

COMPOSITIONS AND METHODS RELATED TO HUMAN NEUTRALIZING ANTIBODIES TO HEPATITIS B

CROSS REFERENCE TO RELATED APPLICATIONS

- [0001] This application claims priority to U.S. provisional patent application no. 62/898,735, filed September 11, 2019, and to U.S. provisional patent application no. 62/982,276, filed February 27, 2020, the entire disclosures of each of which are incorporated herein by reference in their entireties.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

- [0002] This invention was made with government support under grant no. UL1TR001866 awarded by The National Institutes of Health. The government has certain rights in the invention.

SEQUENCE LISTING

- [0003] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on September 9, 2020, is named 076091_00092_SL.txt and is 307,317 bytes in size.

BACKGROUND

- [0004] Despite the existence of effective vaccines, hepatitis B virus (HBV) infection remains a major global health problem with an estimated 257 million people living with the infection. Whereas 95% of adults and 50-75% of children between the ages of 1 and 5 years spontaneously control HBV, only 10% of infants recover naturally. The remainder develop a chronic infection that can lead to liver cirrhosis and hepatocellular carcinoma. Although chronic infection can be suppressed with antiviral medications, there is no effective curative therapy (Dienstag, 2008; Revill et al., 2016; Thomas, 2019).

- [0005] HBV is an enveloped double-stranded DNA virus of the *Hepadnaviridae* family. Its genome is the smallest genome among pathogenic human DNA viruses, with only four open reading frames. Infected liver cells produce both infectious HBV virions (Dane particles) and non-infectious subviral particles (Australia antigen) (Dane et al., 1970; Hu and Liu, 2017). The virion is a 42 nm-diameter particle containing the viral genome and HBV core antigen (HBcAg) encapsidated by a lipid membrane containing the hepatitis B surface

antigen (HBsAg) (Blumberg, 1964; Venkatakrishnan and Zlotnick, 2016). Subviral particles lack the viral genome.

[0006] HBV strains were originally grouped into four HBsAg serotypes (*adr*, *adw*, *ayw*, and *ayr*). Genetic analysis revealed several highly conserved domains and defined eight genotypes A-H, which are highly correlated with the 4 serotypes (Norder et al., 2004). The HBV surface protein, HBsAg, has 4 putative transmembrane domains and can be subdivided into PreS1-, PreS2- and S-regions. The S domain is a cysteine-rich protein consisting of 226 amino acids that contain all 4 of the transmembrane domains (Abou-Jaoude and Sureau, 2007). In addition, the S-protein can be glycosylated at asparagine residue 146 (Julithe et al., 2014).

[0007] Antibodies to HBsAg (anti-HBs) are associated with successful vaccination and recovery from acute infection, while antibodies to HBcAg (anti-HBc) are indicative of past or current HBV infection (Ganem, 1982). Indeed, the most significant difference between chronically infected and naturally recovered individuals is a robust antibody response to HBsAg (Ganem, 1982). Conversely, the inability to produce these antibodies during acute infection is associated with chronicity (Trepo et al., 2014). Whether these associations reflect an etiologic role for anti-HBs antibodies in protecting from or clearing established infection is not known. However, depletion of antibody-producing B lymphocytes in exposed humans by anti-CD20 therapies (e.g. rituximab) is associated with HBV reactivation, indicating that B cells and/or their antibody products play a significant role in controlling the infection (Loomba and Liang, 2017).

[0008] Several human antibodies against HBsAg have been obtained using a variety of methods including: phage display (Kim and Park, 2002; Li et al., 2017; Sankhyan et al., 2016; Wang et al., 2016); humanized mice (Eren et al., 1998); Epstein-Barr virus-induced B cell transformation (Heijntink et al., 2002; Heijntink et al., 1995; Sa'adu et al., 1992); hybridoma technology (Colucci et al., 1986); human B cell cultures (Cerino et al., 2015); and microwell array chips (Jin et al., 2009; Tajiri et al., 2010). However, the donors in these studies were not selected for serum neutralizing activity. Thus, there remains a need for improved approaches and compositions of combatting HBV infection. The present disclosure is pertinent to this need.

BRIEF SUMMARY

[0009] The disclosure provides in part a description of the human humoral immune response to HBsAg in immunized and spontaneously recovered individuals that had been

selected for high levels of serum neutralizing activity. The disclosure demonstrates that these individuals develop closely related bNAbs that target shared non-overlapping epitopes in HBsAg. The crystal structure of one of the antibodies with its peptide target reveals a loop that helps to explain why certain amino acid residues are frequently mutated in escape viruses and why combinations of bNAbs may be needed to control infection. *In vivo* experiments in humanized mice demonstrate that the bNAbs are protective and can be therapeutic when used in combination.

[0010] Any antibody described herein can comprise at least one modification of its constant region. The modification may be made for any one or more amino acids. The modification can have any of a number of desirable effects. In certain approaches, the modification increases *in vivo* half-life of the antibody, or alters the ability of the antibody to bind to Fc receptors, or alters the ability of the antibody to cross placenta or to cross a blood-brain barrier or to cross a blood-testes barrier, or inhibits aggregation of the antibodies, or a combination of said modifications, or wherein the antibody is attached to a label or a substrate. In embodiments, the modification improves the manufacturability of the antibody. In embodiments, any antibody or combination thereof described herein can be present in an immunological assay, such as an enzyme-linked immunosorbent assay (ELISA) assay, or an ELISA assay control. The ELISA assay can be any of a direct ELISA assay, an indirect ELISA assay, a sandwich ELISA assay, or a competition ELISA assay.

[0011] In another aspect the disclosure provides a method for prophylaxis or therapy of a hepatitis viral infection comprising administering to an individual in need thereof an effective amount of at least one antibody described herein, or an antigen binding fragment thereof. The antibody may comprise at least one modification of the constant region. In embodiments, the composition is administered to an individual who is infected with or is at risk of being infected with a hepatitis B virus. In one approach, at least two antibodies are administered, wherein optionally the two antibodies recognize distinct HBV epitopes. In an embodiment, administering at least two distinct antibodies suppresses formation of viruses that are resistant to the antibodies.

[0012] In another aspect the disclosure provides vaccine formulations. In an embodiment a vaccine formulation comprises an isolated or recombinant peptide or a polynucleotide encoding the peptide, wherein the peptide is derived from an epitope that is frequently targeted by HepB immune resistance, and which is located in a loop anchored by oppositely charged residues, as further described herein.

[0013] In another aspect the disclosure provides one or more recombinant expression vectors, and kits comprising the expression vectors. The expression vectors encode at least the heavy chain and the light chain CDRs of any of the antibodies of described herein. Cells comprising the recombinant expression vectors are included, as are methods of making antibodies by culturing cells that comprise expression vectors that express the antibodies, and separating antibodies from the cells. Cell culture media containing such cells and/or antibodies is also included.

BRIEF DESCRIPTION OF THE FIGURES

[0014] Figure 1. Antibody responses in HBV vaccinated and recovered

10 **individuals.** (A) Donor screen. Sera from 159 volunteers were evaluated for anti-HBs binding by ELISA (x-axis) and HBV serum neutralization capacity using HepG2-NTCP cells (y-axis). Serum neutralization capacity on the y-axis was calculated as the reciprocal of the relative percentage of infected HepG2-NTCP cells. The values for unexposed naïve donors are $\cong 1$. Neutralization tests were performed at 1:5 serum dilution in the final assay volume.

