGACAC CCTGAGCAGTGACCTCAGTGTTGGTGGTAAAAACATGTTCTGGTACCAG CAGAAGCCAGGGAGCTCTCCAGGTTATTCCTGTATCACTACTCAGACT CAGACAAGCAGCTGGGACCTGGGGTCCCCAGTCGAGTCTCTGGCTCCAA GGAGACCTCAAGTAACACAGCGTTTTTGTCTATCTCTGGGCTCCAGCCT GAGGACGAGGCCGATTATTACTGCCAGGTGTACGAAAGTAGTGAATTCA CGAGTTCCGAAGTCGACTGTTCCGGCAGTGGCACCAAGGTGACCGTCCTC GGTGAGTCCCCCTTTCTATTCTTTTGGGTCTAGGGTGAGATCTGGGGAG ACTTTTCTGTCCCTTTCTGTCTTACGAGTTCCGAAGTATGGCGCGAGG GAGGC	SEQ ID NO: 6031
hsIGL_0211 _V001_J007 _IGLV01- 36_IGLJ7_F	GCCTTGCCAGCCCGCTCAGTAGGAGACCGTTACTTGGTCCTGGGCCAG TCTGTGCTGACTCAGCCACCCTCGGTGTCTGAAGCCCCCAGGCAGAGGG TCACCATCTCCTGTTCTGGAAGCAGCTCCAACATCGGAAATAATGCTGT AAACTGGTACCAGCAGCTCCCAGGAAAGGCTCCCAAACCTCCTCATCTAT TATGATGATCTGCTGCCCTCAGGGGTCTCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGA TGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGATGATAGGA GACCGTTACTTGTGCTGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTGTAGGAGACCGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6032
hsIGL_0212 _V002_J007 _IGLV01- 40_IGLJ7_F	GCCTTGCCAGCCCGCTCAGGTGTCTACCGTTACTTCTGGGCCAGTCT GTCGTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCA CCATCTCCTGCACTGGGAGCAGCTCCAACATCGGGGCAGGTTATGATGT ACACTGGTACCAGCAGCTTCCAGGAACAGCCCCCAAACCTCCTCATCTAT GGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGA TGAGGCTGATTATTACTGCCAGTCCATGACAGCAGCCTGATGAGTGTCT TACCGTTACTTGTGCTGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTGTGGTGTCTACCGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6033
hsIGL_0213 _V003_J007 _IGLV01-	GCCTTGCCAGCCCGCTCAGGTACAGTGCCTTACTTGGTCCTGGGCCAG TCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGG TCACCATCTCTGTTCTGGAAGCAGCTCCAACATCGGAAGTAATACTGT	SEQ ID NO: 6034

Name	Sequence	SEQ ID NO
44_IGLJ7_F	AAACTGGTACCAGCAGCTCCCAGGAACGGCCCCAAACTCCTCATCTAT AGTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGA TGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGATGAGTACA GTGCGTTACTTGTGCGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTCTGGTACAGTGCCTTACTTCTGATGGCGCGAGG GAGGC	
hsIGL_0214 _V004_J007 _IGLV01- 47_IGLJ7_F	GCCTTGCCAGCCCGCTCAGGGATCATCCGTTACTTGGTCCTGGGCCCAG TCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCGGGCAGAGGG TCACCATCTCTTGTCTGGAAGCAGCTCCAACATCGGAAGTAATTATGT ATACTGGTACCAGCAGCTCCCAGGAACGGCCCCAAACTCCTCATCTAT AGTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGGTCCGAGGA TGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGATGAGGATC ATCCGTTACTTGTGCGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTCTGGGATCATCCGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6035
hsIGL_0215 _V005_J007 _IGLV01- 50- ORF_IGLJ7_ F	GCCTTGCCAGCCCGCTCAGTATTGGCGCGTTACTTCCTGGGCCCAGTCT GTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCA CCATCTCCTGCACTGGGAGCAGCTCCAACATTGGGGCGGGTTATGTTGT ACATTGGTACCAGCAGCTTCCAGGAACAGCCCCAAACTCCTCATCTAT GGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCAATTCTCTGGCTCCA AGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGACTCCAGTCTGAGGA TGAGGCTGATTATTACTGCAAAGCATGGGATAACAGCCTGATGATATTG GCGCGTTACTTGTGCGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTGTATTGGCGCGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6036
hsIGL_0216 _V006_J007 _IGLV01- 51_IGLJ7_F	GCCTTGCCAGCCCGCTCAGAGGCTTGACGTTACTTGGTCCTGGGCCCAG TCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAGG TCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAATTATGT ATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCAAACTCCTCATTTAT GACAATAATAAGCGACCCTCAGGGATTCTGACCGATTCTCTGGCTCCA AGTCTGGCACGTCAGCCACCCTGGGCATCACC GGACTCCAGACTGGGGA CGAGGCCGATTATTACTGCGGAACATGGGATAGCAGCCTGATGAAGGCT TGACGTTACTTGTGCGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTGAGGCTTGACGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6037

Name	Sequence	SEQ ID NO
hsIGL_0217 _V007_J007 _IGLV02- 08_IGLJ7_F	GCCTTGCCAGCCCGCTCAGACACACGTCGTTACTTGTCTGGGCCCAGT CTGCCCTGACTCAGCCTCCCTCCGCGTCCAGGTCTCCTGGACAGTCAGT CACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATAACTAT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCAACTCATGATTT ATGAGGTCAGTAAGCGGCCCTCAGGGGTCCCTGATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGGCTCCAGGCTGAG GATGAGGCTGATTATTACTGTCAGCTCATATGCAGGCAGCAATGAACACA CGTCGTTACTTGTGCGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTGACACACGTCGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6038
hsIGL_0218 _V008_J007 _IGLV02- 11_IGLJ7_F	GCCTTGCCAGCCCGCTCAGTAGACGGACGTTACTTATCCTGGGCTCAGT CTGCCCTGACTCAGCCTCGCTCAGTGTCCGGGTCTCCTGGACAGTCAGT CACCATCTCCTGCACTGGAACCAGCAGTGATGTTGGTGGTTATAACTAT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCAACTCATGATTT ATGATGTCAGTAAGCGGCCCTCAGGGGTCCCTGATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAG GATGAGGCTGATTATTACTGCTGCTCATATGCAGGCAGCTATGATAGAC GGACGTTACTTGTGCGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTGTAGACGGACGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6039
hsIGL_0219 _V009_J007 _IGLV02- 14_IGLJ7_F	GCCTTGCCAGCCCGCTCAGCAGCTCTTCGTTACTTGTCTGGGCCCAGT CTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGAT CACCATCTCCTGCACTGGAACCAGCAGTGATGTTGGGAGTTATAACCTT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCAACTCATGATTT ATGAGGGCAGTAAGCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAG GACGAGGCTGATTATTACTGTCAGCTCATATACAAGCAGCAGTGACAGCT CTTCGTTACTTGTGCGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTGTCAGCTCTTCGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6040
hsIGL_0220 _V010_J007 _IGLV02- 18_IGLJ7_F	GCCTTGCCAGCCCGCTCAGGAGCGATACGTTACTTATCCTGGGCTCAGT CTGCCCTGACTCAGCCTCCCTCCGTGTCCGGGTCTCCTGGACAGTCAGT CACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTAGTTATAACCGT GTCTCCTGGTACCAGCAGCCCCCAGGCACAGCCCCAACTCATGATTT ATGAGGTCAGTAATCGGCCCTCAGGGGTCCCTGATCGCTTCTCTGGGTC CAAGTCTGGCAACACGGCCTCCCTGACCACCTCTGGGCTCCAGGCTGAG GACGAGGCTGATTATTACTGTCAGCTCATATACAAGCAGCAGTGAGAGCG ATACGTTACTTGTGCGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC	SEQ ID NO: 6041

Name	Sequence	SEQ ID NO
	GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTGAGCGATACGTTACTTCTGATGGCGCGAGG GAGGC	
hsIGL_0221 _V011_J007 _IGLV02- 23_IGLJ7_F	GCCTTGCCAGCCCGCTCAGGCATCTGACGTTACTTGTCTGGGCCCAGT CTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGAT CACCATCTCCTGCACTGGAACCAGCAGTGATGTTGGGAGTTATAACCTT GTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCAACTCATGATTT ATGAGGGCAGTAAGCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTC CAAGTCTGGCAACACGGCCTCCCTGACAATCTCTGGGCTCCAGGCTGAG GACGAGGCTGATTATTACTGTCTCATATGCAGGTAGTAGTGAGCATC TGACGTTACTTGTGCACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTGACATCTGACGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6042
hsIGL_0222 _V012_J007 _IGLV02- 33- ORF_IGLJ7_F	GCCTTGCCAGCCCGCTCAGTGCTACACCGTTACTTGTCTGGGCCCAGT CTGCCCTGACTCAGCCTCCTTTTGTGTCCGGGGCTCCTGGACAGTCGGT CACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGGGATTATGATCAT GTCTTCTGGTACCAAAAGCGTCTCAGCACTACCTCCAGACTCCTGATTT ACAATGTCAATACTCGGCCTTCAGGGATCTCTGACCTCTTCTCAGGCTC CAAGTCTGGCAACATGGCTTCCCTGACCATCTCTGGGCTCAAGTCCGAG GTTGAGGCTAATTATCACTGCAGTTATATTCAAGTAGTTATGATGCTA CACCGTTACTTGTGCACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTGTGCTACACCGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6043
hsIGL_0223 _V013_J007 _IGLV03- 01_IGLJ7_F	GCCTTGCCAGCCCGCTCAGAACTGCCACGTTACTTCTCTCCTGTAGGAT CCGTGGCCTCCTATGAGCTGACTCAGCCACCCTCAGTGTCCTGTCCCC AGGACAGACAGCCAGCATCACCTGCTCTGGAGATAAATTGGGGGATAAA TATGCTTGCTGGTATCAGCAGAAGCCAGGCCAGTCCCCGTGTGCTGGTCA TCTATCAAGATAGCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGG CTCCAACCTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCT ATGGATGAGGCTGACTATTACTGTCTAGGCGTGGGACAGCAGTGAACTG CCACGTTACTTGTGCACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTGAACTGCCACGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6044
hsIGL_0224 _V014_J007 _IGLV03- 09- FP_IGLJ7_F	GCCTTGCCAGCCCGCTCAGTTGGACTGCGTTACTTTTTTCTTGAGGTT CTGTGGCCTCCTATGAGCTGACTCAGCCACTCTCAGTGTCAGTGGCCCT GGGACAGGCGGCCAGGATTACCTGTGGGGGAAACAACCTTGGATATAAA AATGTGCACTGGTACCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTCA TCTATAGGGATAACAACCGGCCCTCTGGGATCCCTGAGCGATTCTCTGG	SEQ ID NO: 6045

Name	Sequence	SEQ ID NO
	CTCCAACTCGGGGAACACGGCCACCCTGACCATCAGCAGAGCCCAAGCC GGGGATGAGGCTGACTATTACTGTGAGGTGTGGGACAGCAGTGATTGGA CTGCGTTACTTGTGCGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCCTGTTGGACTGCGTTACTTCTGATGGCGCGAGG GAGGC	
hsIGL_0225 _V015_J007 _IGLV03- 10_IGLJ7_F	GCCTTGCCAGCCCGCTCAGGTAGACACCGTTACTTTTGCAGTCTCTGAG GCCTCCTATGAGCTGACACAGCCACCCTCGGTGTGAGTGTCCCAGGAC AAACGGCCAGGATCACCTGCTCTGGAGATGCATTGCCAAAAAATATGC TTATTGGTACCAGCAGAAGTCAGGCCAGGCCCTGTGCTGGTCATCTAT GAGGACAGCAAACGACCCTCCGGGATCCCTGAGAGATTCTCTGGCTCCA GCTCAGGGACAATGGCCACCTTGACTATCAGTGGGGCCCAGGTGGAGGA TGAAGCTGACTACTACTGTTACTCAACAGACAGCAGTGGTATGAGTAGA CACCGTTACTTGTGCGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCCTGGTAGACACCGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6046
hsIGL_0226 _V016_J007 _IGLV03- 12_IGLJ7_F	GCCTTGCCAGCCCGCTCAGCACTGTACCGTTACTTTTGCAGGCTCTGCG ACCTCCTATGAGCTGACTCAGCCACACTCAGTGTGAGTGGCCACAGCAC AGATGGCCAGGATCACCTGTGGGGGAAACAACATTGGAAGTAAAGTGT GCACTGGTACCAGCAAAAGCCAGGCCAGGACCCTGTGCTGGTCATCTAT AGCGATAGCAACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA ACCCAGGGAACACCGCCACCCTAACCATCAGCAGGATCGAGGCTGGGGA TGAGGCTGACTATTACTGTGAGGTGTGGGACAGTAGTAGTGTGACACTG TACCGTTACTTGTGCGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCCTGCACTGTACCGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6047
hsIGL_0227 _V017_J007 _IGLV03- 16_IGLJ7_F	GCCTTGCCAGCCCGCTCAGGATGATCCCGTTACTTTTGCAGGCTCTGAG GCCTCCTATGAGCTGACACAGCCACCCTCGGTGTGAGTGTCCCTAGGAC AGATGGCCAGGATCACCTGCTCTGGAGAAGCATTGCCAAAAAATATGC TTATTGGTACCAGCAGAAGCCAGGCCAGTTCCCTGTGCTGGTGATATAT AAAGACAGCGAGAGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA GCTCAGGGACAATAGTCACATTGACCATCAGTGGAGTCCAGGCAGAAGA CGAGGCTGACTATTACTGTCTATCAGCAGACAGCAGTGGTATGAGATGA TCCCGTTACTTGTGCGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCCTGGATGATCCCGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6048
hsIGL_0228 _V018_J007	GCCTTGCCAGCCCGCTCAGCGCCAATACGTTACTTTTGCAGGTTCTGTG GTTTCTTCTGAGCTGACTCAGGACCCTGCTGTGTCTGTGGCCTTGGGAC	SEQ ID NO: 6049

Name	Sequence	SEQ ID NO
_IGLV03- 19_IGLJ7_F	AGACAGTCAGGATCACATGCCAAGGAGACAGCCTCAGAAGCTATTATGC AAGCTGGTACCAGCAGAAGCCAGGACAGGCCCTGTACTTGTCTATCTAT GGTAAAAACAACCGGCCCTCAGGGATCCCAGACCGATTCTCTGGCTCCA GCTCAGGAAACACAGCTTCCTTGACCATCACTGGGGCTCAGGCGGAAGA TGAGGCTGACTATTACTGTAACCCCCGGACAGCAGTGGTATGACGCCA ATACGTTACTTGTCTGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTGCGCCAATACGTTACTTCTGATGGCGCGAGG GAGGC	
hsIGL_0229 _V019_J007 _IGLV03- 21_IGLJ7_F	GCCTTGCCAGCCCGCTCAGTCAAGCCTCGTTACTTTTGCAGGCTCTGTG ACCTCCTATGTGCTGACTCAGCCACCCTCAGTGTCAGTGGCCCCAGGAA AGACGGCCAGGATTACCTGTGGGGGAAACAACATTGGAAGTAAAAGTGT GCACTGGTACCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTCTATCTAT TATGATAGCGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA ACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCAAGCCGGGGA TGAGGCCGACTATTACTGTCTAGGTGTGGGACAGTAGTAGTGTGATCAAG CCTCGTTACTTGTCTGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTGTCAAGCCTCGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6050
hsIGL_0230 _V020_J007 _IGLV03- 22- FP_IGLJ7_F	GCCTTGCCAGCCCGCTCAGACGTGTGTCGTTACTTCCTCTCTTGCAGGC TCTGTTGCCCTCCTATGAGCTGACACAGCTACCCTCGGTGTCAGTGTCCC CAGGACAGAAAGCCAGGATCACCTGCTCTGGAGATGTACTGGGGAAAAA TTATGCTGACTGGTACCAGCAGAAGCCAGGCCAGGCCCTGAGTTGGTG ATATACGAAGATAGTGAGCGGTACCCTGGAATCCCTGAACGATTCTCTG GGTCCACCTCAGGGAACACGACCACCCTGACCATCAGCAGGGTCCTGAC CGAAGACGAGGCTGACTATTACTGTTTGTCTGGGAATGAGGTGAACGTG TGTCGTTACTTGTCTGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTGACGTGTGTCGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6051
hsIGL_0231 _V021_J007 _IGLV03- 25_IGLJ7_F	GCCTTGCCAGCCCGCTCAGTCCGTCTACGTTACTTTTGCAGGCTCTGAG GCCTCCTATGAGCTGACACAGCCACCCTCGGTGTCAGTGTCCCCAGGAC AGACGGCCAGGATCACCTGCTCTGGAGATGCATTGCCAAAGCAATATGC TTATTGGTACCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTGATATAT AAAGACAGTGAGAGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA GCTCAGGGACAACAGTCACGTTGACCATCAGTGGAGTCCAGGCAGAAGA TGAGGCTGACTATTACTGTCAATCAGCAGACAGCAGTGGTATGATCCGT CTACGTTACTTGTCTGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTGTCCGTCTACGTTACTTCTGATGGCGCGAGG	SEQ ID NO: 6052

Name	Sequence	SEQ ID NO
	GAGGC	
hsIGL_0232 _V022_J007 _IGLV03- 27_IGLJ7_F	GCCTTGCCAGCCCGCTCAGAAGAGCTGCGTTACTTCTTTTCTTGCAGTC TCTGTGGCCTCCTATGAGCTGACACAGCCATCCTCAGTGTCACTGTCTC CGGGACAGACAGCCAGGATCACCTGCTCAGGAGATGTACTGGCAAAAAA ATATGCTCGGTGGTTCCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTG ATTTATAAAGACAGTGAGCGGCCCTCAGGGATCCCTGAGCGATTCTCCG GCTCCAGCTCAGGGACCACAGTCACCTTGACCATCAGCGGGGCCAGGT TGAGGATGAGGCTGACTATTACTGTTACTCTGCGGCTGACATGAAAGAG CTGCGTTACTTGTGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTGAAGAGCTGCGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6053
hsIGL_0233 _V023_J007 _IGLV04- 03_IGLJ7_F	GCCTTGCCAGCCCGCTCAGTATCGCTCCGTTACTTTGCTGACTCAGCCC CCGTCTGCATCTGCCTTGCTGGGAGCCTCGATCAAGCTCACCTGCACCC TAAGCAGTGAGCACAGCACCTACACCATCGAATGGTATCAACAGAGACC AGGGAGGTCCCCCAGTATATAATGAAGGTTAAGAGTGATGGCAGCCAC AGCAAGGGGGACGGGATCCCCGATCGCTTCATGGGCTCCAGTTCTGGGG CTGACCGCTACCTCACCTTCTCCAACCTCCAGTCTGACGATGAGGCTGA GTATCACTGTGGAGAGAGCCACACGATTGATGGCCAAGTCGTGATATCG CTCCGTTACTTGTGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTGTATCGCTCCGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6054
hsIGL_0234 _V024_J007 _IGLV04- 60_IGLJ7_F	GCCTTGCCAGCCCGCTCAGTCAGATGCCGTTACTTCTCTCTCCAGCCT GTGCTGACTCAATCATCCTCTGCCTCTGCTTCCCTGGGATCCTCGGTCA AGCTCACCTGCACTCTGAGCAGTGGGCACAGTAGCTACATCATCGCATG GCATCAGCAGCAGCCAGGGAAGGCCCTCGGTACTTGATGAAGCTTGAA GGTAGTGAAGCTACAACAAGGGGAGCGGAGTTCCTGATCGCTTCTCAG GCTCCAGCTCTGGGGCTGACCGCTACCTCACCATCTCCAACCTCCAGTT TGAGGATGAGGCTGATTATTACTGTGAGACCTGGGACAGTATGATCAGA TGCCGTTACTTGTGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTGTATGATGCCGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6055
hsIGL_0235 _V025_J007 _IGLV04- 69_IGLJ7_F	GCCTTGCCAGCCCGCTCAGGTGTAGCACGTTACTTCTCTCTCCAGCTT GTGCTGACTCAATCGCCCTCTGCCTCTGCCTCCCTGGGAGCCTCGGTCA AGCTCACCTGCACTCTGAGCAGTGGGCACAGCAGCTACGCCATCGCATG GCATCAGCAGCAGCCAGAGAAGGGCCCTCGGTACTTGATGAAGCTTAAC AGTGATGGCAGCCACAGCAAGGGGGACGGGATCCCTGATCGCTTCTCAG GCTCCAGCTCTGGGGCTGAGCGCTACCTCACCATCTCCAGCCTCCAGTC TGAGGATGAGGCTGACTATTACTGTGAGACCTGGGGCACTGTGAGTGTA	SEQ ID NO: 6056