15 Each dot represents an individual donor. Green indicates unvaccinated and unexposed, black indicates vaccinated, and red indicates spontaneously recovered. The dashed line indicates the no serum control. Top neutralizers (serum neutralization capacity higher than 4) are indicated (top right). Boxed are representative samples shown in Figure 2A. Spearman's rank correlation coefficient (r_s) and significance value (p). (B and C) Dose-dependent HBV neutralization by serum (B) or by purified IgG (C). Two assays were used to measure percent infection: ELISA to measure HBsAg protein in the medium (upper panels) and immunofluorescent staining for HBcAg in HepG2-NTCP cells (lower panels). Dashed line indicates virus-only control. (D) Schematic representation illustrating the three forms of the HBV surface protein: L-, M- and S-protein. These three forms of envelope protein all share

20 the same S-region, with PreS1/PreS2 and PreS2 alone as the N-terminal extensions for L- and M-protein, respectively. (E) S-protein produced in Chinese hamster ovary (CHO) cells blocks serum neutralizing activity. Graphs show infection efficiency as a function of the amount of S-protein added. The concentration of polyclonal IgG antibodies (pAb) is indicated. Upper and lower panels are as in (B) and (C). A representative of at least two experiments is shown.

25 See also Figure 8 and Table S1.

[0015] **Figure 2. S-protein-specific antibodies.** (A) Frequency of S-protein-specific memory B cells. Representative flow cytometry plots displaying the percentage of all IgG⁺ memory B cells that bind to both allophycocyanin- and phycoerythrin-tagged S-protein (S-

protein-APC and S-protein-PE). Flow cytometry plots from other individuals are shown in Figure 9A. Experiments were repeated two times. (B) Dot plot showing the correlation between the frequency of S-protein-binding IgG⁺ memory B cells and the serum neutralizing activity. Spearman's rank correlation coefficient (r_s) and significance value (p). (C) Each pie chart represents the antibodies from an individual donor, and the total number of sequenced antibodies with paired heavy and light chains is indicated in the center. Antibodies with the same combination of IGH and IGL variable gene sequences and closely related CDR3s in each individual are shown. The slices with the same color indicate shared antibodies with the same or similar combination of IGH and IGL variable genes between individuals (Figure 9B). Grey slices indicate antibodies with closely related sequences that are unique to a single donor. In white are singlets. (D) V(D)J alignments for representative IGHV3-30/IGLV3-21, IGHV3-33/IGLV3-21 and IGHV3-23/IGLV3-21 antibodies from donors #60/#146 (H006 and H008), #146/#13 (H014 and H012), and #13/#60/#146 (H021, H003 and H004) respectively. Boxed grey residues are shared between antibodies. See also Figure 9 and Table S2. Figure discloses SEQ ID NOS 1438-1451, respectively, in order of appearance.

[0016] Figure 3. Broad cross-reactivity. (A) Binding to S-protein (*adr* serotype). 50% effective concentration (EC₅₀ in ng/ml) required for binding of the indicated human monoclonal antibodies to the S-protein. Libivirumab (Eren et al., 2000; Eren et al., 1998) and anti-HIV antibody 10-1074 (Mouquet et al., 2012) were used as positive and negative controls, respectively. All antibodies were tested. (B) Comparative binding of the mature and unmutated common ancestor (UCA) of antibodies H006, H019, and H020 to S-protein by ELISA. (C) Anti-HBs antibody binding to 5 different serotypes of HBsAg. Similar to panel (A), EC₅₀ values are color-coded: red, ≤50 ng/ml; orange, 50 to 100 ng/ml; yellow, 100 to 200 ng/ml; and white, > 200 ng/ml. The abbreviation b.d. indicates below detection. All antibodies were tested. All experiments were performed at least two times. See also Figure 10.

[0017] Figure 4. HBsAg epitopes. (A) Competition ELISA defines 3 groups of antibodies. Results of competition ELISA shown as percent of binding by biotinylated antibodies and illustrated by colors: black, 0-25%; dark grey, 26-50%; light grey, 51-75%; white, >76%. Weak binders (H002, H012, H013, H014, H018) were excluded. Representative of two experiments. (B) Results of ELISA on alanine scanning mutants of S-protein. Only the amino acids vital for antibody binding are shown. Binding to mutants relative to wild-type S-protein: black, 0-25%; dark grey, 26-50%; light grey, 51-75%; white, >75%. Additional details are provided in Figure 11. (C) Results of ELISA on human escape

mutations of S-protein. Wild-type S-protein and empty vector serve as a positive and negative controls, respectively. Binding to mutants relative to wild-type S-protein: black, 0-25%; dark grey, 26-50%; light grey, 51-75%; white, >75%. Amino acid mutations in bold represent frequently observed mutations in humans (Ma and Wang, 2012). The antibodies tested in (B and C) were selected from Group-I, -II, -III based on their neutralizing activity (Figure 5A-5C). All experiments were performed at least two times. See also Figure 11.

[0018] Figure 5. *In vitro* neutralization by the monoclonal antibodies. (A and B) *In vitro* neutralization assays using HepG2-NTCP cells. Percent infection in the presence of the indicated concentrations of bNAbs measured by ELISA of HBsAg in medium (A) and anti-HBcAg immunofluorescence (B). Anti-HIV antibody 10-1074 (Mouquet et al., 2012) and libivirumab (Eren et al., 2000; Eren et al., 1998) were used as negative and positive controls respectively. The corresponding IC₅₀s are shown in the left and middle column of panel (C). All experiments were repeated a minimum of two times. (C) bNAb 50% maximal inhibitory concentration (IC₅₀) calculated based on HBsAg ELISA (left column) and HBcAg immunofluorescence (middle column) for the *in vitro* neutralization assays using HepG2-NTCP cells, or HBeAg ELISA (right column) for *in vitro* neutralization using primary human hepatocytes. The abbreviation b.d. and n.d. indicate below detection and not done respectively. (D) *In vitro* neutralization using primary human hepatocytes. The levels of HBeAg in medium were measured by ELISA. The calculated IC₅₀ values are shown in the right column of panel (C). Experiments were repeated three times. (E) *In vitro* neutralization assay using HepG2-NTCP cells. IgG antibodies were compared to their corresponding Fab fragments. Concentrations of Fab fragments were adjusted to correspond to IgG. Experiment was performed two times. See also Figure 12.

[0019] Figure 6. Crystal structure of H015 bound to its recognition motif. A single crystal was used to obtain a high resolution (1.78 Å) structure. (A) Synthetic peptides (SEQ ID NOS 1452-1455, respectively, in order of appearance) spanning the antigenic loop region were subjected to ELISA for antibody binding. Among the tested antibodies, only H015 binds peptides-11 and -12. Experiments were performed three times and details are in Figure 13A. (B and C) The peptide binds to CDR1 (R31), CDR2 (W52 and F53) and CDR3 (E99, P101, L103, and L104) of H015 heavy chain (green) and CDR3 (P95) of the light chain (cyan) (B). The interacting residues (C) on the heavy chain (green) are R31 (main chain), W52, F53 (main chain), E99, P101 (main chain), L103 (main chain), L104 (hydrophobic). One contact with the light chain (cyan) is with P95. (D) Electron density map of the bound peptide as seen in the 2Fo-Fc map contoured at 1 RMSD indicating high occupancy (92%).

(E) The recognition motif, KPSDGN (SEQ ID NO: 1), adopts a sharp hairpin conformation due to the salt-bridge between K141 and D144 and is facilitated by kinks at P142 and G145. Glycine 145 (G145, circled) is the residue that escapes the immune system when mutated to an arginine. See also Figure 13.

- 5 **[0020] Figure 7. Anti-HBs bNAbs are protective and therapeutic *in vivo*.** (A and E) Diagram of the prophylaxis and treatment protocols, respectively. (B) Prophylaxis with isotype control antibody 10-1074 (Mouquet et al., 2012). (C and D) Prophylaxis with H020 and H007 respectively. The dashed line in (B-D) indicates the detection limit. (F) Treatment of viremic huFNRG mice with control antibody 10-1074. (G and H) Treatment of viremic
- 10 huFNRG mice with H020 alone or H007 alone, respectively. HBV DNA levels in serum were monitored on a weekly basis. Two independent experiments comprising a total of 5 to 8 mice were combined and displayed. (I) Mutations in the S-protein sequence from the indicated mice (red arrows) in (G), (H) and (J). S-protein sequence chromatograms are shown in Figure 14. (J-L) Treatment of viremic huFNRG mice with combination of anti-HBs bNAbs H006 +
- 15 H007 (J), or H017 + H019 (K), or H016 + H017 + H019 (L), respectively. Sequencing showed that none of the mice in (K) and (J) carried viruses with escape mutations in the S-protein. See also Figure 14.