Name	Sequence	SEQ ID NO
	GCACGTTACTTGTGCGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTCTGGTGTAGCACGTTACTTCTGATGGCGCGAGG GAGGC	
hsIGL_0236 _V026_J007 _IGLV05- 37_IGLJ7_F	GCCTTGCCAGCCCGCTCAGTGGCAGTTCGTTACTTTGTGCTGACTCAGC CACCTTCCTCCTCCGCATCTCCTGGAGAATCCGCCAGACTCACCTGCAC CTTGCCAGTGACATCAATGTTGGTAGCTACAACATATACTGGTACCAG CAGAAGCCAGGGAGCCCTCCCAGGTATCTCCTGTACTACTACTCAGACT CAGATAAGGGCCAGGGCTCTGGAGTCCCCAGCCGCTTCTCTGGATCCAA AGATGCTTCAGCCAATACAGGGATTTTACTCATCTCCGGGCTCCAGTCT GAGGATGAGGCTGACTATTACTGTATGATTTGGCCAAGCAATGATGGCA GTTTCGTTACTTGTGCGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTCTGTGGCAGTTCGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6057
hsIGL_0237 _V027_J007 _IGLV05- 39_IGLJ7_F	GCCTTGCCAGCCCGCTCAGCAGTCCAACGTTACTTTGTGCTGACTCAGC CAACCTCCCTCTCAGCATCTCCTGGAGCATCAGCCAGATTCACCTGCAC CTTGCGCAGCGGCATCAATGTTGGTACCTACAGGATATACTGGTACCAG CAGAAATCCAGGGAGTCTTCCCCGGTATCTCCTGAGGTACAAATCAGACT CAGATAAGCAGCAGGGCTCTGGAGTCCCCAGCCGCTTCTCTGGATCCAA AGATGCTTCAACCAATGCAGGCCTTTTACTCATCTCTGGGCTCCAGTCT GAAGATGAGGCTGACTATTACTGTGCCATTTGGTACAGCAGTGACAGTC CAACGTTACTTGTGCGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTCTGCAGTCCAACGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6058
hsIGL_0238 _V028_J007 _IGLV05- 45_IGLJ7_F	GCCTTGCCAGCCCGCTCAGTACGTACGCGTTACTTTGTGCTGACTCAGC CGTCTTCCCTCTCTGCATCTCCTGGAGCATCAGCCAGTCTCACCTGCAC CTTGCGCAGTGGCATCAATGTTGGTACCTACAGGATATACTGGTACCAG CAGAAGCCAGGGAGTCTTCCCCAGTATCTCCTGAGGTACAAATCAGACT CAGATAAGCAGCAGGGCTCTGGAGTCCCCAGCCGCTTCTCTGGATCCAA AGATGCTTCGGCCAATGCAGGGATTTTACTCATCTCTGGGCTCCAGTCT GAGGATGAGGCTGACTATTACTGTATGATTTGGCACAGCAGTGATACGT ACGCGTTACTTGTGCGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTCTGTACGTACGCGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6059
hsIGL_0239 _V029_J007 _IGLV05- 52_IGLJ7_F	GCCTTGCCAGCCCGCTCAGAGTACCGACGTTACTTTGACTCAGCCATCT TCCATTCTGCATCTTCTGGAGCATCAGTCAGACTCACCTGCATGCTGA GCAGTGGCTTCAGTGTGGGGACTTCTGGATAAGGTGGTACCAACAAAA GCCAGGGAACCTCCCCGGTATCTCCTGTACTACCACTCAGACTCCAAT	SEQ ID NO: 6060

Name	Sequence	SEQ ID NO
	AAGGGCCAAGGCTCTGGAGTTCCAGCCGCTTCTCTGGATCCAACGATG CATCAGCCAATGCAGGGATTCTGCGTATCTCTGGGCTCCAGCCTGAGGA TGAGGCTGACTATTACTGTGGTACATGGCACAGCAACTCTATGAAGTAC CGACGTTACTTGTGCGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTGAGTACCGACGTTACTTCTGATGGCGCGAGG GAGGC	
hsIGL_0240 _V030_J007 _IGLV07- 43_IGLJ7_F	GCCTTGCCAGCCCGCTCAGATCCATGGCGTTACTTAGGGTCCAATTCTC AGACTGTGGTGACTCAGGAGCCCTCACTGACTGTGTCCCCAGGAGGGAC AGTCACTCTCACCTGTGCTTCCAGCACTGGAGCAGTCACCACTGGTTAC TATCCAAACTGGTTCCAGCAGAAACCTGGACAAGCACCCAGGGCACTGA TTTATAGTACAAGCAACAAACACTCCTGGACCCCTGCCCGGTTCTCAGG CTCCCTCCTTGGGGGGCAAAGCTGCCCTGACACTGTCAGGTGTGCAGCCT GAGGACGAGGCTGAGTATTACTGCCTGCTCTACTATGGTGGTGAATCCA TGCGCTTACTTGTGCGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTGATCCATGGCGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6061
hsIGL_0241 _V031_J007 _IGLV07- 46- FP_IGLJ7_F	GCCTTGCCAGCCCGCTCAGGTAGCAGTCGTTACTTAGGGTCCAATTCCC AGGCTGTGGTGACTCAGGAGCCCTCACTGACTGTGTCCCCAGGAGGGAC AGTCACTCTCACCTGTGGCTCCAGCACTGGAGCTGTCACCACTGGTTCAT TATCCCTACTGGTTCCAGCAGAAGCCTGGCCAAGCCCCCAGGACACTGA TTTATGATACAAGCAACAAACACTCCTGGACACCTGCCCGGTTCTCAGG CTCCCTCCTTGGGGGGCAAAGCTGCCCTGACCCTTTTGGGTGCGCAGCCT GAGGATGAGGCTGAGTATTACTGCTTGCTCTCCTATAGTGGTGAGTAGC AGTCGTTACTTGTGCGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTGGTAGCAGTCGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6062
hsIGL_0242 _V032_J007 _IGLV08- 61_IGLJ7_F	GCCTTGCCAGCCCGCTCAGATCTTCGTCGTTACTTGAGTGGATTCTCAG ACTGTGGTGACCCAGGAGCCATCGTTCTCAGTGTCCCCTGGAGGGACAG TCACACTCACTTGTGGCTTGAGCTCTGGCTCAGTCTCTACTAGTTACTA CCCCAGCTGGTACCAGCAGACCCAGGCCAGGCTCCACGCACGCTCATC TACAGCACAAACACTCGCTCTTCTGGGGTCCCTGATTGCTTCTCTGGCT CCATCCTTGGGAACAAAGCTGCCCTCACCATCACGGGGGGCCAGGCAGA TGATGAATCTGATTATTACTGTGTGCTGTATATGGGTAGTGTGAATCTT CGTCGTTACTTGTGCGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTGATCTTCGTCGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6063
hsIGL_0243	GCCTTGCCAGCCCGCTCAGTCCACAGTCGTTACTTTGACTCAGCCACCT	SEQ ID NO:

Name	Sequence	SEQ ID NO
_V033_J007 _IGLV09- 49_IGLJ7_F	TCTGCATCAGCCTCCCTGGGAGCCTCGGTCACACTCACCTGCACCCTGA GCAGCGGCTACAGTAATTATAAAGTGGACTGGTACCAGCAGAGACCAGG GAAGGGCCCCCGGTTTGTGATGCGAGTGGGCACCTGGTGGGATTGTGGGA TCCAAGGGGGATGGCATCCCTGATCGCTTCTCAGTCTTGGGCTCAGGCC TGAATCGGTACCTGACCATCAAGAACATCCAGGAAGAAGATGAGAGTGA CTACCACTGTGGGGCAGACCATGGCAGTGGGAGCAACTTCGTGATCCAC AGTCGTTACTTGTGCGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTGTCCACAGTCGTTACTTCTGATGGCGCGAGG GAGGC	6064
hsIGL_0244 _V034_J007 _IGLV10- 54- FP_IGLJ7_F	GCCTTGCCAGCCCGCTCAGATGACACCCGTTACTTTGTCAGTGGTCCAG GCAGGGCTGACTCAGCCACCCTCGGTCTCCAAGGGCTTGAGACAGACCG CCACACTCACCTGCACTGGGAACAGCAACAATGTTGGCAACCAAGGAGC AGCTTGGCCTGAGCAGCACCAGGGCCACCCTCCCAAACCTCCTATCCTAC AGGAATAACAACCGGCCCTCAGGGATCTCAGAGAGATTATCTGCATCCA GGTCAGGAAACACAGCCTCCCTGACCATTACTGGACTCCAGCCTGAGGA CGAGGCTGACTATTACTGCTCAGCATGGGACAGCAGCCTCATGAATGAC ACCCGTTACTTGTGCGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTGTGATGACACCCGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6065
hsIGL_0245 _V035_J007 _IGLV11- 55- ORF_IGLJ7_ F	GCCTTGCCAGCCCGCTCAGCTTACGACGTTACTTCGTGCTGACTCAGC CGCCCTCTCTGTCTGCATCCCCGGGAGCAACAGCCAGACTCCCCCTGCAC CCTGAGCAGTGACCTCAGTGTGGTGGTAAAAACATGTTCTGGTACCAG CAGAAGCCAGGGAGCTCTCCCAGGTTATTCCTGTATCACTACTCAGACT CAGACAAGCAGCTGGGACCTGGGGTCCCCAGTCGAGTCTCTGGCTCCAA GGAGACCTCAAGTAACACAGCGTTTTTTGCTCATCTCTGGGCTCCAGCCT GAGGACGAGGCCGATTATTACTGCCAGGTGTACGAAAGTAGTGACTTCA CGACGTTACTTGTGCGACTGTTTCGGAGGAGGCACCCAGCTGACCGTCCTC GGTAAGTCTCCCCGCTTCTCTCCTCTTTGAGATCCCAAGTTAAACACGG GGAGTTTTTCCCTTTCTGTGCTTACGACGTTACTTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6066

Bias Control Sequences for hs-IgK

Name	Sequence	SEQ ID NO
hsIGK_0001 _V001_J001 _IGKV1-05- F_IGKJ1	GCCTTGCCAGCCCGCTCAGGTTCCGAAGACACTCTCCAATCTCAGGTGC CAAATGTGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCCAGTCAGAGTATTAGTA GCTGGTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCCTAAGCTCCT GATCTATAAGGCGTCTAGTTTAGAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGAATTCACCTCTCACCATCAGCAGCCTGCAGC CTGATGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTGAGTTCC GAAGACACTCTGTGACCGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA CGTGAGTAGAATTTAAACTTTGCTTCCTCAGTTGTCTGTGTCTTCTGTT CCCTGTGTCTATGAAGTGAGTTCCGAAGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6067
hsIGK_0002 _V002_J001 _IGKV1-06- F_IGKJ1	GCCTTGCCAGCCCGCTCAGCGTTACTTGACACTCTCCAATCTCAGGTGC CAGATGTGCCATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAA ATGATTTAGGCTGGTATCAGCAGAAACCAGGGAAAGCCCCCTAAGCTCCT GATCTATGCTGCATCCAGTTTACAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGCACAGATTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGTCTACAAGATTACAATTGACGTTA CTTGACACTCTGTGACCGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA CGTGAGTAGAATTTAAACTTTGCTTCCTCAGTTGTCTGTGTCTTCTGTT CCCTGTGTCTATGAAGTGACGTTACTTGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6068
hsIGK_0003 _V003_J001 _IGKV1-08- F_IGKJ1	GCCTTGCCAGCCCGCTCAGTAGGAGACGACACTCTCCAATCTCAGGTGC CAGATGTGCCATCCGGATGACCCAGTCTCCATCCTCATTCCTCTGCATCT ACAGGAGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCA GTTATTTAGCCTGGTATCAGCAAAAACCAGGGAAAGCCCCCTAAGCTCCT GATCTATGCTGCATCCACTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCTGCCTGCAGT CTGAAGATTTTGCAACTTATTACTGTCAACAGTATTATAGTTGATAGGA GACGACACTCTGTGACCGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA CGTGAGTAGAATTTAAACTTTGCTTCCTCAGTTGTCTGTGTCTTCTGTT CCCTGTGTCTATGAAGTGATAGGAGACGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6069
hsIGK_0004 _V004_J001 _IGKV1-09- F_IGKJ1	GCCTTGCCAGCCCGCTCAGGTGTCTACGACACTCTCCAATCTCAGGTGC CAGATGTGACATCCAGTTGACCCAGTCTCCATCCTTCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCCAGTCAGGGCATTAGCA GTTATTTAGCCTGGTATCAGCAAAAACCAGGGAAAGCCCCCTAAGCTCCT GATCTATGCTGCATCCACTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGAATTCACCTCTCACAATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGTCAACAGCTTAATAGTTGAGTGTC	SEQ ID NO: 6070

Name	Sequence	SEQ ID NO
	TACGACACTCTGTGACCGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA CGTGAGTAGAATTTAAACTTTTGCTTCCTCAGTTGTCTGTGTCTTCTGTT CCCTGTGTCTATGAAGTGAGTGTCTACGACACTCTCTGATGGCGCGAGG GAGGC	
hsIGK_0005 _V005_J001 _IGKV1-12- F_IGKJ1	GCCTTGCCAGCCCGCTCAGGTACAGTGGACACTCTCCAATCTCAGGTTT CAGATGCGACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGTGCGGGCGAGTCAGGGTATTAGCA GCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCCTAAGCTCCT GATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAACAGTTGAGTACA GTGGACACTCTGTGACCGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA CGTGAGTAGAATTTAAACTTTTGCTTCCTCAGTTGTCTGTGTCTTCTGTT CCCTGTGTCTATGAAGTGAGTACAGTGGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6071
hsIGK_0006 _V006_J001 _IGKV1-13- FP_IGKJ1	GCCTTGCCAGCCCGCTCAGGGATCATCGACACTCTCCAATCTCAGGTGC CAGATGTGCCATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGCA GTGCTTTAGCCTGATATCAGCAGAAACCAGGGAAAGCTCCTAAGCTCCT GATCTATGATGCCTCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGTCAACAGTTTAATAATTGAGGATC ATCGACACTCTGTGACCGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA CGTGAGTAGAATTTAAACTTTTGCTTCCTCAGTTGTCTGTGTCTTCTGTT CCCTGTGTCTATGAAGTGAGGATCATCGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6072
hsIGK_0007 _V007_J001 _IGKV1-16- F_IGKJ1	GCCTTGCCAGCCCGCTCAGTATTGGCGGACACTCTCCAATCTCAGGTGC CAGATGTGACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGTGCGGGCGAGTCAGGGCATTAGCA ATTATTTAGCCTGGTTTCAGCAGAAACCAGGGAAAGCCCCCTAAGTCCCT GATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAAGTTTCAGC GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTGATATTG GCGGACACTCTGTGACCGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA CGTGAGTAGAATTTAAACTTTTGCTTCCTCAGTTGTCTGTGTCTTCTGTT CCCTGTGTCTATGAAGTGATATTGGCGGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6073
hsIGK_0008 _V008_J001 _IGKV1-17- F_IGKJ1	GCCTTGCCAGCCCGCTCAGAGGCTTGAGACACTCTCCAATCTCAGGTGC CAGGTGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAA ATGATTTAGGCTGGTATCAGCAGAAACCAGGGAAAGCCCCCTAAGCGCCT	SEQ ID NO: 6074

Name	Sequence	SEQ ID NO
	GATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGAATTCACCTCTCACAATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGTCTACAGCATAATAGTTGAAGGCT TGAGACACTCTGTGACCGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA CGTGAGTAGAATTTAAACTTTGCTTCCTCAGTTGTCTGTGTCTTCTGTT CCCTGTGTCTATGAAGTGAAGGCTTGAGACACTCTCTGATGGCGCGAGG GAGGC	
hsIGK_0009 _V009_J001 _IGKV1-27- F_IGKJ1	GCCTTGCCAGCCCGCTCAGACACACGTGACACTCTCTAATATCAGATAC CAGATGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCGAGTCAGGGCATTAGCA ATTATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCT GATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTTTCAGT GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTTGAACACA CGTGACACTCTGTGACCGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA CGTGAGTAGAATTTAAACTTTGCTTCCTCAGTTGTCTGTGTCTTCTGTT CCCTGTGTCTATGAAGTGAACACACGTGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6075
hsIGK_0010 _V010_J001 _IGKV1-33- F_IGKJ1	GCCTTGCCAGCCCGCTCAGTAGACGGAGACACTCTCTAATCGCAGGTGC CAGATGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCAGGCGAGTCAGGACATTAGCA ACTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT GATCTACGATGCATCCAATTTGGAACAGGGGTCCCATCAAGGTTTCAGT GGAAGTGGATCTGGGACAGATTTTACTTTTACCATCAGCAGCCTGCAGC CTGAAGATATTGCAACATATTACTGTCAACAGTATGATAATTGATAGAC GGAGACACTCTGTGACCGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA CGTGAGTAGAATTTAAACTTTGCTTCCTCAGTTGTCTGTGTCTTCTGTT CCCTGTGTCTATGAAGTGATAGACGGAGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6076
hsIGK_0011 _V011_J001 _IGKV1-37- O_IGKJ1	GCCTTGCCAGCCCGCTCAGCAGCTCTTGACACTCTCCAATCTCAGGTGC CAGATGTGACATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGTGAGTCAGGGCATTAGCA GTTATTTAAATTGGTATCGGCAGAAACCAGGGAAAGTTCCTAAGCTCCT GATCTATAGTGCATCCAATTTGCAATCTGGAGTCCCATCTCGGTTTCAGT GGCAGTGGATCTGGGACAGATTTCACTCTCACTATCAGCAGCCTGCAGC CTGAAGATGTTGCAACTTATTACGGTCAACGGACTTACAATTGACAGCT CTTGACACTCTGTGACCGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA CGTGAGTAGAATTTAAACTTTGCTTCCTCAGTTGTCTGTGTCTTCTGTT CCCTGTGTCTATGAAGTGACAGCTCTTGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6077
hsIGK_0012	GCCTTGCCAGCCCGCTCAGGAGCGATAGACACTCTCCAATCTCAGGTGC	SEQ ID NO:

Name	Sequence	SEQ ID NO
_V012_J001 _IGKV1-39- FP_IGKJ1	CAGATGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGAGCATTAGCA GCTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT GATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAAGT GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAAC CTGAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTTGAGAGCG ATAGACACTCTGTGACCGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA CGTGAGTAGAATTTAAACTTTGCTTCCTCAGTTGTCTGTGTCTTCTGTT CCCTGTGTCTATGAAGTGAGAGCGATAGACACTCTCTGATGGCGCGAGG GAGGC	6078
hsIGK_0013 _V013_J001 _IGKV1- NL1- F_IGKJ1	GCCTTGCCAGCCCGCTCAGGCATCTGAGACACTCTCCAATCTCAGGTAC CAGATGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCGAGTCAGGGCATTAGCA ATTCTTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT GCTCTATGCTGCATCCAGATTGGAAAGTGGGGTCCCATCCAGGTTCAAGT GGCAGTGGATCTGGGACGGATTACACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGTCAACAGTATTATAGTTGAGCATC TGAGACACTCTGTGACCGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA CGTGAGTAGAATTTAAACTTTGCTTCCTCAGTTGTCTGTGTCTTCTGTT CCCTGTGTCTATGAAGTGAGCATCTGAGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6079
hsIGK_0014 _V014_J001 _IGKV2-24- F_IGKJ1	GCCTTGCCAGCCCGCTCAGTGCTACACGACACTCTAGTGGGGATATTGT GATGACCCAGACTCCACTCTCCTCACCTGTCACCCCTGGACAGCCGGCC TCCATCTCCTGCAGGTCTAGTCAAAGCCTCGTACACAGTGATGGAAACA CCTACTTGAGTTGGCTTCAGCAGAGGCCAGGCCAGCCTCCAAGACTCCT AATTTATAAGATTTCTAACCGGTTCTCTGGGGTCCCAGACAGATTCAAGT GGCAGTGGGGCAGGGACAGATTTCACTGAAAATCAGCAGGGTGGAAAG CTGAGGATGTCGGGGTTTATTACTGCATGCAAGCTACACAATGATGCTA CACGACACTCTGTGACCGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA CGTGAGTAGAATTTAAACTTTGCTTCCTCAGTTGTCTGTGTCTTCTGTT CCCTGTGTCTATGAAGTGATGCTACACGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6080
hsIGK_0015 _V015_J001 _IGKV2-28- F_IGKJ1	GCCTTGCCAGCCCGCTCAGAACTGCCAGACACTCTAGTGGGGATATTGT GATGACTCAGTCTCCACTCTCCCTGCCCCGTACCCCTGGAGAGCCGGCC TCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACA ACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCT GATCTATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTCAAGT GGCAGTGGATCAGGCACAGATTTTCACTGAAAATCAGCAGAGTGGAGG CTGAGGATGTTGGGGTTTATTACTGCATGCAAGCTCTACAATGAAACTG CCAGACACTCTGTGACCGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA CGTGAGTAGAATTTAAACTTTGCTTCCTCAGTTGTCTGTGTCTTCTGTT	SEQ ID NO: 6081

Name	Sequence	SEQ ID NO
	CCCTGTGTCTATGAAGTGAACTGCCAGACACTCTCTGATGGCGCGAGG GAGGC	
hsIGK_0016 _V016_J001 _IGKV2-29- FP_IGKJ1	GCCTTGCCAGCCCGCTCAGTTGGACTGGACACTCTAGTGCGGATATTGT GATGACCCAGACTCCACTCTCTGTCCGTCACCCCTGGACAGCCGGCC TCCATCTCCTGCAAGTCTAGTCAGAGCCTCCTGCATAGTGATGGAAAGA CCTATTTGTATTGGTACCTGCAGAAGCCAGGCCAGTCTCCACAGCTCCT GATCTATGAAGTTTCCAGCCGGTTCTCTGGAGTGCCAGATAGGTTTCAGT GGCAGCGGGTCAGGGACAGATTTCACTGAAAATCAGCCGGGTGGAGG CTGAGGATGTTGGGGTTTATTACTGAATGCAAGGTATACACTGATTGGA CTGGACACTCTGTGACCGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA CGTGAGTAGAATTTAACTTTGCTTCCTCAGTTGTCTGTGTCTTCTGTT CCCTGTGTCTATGAAGTGATTGGACTGGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6082
hsIGK_0017 _V017_J001 _IGKV2-30- F_IGKJ1	GCCTTGCCAGCCCGCTCAGGTAGACACGACACTCTAGTGGGGATGTTGT GATGACTCAGTCTCCACTCTCCCTGCCCCTCACCCCTGGACAGCCGGCC TCCATCTCCTGCAGGTCTAGTCAAAGCCTCGTATACAGTGATGGAAACA CCTACTTGAATTGGTTTTCAGCAGAGGCCAGGCCAATCTCCAAGGCGCCT AATTTATAAGGTTTCTAACCGGGACTCTGGGGTCCCAGACAGATTTCAGC GGCAGTGGGTCAGGCACTGATTTCACTGAAAATCAGCAGGGTGGAGG CTGAGGATGTTGGGGTTTATTACTGCATGCAAGGTACACACTGAGTAGA CACGACACTCTGTGACCGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA CGTGAGTAGAATTTAACTTTGCTTCCTCAGTTGTCTGTGTCTTCTGTT CCCTGTGTCTATGAAGTGAGTAGACACGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6083
hsIGK_0018 _V018_J001 _IGKV2-40- F_IGKJ1	GCCTTGCCAGCCCGCTCAGCACTGTACGACACTCTGAGGATATTGTGAT GACCCAGACTCCACTCTCCCTGCCCCTCACCCCTGGAGAGCCGGCCTCC ATCTCCTGCAGGTCTAGTCAGAGCCTCTTGGATAGTGATGATGGAAACA CCTATTTGGACTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCT GATCTATACGCTTTCTATCGGGCCTCTGGAGTCCCAGACAGGTTTCAGT GGCAGTGGGTCAGGCACTGATTTCACTGAAAATCAGCAGGGTGGAGG CTGAGGATGTTGGAGTTTATTACTGCATGCAACGTATAGAGTGACACTG TACGACACTCTGTGACCGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA CGTGAGTAGAATTTAACTTTGCTTCCTCAGTTGTCTGTGTCTTCTGTT CCCTGTGTCTATGAAGTGACACTGTACGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6084
hsIGK_0019 _V019_J001 _IGKV3-07- F_IGKJ1	GCCTTGCCAGCCCGCTCAGGATGATCCGACACTCTATCTCAGATACCAC CGGAGAAATTGTAATGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCA GGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTATCCTGGTACCAGCAGAAACCTGGGCAGGCTCCCAGGCTCCT CATCTATGGTGCATCCACCAGGGCCACTGGCATCCCAGCCAGGTTTCAGT GGCAGTGGGTCTGGGACAGACTTCACTCTACCATCAGCAGCCTGCAGC	SEQ ID NO: 6085