- [0021] Figure 8. Characterization of Antibody Immune Response Against HBV, Related to Figure 1.** (A) Schematic representation of different stages of HBV infection.
- 20 Vaccinated or infected naturally recovered individuals were recruited for this study. (B) Sera (1:50 dilution in the final assay volume) from 159 volunteers were screened, see also Figure 1A. (C-E) Comparison of anti-HBs ELISA titers (upper panel) and their serum neutralization capacity (lower panel) between different groups of individuals. Vaccinated or recovered individuals show statistically higher anti-HBs titers (upper panel, C) and more potent
- 25 neutralizing activity (lower panel, C) than the uninfected unvaccinated individuals. Younger individuals (≤ 45 years old) showed slightly higher antibody immune response against HBsAg (D). No difference was found between genders (E).

- [0022] Figure 9. Antibody Cloning and Sequence Analysis of Anti-HBs, Related to Figure 2.** (A) Frequency of S-protein-specific memory B cells in peripheral blood
- 30 mononuclear cells of all twelve donors. Details are similar to Figure 2A. (B) Pie charts show the distribution of anti-HBs antibodies. Figure legends are similar to Figure 2C. VH and VL genes for each slice are shown and the 20 chosen anti-HBs antibodies are labeled. (C) Phylogenetic tree of all cloned anti-HBs antibodies based on IGH Fab region. IGH Fab

regions from 244 memory B cells sorted with HBsAg were aligned followed by tree construction.

[0023] Figure 10. Autoreactivity of 20 anti-HBs antibodies, Related to Figure 3.

(A) Autoreactivity of monoclonal antibodies. Positive control antibody efficiently stained the nucleus of HEp-2 cells. Twenty anti-HBs antibodies, as well as anti-HBs antibody libivirumab and anti-HIV antibody 10-1074, were also tested. (B) Polyreactivity profiles of 20 anti-HBs antibodies. ELISA measures antibody binding to the following antigens: double-stranded DNA (dsDNA), insulin, keyhole limpet hemocyanin (KLH), lipopolysaccharides (LPS), and single-stranded DNA (ssDNA). Red and green lines represent positive control antibody ED38 and negative control antibody mGO53 respectively, while dashed lines show cut-off values for positive reactivity (Gitlin et al., 2016).

[0024] Figure 11. Alanine Scanning and Peptide Screening, Related to Figure 4.

(A) Results of ELISA on alanine scanning mutants of HBsAg. Binding to mutants was normalized to wild-type S-protein: black, 0-25%; dark grey, 26-50%; light grey, 51-75%; white, >76%. Experiments were performed three times. Underlined cysteines, alanines, and amino acids known to be critical for S-protein production were not mutated (Salisse and Bureau, 2009). Figure discloses SEQ ID NO: 1456. (B) Schematic diagram of alanine scanning results. Figure discloses the primary amino acid sequence as SEQ ID NO: 1456 and the sequence containing alanine mutations as SEQ ID NO: 1457.

[0025] Figure 12. *In Vitro* Neutralization Assay of anti-HBs bNAb Unmutated Common Ancestor Antibodies or Combinations, Related to Figure 5. (A-B) *In vitro* neutralization assay of anti-HBs bNAbs and their corresponding unmutated common ancestor (UCA) antibodies. The relative infection rates were calculated based on either HBsAg protein level in culture medium (A) or HBcAg staining intracellularly (B). (C) *In vitro* neutralization assay of anti-HBs bNAbs recognizing different epitopes and the same total amount of antibody combination at 1:1 or 1:1:1 ratio.

[0026] Figure 13. Detailed Information of Crystal Structure of H015 and Its Linear Epitope, Related to Figure 6. (A) Synthesized peptides (SEQ ID NOS 1458-1476, respectively, in order of appearance) for antigenic loop region were subjected to ELISA for antibody binding. Among the tested antibodies, only H015 binds peptide-11 and -12. (B) Data collection and refinement statistics for H015 Fab are summarized. Statistics for the highest-resolution shell are shown in parentheses. Refinement program PHENIX 1.16. (C) The green/red density is the unbiased omit map. Red is negative density equated to noise. (D) Table of contacts within the peptide and between Fab fragment and peptide.

[0027] Figure 14. HBV DNA levels and S-protein Sequences in Antibody-Treated huFNRG Mice, Related to Figure 7.

(A) HBV DNA levels in representative individual huFNRG mice treated by control antibody 10-1074, anti-HBs bNAb H020, anti-HBs bNAb H007, combination of anti-HBs bNAb (H006 + H007), (H017 + H019), and (H016 + H017 + H019). HBV DNA levels in mouse sera were monitored on a weekly basis. The mice without arrows bear no escape mutations at the last time point. (B) Part of the S-protein sequences from the indicated mice (arrows and numbers) are shown below as chromatograms, with mutations marked by arrowheads. (B) discloses the S-protein amino acid and nucleotide sequences as SEQ ID NOS 1477 and 1478, respectively. The sequences represented by the subsequent chromatograms that disclose amino acid residues and nucleotides are SEQ ID NOS 1479, 1480, 1480, 1480-1482, 1479, 1478, 1480, 1480, 1478, 1480, and 1483-1488, respectively, in order of columns. (C-D) HBsAg levels in mouse sera before and after antibody infusion. Mice were treated by anti-HBs combination H017 + H019 (C) (see Figure 7K) and H016 + H017 + H019 (D) (see Figure 7L). Each line represents a mouse with concentrations of serum HBsAg level expressed in NCU/ml (national clinical units per milliliter).

DETAILED DESCRIPTION OF THE DISCLOSURE

[0028] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs.

[0029] Every numerical range given throughout this specification includes its upper and lower values, as well as every narrower numerical range that falls within it, as if such narrower numerical ranges were all expressly written herein.

[0030] This disclosure includes every nucleotide sequence described herein, and in the tables and figures, and all sequences that are complementary to them, RNA equivalents of DNA sequences, all amino acid sequences described herein, and all polynucleotide sequences encoding the amino acid sequences. Every antibody sequence and functional fragments of them are included. Polynucleotide and amino acid sequences having from 80-99% similarity, inclusive, and including ranges of numbers there between, with the sequences provided here are included in the invention. All of the amino acid sequences described herein can include amino acid substitutions, such as conservative substitutions, that do not adversely affect the function of the protein or polypeptide that comprises the amino acid sequences. It will be recognized that when reference herein is made to an “antibody” it does not necessarily mean

a single antibody molecule. For example, “administering an antibody” includes administering a plurality of the same antibodies. Likewise, a composition comprising an “antibody” can comprise a plurality of the same antibodies.

5 [0031] For amino acid and polynucleotide sequences of this disclosure, contiguous segments of the sequences are included, and can range from 2 amino acids, up to full-length protein sequences. Polynucleotide sequences encoding such segments are also included.

[0032] The disclosure includes DNA and RNA sequences encoding the antibodies and antigen fragments thereof, and any virus peptides described herein for use in prophylactic and therapeutic approaches as protein or DNA and/or RNA vaccines, which may be
10 formulated and/or delivered according to known approaches, given the benefit of this disclosure. The disclosure includes a cDNA sequences encoding the antibodies, antigen binding fragments thereof, and any viral proteins or peptides described herein. Expression vectors that contain cDNAs are also included, and encode said antibodies, antigen binding fragments thereof, and viral proteins and peptides.

15 [0033] All sequences from the figures, text, and tables of this application or patent include every amino acid sequence associated with every Donor ID, and all possible combinations of the amino acid sequences given for all complementarity determining regions (CDRs), e.g., all combinations of heavy chain CDR1, CDR2, CDR3 sequences, and all combinations of light chain CDR1, CDR2, and CDR3 sequences, including heavy chain
20 sequences, and light chain sequences that are either lambda or kappa light chain sequences. The disclosure includes all combinations of antibodies described herein. One or more antibodies may also be excluded from any combination of antibodies.

[0034] The disclosure includes antibodies described herein, which are present in an *in vitro* complex with one or more hepatitis B proteins.

25 [0035] In embodiments, the disclosure provides an isolated or recombinant antibody that binds with specificity to a hepatitis B virus epitope, and wherein the antibody optionally comprises a modification of its amino acid sequence, including but not limited to a modification of its constant region.

[0036] In embodiments, one or more antibodies described herein bind with specificity
30 to an epitope present in the HBsAg protein or the S-protein in the unmutated, or mutated form.

[0037] In embodiments, the antibodies described herein bind to a hepatitis B protein that comprises one or more HepB escape mutations. In embodiments, the antibodies bind to a hepatitis B virus protein that comprises a mutation that is a substitution of a large positively

charged residue for a small neutral residue. In embodiments, the mutation is present in the so-called “a” determinant area, which is known in the art. In embodiments, the epitope is present in the major hydrophilic region of the HBsAg protein. In embodiments, the epitope to which the antibodies bind is present in the S-protein, including but not necessarily limited to the predicted or actual extracellular domain of the S-protein.

[0038] In embodiments, the epitope to which the described antibodies bind is common to HBsAg L-protein, M-protein, or S-protein. In embodiments, the antibodies bind to an epitope present in the L-protein version of HBsAg, which comprises the amino acid sequence that is accessible via Accession number: AAL66340.1 as that amino acid sequence exists in the database as of the filing date of this application or patent. In an embodiment, this amino acid sequence is:

MGGWSSKPRQGMGTNLSVPNPLGFFPDHQLDPAFGANSNNPDWDFNPKNKDHWPENQVG
AGAFGPGFTPPHGGLLGWSPQAQGILTTVPVAPPPASTNRQSGRQPTPISPPLRDSHPQAMQ
WNSTTFHQALLDPRVRGLYFPAGGSSSGTVNPVPTTASPISSIFSRTGDPAPNMESTTSGFLGP
LLVLQAGFFLLTRILTIPQSLDSWWTSLNFLGGAPTCPGQNSQSPTSNNHSPTSCPPICPGYRWM
CLRRFIIFLIFLLCLIFLLVLLDYQGMLPVCPLLPGTSTTSTGPCKTCTSPAQGTSMFPSCCCTKP
SDGNCTCIPISSWAFARFLWEWASVRFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWG
PCLYNILSPFLPLLPIFFCLWVYI (SEQ ID NO: 2).

[0039] In embodiments, the disclosure includes use of only two proteins, or at least two proteins. In an embodiment, the S proteins may be used as bait to sort B cells purified from Chinese hamster ovary (CHO) cells, or any other suitable cell type, including but not limited to human cell cultures. In embodiments, the S protein comprises or consists of the amino acid sequence available under Uniprot ID_P30019, the amino acid sequence of which is incorporated herein as it exists in the database at the filing date of this application or patent. In an embodiment, the S protein comprises the sequence:

MENTASGFLGPLLVLQAGFFLLTRILTIPQSLDSWWTSLNFLGGAPTCPGQNSQSPTSNNHSPTS
CPPICPGYRWMCLRRFIIFLIFLLCLIFLLVLLDYHGMLPVCPLLPGTSTTSTGPCKTCTIPAQG
TSMFPSCCCTKPSDGNCTCIPISSWAFARFLWEWASVRFSWLSLLVPFVQWFVGLSPTVWLS
VIWMMWYWGPSLYNILSPFLPLLPIFFCLWVYI (SEQ ID NO: 3).

[0040] In non-limiting embodiments, the S polynucleotide sequence used for alanine scanning comprises:

ATGGAGAACATCACATCAGGATTCCTAGGACCCCTGCTCGTGTTACAGGCGGGGTTTTCTTG
 TTGACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAATTTTCTA
 GGGGGATCTCCCGTGTGTCTTGGCCAAAATTCGCAGTCCCCAACCTCCAATCACTCACCAACC
 TCCTGTCCTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTTTATCATATTCCTC
 5 TTCATCCTGCTGCTATGCCTCATCTTCTTATTGGTTCTTCTGGATTATCAAGGTATGTTGCCC
 GTTTGTCTCTAATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACCTGCACGACT
 CCTGCTCAAGGCAACTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGATGGAAATTGC
 ACCTGTATTCCCATCCCATCGTCCTGGGCTTTTCGCAAAATACCTATGGGAGTGGGCCTCAGTC
 CGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTTCAGTGGTTTCGTAGGGCTTTCCCCCACT
 10 GTTTGGCTTTTCAGCTATATGGATGATGTGGTATTGGGGGCCAAGTCTGTACAGCATCGTGAG
 TCCCTTTATACCGCTGTTACCAATTTTCTTTTGTCTCTGGGTATACATTTAA (SEQ ID NO:
 4).

[0041] The amino acid sequence encoded by the DNA sequence immediately above is:

15 MENITSGFLGPLLVLQAGFLLTRILTIPQSLDSWWTSLNFLGGSPVCLGQNSQSPTSNNHSPTSC
 PPICPGYRWMCLRRFIIFLLFILLCLIFLLVLDYQGMLPVCPLIPGSTTTSTGPCKTCTTPAQGN
 SMFPSCCCTKPTDGNCTCIPISSWAFAYLWEWASVRFSWLSLLVPFVQWFVGLSPTVWLS
 AIWMMWYWGPSLYSIVSPFIPLPIFFCLWVYI (SEQ ID NO: 5).

[0042] In embodiments, antibodies of this disclosure bind to an epitope present in any
 20 of the foregoing amino sequences, including linear and confirmation epitopes that may be
 formed by proteins comprising or consisting of said sequences.

[0043] In an embodiment, the isolated or recombinant antibody or antigen binding
 fragment thereof binds with specificity to an epitope comprised by a structurally defined
 peptide loop, as further described herein. In embodiments, the loop is as generally depicted in
 25 Figure 6, which comprises a partial structure of HepB surface protein, and demonstrates the
 existence of a loop that includes the most frequently targeted residue found in human escapes
 G145. Without intending to be bound by any particular theory, it is considered that this
 structure explains why this mutant can escape, and also why additional commonly found
 escape mutants exist. Further, the structure and the antibody peptide complex represents a
 30 new and previously undiscovered target for drug discovery. Thus, in embodiments, the
 disclosure provides for screening drug candidates that can interfere with formation of this
 structure, and thus which may also interfere with the viability of the virus. Those skilled in

the art will recognize from the present disclosure how to design an assay to determine whether or not drug candidates could interfere with the complex, and how antibodies described in herein may be used in such an assay.

5 **[0044]** In embodiments, antibodies described herein bind with specificity to an amino acid sequence comprised by any peptide sequence described herein. In embodiments, the peptide comprises the sequence KPSDG (SEQ ID NO: 6), or mutants thereof. In embodiments, antibodies described herein bind with specificity to an epitope in an amino acid sequence that comprises the sequence PSSSSTKPSDGNSTS (SEQ ID NO: 7), or mutants thereof. Additional and non-limiting examples of peptides of this disclosure include those
10 shown on Figure 6, e.g., peptide-11 and peptide-12.