Name	Sequence	SEQ ID NO
	CTGAAGATTTTGCAGTTTATTACTGTCAGCAGGATTATAACTGAGATGA TCCGACACTCTGTGACCGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA CGTGAGTAGAATTTAACTTTGCTTCCTCAGTTGTCTGTGTCTTCTGTT CCCTGTGTCTATGAAGTGAGATGATCCGACACTCTCTGATGGCGCGAGG GAGGC	
hsIGK_0020 _V020_J001 _IGKV3-11- F_IGKJ1	GCCTTGCCAGCCCGCTCAGCGCCAATAGACACTCTCCAATTTTCAGATAC CACCGGAGAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCT CCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTAGCA GCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTTCAGT GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGC CTGAAGATTTTGCAGTTTATTACTGTCAGCAGCGTAGCAACTGACGCCA ATAGACACTCTGTGACCGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA CGTGAGTAGAATTTAACTTTGCTTCCTCAGTTGTCTGTGTCTTCTGTT CCCTGTGTCTATGAAGTGACGCCAATAGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6086
hsIGK_0021 _V021_J001 _IGKV3-15- F_IGKJ1	GCCTTGCCAGCCCGCTCAGTCAAGCCTGACACTCTCCAATTTTCAGATAC CACTGGAGAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTAGCA GCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTTCAGT GGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGT CTGAAGATTTTGCAGTTTATTACTGTCAGCAGTATAATAACTGATCAAG CCTGACACTCTGTGACCGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA CGTGAGTAGAATTTAACTTTGCTTCCTCAGTTGTCTGTGTCTTCTGTT CCCTGTGTCTATGAAGTGATCAAGCCTGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6087
hsIGK_0022 _V022_J001 _IGKV3-20- F_IGKJ1	GCCTTGCCAGCCCGCTCAGACGTGTGTGACACTCTATCTCAGATACCAC CGGAGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCA GGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTTCAGT GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGC CTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTGAACGTG TGTGACACTCTGTGACCGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA CGTGAGTAGAATTTAACTTTGCTTCCTCAGTTGTCTGTGTCTTCTGTT CCCTGTGTCTATGAAGTGAACGTGTGTGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6088
hsIGK_0023 _V023_J001 _IGKV3-	GCCTTGCCAGCCCGCTCAGTCCGTCTAGACACTCTCCAATTTTCAGATAC CACCGGAGAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCT CCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGGGTGTAGCA	SEQ ID NO: 6089

Name	Sequence	SEQ ID NO
NL4- FNG_IGKJ1	GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTTCAGT GGCAGTGGGCCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGC CTGAAGATTTTGCAGTTTATTACTGTCTCAGCAGCGTAGCAACTGATCCGT CTAGACACTCTGTCTGACCGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA CGTGAGTAGAATTTAAACTTTTGCTTCCTCAGTTGTCTGTGTCTTCTGTT CCCTGTGTCTATGAAGTGATCCGTCTAGACACTCTCTGATGGCGCGAGG GAGGC	
hsIGK_0024 _V024_J001 _IGKV4-01- F_IGKJ1	GCCTTGCCAGCCCGCTCAGAAGAGCTGGACACTCTGGGGACATCGTGAT GACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGA ACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCT CATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTTCAGT GGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGG CTGAAGATGTGGCAGTTTATTACTGTCTCAGCAATATTATAGTTGAAAAGAG CTGGACACTCTGTCTGACCGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA CGTGAGTAGAATTTAAACTTTTGCTTCCTCAGTTGTCTGTGTCTTCTGTT CCCTGTGTCTATGAAGTGAAAGAGCTGGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6090
hsIGK_0025 _V025_J001 _IGKV5-02- F_IGKJ1	GCCTTGCCAGCCCGCTCAGTATCGCTCGACACTCTCCATAATCAGATAC CAGGGCAGAAACGACACTCACGCAGTCTCCAGCATTCATGTCTCAGCGACT CCAGGAGACAAAGTCAACATCTCCTGCAAAGCCAGCCAAGACATTGATG ATGATATGAAGTGGTACCAACAGAAACCAGGAGAAGCTGCTATTTTCAT TATTCAGAAGCTACTACTCTCGTTCCCTGGAATCCACCTCGATTTCAGT GGCAGCGGGTATGGAACAGATTTTACCCTCACAATTAATAACATAGAAT CTGAGGATGCTGCATATTACTTCTGTCTACAACATGATAATTGATATCG CTCGACACTCTGTCTGACCGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA CGTGAGTAGAATTTAAACTTTTGCTTCCTCAGTTGTCTGTGTCTTCTGTT CCCTGTGTCTATGAAGTGATATCGCTCGACACTCTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6091
hsIGK_0026 _V001_J002 _IGKV1-05- F_IGKJ2	GCCTTGCCAGCCCGCTCAGGTTCCGAATTCGGAACCCAATCTCAGGTGC CAAATGTGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCCAGTCAGAGTATTAGTA GCTGGTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT GATCTATAAGGCGTCTAGTTTAGAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGAATTCACCTCTCACCATCAGCAGCCTGCAGC CTGATGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTGAGTTCC GAATTCGGAACGTCGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGTAAGTACTTTTTTCCACTGATTCTTCACTGTTGCTAATTAGTTTAC TTTGTGTTCCCTTTGTGTGGGTTCGGAATTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6092

Name	Sequence	SEQ ID NO
hsIGK_0027 _V002_J002 _IGKV1-06- F_IGKJ2	GCCTTGCCAGCCCGCTCAGCGTTACTTTTCGGAACCCAATCTCAGGTGC CAGATGTGCCATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAA ATGATTTAGGCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT GATCTATGCTGCATCCAGTTTACAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGCACAGATTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGTCTACAAGATTACAATTGACGTTA CTTTTCGGAACGTCGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGTAAGTACTTTTTTCCACTGATTCTTCACTGTTGCTAATTAGTTTAC TTTGTGTTCCCTTTGTGTGGCGTTACTTTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6093
hsIGK_0028 _V003_J002 _IGKV1-08- F_IGKJ2	GCCTTGCCAGCCCGCTCAGTAGGAGACTTCGGAACCCAATCTCAGGTGC CAGATGTGCCATCCGGATGACCCAGTCTCCATCCTCATTCTCTGCATCT ACAGGAGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCA GTTATTTAGCCTGGTATCAGCAAAAACCAGGGAAAGCCCCTAAGCTCCT GATCTATGCTGCATCCACTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCTGCCTGCAGT CTGAAGATTTTGCAACTTATTACTGTCAACAGTATTATAGTTGATAGGA GACTTCGGAACGTCGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGTAAGTACTTTTTTCCACTGATTCTTCACTGTTGCTAATTAGTTTAC TTTGTGTTCCCTTTGTGTGGTAGGAGACTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6094
hsIGK_0029 _V004_J002 _IGKV1-09- F_IGKJ2	GCCTTGCCAGCCCGCTCAGGTGTCTACTTCGGAACCCAATCTCAGGTGC CAGATGTGACATCCAGTTGACCCAGTCTCCATCCTTCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGGCCAGTCAGGGCATTAGCA GTTATTTAGCCTGGTATCAGCAAAAACCAGGGAAAGCCCCTAAGCTCCT GATCTATGCTGCATCCACTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGAATTCACTCTCACAATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGTCAACAGCTTAATAGTTGAGTGTC TACTTCGGAACGTCGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGTAAGTACTTTTTTCCACTGATTCTTCACTGTTGCTAATTAGTTTAC TTTGTGTTCCCTTTGTGTGGGTGTCTACTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6095
hsIGK_0030 _V005_J002 _IGKV1-12- F_IGKJ2	GCCTTGCCAGCCCGCTCAGGTACAGTGTTTCGGAACCCAATCTCAGGTTC CAGATGCGACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCA GCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT GATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAACAGTTGAGTACA GTGTTTCGGAACGTCGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA	SEQ ID NO: 6096

Name	Sequence	SEQ ID NO
	ACGTAAGTACTTTTTTCCACTGATTCTTCACTGTTGCTAATTAGTTTAC TTTGTGTTCCCTTTGTGTGGGTACAGTGTTCGGAACCTGATGGCGCGAGG GAGGC	
hsIGK_0031 _V006_J002 _IGKV1-13- FP_IGKJ2	GCCTTGCCAGCCCGCTCAGGGATCATCTTCGGAACCCAATCTCAGGTGC CAGATGTGCCATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGGCAAGTCAGGGCATTAGCA GTGCTTTAGCCTGATATCAGCAGAAACCAGGGAAAGCTCCTAAGCTCCT GATCTATGATGCCTCCAGTTTGGAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGTCAACAGTTTAATAATTGAGGATC ATCTTCGGAACGTCGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGTAAGTACTTTTTTCCACTGATTCTTCACTGTTGCTAATTAGTTTAC TTTGTGTTCCCTTTGTGTGGGTACATCTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6097
hsIGK_0032 _V007_J002 _IGKV1-16- F_IGKJ2	GCCTTGCCAGCCCGCTCAGTATTGGCGTTCGGAACCCAATCTCAGGTGC CAGATGTGACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGCATTAGCA ATTATTTAGCCTGGTTTTCAGCAGAAACCAGGGAAAGCCCTAAGTCCCT GATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAAGTTTCAGC GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTGATATTG GCGTTCGGAACGTCGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGTAAGTACTTTTTTCCACTGATTCTTCACTGTTGCTAATTAGTTTAC TTTGTGTTCCCTTTGTGTGGTATTGGCGTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6098
hsIGK_0033 _V008_J002 _IGKV1-17- F_IGKJ2	GCCTTGCCAGCCCGCTCAGAGGCTTGATTTCGGAACCCAATCTCAGGTGC CAGGTGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGGCAAGTCAGGGCATTAGAA ATGATTTAGGCTGGTATCAGCAGAAACCAGGGAAAGCCCTAAGCGCCT GATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGAATTCATCTCACAATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGTCTACAGCATAATAGTTGAAGGCT TGATTTCGGAACGTCGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGTAAGTACTTTTTTCCACTGATTCTTCACTGTTGCTAATTAGTTTAC TTTGTGTTCCCTTTGTGTGGAGGCTTGATTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6099
hsIGK_0034 _V009_J002 _IGKV1-27- F_IGKJ2	GCCTTGCCAGCCCGCTCAGACACAGTTTTCGGAACCTAATATCAGATAC CAGATGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCGAGTCAGGGCATTAGCA ATTATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGTTCTAAGCTCCT GATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTTTCAGT	SEQ ID NO: 6100

Name	Sequence	SEQ ID NO
	GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTTGAACACA CGTTTCGGAACGTCGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGTAAGTACTTTTTTCCACTGATTCTTCACTGTTGCTAATTAGTTTAC TTTGTGTTCCCTTTGTGTGGACACACGTTTCGGAACCTGATGGCGCGAGG GAGGC	
hsIGK_0035 _V010_J002 _IGKV1-33- F_IGKJ2	GCCTTGCCAGCCCGCTCAGTAGACGGATTTCGGAACCTAATCGCAGGTGC CAGATGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCAGGCGAGTCAGGACATTAGCA ACTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT GATCTACGATGCATCCAATTTGGAAACAGGGGTCCCATCAAGGTTCACT GGAAGTGGATCTGGGACAGATTTTACTTTTACCATCAGCAGCCTGCAGC CTGAAGATATTGCAACATATTACTGTCAACAGTATGATAATTGATAGAC GGATTTCGGAACGTCGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGTAAGTACTTTTTTCCACTGATTCTTCACTGTTGCTAATTAGTTTAC TTTGTGTTCCCTTTGTGTGGTAGACGGATTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6101
hsIGK_0036 _V011_J002 _IGKV1-37- O_IGKJ2	GCCTTGCCAGCCCGCTCAGCAGCTCTTTTCGGAACCCAATCTCAGGTGC CAGATGTGACATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGTGAGTCAGGGCATTAGCA GTTATTTAAATTGGTATCGGCAGAAACCAGGGAAAGTTCCTAAGCTCCT GATCTATAGTGCATCCAATTTGCAATCTGGAGTCCCATCTCGGTTCACT GGCAGTGGATCTGGGACAGATTTTCACTCTCACTATCAGCAGCCTGCAGC CTGAAGATGTTGCAACTTATTACGGTCAACGGACTTACAATTGACAGCT CTTTTCGGAACGTCGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGTAAGTACTTTTTTCCACTGATTCTTCACTGTTGCTAATTAGTTTAC TTTGTGTTCCCTTTGTGTGGCAGCTCTTTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6102
hsIGK_0037 _V012_J002 _IGKV1-39- FP_IGKJ2	GCCTTGCCAGCCCGCTCAGGAGCGATATTCGGAACCCAATCTCAGGTGC CAGATGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGAGCATTAGCA GCTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT GATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCACT GGCAGTGGATCTGGGACAGATTTTCACTCTCACCATCAGCAGTCTGCAAC CTGAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTTGAGAGCG ATATTTCGGAACGTCGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGTAAGTACTTTTTTCCACTGATTCTTCACTGTTGCTAATTAGTTTAC TTTGTGTTCCCTTTGTGTGGGAGCGATATTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6103
hsIGK_0038 _V013_J002	GCCTTGCCAGCCCGCTCAGGCATCTGATTTCGGAACCCAATCTCAGGTAC CAGATGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT	SEQ ID NO: 6104

Name	Sequence	SEQ ID NO
_IGKV1- NL1- F_IGKJ2	GTAGGAGACAGAGTCACCATCACTTGCCGGGCGAGTCAGGGCATTAGCA ATTCTTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT GCTCTATGCTGCATCCAGATTGGAAAGTGGGGTCCCATCCAGGTTTCAGT GGCAGTGGATCTGGGACGGATTACACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGTCAACAGTATTATAGTTGAGCATC TGATTTCGGAACGTCGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGTAAGTACTTTTTTCCACTGATTCTTCACTGTTGCTAATTAGTTTAC TTTGTGTTCCCTTTGTGTGGGCATCTGATTTCGGAACCTGATGGCGCGAGG GAGGC	
hsIGK_0039 _V014_J002 _IGKV2-24- F_IGKJ2	GCCTTGCCAGCCCGCTCAGTGCTACACTTCGGAACAGTGGGGATATTGT GATGACCCAGACTCCACTCTCCTCACCTGTCACCCTTGGACAGCCGGCC TCCATCTCCTGCAGGTCTAGTCAAAGCCTCGTACACAGTGATGGAAACA CCTACTTGAGTTGGCTTCAGCAGAGGCCAGGCCAGCCTCCAAGACTCCT AATTTATAAGATTTCTAACCGTTCTCTGGGGTCCCAGACAGATTTCAGT GGCAGTGGGGCAGGGACAGATTTACACTGAAAATCAGCAGGGTGGAAAG CTGAGGATGTCGGGGTTTATTACTGCATGCAAGCTACACAATGATGCTA CACTTCGGAACGTCGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGTAAGTACTTTTTTCCACTGATTCTTCACTGTTGCTAATTAGTTTAC TTTGTGTTCCCTTTGTGTGGTGCTACACTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6105
hsIGK_0040 _V015_J002 _IGKV2-28- F_IGKJ2	GCCTTGCCAGCCCGCTCAGAACTGCCATTTCGGAACAGTGGGGATATTGT GATGACTCAGTCTCCACTCTCCCTGCCCCGTACCCCTGGAGAGCCGGCC TCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACA ACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCT GATCTATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTTCAGT GGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGG CTGAGGATGTTGGGGTTTATTACTGCATGCAAGCTCTACAATGAACTG CCATTTCGGAACGTCGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGTAAGTACTTTTTTCCACTGATTCTTCACTGTTGCTAATTAGTTTAC TTTGTGTTCCCTTTGTGTGGAAGTCCATTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6106
hsIGK_0041 _V016_J002 _IGKV2-29- FP_IGKJ2	GCCTTGCCAGCCCGCTCAGTTGGACTGTTTCGGAACAGTGCGGATATTGT GATGACCCAGACTCCACTCTCTGTCCGTACCCCTGGACAGCCGGCC TCCATCTCCTGCAAGTCTAGTCAGAGCCTCCTGCATAGTGATGGAAAGA CCTATTTGTATTGGTACCTGCAGAAGCCAGGCCAGTCTCCACAGCTCCT GATCTATGAAGTTTCCAGCCGGTTCTCTGGAGTGCCAGATAGGTTTCAGT GGCAGCGGGTCAGGGACAGATTTACACTGAAAATCAGCCGGGTGGAGG CTGAGGATGTTGGGGTTTATTACTGAATGCAAGGTATACACTGATTGGA CTGTTTCGGAACGTCGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGTAAGTACTTTTTTCCACTGATTCTTCACTGTTGCTAATTAGTTTAC TTTGTGTTCCCTTTGTGTGGTTGGACTGTTTCGGAACCTGATGGCGCGAGG	SEQ ID NO: 6107

Name	Sequence	SEQ ID NO
	GAGGC	
hsIGK_0042 _V017_J002 _IGKV2-30- F_IGKJ2	GCCTTGCCAGCCCGCTCAGGTAGACACTTCGGAACAGTGGGGATGTTGT GATGACTCAGTCTCCACTCTCCCTGCCCCGTCACCCCTGGACAGCCGGCC TCCATCTCCTGCAGGTCTAGTCAAAGCCTCGTATACAGTGATGGAAACA CCTACTTGAATTGGTTTCAGCAGAGGCCAGGCCAATCTCCAAGGCGCCT AATTTATAAGGTTTCTAACCGGGACTCTGGGGTCCCAGACAGATTTCAGC GGCAGTGGGTGAGCACTGATTTACACTGAAAATCAGCAGGGTGGAGG CTGAGGATGTTGGGGTTTATTACTGCATGCAAGGTACACACTGAGTAGA CACTTCGGAACGTCGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGTAAGTACTTTTTTCCACTGATTCTTCACTGTTGCTAATTAGTTTAC TTTGTGTTCCCTTGTGTGGGTAGACACTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6108
hsIGK_0043 _V018_J002 _IGKV2-40- F_IGKJ2	GCCTTGCCAGCCCGCTCAGCACTGTACTTCGGAACGAGGATATTGTGAT GACCCAGACTCCACTCTCCCTGCCCCGTCACCCCTGGAGAGCCGGCCTCC ATCTCCTGCAGGTCTAGTCAGAGCCTCTTGGATAGTGATGATGGAAACA CCTATTTGGACTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCT GATCTATACGCTTTCCTATCGGGCCTCTGGAGTCCCAGACAGGTTTCAGT GGCAGTGGGTGAGCACTGATTTACACTGAAAATCAGCAGGGTGGAGG CTGAGGATGTTGGAGTTTATTACTGCATGCAACGTATAGAGTGACACTG TACTTCGGAACGTCGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGTAAGTACTTTTTTCCACTGATTCTTCACTGTTGCTAATTAGTTTAC TTTGTGTTCCCTTGTGTGGCACTGTACTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6109
hsIGK_0044 _V019_J002 _IGKV3-07- F_IGKJ2	GCCTTGCCAGCCCGCTCAGGATGATCCTTCGGAACATCTCAGATACCAC CGGAGAAATTGTAATGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCA GGGGAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTATCCTGGTACCAGCAGAAACCTGGGCAGGCTCCCAGGCTCCT CATCTATGGTGCATCCACCAGGGCCACTGGCATCCCAGCCAGGTTTCAGT GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAGTTTATTACTGTCAGCAGGATTATAACTGAGATGA TCCTTCGGAACGTCGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGTAAGTACTTTTTTCCACTGATTCTTCACTGTTGCTAATTAGTTTAC TTTGTGTTCCCTTGTGTGGGATGATCCTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6110
hsIGK_0045 _V020_J002 _IGKV3-11- F_IGKJ2	GCCTTGCCAGCCCGCTCAGCGCCAATATTCGGAACCAATTTTCAGATAC CACCGGAGAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCT CCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCA GCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTTCAGT GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGC CTGAAGATTTTGCAGTTTATTACTGTCAGCAGCGTAGCAACTGACGCCA	SEQ ID NO: 6111