[0045] In embodiments, the disclosure comprises compositions and methods that involve use of more than one distinct antibody or antigen binding fragment thereof. In embodiments, the methods of this disclosure comprise administering a combination of antibodies or antigen binding fragment thereof which bind distinct hepatitis B epitopes. In
15 embodiments, distinct antibodies recognize epitopes present in two dominant non-overlapping antigenic sites on the HBsAg, or epitopes present on the S-protein. In embodiments, the disclosure provides for use of a combination of the Group-I and Group-II antibodies described herein. Thus, the disclosure comprises co-administration or sequential administration of a combination of antibodies. In an embodiment, administration of a
20 combination of distinct antibodies suppresses formation of viruses that are resistant to the effects of any one of the antibodies alone. In embodiments, the disclosure includes administering a combination comprising at least one Group I antibody and at least one Group II antibody, wherein at least one of the antibodies is G145R mutation resistant. In non-limiting embodiments, antibodies that are provided by the present disclosure, and which can
25 be administered to an individual in need thereof, comprise at least one of H006, H007, H0017, H0019, or H020. Further, H005, H008 and H009 are similar to H006, and therefore may be used as alternatives to H006.

[0046] All combinations of H and L chains described herein are included, including all kappa and lambda light chains. In embodiments, a single antibody of this disclosure may
30 comprise an H+L chain from one antibody, and an H+L chain from another antibody. In embodiments, the antibodies comprise modifications that are not coded for in any B cells obtained from an individual, and/or the antibodies are not produced by immune cells in an individual from which a biological sample from the individual is used at least in part to identify and/or generate and/or characterize the antibodies of this disclosure. In embodiments,

antibodies provided by this disclosure can be made recombinantly, and can be expressed with a constant region of choice, which may be different from a constant region that was coded for in any sample from which the amino acid sequences of the antibodies were deduced.

[0047] As discussed above, in embodiments, the disclosure includes a combination of antibodies or antigen binding fragments thereof, or a composition comprising or consisting of said antibodies or antigen binding fragments thereof. In embodiments, a combination of antibodies of this disclosure are effective in preventing viral escape by mutation. In this regard, the disclosure includes data demonstrating that not all antibody combinations are effective in preventing escape by mutation, such as the combination of H006 and H007, which are ineffective. Thus, in embodiments, a combinations of antibodies or antigen binding fragments collectively target more than one commonly occurring escape mutation, examples of which escape mutations are known in the art and are described herein. Accordingly, combinations of antibodies and antigen binding fragments thereof of this disclosure may target non-overlapping groups of common escape mutations. In embodiments, the disclosure thus includes a proviso that excludes any combination of antibodies that collectively only target separate epitopes but have overlapping sensitivity to commonly occurring escape mutations.

[0048] In embodiments, at least one antibody or antigen binding fragment thereof included in this disclosure, and in the combinations and methods of this disclosure, has greater virus neutralizing activity than a control neutralizing activity value, such as the neutralizing capability of libivirumab. In embodiments, at least one antibody or antigen binding fragment of this disclosure exhibits a viral neutralizing activity with an IC_{50} values that is less than 128 ng/ml, or less than 35 ng/ml, or less than 5 ng/ml, and including all integers and ranges of integers between 128 and 5 ng/ml. Such neutralizing activity can be determined using known approaches, such as by ELISA or immunofluorescence assays, and as further described in Example 5 of this disclosure. In embodiments, an antibody or antigen binding fragment thereof that is encompassed by this disclosure includes but is not limited to antibodies or antigen binding fragments selected from the H016, H017 and H019 antibodies, as defined by their CDRs. In an embodiment, the disclosure includes combinations of these antibodies, and can include antigen binding fragments thereof. In embodiments, the combination of antibodies comprises the H017 and H019 antibodies, and/or antigen binding fragments thereof. In an embodiment, the combination optionally further comprises the H016 antibody or an antigen binding fragment thereof. In embodiments, a combination of the disclosure comprises a combination that consists of only the H017 and H019 antibodies or

antigen binding fragments thereof. In embodiments, a combination of the disclosure comprises a combination that consists of only the H016, H017, and H019 antibodies or antigen binding fragments thereof. Methods of administration of the described antibody combinations, and all other antibodies and antigen binding fragments thereof described
5 herein, sequentially and concurrently are included within the scope of this disclosure. Thus, the disclosure includes administering to an individual in need concurrently or sequentially a combination of antibodies or antigen binding fragments thereof, which in certain embodiments comprise or consist of H017 and H019, or H016, H017, and H019 and antigen binding fragments thereof. Additional antibodies and antibody combinations, including
10 antigen binding fragments thereof, include but are not limited to antibodies and antigen binding fragments thereof that comprise the heavy and light chain CDRs of H004, H005, and H009, and H020.

[0049] With respect to the H016, H017, and H019 antibodies, as can be seen from Table S2, the H016 antibody comprises a heavy chain CDR1 with the amino acid sequence
15 GFTFPSHT (SEQ ID NO: 8), a heavy chain CDR2 with the amino acid sequence ISTTSEAI (SEQ ID NO: 9), and a heavy chain CDR3 with the amino acid sequence ARVGLALTISGYWYFDL (SEQ ID NO: 10). The H016 antibody comprises a kappa light chain CDR1 with the amino acid sequence QSISSN (SEQ ID NO: 11), a kappa light chain with the CDR2 amino acid sequence RAS, and a kappa light chain with the CDR3 amino acid
20 sequence QQYDHWPLT (SEQ ID NO: 12).

[0050] As can be seen from Table S2, the H017 antibody comprises a heavy chain CDR1 with the amino acid sequence GFTFSNYW (SEQ ID NO: 13), a heavy chain CDR2 with the amino acid sequence ISTDGSST (SEQ ID NO: 14), and a heavy chain CDR3 with the amino acid sequence ARGSTYYFGSGSVDY (SEQ ID NO: 15). The H017 antibody
25 comprises a lambda light chain with the CDR1 sequence SSDIGVYNY (SEQ ID NO: 16), a lambda light chain with the CDR2 sequence DVT, and a lambda light chain with the CDR3 sequence SSYRGSSSTPYV (SEQ ID NO: 17).

[0051] As can be seen from Table S2, the H019 antibody comprises a heavy chain CDR1 with the amino acid sequence GGSITTGDYY (SEQ ID NO: 18), a heavy chain CDR2
30 with the amino acid sequence IYYSGST (SEQ ID NO: 19), and a heavy chain CDR3 with the amino acid sequence AIYMDEAWAFE (SEQ ID NO: 20). The H019 antibody comprises a lambda light chain CDR1 with the amino acid sequence QSIGNY (SEQ ID NO: 21), a lambda light chain with the CDR2 amino acid sequence AVS, and a lambda light chain with the CDR3 amino acid sequence QQSYTISLFT (SEQ ID NO: 22).

[0052] In certain embodiments, the antibodies contain one or more modifications, such as non-naturally occurring mutations. As non-limiting examples, in certain approaches the Fc region of the antibodies can be changed, and may be of any isotype, including but not limited to any IgG type, or an IgA type, etc. Antibodies of this disclosure can be modified to improve certain biological properties of the antibody, e.g., to improve stability, to modify effector functions, to improve or prevent interaction with cell-mediated immunity and transfer across tissues (placenta, blood-brain barrier, blood-testes barrier), and for improved recycling, half-life and other effects, such as manufacturability and delivery.

[0053] In embodiments, an antibody of this disclosure can be modified by using techniques known in the art, such as those described in Buchanan, et al., Engineering a therapeutic IgG molecule to address cysteinylolation, aggregation and enhance thermal stability and expression mAbs 5:2, 255–262; March/April 2013, and in Zalevsky J. et al., (2010) Nature Biotechnology, Vol. 28, No.2, p157-159, and Ko, S-Y, et al., (2014) Nature, Vol. 514, p642-647, and Horton, H. et al., Cancer Res 2008; 68: (19), October 1, 2008, from which the descriptions are incorporated herein by reference. In certain embodiments an antibody modification increases in vivo half-life of the antibody (e.g. LS mutations), or alters the ability of the antibody to bind to Fc receptors (e.g. GRLR mutations), or alters the ability to cross the placenta or to cross the blood-brain barrier or to cross the blood-testes barrier. Thus, in certain embodiments an antibody modification comprises a change of G to R, L to R, M to L, or N to S, or any combination thereof.