Name	Sequence	SEQ ID NO
	ATATTCGGAACGTCGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGTAAGTACTTTTTTCCACTGATTCTTCACTGTTGCTAATTAGTTTAC TTTGTGTTTCCTTTGTGTGGCGCCAATATTCGGAACCTGATGGCGCGAGG GAGGC	
hsIGK_0046 _V021_J002 _IGKV3-15- F_IGKJ2	GCCTTGCCAGCCCGCTCAGTCAAGCCTTTCGGAACCCAATTCAGATAC CACTGGAGAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTAGCA GCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCACT GGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGT CTGAAGATTTTGCAGTTTATTACTGTCAGCAGTATAATAACTGATCAAG CCTTTCGGAACGTCGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGTAAGTACTTTTTTCCACTGATTCTTCACTGTTGCTAATTAGTTTAC TTTGTGTTTCCTTTGTGTGGTCAAGCCTTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6112
hsIGK_0047 _V022_J002 _IGKV3-20- F_IGKJ2	GCCTTGCCAGCCCGCTCAGACGTGTGTTTCGGAACATCTCAGATACCAC CGGAGAAATGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCA GGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCACT GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGC CTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTGAACGTG TGTTTCGGAACGTCGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGTAAGTACTTTTTTCCACTGATTCTTCACTGTTGCTAATTAGTTTAC TTTGTGTTTCCTTTGTGTGGACGTGTGTTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6113
hsIGK_0048 _V023_J002 _IGKV3- NL4- FNG_IGKJ2	GCCTTGCCAGCCCGCTCAGTCCGTCTATTCGGAACCCAATTCAGATAC CACCGGAGAAATGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCT CCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGGGTGTAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTCACT GGCAGTGGGCCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGC CTGAAGATTTTGCAGTTTATTACTGTCAGCAGCGTAGCAACTGATCCGT CTATTCGGAACGTCGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGTAAGTACTTTTTTCCACTGATTCTTCACTGTTGCTAATTAGTTTAC TTTGTGTTTCCTTTGTGTGGTCCGTCTATTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6114
hsIGK_0049 _V024_J002 _IGKV4-01- F_IGKJ2	GCCTTGCCAGCCCGCTCAGAAGAGCTGTTTCGGAACGGGGACATCGTGAT GACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGA ACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCT	SEQ ID NO: 6115

Name	Sequence	SEQ ID NO
	CATTTACTGGGCATCTACCCGGAATCCGGGGTCCCTGACCGATTTCAGT GGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGG CTGAAGATGTGGCAGTTTATTACTGTCTAGCAATATTATAGTTGAAAGAG CTGTTTCGGAACGTCGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGTAAGTACTTTTTTCCACTGATTCTTCACTGTTGCTAATTAGTTTAC TTTGTGTTCCCTTTGTGTGGAAGAGCTGTTTCGGAACCTGATGGCGCGAGG GAGGC	
hsIGK_0050 _V025_J002 _IGKV5-02- F_IGKJ2	GCCTTGCCAGCCCGCTCAGTATCGCTCTTCGGAACCCATAATCAGATAC CAGGGCAGAAACGACACTCACGCAGTCTCCAGCATTTCATGTCAGCGACT CCAGGAGACAAAGTCAACATCTCCTGCAAAGCCAGCCAAGACATTGATG ATGATATGAACTGGTACCAACAGAAACCAGGAGAAGCTGCTATTTTCAT TATTCAAGAAGCTACTACTCTCGTTCCTGGAATCCACCTCGATTTCAGT GGCAGCGGGTATGGAACAGATTTTACCCTCACAATTAATAACATAGAAT CTGAGGATGCTGCATATTACTTCTGTCTACAACATGATAATTGATATCG CTCTTCGGAACGTCGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGTAAGTACTTTTTTCCACTGATTCTTCACTGTTGCTAATTAGTTTAC TTTGTGTTCCCTTTGTGTGGTATCGCTCTTCGGAACCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6116
hsIGK_0051 _V001_J003 _IGKV1-05- F_IGKJ3	GCCTTGCCAGCCCGCTCAGGTTCCGAAAAGTAACGCCAATCTCAGGTGC CAAATGTGACATCCAGATGACCCAGTCTCCTTCCACCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGGCCAGTCAGAGTATTAGTA GCTGGTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT GATCTATAAGGCGTCTAGTTTAGAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGAATTCCTCTCACCATCAGCAGCCTGCAGC CTGATGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTGAGTTCC GAAAAGTAACGGTCGACCTTTTCGGCCCTGGGACCAAAGTGATATCAAA CGTAAGTACATCTGTCTCAATTATTTCGTGAGATTTTAGTGCCATTGTAT CATTTGTGCAAGTTTTGTGGTTCCGAAAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6117
hsIGK_0052 _V002_J003 _IGKV1-06- F_IGKJ3	GCCTTGCCAGCCCGCTCAGCGTTACTTAAGTAACGCCAATCTCAGGTGC CAGATGTGCCATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAA ATGATTTAGGCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT GATCTATGCTGCATCCAGTTTACAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGCACAGATTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGTCTACAAGATTACAATTGACGTTA CTTAAGTAACGGTCGACCTTTTCGGCCCTGGGACCAAAGTGATATCAAA CGTAAGTACATCTGTCTCAATTATTTCGTGAGATTTTAGTGCCATTGTAT CATTTGTGCAAGTTTTGTGCGTTACTTAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6118
hsIGK_0053	GCCTTGCCAGCCCGCTCAGTAGGAGACAAGTAACGCCAATCTCAGGTGC	SEQ ID NO:

Name	Sequence	SEQ ID NO
_V003_J003 _IGKV1-08- F_IGKJ3	CAGATGTGCCATCCGGATGACCCAGTCTCCATCCTCATTCTCTGCATCT ACAGGAGACAGAGTCACCATCACTTGTGCGGGCGAGTCAGGGTATTAGCA GTTATTTAGCCTGGTATCAGCAAAAACCAGGGAAAGCCCCCTAAGCTCCT GATCTATGCTGCATCCACTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCTGCCTGCAGT CTGAAGATTTTGCAACTTATTACTGTCAACAGTATTATAGTTGATAGGA GACAAGTAACGGTCGACCTTTTCGGCCCTGGGACCAAAGTGGATATCAAA CGTAAGTACATCTGTCTCAATTATTCGTGAGATTTTAGTGCCATTGTAT CATTTGTGCAAGTTTTGTGTAGGAGACAAGTAACGCTGATGGCGCGAGG GAGGC	6119
hsIGK_0054 _V004_J003 _IGKV1-09- F_IGKJ3	GCCTTGCCAGCCCCTCAGGTGTCTACAAGTAACGCCAATCTCAGGTGC CAGATGTGACATCCAGTTGACCCAGTCTCCATCCTTCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGC CGGGCCAGTCAGGGCATTAGCA GTTATTTAGCCTGGTATCAGCAAAAACCAGGGAAAGCCCCCTAAGCTCCT GATCTATGCTGCATCCACTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGAATTCACTCTCACAATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGTCAACAGCTTAATAGTTGAGTGTCT TACAAGTAACGGTCGACCTTTTCGGCCCTGGGACCAAAGTGGATATCAAA CGTAAGTACATCTGTCTCAATTATTCGTGAGATTTTAGTGCCATTGTAT CATTTGTGCAAGTTTTGTGGTGTCTACAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6120
hsIGK_0055 _V005_J003 _IGKV1-12- F_IGKJ3	GCCTTGCCAGCCCCTCAGGTACAGTGAAGTAACGCCAATCTCAGGTTC CAGATGCGACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGTGCGGGCGAGTCAGGGTATTAGCA GCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCCTAAGCTCCT GATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAACAGTTGAGTACA GTGAAGTAACGGTCGACCTTTTCGGCCCTGGGACCAAAGTGGATATCAAA CGTAAGTACATCTGTCTCAATTATTCGTGAGATTTTAGTGCCATTGTAT CATTTGTGCAAGTTTTGTGGTACAGTGAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6121
hsIGK_0056 _V006_J003 _IGKV1-13- FP_IGKJ3	GCCTTGCCAGCCCCTCAGGGATCATCAAGTAACGCCAATCTCAGGTGC CAGATGTGCCATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGC CGGGCAAGTCAGGGCATTAGCA GTGCTTTAGCCTGATATCAGCAGAAACCAGGGAAAGCTCCTAAGCTCCT GATCTATGATGCCTCCAGTTTGGAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGTCAACAGTTTAATAATTGAGGATC ATCAAGTAACGGTCGACCTTTTCGGCCCTGGGACCAAAGTGGATATCAAA CGTAAGTACATCTGTCTCAATTATTCGTGAGATTTTAGTGCCATTGTAT	SEQ ID NO: 6122

Name	Sequence	SEQ ID NO
	CATTTGTGCAAGTTTTGTGGGATCATCAAGTAACGCTGATGGCGCGAGG GAGGC	
hsIGK_0057 _V007_J003 _IGKV1-16- F_IGKJ3	GCCTTGCCAGCCCGCTCAGTATTGGCGAAGTAACGCCAATCTCAGGTGC CAGATGTGACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGTCTGGGCGAGTCAGGGCATTAGCA ATTATTTAGCCTGGTTTTAGCAGAAACCAGGGAAAGCCCCTAAGTCCCT GATCTATGCTGCATCCAGTTTTGCAAAGTGGGGTCCCATCAAAGTTCAGC GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTGATATTG GCGAAGTAACGGTCGACCTTTTCGGCCCTGGGACCAAAGTGATATCAAA CGTAAGTACATCTGTCTCAATTATTCGTGAGATTTTAGTGCCATTGTAT CATTTGTGCAAGTTTTGTGTATTGGCGAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6123
hsIGK_0058 _V008_J003 _IGKV1-17- F_IGKJ3	GCCTTGCCAGCCCGCTCAGAGGCTTGAAAGTAACGCCAATCTCAGGTGC CAGGTGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAA ATGATTTAGGCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCT GATCTATGCTGCATCCAGTTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGAATTCCTCTCACAATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGTCTACAGCATAATAGTTGAAGGCT TGAAAGTAACGGTCGACCTTTTCGGCCCTGGGACCAAAGTGATATCAAA CGTAAGTACATCTGTCTCAATTATTCGTGAGATTTTAGTGCCATTGTAT CATTTGTGCAAGTTTTGTGAGGCTTGAAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6124
hsIGK_0059 _V009_J003 _IGKV1-27- F_IGKJ3	GCCTTGCCAGCCCGCTCAGACACACGTAAGTAACGCTAATATCAGATAC CAGATGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCGAGTCAGGGCATTAGCA ATTATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGTTCCCTAAGCTCCT GATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTTTCAGT GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTTGAACACA CGTAAGTAACGGTCGACCTTTTCGGCCCTGGGACCAAAGTGATATCAAA CGTAAGTACATCTGTCTCAATTATTCGTGAGATTTTAGTGCCATTGTAT CATTTGTGCAAGTTTTGTGACACACGTAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6125
hsIGK_0060 _V010_J003 _IGKV1-33- F_IGKJ3	GCCTTGCCAGCCCGCTCAGTAGACGGAAAGTAACGCTAATCGCAGGTGC CAGATGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCAGGCGAGTCAGGACATTAGCA ACTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCCTAAGCTCCT GATCTACGATGCATCCAATTTGGAAACAGGGGTCCCATCAAGGTTTCAGT GGAAGTGGATCTGGGACAGATTTTACTTTTACCATCAGCAGCCTGCAGC	SEQ ID NO: 6126

Name	Sequence	SEQ ID NO
	CTGAAGATATTGCAACATATTACTGTCAACAGTATGATAATTGATAGAC GGAAAGTAACGGTCGACCTTTTCGGCCCTGGGACCAAAGTGGATATCAAA CGTAAGTACATCTGTCTCAATTATTCGTGAGATTTTAGTGCCATTGTAT CATTTGTGCAAGTTTGTGTAGACGGAAAGTAACGCTGATGGCGCGAGG GAGGC	
hsIGK_0061 _V011_J003 _IGKV1-37- O_IGKJ3	GCCTTGCCAGCCCGCTCAGCAGCTCTTAAGTAACGCCAATCTCAGGTGC CAGATGTGACATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGTGAGTCAGGGCATTAGCA GTTATTTAAATTGGTATCGGCAGAAACCAGGGAAAGTTCCTAAGCTCCT GATCTATAGTGCATCCAATTTGCAATCTGGAGTCCCATCTCGGTTTCAGT GGCAGTGGATCTGGGACAGATTTCACTCTCACTATCAGCAGCCTGCAGC CTGAAGATGTTGCAACTTATTACGGTCAACGGACTTACAATTGACAGCT CTTAAGTAACGGTCGACCTTTTCGGCCCTGGGACCAAAGTGGATATCAAA CGTAAGTACATCTGTCTCAATTATTCGTGAGATTTTAGTGCCATTGTAT CATTTGTGCAAGTTTGTGTCAGCTCTTAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6127
hsIGK_0062 _V012_J003 _IGKV1-39- FP_IGKJ3	GCCTTGCCAGCCCGCTCAGGAGCGATAAAGTAACGCCAATCTCAGGTGC CAGATGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGAGCATTAGCA GCTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT GATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGT GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAAC CTGAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTTGAGAGCG ATAAAGTAACGGTCGACCTTTTCGGCCCTGGGACCAAAGTGGATATCAAA CGTAAGTACATCTGTCTCAATTATTCGTGAGATTTTAGTGCCATTGTAT CATTTGTGCAAGTTTGTGGAGCGATAAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6128
hsIGK_0063 _V013_J003 _IGKV1- NL1- F_IGKJ3	GCCTTGCCAGCCCGCTCAGGCATCTGAAAGTAACGCCAATCTCAGGTAC CAGATGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCGAGTCAGGGCATTAGCA ATTCTTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT GCTCTATGCTGCATCCAGATTGGAAGTGGGGTCCCATCCAGGTTTCAGT GGCAGTGGATCTGGGACGGATTACACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGTCAACAGTATTATAGTTGAGCATC TGAAAGTAACGGTCGACCTTTTCGGCCCTGGGACCAAAGTGGATATCAAA CGTAAGTACATCTGTCTCAATTATTCGTGAGATTTTAGTGCCATTGTAT CATTTGTGCAAGTTTGTGGCATCTGAAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6129
hsIGK_0064 _V014_J003 _IGKV2-24-	GCCTTGCCAGCCCGCTCAGTGCTACACAAGTAACGAGTGGGGATATTGT GATGACCCAGACTCCACTCTCCTCACCTGTCACCCTTGGACAGCCGGCC TCCATCTCCTGCAGGTCTAGTCAAAGCCTCGTACACAGTGATGGAAACA	SEQ ID NO: 6130

Name	Sequence	SEQ ID NO
F_IGKJ3	CCTACTTGAGTTGGCTTCAGCAGAGGCCAGGCCAGCCTCCAAGACTCCT AATTTATAAGATTCTAACCGGTTCTCTGGGGTCCCAGACAGATTTCAGT GGCAGTGGGGCAGGGACAGATTTACACTGAAAATCAGCAGGGTGGAG CTGAGGATGTCGGGGTTTATTACTGCATGCAAGCTACACAATGATGCTA CACAAGTAACGGTCGACCTTTTCGGCCCTGGGACCAAAGTGGATATCAAA CGTAAGTACATCTGTCTCAATTATTCGTGAGATTTTAGTGCCATTGTAT CATTTGTGCAAGTTTGTGTGCTACACAAGTAACGCTGATGGCGCGAGG GAGGC	
hsIGK_0065 _V015_J003 _IGKV2-28- F_IGKJ3	GCCTTGCCAGCCCGCTCAGAACTGCCAAAGTAACGAGTGGGGATATTGT GATGACTCAGTCTCCACTCTCCCTGCCCCGTACCCCTGGAGAGCCGGCC TCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACA ACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCT GATCTATTTGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTTCAGT GGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGG CTGAGGATGTTGGGGTTTATTACTGCATGCAAGCTCTACAATGAACTG CCAAAGTAACGGTCGACCTTTTCGGCCCTGGGACCAAAGTGGATATCAAA CGTAAGTACATCTGTCTCAATTATTCGTGAGATTTTAGTGCCATTGTAT CATTTGTGCAAGTTTGTGAACTGCCAAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6131
hsIGK_0066 _V016_J003 _IGKV2-29- FP_IGKJ3	GCCTTGCCAGCCCGCTCAGTTGGACTGAAGTAACGAGTGCGGATATTGT GATGACCCAGACTCCACTCTCTGTCCGTACCCCTGGACAGCCGGCC TCCATCTCCTGCAAGTCTAGTCAGAGCCTCCTGCATAGTGATGGAAAGA CCTATTTGTATTGGTACCTGCAGAAGCCAGGCCAGTCTCCACAGCTCCT GATCTATGAAGTTTCCAGCCGGTTCTCTGGAGTGCCAGATAGGTTTCAGT GGCAGCGGGTCAGGGACAGATTTACACTGAAAATCAGCCGGGTGGAGG CTGAGGATGTTGGGGTTTATTACTGAATGCAAGGTATACACTGATTGGA CTGAAGTAACGGTCGACCTTTTCGGCCCTGGGACCAAAGTGGATATCAAA CGTAAGTACATCTGTCTCAATTATTCGTGAGATTTTAGTGCCATTGTAT CATTTGTGCAAGTTTGTGTTGGACTGAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6132
hsIGK_0067 _V017_J003 _IGKV2-30- F_IGKJ3	GCCTTGCCAGCCCGCTCAGGTAGACACAAGTAACGAGTGGGGATGTTGT GATGACTCAGTCTCCACTCTCCCTGCCCCGTACCCCTGGACAGCCGGCC TCCATCTCCTGCAGGTCTAGTCAAAGCCTCGTATACAGTGATGGAAACA CCTACTTGAATTGGTTTCAGCAGAGGCCAGGCCAATCTCCAAGGCGCCT AATTTATAAGGTTTCTAACCGGGACTCTGGGGTCCCAGACAGATTTCAGC GGCAGTGGGTGAGGCACTGATTTACACTGAAAATCAGCAGGGTGGAGG CTGAGGATGTTGGGGTTTATTACTGCATGCAAGGTACACACTGAGTAGA CACAAGTAACGGTCGACCTTTTCGGCCCTGGGACCAAAGTGGATATCAAA CGTAAGTACATCTGTCTCAATTATTCGTGAGATTTTAGTGCCATTGTAT CATTTGTGCAAGTTTGTGGTAGACACAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6133

Name	Sequence	SEQ ID NO
hsIGK_0068 _V018_J003 _IGKV2-40- F_IGKJ3	GCCTTGCCAGCCCCTCAGCACTGTACAAGTAACGGAGGATATTGTGAT GACCCAGACTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCC ATCTCCTGCAGGTCTAGTCAGAGCCTCTTGGATAGTGATGATGGAACA CCTATTTGGACTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCT GATCTATACGCTTTCCTATCGGGCCTCTGGAGTCCCAGACAGGTTTCAGT GGCAGTGGGTCAGGCACTGATTTTCACTGAAAATCAGCAGGGTGGAGG CTGAGGATGTTGGAGTTTATTACTGCATGCAACGTATAGAGTGACACTG TACAAGTAACGGTCGACCTTTCGGCCCTGGGACCAAAGTGATATCAAA CGTAAGTACATCTGTCTCAATTATTCGTGAGATTTTAGTGCCATTGTAT CATTTGTGCAAGTTTTGTGCACTGTACAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6134
hsIGK_0069 _V019_J003 _IGKV3-07- F_IGKJ3	GCCTTGCCAGCCCCTCAGGATGATCCAAGTAACGATCTCAGATACCAC CGGAGAAATTGTAATGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCA GGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTATCCTGGTACCAGCAGAAACCTGGGCAGGCTCCCAGGCTCCT CATCTATGGTGCATCCACCAGGGCCACTGGCATCCCAGCCAGGTTTCAGT GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAGTTTATTACTGTCAGCAGGATTATAACTGAGATGA TCCAAGTAACGGTCGACCTTTCGGCCCTGGGACCAAAGTGATATCAAA CGTAAGTACATCTGTCTCAATTATTCGTGAGATTTTAGTGCCATTGTAT CATTTGTGCAAGTTTTGTGGATGATCCAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6135
hsIGK_0070 _V020_J003 _IGKV3-11- F_IGKJ3	GCCTTGCCAGCCCCTCAGCGCCAATAAAGTAACGCCAATTTTCAGATAC CACCGGAGAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCT CCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCA GCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTTCAGT GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGC CTGAAGATTTTGCAGTTTATTACTGTCAGCAGCGTAGCAACTGACGCCA ATAAAGTAACGGTCGACCTTTCGGCCCTGGGACCAAAGTGATATCAAA CGTAAGTACATCTGTCTCAATTATTCGTGAGATTTTAGTGCCATTGTAT CATTTGTGCAAGTTTTGTGCGCCAATAAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6136
hsIGK_0071 _V021_J003 _IGKV3-15- F_IGKJ3	GCCTTGCCAGCCCCTCAGTCAAGCCTAAGTAACGCCAATTTTCAGATAC CACTGGAGAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTTCAGT GGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGT CTGAAGATTTTGCAGTTTATTACTGTCAGCAGTATAATAACTGATCAAG CCTAAGTAACGGTCGACCTTTCGGCCCTGGGACCAAAGTGATATCAAA	SEQ ID NO: 6137

Name	Sequence	SEQ ID NO
	CGTAAGTACATCTGTCTCAATTATTCGTGAGATTTTAGTGCCATTGTAT CATTGTGCAAGTTTTGTGTCAAGCCTAAGTAACGCTGATGGCGCGAGG GAGGC	
hsIGK_0072 _V022_J003 _IGKV3-20- F_IGKJ3	GCCTTGCCAGCCCGCTCAGACGTGTGTAAGTAACGATCTCAGATACCAC CGGAGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCA GGGAAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTTCAGT GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGC CTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTGAACGTG TGTAAGTAACGGTCGACCTTTTCGGCCCTGGGACCAAAGTGATATCAAA CGTAAGTACATCTGTCTCAATTATTCGTGAGATTTTAGTGCCATTGTAT CATTGTGCAAGTTTTGTGTACGTGTGTAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6138
hsIGK_0073 _V023_J003 _IGKV3- NL4- FNG_IGKJ3	GCCTTGCCAGCCCGCTCAGTCCGTCTAAAGTAACGCCAATTCAGATAC CACCGGAGAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCT CCAGGGGAAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGGGTGTTAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTTCAGT GGCAGTGGGCCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGC CTGAAGATTTTGCAGTTTATTACTGTCAGCAGCGTAGCAACTGATCCGT CTAAAGTAACGGTCGACCTTTTCGGCCCTGGGACCAAAGTGATATCAAA CGTAAGTACATCTGTCTCAATTATTCGTGAGATTTTAGTGCCATTGTAT CATTGTGCAAGTTTTGTGTCCGTCTAAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6139
hsIGK_0074 _V024_J003 _IGKV4-01- F_IGKJ3	GCCTTGCCAGCCCGCTCAGAAGAGCTGAAGTAACGGGGGACATCGTGAT GACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC ATCAACTGCAAGTCCAGCCAGAGTGTATTTATACAGCTCCAACAATAAGA ACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCT CATTACTGGGCATCTACCCGGAATCCGGGGTCCCTGACCGATTTCAGT GGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGG CTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTTGAAAGAG CTGAAGTAACGGTCGACCTTTTCGGCCCTGGGACCAAAGTGATATCAAA CGTAAGTACATCTGTCTCAATTATTCGTGAGATTTTAGTGCCATTGTAT CATTGTGCAAGTTTTGTGAAGAGCTGAAGTAACGCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6140
hsIGK_0075 _V025_J003 _IGKV5-02- F_IGKJ3	GCCTTGCCAGCCCGCTCAGTATCGCTCAAGTAACGCCATAATCAGATAC CAGGGCAGAAACGACACTCACGCAGTCTCCAGCATTTCATGTCAGCGACT CCAGGAGACAAAGTCAACATCTCCTGCAAAGCCAGCCAAGACATTGATG ATGATATGAAGTGGTACCAACAGAAACCAGGAGAAGCTGCTATTTTCAT TATTCAAGAAGCTACTACTCTCGTTCCTGGAATCCCACCTCGATTTCAGT	SEQ ID NO: 6141

Name	Sequence	SEQ ID NO
	GGCAGCGGGTATGGAACAGATTTTACCCTCACAAATTAATAACATAGAAT CTGAGGATGCTGCATATTACTTCTGTCTACAACATGATAATTGATATCG CTCAAGTAACGGTCGACCTTTTCGGCCCTGGGACCAAAGTGGATATCAAA CGTAAGTACATCTGTCTCAATTATTCGTGAGATTTTAGTGCCATTGTAT CATTTGTGCAAGTTTGTGTATCGCTCAAGTAACGCTGATGGCGCGAGG GAGGC	
hsIGK_0076 _V001_J004 _IGKV1-05- F_IGKJ4	GCCTTGCCAGCCCGCTCAGGTTCCGAAGTCTCCTACCAATCTCAGGTGC CAAATGTGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCCAGTCAGAGTATTAGTA GCTGGTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT GATCTATAAGGCGTCTAGTTTAGAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGAATTCACCTCTCACCATCAGCAGCCTGCAGC CTGATGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTGAGTTCC GAAGTCTCCTAGTCGACCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA CGTAAGTGCACTTTCCTAATGCTTTTTCTTATAAGGTTTTAAATTTGGA GCGTTTTTGTGTTTGAGATGTTCCGAAGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 6142
hsIGK_0077 _V002_J004 _IGKV1-06- F_IGKJ4	GCCTTGCCAGCCCGCTCAGCGTTACTTGTCTCCTACCAATCTCAGGTGC CAGATGTGCCATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAA ATGATTTAGGCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT GATCTATGCTGCATCCAGTTTACAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGCACAGATTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGTCTACAAGATTACAATTGACGTTA CTTGTCTCCTAGTCGACCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA CGTAAGTGCACTTTCCTAATGCTTTTTCTTATAAGGTTTTAAATTTGGA GCGTTTTTGTGTTTGAGATCGTTACTTGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 6143
hsIGK_0078 _V003_J004 _IGKV1-08- F_IGKJ4	GCCTTGCCAGCCCGCTCAGTAGGAGACGTCTCCTACCAATCTCAGGTGC CAGATGTGCCATCCGGATGACCCAGTCTCCATCCTCATTCTCTGCATCT ACAGGAGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCA GTTATTTAGCCTGGTATCAGCAAAAACCAGGGAAAGCCCCTAAGCTCCT GATCTATGCTGCATCCACTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCTGCCTGCAGT CTGAAGATTTTGCAACTTATTACTGTCAACAGTATTATAGTTGATAGGA GACGTCTCCTAGTCGACCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA CGTAAGTGCACTTTCCTAATGCTTTTTCTTATAAGGTTTTAAATTTGGA GCGTTTTTGTGTTTGAGATTAGGAGACGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 6144
hsIGK_0079 _V004_J004	GCCTTGCCAGCCCGCTCAGGTGTCTACGTCTCCTACCAATCTCAGGTGC CAGATGTGACATCCAGTTGACCCAGTCTCCATCCTTCTGTCTGCATCT	SEQ ID NO: 6145

Name	Sequence	SEQ ID NO
_IGKV1-09-F_IGKJ4	GTAGGAGACAGAGTCACCATCACTTGCCGGGCCAGTCAGGGCATTAGCA GTTATTTAGCCTGGTATCAGCAAAAACCAGGGAAAGCCCCTAAGCTCCT GATCTATGCTGCATCCACTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGAATTCCTCTCACAATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGTCAACAGCTTAATAGTTGAGTGTC TACGTCTCCTAGTCGACCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA CGTAAGTGCACCTTCCTAATGCTTTTTCTTATAAGGTTTTAAATTTGGA GCGTTTTTGTGTTTGAGATGTGTCTACGTCTCCTACTGATGGCGCGAGG GAGGC	
hsIGK_0080_V005_J004_IGKV1-12-F_IGKJ4	GCCTTGCCAGCCCGCTCAGGTACAGTGGTCTCCTACCAATCTCAGGTTC CAGATGCGACATCCAGATGACCCAGTCTCCATCTTCCGTGCTGCATCT GTAGGAGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCA GCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT GATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAACAGTTGAGTACA GTGGTCTCCTAGTCGACCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA CGTAAGTGCACCTTCCTAATGCTTTTTCTTATAAGGTTTTAAATTTGGA GCGTTTTTGTGTTTGAGATGTACAGTGGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 6146
hsIGK_0081_V006_J004_IGKV1-13-FP_IGKJ4	GCCTTGCCAGCCCGCTCAGGGATCATCGTCTCCTACCAATCTCAGGTGC CAGATGTGCCATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGCA GTGCTTTAGCCTGATATCAGCAGAAACCAGGGAAAGCTCCTAAGCTCCT GATCTATGATGCCTCCAGTTTGGAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGTCAACAGTTTAATAATTGAGGATC ATCGTCTCCTAGTCGACCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA CGTAAGTGCACCTTCCTAATGCTTTTTCTTATAAGGTTTTAAATTTGGA GCGTTTTTGTGTTTGAGATGGATCATCGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 6147
hsIGK_0082_V007_J004_IGKV1-16-F_IGKJ4	GCCTTGCCAGCCCGCTCAGTATTGGCGGTCTCCTACCAATCTCAGGTGC CAGATGTGACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGCATTAGCA ATTATTTAGCCTGGTTTCAGCAGAAACCAGGGAAAGCCCCTAAGTCCCT GATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAAGTTTCAGC GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTGATATTG GCGGTCTCCTAGTCGACCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA CGTAAGTGCACCTTCCTAATGCTTTTTCTTATAAGGTTTTAAATTTGGA GCGTTTTTGTGTTTGAGATTATTGGCGGTCTCCTACTGATGGCGCGAGG	SEQ ID NO: 6148

Name	Sequence	SEQ ID NO
	GAGGC	
hsIGK_0083 _V008_J004 _IGKV1-17- F_IGKJ4	GCCTTGCCAGCCCGCTCAGAGGCTTGAGTCTCCTACCAATCTCAGGTGC CAGGTGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAA ATGATTTAGGCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCT GATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGAATTCCTCTCACAATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGTCTACAGCATAATAGTTGAAGGCT TGAGTCTCCTAGTCGACCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA CGTAAGTGCACTTTCCTAATGCTTTTTCTTATAAGGTTTTAAATTTGGA GCGTTTTTGTGTTTGAGATAGGCTTGAGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 6149
hsIGK_0084 _V009_J004 _IGKV1-27- F_IGKJ4	GCCTTGCCAGCCCGCTCAGACACACGTGTCTCCTACTAATATCAGATAC CAGATGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCGAGTCAGGGCATTAGCA ATTATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCT GATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTTTCAGT GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTTGAACACA CGTGTCTCCTAGTCGACCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA CGTAAGTGCACTTTCCTAATGCTTTTTCTTATAAGGTTTTAAATTTGGA GCGTTTTTGTGTTTGAGATACACACGTGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 6150
hsIGK_0085 _V010_J004 _IGKV1-33- F_IGKJ4	GCCTTGCCAGCCCGCTCAGTAGACGGAGTCTCCTACTAATCGCAGGTGC CAGATGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCAGGCGAGTCAGGACATTAGCA ACTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT GATCTACGATGCATCCAATTTGGAACAGGGGTCCCATCAAGGTTTCAGT GGAAGTGGATCTGGGACAGATTTTACTTTTACCATCAGCAGCCTGCAGC CTGAAGATATTGCAACATATTACTGTCAACAGTATGATAATTGATAGAC GGAGTCTCCTAGTCGACCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA CGTAAGTGCACTTTCCTAATGCTTTTTCTTATAAGGTTTTAAATTTGGA GCGTTTTTGTGTTTGAGATTAGACGGAGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 6151
hsIGK_0086 _V011_J004 _IGKV1-37- O_IGKJ4	GCCTTGCCAGCCCGCTCAGCAGCTCTTGCTCTCCTACCAATCTCAGGTGC CAGATGTGACATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGTGAGTCAGGGCATTAGCA GTTATTTAAATTGGTATCGGCAGAAACCAGGGAAAGTTCCTAAGCTCCT GATCTATAGTGCATCCAATTTGCAATCTGGAGTCCCATCTCGGTTTCAGT GGCAGTGGATCTGGGACAGATTTTCACTCTCACTATCAGCAGCCTGCAGC CTGAAGATGTTGCAACTTATTACGGTCAACGGACTTACAATTGACAGCT	SEQ ID NO: 6152

Name	Sequence	SEQ ID NO
	CTTGTCTCCTAGTCGACCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA CGTAAGTGCACTTTCCTAATGCTTTTTCTTATAAGGTTTTAAATTTGGA GCGTTTTTGTGTTTGAGATCAGCTCTTGTCTCCTACTGATGGCGCGAGG GAGGC	
hsIGK_0087 _V012_J004 _IGKV1-39- FP_IGKJ4	GCCTTGCCAGCCCGCTCAGGAGCGATAGTCTCCTACCAATCTCAGGTGC CAGATGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGAGCATTAGCA GCTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT GATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGT GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAAC CTGAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTTGAGAGCG ATAGTCTCCTAGTCGACCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA CGTAAGTGCACTTTCCTAATGCTTTTTCTTATAAGGTTTTAAATTTGGA GCGTTTTTGTGTTTGAGATGAGCGATAGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 6153
hsIGK_0088 _V013_J004 _IGKV1- NL1- F_IGKJ4	GCCTTGCCAGCCCGCTCAGGCATCTGAGTCTCCTACCAATCTCAGGTAC CAGATGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCGAGTCAGGGCATTAGCA ATTCTTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT GCTCTATGCTGCATCCAGATTGGAAGTGGGGTCCCATCCAGGTTTCAGT GGCAGTGGATCTGGGACGGATTACACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGTCAACAGTATTATAGTTGAGCATC TGAGTCTCCTAGTCGACCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA CGTAAGTGCACTTTCCTAATGCTTTTTCTTATAAGGTTTTAAATTTGGA GCGTTTTTGTGTTTGAGATGCATCTGAGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 6154
hsIGK_0089 _V014_J004 _IGKV2-24- F_IGKJ4	GCCTTGCCAGCCCGCTCAGTGCTACACGTCTCCTAAGTGGGGATATTGT GATGACCCAGACTCCACTCTCCTCACCTGTCACCCTTGACAGCCGGCC TCCATCTCCTGCAGGTCTAGTCAAAGCCTCGTACACAGTGATGGAAACA CCTACTTGAGTTGGCTTCAGCAGAGGCCAGGCCAGCCTCCAAGACTCCT AATTTATAAGATTTCTAACCGGTTCTCTGGGGTCCCAGACAGATTTCAGT GGCAGTGGGGCAGGGACAGATTTACACTGAAAAATCAGCAGGGTGGAAAG CTGAGGATGTCGGGGTTTATTACTGCATGCAAGCTACACAATGATGCTA CACGTCTCCTAGTCGACCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA CGTAAGTGCACTTTCCTAATGCTTTTTCTTATAAGGTTTTAAATTTGGA GCGTTTTTGTGTTTGAGATTGCTACACGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 6155
hsIGK_0090 _V015_J004 _IGKV2-28- F_IGKJ4	GCCTTGCCAGCCCGCTCAGAACTGCCAGTCTCCTAAGTGGGGATATTGT GATGACTCAGTCTCCACTCTCCCTGCCCCGTACCCCTGGAGAGCCGGCC TCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACA ACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCT	SEQ ID NO: 6156

Name	Sequence	SEQ ID NO
	GATCTATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTTCAGT GGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGG CTGAGGATGTTGGGGTTTATTACTGCATGCAAGCTCTACAATGAAACTG CCAGTCTCCTAGTCGACCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA CGTAAGTGCACCTTTCCTAATGCTTTTTCTTATAAGGTTTTAAATTTGGA GCGTTTTTGTGTTTGAGATAACTGCCAGTCTCCTACTGATGGCGCGAGG GAGGC	
hsIGK_0091 _V016_J004 _IGKV2-29- FP_IGKJ4	GCCTTGCCAGCCCCTCAGTTGGACTGGTCTCCTAAGTGC GGATATTGT GATGACCCAGACTCCACTCTCTGTCCGTACCCCTGGACAGCCGGCC TCCATCTCCTGCAAGTCTAGTCAGAGCCTCCTGCATAGTGATGGAAAGA CCTATTTGTATTGGTACCTGCAGAAGCCAGGCCAGTCTCCACAGCTCCT GATCTATGAAGTTTCCAGCCGGTTCTCTGGAGTGCCAGATAGGTTTCAGT GGCAGCGGGTCAGGGACAGATTTACACTGAAAATCAGCCGGGTGGAGG CTGAGGATGTTGGGGTTTATTACTGAATGCAAGGTATACACTGATTGGA CTGGTCTCCTAGTCGACCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA CGTAAGTGCACCTTTCCTAATGCTTTTTCTTATAAGGTTTTAAATTTGGA GCGTTTTTGTGTTTGAGATTTGGACTGGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 6157
hsIGK_0092 _V017_J004 _IGKV2-30- F_IGKJ4	GCCTTGCCAGCCCCTCAGGTAGACACGTCTCCTAAGTGGGGATGTTGT GATGACTCAGTCTCCACTCTCCCTGCCCCTACCCCTGGACAGCCGGCC TCCATCTCCTGCAGGTCTAGTCAAAGCCTCGTATACAGTGATGGAAACA CCTACTTGAATTGGTTTCAGCAGAGGCCAGGCCAATCTCCAAGGCGCCT AATTTATAAGGTTTCTAACC GG GACTCTGGGGTCCCAGACAGATTTCAGC GGCAGTGGGT CAGGCACTGATTTACACTGAAAATCAGCAGGGTGGAGG CTGAGGATGTTGGGGTTTATTACTGCATGCAAGGTACACACTGAGTAGA CACGTCTCCTAGTCGACCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA CGTAAGTGCACCTTTCCTAATGCTTTTTCTTATAAGGTTTTAAATTTGGA GCGTTTTTGTGTTTGAGATGTAGACACGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 6158
hsIGK_0093 _V018_J004 _IGKV2-40- F_IGKJ4	GCCTTGCCAGCCCCTCAGCACTGTACGTCTCCTAGAGGATATTGTGAT GACCCAGACTCCACTCTCCCTGCCCCTACCCCTGGAGAGCCGGCCTCC ATCTCCTGCAGGTCTAGTCAGAGCCTCTTGGATAGTGATGATGGAAACA CCTATTTGGACTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCT GATCTATACGCTTTCCTATCGGGCCTCTGGAGTCCCAGACAGGTTTCAGT GGCAGTGGGT CAGGCACTGATTTACACTGAAAATCAGCAGGGTGGAGG CTGAGGATGTTGGAGTTTATTACTGCATGCAACGTATAGAGTGACACTG TACGTCTCCTAGTCGACCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA CGTAAGTGCACCTTTCCTAATGCTTTTTCTTATAAGGTTTTAAATTTGGA GCGTTTTTGTGTTTGAGATCACTGTACGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 6159
hsIGK_0094	GCCTTGCCAGCCCCTCAGGATGATCCGTCTCCTAATCTCAGATACCAC	SEQ ID NO:

Name	Sequence	SEQ ID NO
_V019_J004 _IGKV3-07- F_IGKJ4	CGGAGAAATTGTAATGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCA GGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTATCCTGGTACCAGCAGAAACCTGGGCAGGCTCCCAGGCTCCT CATCTATGGTGCATCCACCAGGGCCACTGGCATCCCAGCCAGGTTTCAGT GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAGTTTATTACTGTCAGCAGGATTATAACTGAGATGA TCCGTCTCCTAGTCGACCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA CGTAAGTGCACTTTCCTAATGCTTTTTTCTTATAAGGTTTTAAATTTGGA GCGTTTTTGTGTTTGAGATGATGATCCGTCTCCTACTGATGGCGCGAGG GAGGC	6160
hsIGK_0095 _V020_J004 _IGKV3-11- F_IGKJ4	GCCTTGCCAGCCCGCTCAGCGCCAATAGTCTCCTACCAATTTTCAGATAC CACCGGAGAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCT CCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCA GCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTTCAGT GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGC CTGAAGATTTTGCAGTTTATTACTGTCAGCAGCGTAGCAACTGACGCCA ATAGTCTCCTAGTCGACCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA CGTAAGTGCACTTTCCTAATGCTTTTTTCTTATAAGGTTTTAAATTTGGA GCGTTTTTGTGTTTGAGATCGCCAATAGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 6161
hsIGK_0096 _V021_J004 _IGKV3-15- F_IGKJ4	GCCTTGCCAGCCCGCTCAGTCAAGCCTGTCTCCTACCAATTTTCAGATAC CACTGGAGAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTTCAGT GGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGT CTGAAGATTTTGCAGTTTATTACTGTCAGCAGTATAATAACTGATCAAG CCTGTCTCCTAGTCGACCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA CGTAAGTGCACTTTCCTAATGCTTTTTTCTTATAAGGTTTTAAATTTGGA GCGTTTTTGTGTTTGAGATTCAAGCCTGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 6162
hsIGK_0097 _V022_J004 _IGKV3-20- F_IGKJ4	GCCTTGCCAGCCCGCTCAGACGTGTGTGTCTCCTAATCTCAGATACCAC CGGAGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCA GGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTTCAGT GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGC CTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTGAACGTG TGTGTCTCCTAGTCGACCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA CGTAAGTGCACTTTCCTAATGCTTTTTTCTTATAAGGTTTTAAATTTGGA	SEQ ID NO: 6163

Name	Sequence	SEQ ID NO
	GCGTTTTTGTGTTTGAGATACGTGTGTGTCTCCTACTGATGGCGCGAGG GAGGC	
hsIGK_0098 _V023_J004 _IGKV3- NL4- FNG_IGKJ4	GCCTTGCCAGCCCGCTCAGTCCGTCTAGTCTCCTACCAATTTAGATAC CACCGGAGAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCT CCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGGGTGTTAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTCACT GGCAGTGGGCCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGC CTGAAGATTTTGCAGTTTATTACTGTGTCAGCAGCGTAGCAACTGATCCGT CTAGTCTCCTAGTCGACCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA CGTAAGTGCACCTTTCCTAATGCTTTTTTCTTATAAGGTTTTAAATTTGGA GCGTTTTTGTGTTTGAGATTCCGTCTAGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 6164
hsIGK_0099 _V024_J004 _IGKV4-01- F_IGKJ4	GCCTTGCCAGCCCGCTCAGAAGAGCTGGTCTCCTAGGGGACATCGTGAT GACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC ATCAACTGCAAGTCCAGCCAGAGTGTATTTATACAGCTCCAACAATAAGA ACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCT CATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCACT GGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGG CTGAAGATGTGGCAGTTTATTACTGTGTCAGCAATATTATAGTTGAAAGAG CTGGTCTCCTAGTCGACCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA CGTAAGTGCACCTTTCCTAATGCTTTTTTCTTATAAGGTTTTAAATTTGGA GCGTTTTTGTGTTTGAGATAAGAGCTGGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 6165
hsIGK_0100 _V025_J004 _IGKV5-02- F_IGKJ4	GCCTTGCCAGCCCGCTCAGTATCGCTCGTCTCCTACCATAATCAGATAC CAGGGCAGAAACGACACTCACGCAGTCTCCAGCATTATGTCAGCGACT CCAGGAGACAAAGTCAACATCTCCTGCAAAGCCAGCCAAGACATTGATG ATGATATGAACTGGTACCAACAGAAACCAGGAGAAGCTGCTATTTTCAT TATTCAAGAAGCTACTACTCTCGTTCCTGGAATCCCACCTCGATTCACT GGCAGCGGGTATGGAACAGATTTTACCCTCACAATTAATAACATAGAAT CTGAGGATGCTGCATATTACTTCTGTCTACAACATGATAATTGATATCG CTCGTCTCCTAGTCGACCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA CGTAAGTGCACCTTTCCTAATGCTTTTTTCTTATAAGGTTTTAAATTTGGA GCGTTTTTGTGTTTGAGATTATCGCTCGTCTCCTACTGATGGCGCGAGG GAGGC	SEQ ID NO: 6166
hsIGK_0101 _V001_J005 _IGKV1-05- F_IGKJ5	GCCTTGCCAGCCCGCTCAGGTTCCGAAAGAGTGTCCTCAATCTCAGGTGC CAAATGTGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGGCCAGTCAGAGTATTAGTA GCTGGTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT GATCTATAAGGCGTCTAGTTTGTAGAAAGTGGGGTCCCATCAAGGTTCAAGC GGCAGTGGATCTGGGACAGAATTCCTCTCACCATCAGCAGCCTGCAGC	SEQ ID NO: 6167