[0054] In embodiments bi-specific antibodies are provided by modifying and/or combining segments of antibodies as described herein, such as by combining heavy and light chain pairs from distinct antibodies into a single antibody. Suitable methods of making bispecific antibodies are known in the art, such as in Kontermann, E. et al., Bispecific antibodies, Drug Discovery Today, Volume 20, Issue 7, July 2015, Pages 838-847, the description of which is incorporated herein by reference.

[0055] In embodiments, any antibody described herein comprises a modified heavy chain, a modified light chain, a modified constant region, or a combination thereof, thus rendering them distinct from antibodies produced by humans. In embodiments, the modification is made in a hypervariable region, and/or in a framework region (FR).

[0056] In embodiments, mutations to an antibody described herein, including but not limited to the antibodies described, comprise modifications relative to the antibodies originally produced in humans. Such modifications include but are not necessarily limited to the heavy chain to increase the antibody half-life.

[0057] In embodiments, antibodies of this disclosure have variable regions that are described herein, and may comprise or consist of any of these sequences, and may include sequences that have from 80-99% similarity, inclusive, and including ranges of numbers there between, with the sequences expressly disclosed herein, provided antibodies that have
5 differing sequences retain the same or similar binding affinity as an antibody with an unmodified sequence. In embodiments, the sequences are at least 95%, 96%, 97%, 98% or 99% similar to an expressly disclosed sequence herein.

[0058] Antibodies comprising the sequences described in Table S2 have been isolated and characterized for at least binding affinity, and as otherwise described herein, such as for
10 virus neutralizing activity. Thus, in embodiments the disclosure provides neutralizing antibodies. The term “neutralizing antibody” refers to an antibody or a plurality of antibodies that inhibits, reduces or completely prevents viral infection. Whether any particular antibody is a neutralizing antibody can be determined by in vitro assays described in the examples below, and as is otherwise known in the art. The term “broadly neutralizing” antibody refers
15 to an antibody that can neutralize more than one strain or serotype of a virus.

[0059] Antibodies of this disclosure can be provided as intact immunoglobulins, or as antigen binding fragments of immunoglobulins, including but not necessarily limited to antigen-binding (Fab) fragments, Fab' fragments, (Fab')₂ fragments, Fd (N-terminal part of the heavy chain) fragments, Fv fragments (the two variable domains), dAb fragments, single
20 domain fragments or single monomeric variable antibody domains, isolated CDR regions, single-chain variable fragment (scFv), and other antibody fragments that retain virus-binding capability and preferably virus neutralizing activity as further described below. In embodiments, the variable regions, including but not necessarily limited to the described CDRs, may be used as a component of a Bi-specific T-cell engager (BiTE), bispecific killer
25 cell engager (BiKE), or a chimeric antigen receptor (CAR), such as for producing chimeric antigen receptor T cells (e.g. CAR T cells). In embodiments, the disclosure includes tri-valent antibodies, which can bind with specificity to three different epitopes.

[0060] Antibodies and antigens of this disclosure can be provided in pharmaceutical formulations. It is considered that administering a DNA or RNA polynucleotide encoding any
30 protein described herein (including peptides and polypeptides), such as antibodies and antigens described herein, is also a method of delivering such proteins to an individual, provided the protein is expressed in the individual. Methods of delivering DNA and RNAs encoding proteins are known in the art and can be adapted to deliver the protein, particularly the described antigens, given the benefit of the present disclosure. Similarly, the antibodies of

this disclosure can be administered as DNA molecules encoding for such antibodies using any suitable expression vector(s), or as RNA molecules encoding the antibodies.

[0061] Pharmaceutical formulations containing antibodies or viral antigens or polynucleotides encoding them can be prepared by mixing them with pharmaceutically acceptable carriers. Pharmaceutically acceptable carriers include solvents, dispersion media, isotonic agents and the like. The carrier can be liquid, semi-solid, e.g. pastes, or solid carriers. Examples of carriers include water, saline solutions or other buffers (such as phosphate, citrate buffers), oil, alcohol, proteins (such as serum albumin, gelatin), carbohydrates (such as monosaccharides, disaccharides, and other carbohydrates including glucose, sucrose, trehalose, mannose, mannitol, sorbitol or dextrans), gel, lipids, liposomes, resins, porous matrices, binders, fillers, coatings, stabilizers, preservatives, liposomes, antioxidants, chelating agents such as EDTA; salt forming counter-ions such as sodium; non-ionic surfactants such as TWEEN, PLURONICS or polyethylene glycol (PEG), or combinations thereof. In embodiments, a pharmaceutical/vaccine formulation exhibits an improved activity relative to a control, such as antibodies that are delivered without adding additional agents, or a particular added agent improves the activity of the antibodies.

[0062] The formulation can contain more than one antibody type or antigen, and thus mixtures of antibodies, and mixtures of antigens, and combinations thereof as described herein can be included. These components can be combined with a carrier in any suitable manner, e.g., by admixture, solution, suspension, emulsification, encapsulation, absorption and the like, and can be made in formulations such as tablets, capsules, powder (including lyophilized powder), syrup, suspensions that are suitable for injections, ingestions, infusion, or the like. Sustained-release preparations can also be prepared.

[0063] The antibodies and vaccine components of this disclosure are employed for the treatment and/or prevention of hepatitis B virus infection in a subject, as well as for inhibition and/or prevention of their transmission from one individual to another.

[0064] The term "treatment" of viral infection refers to effective inhibition of the viral infection so as to delay the onset, slow down the progression, reduce viral load, and/or ameliorate the symptoms caused by the infection.

[0065] The term "prevention" of viral infection means the onset of the infection is delayed, and/or the incidence or likelihood of contracting the infection is reduced or eliminated.

[0066] In embodiments, to treat and/or prevent viral infection, a therapeutic amount of an antibody or antigen vaccine disclosed herein is administered to a subject in need

thereof. The term "therapeutically effective amount" means the dose required to effect an inhibition of infection so as to treat and/or prevent the infection.

[0067] The dosage of an antibody or antigen vaccine depends on the disease state and other clinical factors, such as weight and condition of the subject, the subject's response to the therapy, the type of formulations and the route of administration. The precise dosage to be therapeutically effective and non-detrimental can be determined by those skilled in the art. As a general rule, a suitable dose of an antibody for the administration to adult humans parenterally is in the range of about 0.1 to 20 mg/kg of patient body weight per day, once a week, or even once a month, with the typical initial range used being in the range of about 2 to 10 mg/kg. Since the antibodies will eventually be cleared from the bloodstream, re-administration may be required. Alternatively, implantation or injection of the antibodies provided in a controlled release matrix can be employed.