Name	Sequence	SEQ ID NO
	CTGATGATTTTGGCACTTATTACTGCCAACAGTATAATAGTTGAGTTCC GAAAGAGTGTCTGCGACCCCTTCGGCCAAGGGACACGACTGGAGATTAAA CGTAAGTAATTTTCACTATTGTCTTCTGAAATTTGGGTCTGATGGCCA GTATTGACTTTTAGAGGCTGTTCCGAAAGAGTGTCTGATGGCGCGAGG GAGGC	
hsIGK_0102 _V002_J005 _IGKV1-06- F_IGKJ5	GCCTTGCCAGCCCGCTCAGCGTTACTTAGAGTGTCCCAATCTCAGGTGC CAGATGTGCCATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAA ATGATTTAGGCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT GATCTATGCTGCATCCAGTTTACAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGCACAGATTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGGCACTTATTACTGTCTACAAGATTACAATTGACGTTA CTTAGAGTGTCTGCGACCCCTTCGGCCAAGGGACACGACTGGAGATTAAA CGTAAGTAATTTTCACTATTGTCTTCTGAAATTTGGGTCTGATGGCCA GTATTGACTTTTAGAGGCTCGTTACTTAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6168
hsIGK_0103 _V003_J005 _IGKV1-08- F_IGKJ5	GCCTTGCCAGCCCGCTCAGTAGGAGACAGAGTGTCCCAATCTCAGGTGC CAGATGTGCCATCCGGATGACCCAGTCTCCATCCTCATTCTCTGCATCT ACAGGAGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCA GTTATTTAGCCTGGTATCAGCAAAAACCAGGGAAAGCCCCTAAGCTCCT GATCTATGCTGCATCCACTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCTGCCTGCAGT CTGAAGATTTTGGCACTTATTACTGTCAACAGTATTATAGTTGATAGGA GACAGAGTGTCTGCGACCCCTTCGGCCAAGGGACACGACTGGAGATTAAA CGTAAGTAATTTTCACTATTGTCTTCTGAAATTTGGGTCTGATGGCCA GTATTGACTTTTAGAGGCTTAGGAGACAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6169
hsIGK_0104 _V004_J005 _IGKV1-09- F_IGKJ5	GCCTTGCCAGCCCGCTCAGGTGTCTACAGAGTGTCCCAATCTCAGGTGC CAGATGTGACATCCAGTTGACCCAGTCTCCATCCTTCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCCAGTCAGGGCATTAGCA GTTATTTAGCCTGGTATCAGCAAAAACCAGGGAAAGCCCCTAAGCTCCT GATCTATGCTGCATCCACTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGAATTCCTCTCACAATCAGCAGCCTGCAGC CTGAAGATTTTGGCACTTATTACTGTCAACAGCTTAATAGTTGAGTGTC TACAGAGTGTCTGCGACCCCTTCGGCCAAGGGACACGACTGGAGATTAAA CGTAAGTAATTTTCACTATTGTCTTCTGAAATTTGGGTCTGATGGCCA GTATTGACTTTTAGAGGCTGTGTCTACAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6170
hsIGK_0105 _V005_J005 _IGKV1-12-	GCCTTGCCAGCCCGCTCAGGTACAGTGAGAGTGTCCCAATCTCAGGTTC CAGATGCGACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCA	SEQ ID NO: 6171

Name	Sequence	SEQ ID NO
F_IGKJ5	GCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCCTAAGCTCCT GATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAACAGTTGAGTACA GTGAGAGTGTCTGCGACCCCTTCGGCCAAGGGACACGACTGGAGATTAAA CGTAAGTAATTTTTCCTACTATTGTCTTCTGAAATTTGGGTCTGATGGCCA GTATTGACTTTTAGAGGCTGTACAGTGAGAGTGTCTGATGGCGCGAGG GAGGC	
hsIGK_0106 _V006_J005 _IGKV1-13- FP_IGKJ5	GCCTTGCCAGCCCGCTCAGGGATCATCAGAGTGTCCCAATCTCAGGTGC CAGATGTGCCATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGCA GTGCTTTAGCCTGATATCAGCAGAAACCAGGGAAAGCTCCTAAGCTCCT GATCTATGATGCCTCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGTCAACAGTTTAATAATTGAGGATC ATCAGAGTGTCTGCGACCCCTTCGGCCAAGGGACACGACTGGAGATTAAA CGTAAGTAATTTTTCCTACTATTGTCTTCTGAAATTTGGGTCTGATGGCCA GTATTGACTTTTAGAGGCTGGATCATCAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6172
hsIGK_0107 _V007_J005 _IGKV1-16- F_IGKJ5	GCCTTGCCAGCCCGCTCAGTATTGGCGAGAGTGTCCCAATCTCAGGTGC CAGATGTGACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGTCTGGGCGAGTCAGGGCATTAGCA ATTATTTAGCCTGGTTTCAGCAGAAACCAGGGAAAGCCCCCTAAGTCCCT GATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAAGTTTCAGC GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTGATATTG GCGAGAGTGTCTGCGACCCCTTCGGCCAAGGGACACGACTGGAGATTAAA CGTAAGTAATTTTTCCTACTATTGTCTTCTGAAATTTGGGTCTGATGGCCA GTATTGACTTTTAGAGGCTTATTGGCGAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6173
hsIGK_0108 _V008_J005 _IGKV1-17- F_IGKJ5	GCCTTGCCAGCCCGCTCAGAGGCTTGAAGAGTGTCCCAATCTCAGGTGC CAGGTGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAA ATGATTTAGGCTGGTATCAGCAGAAACCAGGGAAAGCCCCCTAAGCGCCT GATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGC GGCAGTGGATCTGGGACAGAAATTCCTCTCACAATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGTCTACAGCATAATAGTTGAAGGCT TGAAGAGTGTCTGCGACCCCTTCGGCCAAGGGACACGACTGGAGATTAAA CGTAAGTAATTTTTCCTACTATTGTCTTCTGAAATTTGGGTCTGATGGCCA GTATTGACTTTTAGAGGCTAGGCTTGAAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6174

Name	Sequence	SEQ ID NO
hsIGK_0109 _V009_J005 _IGKV1-27- F_IGKJ5	GCCTTGCCAGCCCGCTCAGACACACGTAGAGTGTCCCTAATATCAGATAC CAGATGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCGAGTCAGGGCATTAGCA ATTATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCT GATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTTTCAGT GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTTGAACACA CGTAGAGTGTGTCGACCCCTTCGGCCAAGGGACACGACTGGAGATTAAA CGTAAGTAATTTTCACTATTGTCTTCTGAAATTTGGGTCTGATGGCCA GTATTGACTTTTAGAGGCTACACACGTAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6175
hsIGK_0110 _V010_J005 _IGKV1-33- F_IGKJ5	GCCTTGCCAGCCCGCTCAGTAGACGGAAGAGTGTCCCTAATCGCAGGTGC CAGATGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCAGGCGAGTCAGGACATTAGCA ACTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCCTAAGCTCCT GATCTACGATGCATCCAATTTGAAACAGGGGTCCCATCAAGGTTTCAGT GGAAGTGGATCTGGGACAGATTTTACTTTTACCATCAGCAGCCTGCAGC CTGAAGATATTGCAACATATTACTGTCAACAGTATGATAATTGATAGAC GGAAGAGTGTGTCGACCCCTTCGGCCAAGGGACACGACTGGAGATTAAA CGTAAGTAATTTTCACTATTGTCTTCTGAAATTTGGGTCTGATGGCCA GTATTGACTTTTAGAGGCTTAGACGGAAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6176
hsIGK_0111 _V011_J005 _IGKV1-37- O_IGKJ5	GCCTTGCCAGCCCGCTCAGCAGCTCTTAGAGTGTCCCAATCTCAGGTGC CAGATGTGACATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGTGAGTCAGGGCATTAGCA GTTATTTAAATTGGTATCGGCAGAAACCAGGGAAAGTTCCTAAGCTCCT GATCTATAGTGCATCCAATTTGCAATCTGGAGTCCCATCTCGGTTTCAGT GGCAGTGGATCTGGGACAGATTTCACTCTCACTATCAGCAGCCTGCAGC CTGAAGATGTTGCAACTTATTACGGTCAACGGACTTACAATTGACAGCT CTTAGAGTGTGTCGACCCCTTCGGCCAAGGGACACGACTGGAGATTAAA CGTAAGTAATTTTCACTATTGTCTTCTGAAATTTGGGTCTGATGGCCA GTATTGACTTTTAGAGGCTCAGCTCTTAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6177
hsIGK_0112 _V012_J005 _IGKV1-39- FP_IGKJ5	GCCTTGCCAGCCCGCTCAGGAGCGATAAGAGTGTCCCAATCTCAGGTGC CAGATGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGAGCATTAGCA GCTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCCTAAGCTCCT GATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGT GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAAC CTGAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTTGAGAGCG ATAAGAGTGTGTCGACCCCTTCGGCCAAGGGACACGACTGGAGATTAAA	SEQ ID NO: 6178

Name	Sequence	SEQ ID NO
	CGTAAGTAATTTTTCACATATTGTCTTCTGAAATTTGGGTCTGATGGCCA GTATTGACTTTTAGAGGCTGAGCGATAAGAGTGTCTTGATGGCGCGAGG GAGGC	
hsIGK_0113 _V013_J005 _IGKV1- NL1- F_IGKJ5	GCCTTGCCAGCCCGCTCAGGCATCTGAAGAGTGTCCCAATCTCAGGTAC CAGATGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCT GTAGGAGACAGAGTCACCATCACTTGCCGGGCGAGTCAGGGCATTAGCA ATTCTTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT GCTCTATGCTGCATCCAGATTGGAAAGTGGGGTCCCATCCAGGTTTCAGT GGCAGTGGATCTGGGACGGATTACACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTATTACTGTCAACAGTATTATAGTTGAGCATC TGAAGAGTGTCTGTCGACCCCTTCGGCCAAGGGACACGACTGGAGATTAAA CGTAAGTAATTTTTCACATATTGTCTTCTGAAATTTGGGTCTGATGGCCA GTATTGACTTTTAGAGGCTGCATCTGAAGAGTGTCTTGATGGCGCGAGG GAGGC	SEQ ID NO: 6179
hsIGK_0114 _V014_J005 _IGKV2-24- F_IGKJ5	GCCTTGCCAGCCCGCTCAGTGCTACACAGAGTGTGAGTGGGGATATTGT GATGACCCAGACTCCACTCTCCTCACCTGTCACCCCTGGACAGCCGGCC TCCATCTCCTGCAGGTCTAGTCAAAGCCTCGTACACAGTGATGGAAACA CCTACTTGAGTTGGCTTCAGCAGAGGCCAGGCCAGCCTCCAAGACTCCT AATTTATAAGATTTCTAACCGGTTCTCTGGGGTCCCAGACAGATTTCAGT GGCAGTGGGGCAGGGACAGATTTACACTGAAAATCAGCAGGGTGGAGG CTGAGGATGTCTGGGGTTTATTACTGCATGCAAGCTACACAATGATGCTA CACAGAGTGTCTGTCGACCCCTTCGGCCAAGGGACACGACTGGAGATTAAA CGTAAGTAATTTTTCACATATTGTCTTCTGAAATTTGGGTCTGATGGCCA GTATTGACTTTTAGAGGCTTGCTACACAGAGTGTCTTGATGGCGCGAGG GAGGC	SEQ ID NO: 6180
hsIGK_0115 _V015_J005 _IGKV2-28- F_IGKJ5	GCCTTGCCAGCCCGCTCAGAACTGCCAAGAGTGTGAGTGGGGATATTGT GATGACTCAGTCTCCACTCTCCCTGCCCCGTACCCCTGGAGAGCCGGCC TCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACA ACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCT GATCTATTTGGGTCTTAATCGGGCCTCCGGGGTCCCTGACAGGTTTCAGT GGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGG CTGAGGATGTTGGGGTTTATTACTGCATGCAAGCTCTACAATGAACTG CCAAGAGTGTCTGTCGACCCCTTCGGCCAAGGGACACGACTGGAGATTAAA CGTAAGTAATTTTTCACATATTGTCTTCTGAAATTTGGGTCTGATGGCCA GTATTGACTTTTAGAGGCTAACTGCCAAGAGTGTCTTGATGGCGCGAGG GAGGC	SEQ ID NO: 6181
hsIGK_0116 _V016_J005 _IGKV2-29- FP_IGKJ5	GCCTTGCCAGCCCGCTCAGTTGGACTGAGAGTGTGAGTGGGATATTGT GATGACCCAGACTCCACTCTCTGTCCGTACCCCTGGACAGCCGGCC TCCATCTCCTGCAAGTCTAGTCAGAGCCTCCTGCATAGTGATGGAAAGA CCTATTTGTATTGGTACCTGCAGAAGCCAGGCCAGTCTCCACAGCTCCT GATCTATGAAGTTTCCAGCCGGTTCTCTGGAGTGCCAGATAGGTTTCAGT	SEQ ID NO: 6182

Name	Sequence	SEQ ID NO
	GGCAGCGGGTCAGGGACAGATTTACACTGAAAATCAGCCGGGTGGAGG CTGAGGATGTTGGGGTTTATTACTGAATGCAAGGTATACACTGATTGGA CTGAGAGTGTCTCGACCCCTTCGGCCAAGGGACACGACTGGAGATTAAA CGTAAGTAATTTTCACTATTGTCTTCTGAAATTTGGGTCTGATGGCCA GTATTGACTTTTAGAGGCTTTGGACTGAGAGTGTCTGATGGCGCGAGG GAGGC	
hsIGK_0117 _V017_J005 _IGKV2-30- F_IGKJ5	GCCTTGCCAGCCCGCTCAGGTAGACACAGAGTGTCTAGTGGGGATGTTGT GATGACTCAGTCTCCACTCTCCCTGCCCCGTACCCCTTGACAGCCGGCC TCCATCTCCTGCAGGTCTAGTCAAAGCCTCGTATACAGTGATGGAAACA CCTACTTGAATTGGTTTCAGCAGAGGCCAGGCCAATCTCCAAGGCGCCT AATTTATAAGGTTTCTAACCAGGACTCTGGGGTCCCAGACAGATTGAGC GGCAGTGGGTGAGGCACTGATTTACACTGAAAATCAGCAGGGTGGAGG CTGAGGATGTTGGGGTTTATTACTGCATGCAAGGTACACACTGAGTAGA CACAGAGTGTCTCGACCCCTTCGGCCAAGGGACACGACTGGAGATTAAA CGTAAGTAATTTTCACTATTGTCTTCTGAAATTTGGGTCTGATGGCCA GTATTGACTTTTAGAGGCTGTAGACACAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6183
hsIGK_0118 _V018_J005 _IGKV2-40- F_IGKJ5	GCCTTGCCAGCCCGCTCAGCACTGTACAGAGTGTCTGAGGATATTGTGAT GACCCAGACTCCACTCTCCCTGCCCCGTACCCCTGGAGAGCCGGCCTCC ATCTCCTGCAGGTCTAGTCAGAGCCTCTTGATAGTGATGATGGAAACA CCTATTTGGACTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCT GATCTATACGCTTTCCTATCGGGCCTCTGGAGTCCCAGACAGGTTGAGT GGCAGTGGGTGAGGCACTGATTTACACTGAAAATCAGCAGGGTGGAGG CTGAGGATGTTGGAGTTTATTACTGCATGCAACGTATAGAGTGACACTG TACAGAGTGTCTCGACCCCTTCGGCCAAGGGACACGACTGGAGATTAAA CGTAAGTAATTTTCACTATTGTCTTCTGAAATTTGGGTCTGATGGCCA GTATTGACTTTTAGAGGCTCACTGTACAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6184
hsIGK_0119 _V019_J005 _IGKV3-07- F_IGKJ5	GCCTTGCCAGCCCGCTCAGGATGATCCAGAGTGTCTCTCAGATACCAC CGGAGAAATTGTAATGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCA GGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTATCCTGGTACCAGCAGAAACCTGGGCAGGCTCCCAGGCTCCT CATCTATGGTGCATCCACCAGGGCCACTGGCATCCCAGCCAGGTTGAGT GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAGTTTATTACTGTCTCAGCAGGATTATACTGAGATGA TCCAGAGTGTCTCGACCCCTTCGGCCAAGGGACACGACTGGAGATTAAA CGTAAGTAATTTTCACTATTGTCTTCTGAAATTTGGGTCTGATGGCCA GTATTGACTTTTAGAGGCTGATGATCCAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6185
hsIGK_0120 _V020_J005	GCCTTGCCAGCCCGCTCAGCGCCAATAAGAGTGTCCCAATTCAGATAC CACCGGAGAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCT	SEQ ID NO: 6186

Name	Sequence	SEQ ID NO
_IGKV3-11-F_IGKJ5	CCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCA GCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTTCAGT GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGC CTGAAGATTTTGCAGTTTATTACTGTCAGCAGCGTAGCAACTGACGCCA ATAAGAGTGTCGTCGACCCTTCGGCCAAGGGACACGACTGGAGATTAAA CGTAAGTAATTTTTCCTACTATTGTCTTCTGAAATTTGGGTCTGATGGCCA GTATTGACTTTTAGAGGCTCGCCAATAAGAGTGTCCTGATGGCGCGAGG GAGGC	
hsIGK_0121_V021_J005_IGKV3-15-F_IGKJ5	GCCTTGCCAGCCCCTCAGTCAAGCCTAGAGTGTCCTCAATTTTCAGATAC CACTGGAGAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTTCAGT GGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGT CTGAAGATTTTGCAGTTTATTACTGTCAGCAGTATAATAACTGATCAAG CCTAGAGTGTCGTCGACCCTTCGGCCAAGGGACACGACTGGAGATTAAA CGTAAGTAATTTTTCCTACTATTGTCTTCTGAAATTTGGGTCTGATGGCCA GTATTGACTTTTAGAGGCTTCAAGCCTAGAGTGTCCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6187
hsIGK_0122_V022_J005_IGKV3-20-F_IGKJ5	GCCTTGCCAGCCCCTCAGACGTGTGTAGAGTGTCATCTCAGATACCAC CGGAGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCA GGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTTCAGT GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGC CTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTGAACGTG TGTAAGAGTGTCGTCGACCCTTCGGCCAAGGGACACGACTGGAGATTAAA CGTAAGTAATTTTTCCTACTATTGTCTTCTGAAATTTGGGTCTGATGGCCA GTATTGACTTTTAGAGGCTACGTGTGTAGAGTGTCCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6188
hsIGK_0123_V023_J005_IGKV3-NL4-FNG_IGKJ5	GCCTTGCCAGCCCCTCAGTCCGTCTAAGAGTGTCCTCAATTTTCAGATAC CACCGGAGAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCT CCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGGGTGTTAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTTCAGT GGCAGTGGGCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGC CTGAAGATTTTGCAGTTTATTACTGTCAGCAGCGTAGCAACTGATCCGT CTAAGAGTGTCGTCGACCCTTCGGCCAAGGGACACGACTGGAGATTAAA CGTAAGTAATTTTTCCTACTATTGTCTTCTGAAATTTGGGTCTGATGGCCA GTATTGACTTTTAGAGGCTTCCGTCTAAGAGTGTCCTGATGGCGCGAGG	SEQ ID NO: 6189

Name	Sequence	SEQ ID NO
	GAGGC	
hsIGK_0124 _V024_J005 _IGKV4-01- F_IGKJ5	GCCTTGCCAGCCCGCTCAGAAGAGCTGAGAGTGTCTGGGGACATCGTGAT GACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGA ACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCT CATTTACTGGGCATCTACCCGGAATCCGGGGTCCCTGACCGATTTCAGT GGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGG CTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTTGAAAGAG CTGAGAGTGTCTGTCGACCCTTCGGCCAAGGGACACGACTGGAGATTAAA CGTAAGTAATTTTCACTATTGTCTTCTGAAATTTGGGTCTGATGGCCA GTATTGACTTTTAGAGGCTAAGAGCTGAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6190
hsIGK_0125 _V025_J005 _IGKV5-02- F_IGKJ5	GCCTTGCCAGCCCGCTCAGTATCGCTCAGAGTGTCCATAATCAGATAC CAGGGCAGAAACGACACTCACGCAGTCTCCAGCATTTCATGTCAGCGACT CCAGGAGACAAAGTCAACATCTCCTGCAAAGCCAGCCAAGACATTGATG ATGATATGAACTGGTACCAACAGAAACCAGGAGAAGCTGCTATTTTCAT TATTCAAGAAGCTACTACTCTCGTTCCTGGAATCCACCTCGATTTCAGT GGCAGCGGGTATGGAACAGATTTTACCCTCACAATTAATAACATAGAAT CTGAGGATGCTGCATATTACTTCTGTCTACAACATGATAATTGATATCG CTCAGAGTGTCTGTCGACCCTTCGGCCAAGGGACACGACTGGAGATTAAA CGTAAGTAATTTTCACTATTGTCTTCTGAAATTTGGGTCTGATGGCCA GTATTGACTTTTAGAGGCTTATCGCTCAGAGTGTCTGATGGCGCGAGG GAGGC	SEQ ID NO: 6191

Primer Sequences for hs-TCRB-P10

Target	Gene specific primer sequence	Primer With Universal Sequence	SEQ ID NO
TCRBV01	GAATGCCCTGACAGCTCTCGC TTATA	GGGCTGGCAAGCCACGTTTGGTGG AATGCCCTGACAGCTCTCGCTTAT A	SEQ ID NO: 6192
TCRBV02	CTCAGAGAAGTCTGAAATATT CGATGATCAATTCTCAGTTG	GGGCTGGCAAGCCACGTTTGGTGC TCAGAGAAGTCTGAAATATTCGAT GATCAATTCTCAGTTG	SEQ ID NO: 6193
TCRBV03-1	CCAAATCGMTTCTCACCTAAA TCTCCAGACAAAAG	GGGCTGGCAAGCCACGTTTGGTGC CAAATCGMTTCTCACCTAAATCTC CAGACAAAAG	SEQ ID NO: 6194
TCRBV03-2	CACCTGACTCTCCAGACAAAAG CTCAT	GGGCTGGCAAGCCACGTTTGGTGC ACCTGACTCTCCAGACAAAAGCTCA T	SEQ ID NO: 6195
TCRBV04- 1/2/3	CCTGAATGCCCCAACAGCTCT C	GGGCTGGCAAGCCACGTTTGGTGC CTGAATGCCCCAACAGCTCTC	SEQ ID NO: 6196
TCRBV05-1	GATTCTCAGGGCGCCAGTTCT CTA	GGGCTGGCAAGCCACGTTTGGTGG ATTCTCAGGGCGCCAGTTCTCTA	SEQ ID NO: 6197
TCRBV05-2	CCTAATTGATTCTCAGCTCAC CACGTCCATA	GGGCTGGCAAGCCACGTTTGGTGC CTAATTGATTCTCAGCTCACCACG TCCATA	SEQ ID NO: 6198
TCRBV05-3	TCAGGGCGCCAGTTCCATG	GGGCTGGCAAGCCACGTTTGGTGT CAGGGCGCCAGTTCCATG	SEQ ID NO: 6199
TCRBV05-4	TCCTAGATTCTCAGGTCTCCA GTTCCCTA	GGGCTGGCAAGCCACGTTTGGTGT CCTAGATTCTCAGGTCTCCAGTTC CCTA	SEQ ID NO: 6200
TCRBV05-5	GAGGAACTTCCCTGATCGAT TCTCAGC	GGGCTGGCAAGCCACGTTTGGTGG AGGAACTTCCCTGATCGATTCTC AGC	SEQ ID NO: 6201
TCRBV05-6	CAACTTCCCTGATCGATTCTC AGGTCA	GGGCTGGCAAGCCACGTTTGGTGC AACTTCCCTGATCGATTCTCAGGT CA	SEQ ID NO: 6202
TCRBV05-7	AGGAACTTCCCTGATCAATT CTCAGGTCA	GGGCTGGCAAGCCACGTTTGGTGA GGAACTTCCCTGATCAATTCTCA GGTCA	SEQ ID NO: 6203
TCRBV05-8	GGAACTTCCCTCCTAGATTT TCAGGTCG	GGGCTGGCAAGCCACGTTTGGTGG GAACTTCCCTCCTAGATTTTCAG GTCG	SEQ ID NO: 6204
TCRBV06-1	CCCCAATGGCTACAATGTCTC CAGATT	GGGCTGGCAAGCCACGTTTGGTGC CCCCAATGGCTACAATGTCTCCAGA TT	SEQ ID NO: 6205

Target	Gene specific primer sequence	Primer With Universal Sequence	SEQ ID NO
TCRBV06-2/3	GGAGAGGTCCCTGATGGCTACAA	GGGCTGGCAAGCCACGTTTGGTGG GAGAGGTCCCTGATGGCTACAA	SEQ ID NO: 6206
TCRBV06-4	TCCCTGATGGTTATAGTGTCTCCAGAGC	GGGCTGGCAAGCCACGTTTGGTGT CCCTGATGGTTATAGTGTCTCCAG AGC	SEQ ID NO: 6207
TCRBV06-5	GGAGAAGTCCCCAATGGCTACAATGTC	GGGCTGGCAAGCCACGTTTGGTGG GAGAAGTCCCCAATGGCTACAATG TC	SEQ ID NO: 6208
TCRBV06-6	AAAGGAGAAGTCCCGAATGGCTACAA	GGGCTGGCAAGCCACGTTTGGTGA AAGGAGAAGTCCCGAATGGCTACA A	SEQ ID NO: 6209
TCRBV06-7	GTTCCCAATGGCTACAATGTCTCCAGATC	GGGCTGGCAAGCCACGTTTGGTGG TTCCCAATGGCTACAATGTCTCCA GATC	SEQ ID NO: 6210
TCRBV06-8	GAAGTCCCCAATGGCTACAATGTCTCTAGATT	GGGCTGGCAAGCCACGTTTGGTGG AAGTCCCCAATGGCTACAATGTCT CTAGATT	SEQ ID NO: 6211
TCRBV06-9	GAGAAGTCCCCGATGGCTACAATGTA	GGGCTGGCAAGCCACGTTTGGTGG AGAAGTCCCCGATGGCTACAATGT A	SEQ ID NO: 6212
TCRBV07-1	GTGATCGGTTCTCTGCACAGAGGT	GGGCTGGCAAGCCACGTTTGGTGG TGATCGGTTCTCTGCACAGAGGT	SEQ ID NO: 6213
TCRBV07-2	CGTTTCTCTGCAGAGAGGACTGG	GGGCTGGCAAGCCACGTTTGGTGC GCTTCTCTGCAGAGAGGACTGG	SEQ ID NO: 6214
TCRBV07-3	GGTTCTTTGCAGTCAGGCCTGA	GGGCTGGCAAGCCACGTTTGGTGG GTTCTTTGCAGTCAGGCCTGA	SEQ ID NO: 6215
TCRBV07-4	CAGTGGTCGGTTCTCTGCAGAGG	GGGCTGGCAAGCCACGTTTGGTGC AGTGGTCGGTTCTCTGCAGAGG	SEQ ID NO: 6216
TCRBV07-5	GCTCAGTGATCAATTCTCCACAGAGAGGT	GGGCTGGCAAGCCACGTTTGGTGG CTCAGTGATCAATTCTCCACAGAG AGGT	SEQ ID NO: 6217
TCRBV07-6/7	TTCTCTGCAGAGAGGCCTGAGG	GGGCTGGCAAGCCACGTTTGGTGT TCTCTGCAGAGAGGCCTGAGG	SEQ ID NO: 6218
TCRBV07-8	CCCAGTGATCGCTTCTTTGCAAGAAA	GGGCTGGCAAGCCACGTTTGGTGC CCAGTGATCGCTTCTTTGCAAGAAA	SEQ ID NO: 6219
TCRBV07-9	CTGCAGAGAGGCCTAAGGGATCT	GGGCTGGCAAGCCACGTTTGGTGC TGCAGAGAGGCCTAAGGGATCT	SEQ ID NO: 6220
TCRBV08-1	GAAGGGTACAATGTCTCTGGAACAACAACTCAAG	GGGCTGGCAAGCCACGTTTGGTGG AAGGGTACAATGTCTCTGGAACA AACTCAAG	SEQ ID NO: 6221

Target	Gene specific primer sequence	Primer With Universal Sequence	SEQ ID NO
TCRBV08-2	GGGGTACTGTGTTTCTTGAAA CAAGCTTGAG	GGGCTGGCAAGCCACGTTTGGTGG GGGTACTGTGTTTCTTGAAACAAG CTTGAG	SEQ ID NO: 6222
TCRBV09	CAGTTCCTGACTTGCACTCT GAACTAAAC	GGGCTGGCAAGCCACGTTTGGTGC AGTTCCTGACTTGCACTCTGAAC TAAAC	SEQ ID NO: 6223
TCRBV10-1	ACTAACAAAGGAGAAGTCTCA GATGGCTACAG	GGGCTGGCAAGCCACGTTTGGTGA CTAACAAAGGAGAAGTCTCAGATG GCTACAG	SEQ ID NO: 6224
TCRBV10-2	AGATAAAGGAGAAGTCCCCGA TGGCTA	GGGCTGGCAAGCCACGTTTGGTGA GATAAAGGAGAAGTCCCCGATGGC TA	SEQ ID NO: 6225
TCRBV10-3	GATACTGACAAAGGAGAAGTC TCAGATGGCTATAG	GGGCTGGCAAGCCACGTTTGGTGG ATACTGACAAAGGAGAAGTCTCAG ATGGCTATAG	SEQ ID NO: 6226
TCRBV11- 1/2/3	CTAAGGATCGATTTTCTGCAG AGAGGCTC	GGGCTGGCAAGCCACGTTTGGTGC TAAGGATCGATTTTCTGCAGAGAG GCTC	SEQ ID NO: 6227
TCRBV12-1	TTGATTCTCAGCACAGATGCC TGATGT	GGGCTGGCAAGCCACGTTTGGTGT TGATTCTCAGCACAGATGCCTGAT GT	SEQ ID NO: 6228
TCRBV12-2	ATTCTCAGCTGAGAGGCCTGA TGG	GGGCTGGCAAGCCACGTTTGGTGA TTCTCAGCTGAGAGGCCTGATGG	SEQ ID NO: 6229
TCRBV12- 3/4	GGATCGATTCTCAGCTAAGAT GCCTAATGC	GGGCTGGCAAGCCACGTTTGGTGG GATCGATTCTCAGCTAAGATGCCT AATGC	SEQ ID NO: 6230
TCRBV12-5	CTCAGCAGAGATGCCTGATGC AACTTTA	GGGCTGGCAAGCCACGTTTGGTGC TCAGCAGAGATGCCTGATGCAACT TTA	SEQ ID NO: 6231
TCRBV13	CTGATCGATTCTCAGCTCAAC AGTTCAGT	GGGCTGGCAAGCCACGTTTGGTGC TGATCGATTCTCAGCTCAACAGTT CAGT	SEQ ID NO: 6232
TCRBV14	TAGCTGAAAGGACTGGAGGGA CGTAT	GGGCTGGCAAGCCACGTTTGGTGT AGCTGAAAGGACTGGAGGGACGTA T	SEQ ID NO: 6233
TCRBV15	CCAGGAGGCCGAACACTTCTT TCT	GGGCTGGCAAGCCACGTTTGGTGC CAGGAGGCCGAACACTTCTTCT	SEQ ID NO: 6234
TCRBV16	GCTAAGTGCCTCCCAAATTCA CCCT	GGGCTGGCAAGCCACGTTTGGTGG CTAAGTGCCTCCCAAATTCACCCT	SEQ ID NO: 6235

Target	Gene specific primer sequence	Primer With Universal Sequence	SEQ ID NO
TCRBV17	CACAGCTGAAAGACCTAACGG AACGT	GGGCTGGCAAGCCACGTTTGGTGC ACAGCTGAAAGACCTAACGGAACG T	SEQ ID NO: 6236
TCRBV18	CTGCTGAATTTCCCAAAGAGG GCC	GGGCTGGCAAGCCACGTTTGGTGC TGCTGAATTTCCCAAAGAGGGCC	SEQ ID NO: 6237
TCRBV19	AGGGTACAGCGTCTCTCGGG	GGGCTGGCAAGCCACGTTTGGTGA GGGTACAGCGTCTCTCGGG	SEQ ID NO: 6238
TCRBV20	GCCTGACCTTGTCCTCTGCA CA	GGGCTGGCAAGCCACGTTTGGTGG CCTGACCTTGTCCTCTGACA	SEQ ID NO: 6239
TCRBV21	ATGAGCGATTTTGTAGCCCAAT GCTCCA	GGGCTGGCAAGCCACGTTTGGTGA TGAGCGATTTTGTAGCCCAATGCTC CA	SEQ ID NO: 6240
TCRBV22	TGAAGGCTACGTGTCTGCCAA GAG	GGGCTGGCAAGCCACGTTTGGTGT GAAGGCTACGTGTCTGCCAAGAG	SEQ ID NO: 6241
TCRBV23	CTCATCTCAATGCCCCAAGAA CGC	GGGCTGGCAAGCCACGTTTGGTGC TCATCTCAATGCCCCAAGAACGC	SEQ ID NO: 6242
TCRBV24	AGATCTCTGATGGATACAGTG TCTCTCGACA	GGGCTGGCAAGCCACGTTTGGTGA GATCTCTGATGGATACAGTGTCTC TCGACA	SEQ ID NO: 6243
TCRBV25	AGATCTTTCCTCTGAGTCAAC AGTCTCCAGAATA	GGGCTGGCAAGCCACGTTTGGTGA GATCTTTCCTCTGAGTCAACAGTC TCCAGAATA	SEQ ID NO: 6244
TCRBV26	CACTGAAAAAGGAGATATCTC TGAGGGGTATCATG	GGGCTGGCAAGCCACGTTTGGTGC ACTGAAAAAGGAGATATCTCTGAG GGGTATCATG	SEQ ID NO: 6245
TCRBV27	GTTCTGAAGGGTACAAAGTC TCTCGAAAAG	GGGCTGGCAAGCCACGTTTGGTGG TTCCTGAAGGGTACAAAGTCTCTC GAAAAG	SEQ ID NO: 6246
TCRBV28	CTGAGGGGTACAGTGTCTCTA GAGAGA	GGGCTGGCAAGCCACGTTTGGTGC TGAGGGGTACAGTGTCTCTAGAGA GA	SEQ ID NO: 6247
TCRBV29	AGCCGCCCAAACCTAACATTC TCAA	GGGCTGGCAAGCCACGTTTGGTGA GCCGCCCAAACCTAACATTCTCAA	SEQ ID NO: 6248
TCRBV30	CCCAGGACCGGCAGTTCA	GGGCTGGCAAGCCACGTTTGGTGC CCAGGACCGGCAGTTCA	SEQ ID NO: 6249
TCRBVA	TTGATTAGAGACATATCCCTA TTGAAAATATTTCTTGCA	GGGCTGGCAAGCCACGTTTGGTGT TGATTAGAGACATATCCCTATTGA AAATATTTCTTGCA	SEQ ID NO: 6250

Target	Gene specific primer sequence	Primer With Universal Sequence	SEQ ID NO
TCRBVB	AGATGCCCTGAGTCAGCATAG TCATTCTAAC	GGGCTGGCAAGCCACGTTTGGTGA GATGCCCTGAGTCAGCATAGTCAT TCTAAC	SEQ ID NO: 6251
TCRBJ1-1	GTCTTACCTACAACGTGAGT CTGGTGCC	CCGGGAGCTGCATGTGTCAGAGGG TCTTACCTACAACGTGAGTCTGG TGCC	SEQ ID NO: 6252
TCRBJ1-2	CCTTACCTACAACGGTTAACCC TGGTCCC	CCGGGAGCTGCATGTGTCAGAGGC CTTACCTACAACGGTTAACCTGGT CCC	SEQ ID NO: 6253
TCRBJ1-3	CTTACTCACCTACAACAGTGA GCCAACTTCC	CCGGGAGCTGCATGTGTCAGAGGC TTACTCACCTACAACAGTGAGCCA ACTTCC	SEQ ID NO: 6254
TCRBJ1-4	ATACCCAAGACAGAGAGCTGG GTTCC	CCGGGAGCTGCATGTGTCAGAGGA TACCCAAGACAGAGAGCTGGGTTCC	SEQ ID NO: 6255
TCRBJ1-5	AACTTACCTAGGATGGAGAGT CGAGTCCC	CCGGGAGCTGCATGTGTCAGAGGA ACTTACCTAGGATGGAGAGTCGAG TCCC	SEQ ID NO: 6256
TCRBJ1-6	CTGTCACAGTGAGCCTGGTCC C	CCGGGAGCTGCATGTGTCAGAGGC TGTCACAGTGAGCCTGGTCCC	SEQ ID NO: 6257
TCRBJ2-1	CACGGTGAGCCGTGTCCC	CCGGGAGCTGCATGTGTCAGAGGC ACGGTGAGCCGTGTCCC	SEQ ID NO: 6258
TCRBJ2-2	CCAGTACGGTCAGCCTAGAGC C	CCGGGAGCTGCATGTGTCAGAGGC CAGTACGGTCAGCCTAGAGCC	SEQ ID NO: 6259
TCRBJ2-3	CACTGTCAGCCGGGTGCC	CCGGGAGCTGCATGTGTCAGAGGC ACTGTCAGCCGGGTGCC	SEQ ID NO: 6260
TCRBJ2-4	CACTGAGAGCCGGGTCCC	CCGGGAGCTGCATGTGTCAGAGGC ACTGAGAGCCGGGTCCC	SEQ ID NO: 6261
TCRBJ2-5	ACCAGGAGCCGCGTGCC	CCGGGAGCTGCATGTGTCAGAGGA CCAGGAGCCGCGTGCC	SEQ ID NO: 6262
TCRBJ2-6	CACGGTCAGCCTGCTGCC	CCGGGAGCTGCATGTGTCAGAGGC ACGGTCAGCCTGCTGCC	SEQ ID NO: 6263
TCRBJ2-7	GACCGTGAGCCTGGTGCC	CCGGGAGCTGCATGTGTCAGAGGG ACCGTGAGCCTGGTGCC	SEQ ID NO: 6264

Primer Sequences for hs-IGH-D

Target	Gene specific primer sequence	Primer with Universal Sequence	SEQ ID NO
IGHD1- 14_ver10	CGCTAGCTGGGGCTCACAGTG CTCA	GGGCTGGCAAGCCACGTTTGGTGCG CTAGCTGGGGCTCACAGTGCTCA	SEQ ID NO: 6265
IGHD2- 02_ver10	CACTGGGCTCAGAGTCCTCTC CCACAC	GGGCTGGCAAGCCACGTTTGGTGCA CTGGGCTCAGAGTCCTCTCCACAC	SEQ ID NO: 6266
IGHD2- 15_ver10	CCTATACAGCACTGGGCTCAG AGTCCTCTCTGAGAC	GGGCTGGCAAGCCACGTTTGGTGCC TATACAGCACTGGGCTCAGAGTCCT CTCTGAGAC	SEQ ID NO: 6267
IGHD3- 03_ver10	CCTAAGCCAGGGGCAGACCCG AGT	GGGCTGGCAAGCCACGTTTGGTGCC TAAGCCAGGGGCAGACCCGAGT	SEQ ID NO: 6268
IGHD3- 10_ver10	ACAGTGTACAGAGTCCATCA AAAACCCATGCCTGG	GGGCTGGCAAGCCACGTTTGGTGAC AGTGTACAGAGTCCATCAAAAACC CATGCCTGG	SEQ ID NO: 6269
IGHD3- 16_ver10	CACTATCCACATAAGCGAGGG ACAGACCCGAGT	GGGCTGGCAAGCCACGTTTGGTGCA CTATCCACATAAGCGAGGGACAGAC CCGAGT	SEQ ID NO: 6270
IGHD4- 04_ver10	TGCCCTCGATGGCAGGCGGA	GGGCTGGCAAGCCACGTTTGGTGTG CCCTCGATGGCAGGCGGA	SEQ ID NO: 6271
IGHD4- 11_ver10	CCTCTTCCAGGACAGTCCTCA GTGGCATCACAG	GGGCTGGCAAGCCACGTTTGGTGCC TCTTCCAGGACAGTCCTCAGTGGCA TCACAG	SEQ ID NO: 6272
IGHD4- 23_ver10	CAGACCCACCTGCCCTCAATG GCAG	GGGCTGGCAAGCCACGTTTGGTGCA GACCCACCTGCCCTCAATGGCAG	SEQ ID NO: 6273
IGHD5- 12_ver10	TCTCCAGGGAGACACTGTGCA TGTCTGGTACCTAA	GGGCTGGCAAGCCACGTTTGGTGTC TCCAGGGAGACACTGTGCATGTCTG GTACCTAA	SEQ ID NO: 6274
IGHD5- 24_ver10	GGGACACAGTGCATGTCTGGT CCCTGA	GGGCTGGCAAGCCACGTTTGGTGGG GACACAGTGCATGTCTGGTCCCTGA	SEQ ID NO: 6275
IGHD6- 13_ver10	GGACCCCTATTCCAGACACCA GACAGAGGC	GGGCTGGCAAGCCACGTTTGGTGGG ACCCCTATTCCAGACACCAGACAGA GGC	SEQ ID NO: 6276
IGHD6- 19_ver10	CCCCACTCCAGACACCAGACA GAGGG	GGGCTGGCAAGCCACGTTTGGTGCC CCACTCCAGACACCAGACAGAGGG	SEQ ID NO: 6277
IGHD7- 27_ver10	GGGGTCTCCACGTGTTTTGG GGCTAAC	GGGCTGGCAAGCCACGTTTGGTGGG GGTCTCCACGTGTTTTGGGGCTAA C	SEQ ID NO: 6278
IGHD1- 26_ver10	GCTAGCTGGGGCTGCCAGTCC TCA	GGGCTGGCAAGCCACGTTTGGTGGC TAGCTGGGGCTGCCAGTCCTCA	SEQ ID NO: 6279

Primer Sequences for IGK and IGL

Target	Gene specific primer sequence	Primer with Universal Sequence	SEQ ID NO
IGK_V_01-05_F_D10	TCTGCATCTGTAGGAGACA GAGTCACCATCACTTG	GGGCTGGCAAGCCACGTTTGG TGTCTGCATCTGTAGGAGACA GAGTCACCATCACTTG	SEQ ID NO: 6280
IGK_V_01-08_F_D10	TCTGCATCTACAGGAGACA GAGTCACCATCACTTG	GGGCTGGCAAGCCACGTTTGG TGTCTGCATCTACAGGAGACA GAGTCACCATCACTTG	SEQ ID NO: 6281
IGK_V_01-35_P_D10	CTGCATCTGTAAGGAGACA GTGTCACCATCACTTG	GGGCTGGCAAGCCACGTTTGG TGCTGCATCTGTAAGGAGACA GTGTCACCATCACTTG	SEQ ID NO: 6282
IGK_V_1D-08_F_D10	TCTGCATCTACAGGAGACA GAGTCACCATCAGTTG	GGGCTGGCAAGCCACGTTTGG TGTCTGCATCTACAGGAGACA GAGTCACCATCAGTTG	SEQ ID NO: 6283
IGK_V_1D-22_P_D10	ACTGCATCTGTAGGAGAGA GAGTCACCATCACTTG	GGGCTGGCAAGCCACGTTTGG TGA CTGCATCTGTAGGAGAGA GAGTCACCATCACTTG	SEQ ID NO: 6284
IGK_V_1D-35_P_D10	GCATCTGTAAGGAGACAGC GTCACCATCACTTG	GGGCTGGCAAGCCACGTTTGG TGGCATCTGTAAGGAGACAGC GTCACCATCACTTG	SEQ ID NO: 6285
IGK_V_1D-42_F_D10	GTCTGCATCTGTAGGAGAC AGAGTCAGTATCATTTG	GGGCTGGCAAGCCACGTTTGG TGGTCTGCATCTGTAGGAGAC AGAGTCAGTATCATTTG	SEQ ID NO: 6286
IGK_V_02-04_P_D10	GGAGAGCCGGCCTCCATCT CCTG	GGGCTGGCAAGCCACGTTTGG TGGGAGAGCCGGCCTCCATCT CCTG	SEQ ID NO: 6287
IGK_V_02-10_P_D10	CCTGGAGAGCCAGCCTCCA TCTCCTG	GGGCTGGCAAGCCACGTTTGG TGCCTGGAGAGCCAGCCTCCA TCTCCTG	SEQ ID NO: 6288
IGK_V_02-18_P_D10	CTGGAGAGCCGGCCTCCAT CTCTTG	GGGCTGGCAAGCCACGTTTGG TGCTGGAGAGCCGGCCTCCAT CTCTTG	SEQ ID NO: 6289
IGK_V_02-19_P_D10	TCTTCCTTGGAGAGCCATC CTCCATTTCTG	GGGCTGGCAAGCCACGTTTGG TGTCTTCCTTGGAGAGCCATC CTCCATTTCTG	SEQ ID NO: 6290