[0068] The antibodies can be administered to the subject by standard routes, including oral, transdermal, and parenteral (e.g., intravenous, intraperitoneal, intradermal, subcutaneous or intramuscular). In addition, the antibodies and/or the antigen vaccines can be introduced into the body, by injection or by surgical implantation or attachment such that a significant amount of an antibody or the vaccine is able to enter blood stream in a controlled release fashion. In certain embodiments antibodies described herein are incorporated into one or more prophylactic compositions or devices to, for instance, neutralize a virus before it enters cells of the recipient's body. For example, in certain embodiments a composition and/or device comprises a polymeric matrix that may be formed as a gel, and comprises at least one of hydrophilic polymers, hydrophobic polymers, poly(acrylic acids) (PAA), poly(lactic acids) (PLA), carageenans, polystyrene sulfonate, polyamides, polyethylene oxides, cellulose, poly(vinylpyrrolidone) (PVP), poly(vinyl alcohol) (PVA), chitosan, poly(ethylacrylate), methylmethacrylate, chlorotrimethyl ammonium methylmethacrylate, hydroxyapatite, pectin, porcine gastric mucin, poly(sebacic acid) (PSA), hydroxypropyl methylcellulose (HPMC), cellulose acetate phthalate (CAP), magnesium stearate (MS), polyethylene glycol, gum-based polymers and variants thereof, poly (D,L)-lactide (PDLL), polyvinyl acetate and povidone, carboxypolymethylene, and derivatives thereof. In certain aspects the disclosure comprises including antibodies in micro- or nano-particles formed from any suitable biocompatible material, including but not necessarily limited to poly(lactic-co-glycolic acid) (PLGA). Liposomal and microsomal compositions are also included. In certain aspects a gel of this disclosure comprises a carbomer, methylparaben, propylparaben, propylene glycol, sodium carboxymethylcellulose, sorbic acid, dimethicone, a sorbitol solution, or a combination

thereof. In embodiments a gel of this disclosure comprises one or a combination of benzoic acid, BHA, mineral oil, peglicol 5 oleate, pegoxol 7 stearate, and purified water, and can include any combination of these compositions.

[0069] Antibodies of this disclosure can be produced by utilizing techniques available to those skilled in the art. For example, one or distinct DNA molecules encoding one or both of the H and L chains of the antibodies can be constructed based on the coding sequence using standard molecular cloning techniques. The resulting DNAs can be placed into a variety of suitable expression vectors known in the art, which are then transfected into host cells, which are preferably human cells cultured *in vitro*, but may include E. coli or yeast cells, simian COS cells, Chinese Hamster Ovary (CHO) cells, and human embryonic kidney 293 cells, etc. Antibodies can be produced from a single, or separate expression vectors, including but not limited to separate vectors for heavy and light chains, and may include separate vectors for kappa and lambda light chains as appropriate.

[0070] In embodiments, the antibodies may be isolated from cells. In embodiments, the antibodies are recombinant antibodies. "Recombinant" antibodies mean the antibodies are produced by expression within cells from one or more expression vectors.

[0071] In certain approaches the disclosure includes neutralizing antibodies as discussed above, and methods of stimulating the production of such antibodies.

[0072] In certain approaches the disclosure includes vaccinating an individual using a composition described herein, and determining the presence, absence, and/or an amount of neutralizing antibodies produced in response to the vaccination. Thus, methods of determining and monitoring efficacy of a vaccination at least in terms of neutralizing antibody production are included. In an embodiment, subsequent to determining an absence of neutralizing antibodies, and/or an amount of neutralizing antibodies below a suitable reference value, the invention includes administering a composition disclosed herein to the individual. Subsequent administrations and measurements can be made to track the treatment efficacy and make further adjustments to treatment accordingly.

[0073] Antibodies and proteins of this disclosure can be detectably labeled and/or attached to a substrate. Any substrate and detectable label conventionally used in immunological assays and/or devices is included. In embodiments the substrate comprises biotin, or a similar agent that binds specifically with another binding partner to facilitate immobilization and/or detection and/or quantification of antibodies and/or viral proteins.

[0074] In embodiments any type of enzyme-linked immunosorbent (ELISA) assay can be used, and can be performed using polypeptides and/or antibodies of this disclosure for

diagnostic purposes, and can include direct, indirect, and competitive ELISA assays, and adaptations thereof that will be apparent to those skilled in the art given the benefit of this disclosure.

[0075] Any diagnostic result described herein can be compared to any suitable control. Further, any diagnostic result can be fixed in a tangible medium of expression and communicated to a health care provider, or any other recipient. In one aspect the disclosure comprises diagnosing an individual as infected with hepatitis B virus and administering a composition of this invention to the individual.

[0076] In certain embodiments the disclosure includes one or more recombinant expression vectors encoding at least H and L chains of an antibody or antigen binding fragment of this disclosure, cells and cell cultures comprising the expression vectors, methods comprising culturing such cells and separating antibodies from the cell culture, the cell culture media that comprises the antibodies, antibodies that are separated from the cell culture, and kits comprising the expression vectors encoding an antibody and/or a polypeptide of this disclosure. Products containing the antibodies and/or the polypeptides are provided, wherein the antibodies and/or the polypeptides are provided as a pharmaceutical formulation contained in one or more sealed containers, which may be sterile and arranged in any manner by which such agents would be suitable for administration to a human or non-human subject. The products / kits may further comprise one or more articles for use in administering the compositions.

[0077] The following Examples are intended to illustrate but not limit the invention.

Example 1

[0078] Serologic Responses Against HBV

[0079] To select individuals with outstanding antibody responses to HBsAg, we performed ELISA assays on serum obtained from 159 volunteers. These included 15 uninfected and unvaccinated controls (HBsAg⁻, anti-HBs⁻, anti-HBc⁻), 20 infected and spontaneously recovered (HBsAg⁻, anti-HBs^{+/-}, anti-HBc⁺), and 124 vaccinated (HBsAg⁻, anti-HBs^{+/-}, anti-HBc⁻) volunteers. These individuals displayed a broad spectrum of anti-HBs titers (x-axis in Figure 1A and Figure 8B; Table S1). To determine their neutralizing activity, we tested their ability to block HBV infection in sodium taurocholate co-transporting polypeptide (NTCP)-overexpressing HepG2 cells (Michailidis et al., 2017; Yan et al., 2012) (y-axis in Figure 1A and Figure 8B and 8C; Table S1). Sera or antibodies purified from individuals with high levels of neutralizing activity were then compared across a wide range

of dilutions (Figure 1B and 1C). Although anti-HBs ELISA titers positively correlated with neutralizing activity ($r_s=0.492$, $p<0.001$, Spearman's rank correlation), there were notable exceptions as exemplified by volunteers #99 and #49, whose sera failed to neutralize HBV despite high anti-HBs ELISA titers (Figure 1A). Thus, ELISA titers against HBsAg are not
 5 entirely predictive of neutralizing activity *in vitro*.

[0080] The HBV surface protein, HBsAg can be subdivided into PreS1-, PreS2- and S-regions (Figure 1D). To determine which of these regions is the dominant target of the neutralizing response in the selected top neutralizers, we used S-protein to block neutralizing activity *in vitro*. The neutralizing activity in volunteers that received the HBV vaccine, which
 10 is composed of S-protein, was completely blocked by S-protein (black lines in Figure 1E). The same was true for the spontaneously recovered individuals in our cohort despite a reported ability of this population to produce anti-PreS1 or anti-PreS2 antibodies (Coursaget et al., 1988; Li et al., 2017; Sankhyan et al., 2016) (red lines in Figure 1E). These results suggest that the neutralizing antibody response in the selected individuals is directed
 15 primarily against the S-protein irrespective of immunization or infection.

Example 2

[0081] Human Monoclonal Antibodies to HBV

[0082] To characterize the antibodies responsible for neutralizing activity in the selected individuals, we purified S-protein binding class-switched memory B cells (Escolano et al., 2019; Scheid et al., 2009a). Unexposed naïve controls and vaccinated individuals with
 20 low anti-HBs ELISA titers showed background levels of S-protein specific memory B cells (Figure 2A and 9A). In contrast, individuals with high neutralizing activity displayed a distinct population of S-antigen binding B cells constituting 0.03-0.07% of the IgG⁺ memory compartment (CD19-MicroBeads⁺ CD20-PECy7⁺ IgG-Bv421⁺ S-protein-PE⁺ S-protein-
 25 APC⁺ ovalbumin-Alexa Fluor 488⁻) (Figure 2A and 9A). Consistent with the findings in elite HIV-1 neutralizers (Rouers et al., 2017), the fraction of S-protein specific cells was directly correlated to the neutralization titer of the individual ($r_s=0.699$, $p=0.0145$, Spearman's rank correlation) (Figure 2B).