Target	Gene specific primer sequence	Primer with Universal Sequence	SEQ ID NO
IGK_V_02-24_F_D10	GGACAGCCGGCCTCCATCTCCTG	GGGCTGGCAAGCCACGTTTGG TGGGACAGCCGGCCTCCATCTCCTG	SEQ ID NO: 6291
IGK_V_02-28_F_D10	TGGAGAGCCGGCCTCCATCTCCTG	GGGCTGGCAAGCCACGTTTGG TGTGGAGAGCCGGCCTCCATCTCCTG	SEQ ID NO: 6292
IGK_V_02-38_P_D10	ATAATATTTGTACATAACTTTGTACTTCATCTCCTG	GGGCTGGCAAGCCACGTTTGG TGATAATATTTGTACATAACTTTGTACTTCATCTCCTG	SEQ ID NO: 6293
IGK_V_2D-14_P_D10	CCCCTGGAAAGCCAGCCTCTATCTCCTG	GGGCTGGCAAGCCACGTTTGG TGCCCCTGGAAAGCCAGCCTCTATCTCCTG	SEQ ID NO: 6294
IGK_V_2D-19_P_D10	CTCTTCCTTGGAGAGCCATCCTCCATTTCTG	GGGCTGGCAAGCCACGTTTGG TGCTCTTCCTTGGAGAGCCATCCTCCATTTCTG	SEQ ID NO: 6295
IGK_V_2D-24_O_D10	GGACAGCCGGCCTCCATCTCCTT	GGGCTGGCAAGCCACGTTTGG TGGGACAGCCGGCCTCCATCTCCTT	SEQ ID NO: 6296
IGK_V_2D-26_F_D10	CCTGGAGAGCAGGCCTCCATGTCCTG	GGGCTGGCAAGCCACGTTTGG TGCCCTGGAGAGCAGGCCTCCATGTCCTG	SEQ ID NO: 6297
IGK_V_03-07_F_D10	CCAGGGGAAAGAGCCACCTCTCCTG	GGGCTGGCAAGCCACGTTTGG TGCCAGGGGAAAGAGCCACCTCTCCTG	SEQ ID NO: 6298
IGK_V_03-07_P_D10	TCCAGGGGAAAGAGTCACCTCTCCTG	GGGCTGGCAAGCCACGTTTGG TGTCCAGGGGAAAGAGTCACCTCTCCTG	SEQ ID NO: 6299
IGK_V_03-25_P_D10	TCTTTGTCTCTGGAGAAAAAAGCCACCCTGACTTG	GGGCTGGCAAGCCACGTTTGG TGTCTTTGTCTCTGGAGAAAAAAGCCACCCTGACTTG	SEQ ID NO: 6300
IGK_V_03-31_P_D10	TCTCTAGGGGAAAAAGCCACCTCACCTA	GGGCTGGCAAGCCACGTTTGG TGTCTCTAGGGGAAAAAGCCACCTCACCTA	SEQ ID NO: 6301
IGK_V_03-34_P_D10	GGGGAAGGAGCCACCCTCACCTG	GGGCTGGCAAGCCACGTTTGG TGGGGGAAGGAGCCACCCTCACCTG	SEQ ID NO: 6302

Target	Gene specific primer sequence	Primer with Universal Sequence	SEQ ID NO
IGK_V_04-01_F_D10	GGGCGAGAGGGCCACCATC AACTG	GGGCTGGCAAGCCACGTTTGG TGGGGCGAGAGGGCCACCATC AACTG	SEQ ID NO: 6303
IGK_V_05-02_F_D10	GCGACTCCAGGAGACAAAG TCAACATCTCCTG	GGGCTGGCAAGCCACGTTTGG TGGCGACTCCAGGAGACAAAG TCAACATCTCCTG	SEQ ID NO: 6304
IGK_V_06-21_O_D10	CTGTGACTCCAAAGGAGAA AGTCACCATCACCTG	GGGCTGGCAAGCCACGTTTGG TGCTGTGACTCCAAAGGAGAA AGTCACCATCACCTG	SEQ ID NO: 6305
IGK_V_6D-41_F_D10	ACTCCAGGGGAGAAAGTCA CCATCACCTG	GGGCTGGCAAGCCACGTTTGG TGA CTCCAGGGGAGAAAGTCA CCATCACCTG	SEQ ID NO: 6306
IGK_V_07-03_P_D10	CAGGACAGAGGGCCACCAT CACCTG	GGGCTGGCAAGCCACGTTTGG TGCAGGACAGAGGGCCACCAT CACCTG	SEQ ID NO: 6307
IGL_V_R1-20_P_D10	GCAGGACACTCACTCCCC ACCTG	GGGCTGGCAAGCCACGTTTGG TGGCAGGACACTCACTCCCC ACCTG	SEQ ID NO: 6308
IGL_V_R1-63_P_D10	TGGGCCAGAGGGTCACCAT CTCCTG	GGGCTGGCAAGCCACGTTTGG TGTGGGCCAGAGGGTCACCAT CTCCTG	SEQ ID NO: 6309
IGL_V_R1-68_P_D10	GGGCAGGTGGGTACCAGCT CCTG	GGGCTGGCAAGCCACGTTTGG TGGGGCAGGTGGGTACCAGCT CCTG	SEQ ID NO: 6310
IGL_V_R1-70_P_D10	CGTGGGACAGAAGGTCACC CTCTCCTG	GGGCTGGCAAGCCACGTTTGG TGCGTGGGACAGAAGGTCACC CTCTCCTG	SEQ ID NO: 6311
IGL_V_R4-59_P_D10	TCTCTGGGAGCATCTTCCA GACTCACCTG	GGGCTGGCAAGCCACGTTTGG TGTCTCTGGGAGCATCTTCCA GACTCACCTG	SEQ ID NO: 6312
IGL_V_R4-64_P_D10	CACCTCCGGATCAGCCAGA CTCTCCTG	GGGCTGGCAAGCCACGTTTGG TGCACCTCCGGATCAGCCAGA CTCTCCTG	SEQ ID NO: 6313
IGL_V_R4-65_P_D10	CCGGGAGCATGAGCCAGAC TTACCTG	GGGCTGGCAAGCCACGTTTGG TGCCGGGAGCATGAGCCAGAC TTACCTG	SEQ ID NO: 6314

Target	Gene specific primer sequence	Primer with Universal Sequence	SEQ ID NO
IGL_V_R4-66-1_P_D10	CTCTGCACATCTGAGAAAT GCTATAAGACTTCCCTG	GGGCTGGCAAGCCACGTTTGG TGCTCTGCACATCTGAGAAAT GCTATAAGACTTCCCTG	SEQ ID NO: 6315
IGL_V_R5-58_P_D10	TGTGGGAGCCTCGGTCAAG CTTACCTC	GGGCTGGCAAGCCACGTTTGG TGTGTGGGAGCCTCGGTCAAG CTTACCTC	SEQ ID NO: 6316
IGL_V_01-36_F_D10	CCCAGGCAGAGGGTCACCA TCTCCTG	GGGCTGGCAAGCCACGTTTGG TGCCCAGGCAGAGGGTCACCA TCTCCTG	SEQ ID NO: 6317
IGL_V_01-40_F_D10	CCAGGGCAGAGGGTCACCA TCTCCTG	GGGCTGGCAAGCCACGTTTGG TGCCAGGGCAGAGGGTCACCA TCTCCTG	SEQ ID NO: 6318
IGL_V_01-44_F_D10	CCGGGCAGAGGGTCACCAT CTCTTG	GGGCTGGCAAGCCACGTTTGG TGCCGGGCAGAGGGTCACCAT CTCTTG	SEQ ID NO: 6319
IGL_V_01-51_F_D10	CCCCAGGACAGAAGGTCAC CATCTCCTG	GGGCTGGCAAGCCACGTTTGG TGCCCCAGGACAGAAGGTCAC CATCTCCTG	SEQ ID NO: 6320
IGL_V_01-62_P_D10	CCACAAGGCAGAGGCTCAC TGTCTCCTG	GGGCTGGCAAGCCACGTTTGG TGCCACAAGGCAGAGGCTCAC TGTCTCCTG	SEQ ID NO: 6321
IGL_V_02-08_F_D10	GTCTCCTGGACAGTCAGTC ACCATCTCCTG	GGGCTGGCAAGCCACGTTTGG TGGTCTCCTGGACAGTCAGTC ACCATCTCCTG	SEQ ID NO: 6322
IGL_V_02-14_F_D10	GTCTCCTGGACAGTCGATC ACCATCTCCTG	GGGCTGGCAAGCCACGTTTGG TGGTCTCCTGGACAGTCGATC ACCATCTCCTG	SEQ ID NO: 6323
IGL_V_02-33_O_D10	TCCTGGACAGTCGGTCACC ATCTCCTG	GGGCTGGCAAGCCACGTTTGG TGTCTGGACAGTCGGTCACC ATCTCCTG	SEQ ID NO: 6324
IGL_V_02-34_P_D10	CTGGGACTTGGGGTAAACA GTCACCATCTTCTG	GGGCTGGCAAGCCACGTTTGG TGCTGGGACTTGGGGTAAACA GTCACCATCTTCTG	SEQ ID NO: 6325
IGL_V_03-01_F_D10	CCAGGACAGACAGCCAGCA TCACCTG	GGGCTGGCAAGCCACGTTTGG TGCCAGGACAGACAGCCAGCA TCACCTG	SEQ ID NO: 6326

Target	Gene specific primer sequence	Primer with Universal Sequence	SEQ ID NO
IGL_V_03-02_P_D10	CTTTGGGACGTACGGCCAG GATCATCTG	GGGCTGGCAAGCCACGTTTGG TGCTTTGGGACGTACGGCCAG GATCATCTG	SEQ ID NO: 6327
IGL_V_03-04_P_D10	CTTTGGGACAGATGGCCAG GATCACCTG	GGGCTGGCAAGCCACGTTTGG TGCTTTGGGACAGATGGCCAG GATCACCTG	SEQ ID NO: 6328
IGL_V_03-06_P_D10	CCAGGACAGGCAGCCATGA TCACCTG	GGGCTGGCAAGCCACGTTTGG TGCCAGGACAGGCAGCCATGA TCACCTG	SEQ ID NO: 6329
IGL_V_03-07_P_D10	TGGGACAGAGGGCCAGGAT CACCTA	GGGCTGGCAAGCCACGTTTGG TGTGGGACAGAGGGCCAGGAT CACCTA	SEQ ID NO: 6330
IGL_V_03-09_FP_D10	GGGACAGGCGGCCAGGATT ACCTG	GGGCTGGCAAGCCACGTTTGG TGGGGACAGGCGGCCAGGATT ACCTG	SEQ ID NO: 6331
IGL_V_03-10_F_D10	CCAGGACAAACGGCCAGGA TCACCTG	GGGCTGGCAAGCCACGTTTGG TGCCAGGACAAACGGCCAGGA TCACCTG	SEQ ID NO: 6332
IGL_V_03-12_F_D10	CACAGCACAGATGGCCAGG ATCACCTG	GGGCTGGCAAGCCACGTTTGG TGCACAGCACAGATGGCCAGG ATCACCTG	SEQ ID NO: 6333
IGL_V_03-13_P_D10	CCAGGACAGACAGCCAGGA TCAGCTG	GGGCTGGCAAGCCACGTTTGG TGCCAGGACAGACAGCCAGGA TCAGCTG	SEQ ID NO: 6334
IGL_V_03-15_P_D10	CCCCAGGACAGATGACCAG GATCACCTG	GGGCTGGCAAGCCACGTTTGG TGCCCCAGGACAGATGACCAG GATCACCTG	SEQ ID NO: 6335
IGL_V_03-16_F_D10	CCCTAGGACAGATGGCCAG GATCACCTG	GGGCTGGCAAGCCACGTTTGG TGCCCTAGGACAGATGGCCAG GATCACCTG	SEQ ID NO: 6336
IGL_V_03-17_P_D10	GTGTCTGTGGACAGTCAGC AAGGGTAACCTG	GGGCTGGCAAGCCACGTTTGG TGGTGTCTGTGGACAGTCAGC AAGGGTAACCTG	SEQ ID NO: 6337
IGL_V_03-19_F_D10	GGCCTTGGGACAGACAGTC AGGATCACATG	GGGCTGGCAAGCCACGTTTGG TGGGCCTTGGGACAGACAGTC AGGATCACATG	SEQ ID NO: 6338

Target	Gene specific primer sequence	Primer with Universal Sequence	SEQ ID NO
IGL_V_03-21_F_D10	CCCCAGGAAAGACGGCCAG GATTACCTG	GGGCTGGCAAGCCACGTTTGG TGCCCCAGGAAAGACGGCCAG GATTACCTG	SEQ ID NO: 6339
IGL_V_03-22_FP_D10	CCCAGGACAGAAAGCCAGG ATCACCTG	GGGCTGGCAAGCCACGTTTGG TGCCCAGGACAGAAAGCCAGG ATCACCTG	SEQ ID NO: 6340
IGL_V_03-24_P_D10	CAGTAGCTCCAGGACAGAT GACTAGGATCACCTG	GGGCTGGCAAGCCACGTTTGG TGCAGTAGCTCCAGGACAGAT GACTAGGATCACCTG	SEQ ID NO: 6341
IGL_V_03-25_F_D10	CAGGACAGACGGCCAGGAT CACCTG	GGGCTGGCAAGCCACGTTTGG TGCAGGACAGACGGCCAGGAT CACCTG	SEQ ID NO: 6342
IGL_V_03-26_P_D10	CCTGGGACAGTCAGCCAGG GTAACCTG	GGGCTGGCAAGCCACGTTTGG TGCCTGGGACAGTCAGCCAGG GTAACCTG	SEQ ID NO: 6343
IGL_V_03-27_F_D10	CGGGACAGACAGCCAGGAT CACCTG	GGGCTGGCAAGCCACGTTTGG TGCGGGACAGACAGCCAGGAT CACCTG	SEQ ID NO: 6344
IGL_V_03-29_P_D10	CCCAGGACAGACACCCAGG ATCACCTG	GGGCTGGCAAGCCACGTTTGG TGCCCAGGACAGACACCCAGG ATCACCTG	SEQ ID NO: 6345
IGL_V_03-30_P_D10	CCCCATTACAGATGGCCAG GATCACCTG	GGGCTGGCAAGCCACGTTTGG TGCCCCATTACAGATGGCCAG GATCACCTG	SEQ ID NO: 6346
IGL_V_03-31_P_D10	GCCTTGGGATAGACAGCCA GGATCACCTG	GGGCTGGCAAGCCACGTTTGG TGGCCTTGGGATAGACAGCCA GGATCACCTG	SEQ ID NO: 6347
IGL_V_03-32_O_D10	CCTTGGGACAAATGGCCAG GATCACCTG	GGGCTGGCAAGCCACGTTTGG TGCCTTGGGACAAATGGCCAG GATCACCTG	SEQ ID NO: 6348
IGL_V_04-03_F_D10	CTGGGAGCCTCGATCAAGC TCACCTG	GGGCTGGCAAGCCACGTTTGG TGCTGGGAGCCTCGATCAAGC TCACCTG	SEQ ID NO: 6349
IGL_V_04-60_F_D10	CCTGGGATCCTCGGTCAAG CTCACCTG	GGGCTGGCAAGCCACGTTTGG TGCCTGGGATCCTCGGTCAAG CTCACCTG	SEQ ID NO: 6350

Target	Gene specific primer sequence	Primer with Universal Sequence	SEQ ID NO
IGL_V_04-69_F_D10	GGGAGCCTCGGTCAAGCTC ACCTG	GGGCTGGCAAGCCACGTTTGG TGGGGAGCCTCGGTCAAGCTC ACCTG	SEQ ID NO: 6351
IGL_V_05-37_F_D10	TCCTGGAGAATCCGCCAGA CTCACCTG	GGGCTGGCAAGCCACGTTTGG TGTCTGGAGAATCCGCCAGA CTCACCTG	SEQ ID NO: 6352
IGL_V_05-39_F_D10	TCTCCTGGAGCATCAGCCA GATTCACCTG	GGGCTGGCAAGCCACGTTTGG TGTCTCCTGGAGCATCAGCCA GATTCACCTG	SEQ ID NO: 6353
IGL_V_05-45_F_D10	TCCTGGAGCATCAGCCAGT CTCACCTG	GGGCTGGCAAGCCACGTTTGG TGTCTGGAGCATCAGCCAGT CTCACCTG	SEQ ID NO: 6354
IGL_V_05-48_O_D10	TCCTGGAGCATCAGCCAGA CTCACCTG	GGGCTGGCAAGCCACGTTTGG TGTCTGGAGCATCAGCCAGA CTCACCTG	SEQ ID NO: 6355
IGL_V_05-52_F_D10	GCATCTTCTGGAGCATCAG TCAGACTCACCTG	GGGCTGGCAAGCCACGTTTGG TGGCATCTTCTGGAGCATCAG TCAGACTCACCTG	SEQ ID NO: 6356
IGL_V_06-57_F_D10	TCCGGGGAAGACG GTAACC ATCTCCTG	GGGCTGGCAAGCCACGTTTGG TGTCCGGGGAAGACG GTAACC ATCTCCTG	SEQ ID NO: 6357
IGL_V_07-35_P_D10	CCCAGGAGGGACAGTCACT CTCACCTA	GGGCTGGCAAGCCACGTTTGG TGCCCAGGAGGGACAGTCACT CTCACCTA	SEQ ID NO: 6358
IGL_V_07-43_F_D10	CCCAGGAGGGACAGTCACT CTCACCTG	GGGCTGGCAAGCCACGTTTGG TGCCCAGGAGGGACAGTCACT CTCACCTG	SEQ ID NO: 6359
IGL_V_08-61_F_D10	CCCCTGGAGGGACAGTCAC ACTCACTTG	GGGCTGGCAAGCCACGTTTGG TGCCCCTGGAGGGACAGTCAC ACTCACTTG	SEQ ID NO: 6360
IGL_V_09-49_F_D10	TGGGAGCCTCGGTCACT CACCTG	GGGCTGGCAAGCCACGTTTGG TGTGGGAGCCTCGGTCACT CACCTG	SEQ ID NO: 6361
IGL_V_10-54_F_D10	CTTGAGACAGACCGCCACA CTCACCTG	GGGCTGGCAAGCCACGTTTGG TGCTTGAGACAGACCGCCACA CTCACCTG	SEQ ID NO: 6362

Target	Gene specific primer sequence	Primer with Universal Sequence	SEQ ID NO
IGK_J_01_F_D10	TTCTACTCACGTTTGATTT CCACCTTGGTCCC	CCGGGAGCTGCATGTGTCAGA GGTTCTACTCACGTTTGATTT CCACCTTGGTCCC	SEQ ID NO: 6363
IGK_J_02_F_D10	AAGTACTTACGTTTGATCT CCAGCTTGGTCCC	CCGGGAGCTGCATGTGTCAGA GGAAGTACTTACGTTTGATCT CCAGCTTGGTCCC	SEQ ID NO: 6364
IGK_J_03_F_D10	ACAGATGTACTTACGTTTG ATATCCACTTTGGTCCC	CCGGGAGCTGCATGTGTCAGA GGACAGATGTACTTACGTTTG ATATCCACTTTGGTCCC	SEQ ID NO: 6365
IGK_J_04_F_D10	CACTTACGTTTGATCTCCA CCTTGGTCCC	CCGGGAGCTGCATGTGTCAGA GGCACTTACGTTTGATCTCCA CCTTGGTCCC	SEQ ID NO: 6366
IGK_J_05_F_D10	GAAAAATTACTTACGTTTA ATCTCCAGTCGTGTCCC	CCGGGAGCTGCATGTGTCAGA GGGAAAAATTACTTACGTTTA ATCTCCAGTCGTGTCCC	SEQ ID NO: 6367
IGL_J_01_F_D10	CTTACCTAGGACGGTGACC TTGGTCCC	CCGGGAGCTGCATGTGTCAGA GGCTTACCTAGGACGGTGACC TTGGTCCC	SEQ ID NO: 6368
IGL_J_02_F_D10	ACCTAGGACGGTCAGCTTG GTCCC	CCGGGAGCTGCATGTGTCAGA GGACCTAGGACGGTCAGCTTG GTCCC	SEQ ID NO: 6369
IGL_J_04_O_D10	AAGAAGAGACTCATCTAAA ATGATCAGCTGGGTTC	CCGGGAGCTGCATGTGTCAGA GGAAGAAGAGACTCATCTAAA ATGATCAGCTGGGTTC	SEQ ID NO: 6370
IGL_J_05_O_D10	ATCTAGGACGGTCAGCTCC GTCCC	CCGGGAGCTGCATGTGTCAGA GGATCTAGGACGGTCAGCTCC GTCCC	SEQ ID NO: 6371
IGL_J_06_F_D10	GAGGACGGTCACCTTGGTG CC	CCGGGAGCTGCATGTGTCAGA GGGAGGACGGTCACCTTGGTG CC	SEQ ID NO: 6372
IGL_J_07_F_D10	AGGACGGTCAGCTGGGTGC C	CCGGGAGCTGCATGTGTCAGA GGAGGACGGTCAGCTGGGTGC C	SEQ ID NO: 6373
IGK_J_del_F_D10	CTGCAGACTCATGAGGAGT CGCCC	CCGGGAGCTGCATGTGTCAGA GGCTGCAGACTCATGAGGAGT CGCCC	SEQ ID NO: 6374

CLAIMS

1. A method for sequencing mRNA encoding an adaptive immune receptor
comprising reverse transcribing the mRNA to obtain cDNA and amplifying the
5 cDNA with C region primers and V region primers and sequencing the
amplicons.