[0083] Immunoglobulin heavy (*IGH*) and light (*IGL* or *IGK*) chain genes were
 30 amplified from single memory B cells by PCR (Robbiani et al., 2017; Scheid et al., 2009b; von Boehmer et al., 2016). Overall, we obtained 244 paired heavy and light chain variable regions from S-protein-binding memory B cells from eight volunteers with high anti-HBs ELISA titers (Figure 9B and 9C; Table S2). Expanded clones composed of cells producing

antibodies encoded by the same *Ig* variable gene segments with closely related CDR3s were found in each of the top neutralizers #146, #60 and #13 (Figure 2C). Moreover, IGHV3-30/IGLV3-21 was present in #146 and #60; IGHV3-33/IGLV3-21 in #146 and #13; and IGHV3-23/IGLV3-21 in #146, #60 and #13. The variable diversity and joining (V(D)J) region of these antibodies was approximately 80% identical at the amino acid level (Figure 2D). Antibodies with related *Ig* heavy and light chains were also identified between volunteer #55 (HBV infected but recovered) and vaccinated individuals (Figure 2C and 9B). We conclude that top HBV neutralizers produce clones of antigen-binding B cells that express related *Ig* heavy and light chains.

Example 3

[0084] Breadth of Reactivity

[0085] Twenty representative antibodies from 5 individuals, designated as H001 to H020, were selected for expression and further testing (Figure 9B). All 20 antibodies showed reactivity to the S-protein antigen used for B cell selection (HBsAg *adr* CHO) by ELISA with 50% effective concentration (EC₅₀) values ranging from 18-350 ng/ml (Figure 3A). These antibodies carried somatic mutations that enhanced antigen binding as determined by reversion to the inferred unmutated common ancestor (UCA) (Figure 3B). Thus, affinity maturation was essential for their high binding activity.

[0086] Four major serotypes of HBV exist as defined by a constant “a” determinant and two variable and mutually exclusive determinants “d/y” and “w/r” (Bancroft et al., 1972; Le Bouvier, 1971) with a highly statistically significant association between serotypes and genotypes (Kramvis et al., 2008; Norder et al., 2004). To determine whether our antibodies cross-react to different HBsAg serotypes, we performed ELISAs with 5 additional HBsAg antigens: yeast-expressed serotype “*adr*”, “*adw*”, and “*ayw*”, as well as “*ad*” and “*ay*” antigen purified from human blood (Figure 3C). Many of the antibodies tested displayed broad cross-reactivity and EC₅₀ values lower than libivirumab, a human anti-HBs monoclonal antibody that was isolated from HBV-immunized humanized mice and then tested clinically (Eren et al., 2000; Eren et al., 1998; Galun et al., 2002). These antibodies were not polyreactive or autoreactive when tested in polyreactivity ELISA and HEp-2 immunofluorescence assays respectively (Figure 10A and 10B). We conclude that the antibodies tested are broadly cross-reactive with different HBV serotypes.

Example 4

[0087] Antigenic Epitopes on S-protein

[0088] To determine whether the selected antibodies bind to overlapping or non-overlapping epitopes, we performed competition ELISA assays, in which the S-protein was pre-incubated with a selected antibody followed by a second biotinylated antibody. Antibodies that showed weak levels of binding in ELISA (H002, H012, H013, H014, H018) were excluded. As expected, all of the antibodies tested blocked the binding of the autologous biotinylated monoclonal (yellow boxes in Figure 4A), while control human anti-HIV antibody 10-1074 failed to block any of the anti-HBs antibodies. The competition ELISA identified three mutually exclusive groups of monoclonal antibodies, suggesting that there are at least three dominant non-overlapping antigenic sites on HBsAg (red box for Group-I, blue box for Group-II, and H017 in Group-III, Figure 4A). Each of the individuals that had 2 or more antibodies tested in the competition ELISA expressed monoclonal antibodies that targeted 2 of the 3 non-overlapping epitopes (Figure 4A and 9B).

[0089] To further define these epitopes, we produced a series of alanine mutants spanning most of the predicted extracellular domain of the S-protein with the exception of cysteines, alanines, and amino acid residues critical for S-protein production (Salisse and Bureau, 2009) (Figure 1D). ELISA assays with the representative antibodies from each antibody group and the mutant proteins revealed a series of binding patterns partially corresponding to the three groups defined in the competition assays (Figure 4B and 11). For example, mutations I110A and T148A interfered with binding by Group-I antibodies exemplified by H004, H006, H019, and H020, but had little measurable effect on Group-II antibodies exemplified by H007, H015, and H016 or Group-III antibody H017 (Figure 4B and 11).

[0090] However alanine scanning suggested that some residues such as D144 and G145 are critical for binding of monoclonals in both Group-I and Group-II despite their inability to compete with each other for binding to the native antigen (Figure 4B and 11). Without intending to be constrained by any particular theory, it is considered that D144A and G145A mutations alter the overall structure of HBsAg thereby interfering with binding of antibodies that normally target independent sites on the protein.

[0091] In addition to alanine scanning, we also produced 44 common naturally occurring escape variants found in chronically infected individuals (Hsu et al., 2015; Ijaz et al., 2012; Ma and Wang, 2012; Salpini et al., 2015). Whereas alanine scanning showed that some of the antibodies in Group-I and -II were resistant to G145A, the corresponding naturally occurring mutations at the same position, G145E and G145R, revealed decreased binding by most antibodies (Figure 4C). Among the antibodies tested, H017 and H019, in

Groups-I and -III respectively, showed the greatest resistance to G145 mutations and the greatest breadth and complementarity (Figure 4C). We conclude that human anti-HBs monoclonals obtained from the selected individuals recognize distinct epitopes on HBsAg, most of which appear to be non-linear conformational epitopes spanning different regions of the protein.

Example 5

[0092] *In Vitro* Neutralizing Activity

[0093] To determine whether the new monoclonals neutralize HBV *in vitro*, we performed neutralization assays using HepG2-NTCP cells (Figure 5A and 5B). The 50% inhibitory concentration (IC₅₀) values were calculated based on HBsAg/HBeAg ELISA or immunofluorescence staining for HBcAg expression (Michailidis et al., 2017) (Figure 5C). Neutralizing activity was further verified by *in vitro* neutralization assays using primary human hepatocytes (Michailidis et al., 2020) (Figure 5C and 5D). Fourteen of the 20 antibodies tested showed neutralizing activity with IC₅₀ values as low as 5 ng/ml (Figure 5C). By comparison, libivirumab had an IC₅₀ of 35 and 128 ng/ml in the neutralization assays based on ELISA and immunofluorescence assays respectively (Figure 5C). Somatic mutations were essential for potent neutralizing activity as illustrated by the reduced activity of the inferred UCAs (Figure 12A and 12B). In addition, optimal activity required bivalent binding since the IC₅₀ values for Fab fragments were 2 orders of magnitude higher than intact antibodies (Figure 5E). Finally, there was no overt synergy when Group-I, -II, and -III antibodies were combined (Figure 12C). We conclude that half of the new monoclonals were significantly more potent than libivirumab including Group-I H004, H005, H006, H008, H009, H019, and H020 and Group-II H007, H015, and H016 (Figure 5C).

Example 6

25 [0094] Structure of the H015 Antibody/Peptide Complex

[0095] H015 differed from other antibodies in that its binding was inhibited by 5 consecutive alanine mutations spanning positions K141-G145 indicating the existence of a linear epitope. This idea was verified by ELISA against a series of overlapping peptides comprising the predicted extracellular domain of S-protein (Figure 6A and 13A). The data showed that H015 binds to KPSDGN (SEQ ID NO: 23), which is near the center of the putative extracellular domain and contains some of the most frequently mutated amino acids during natural infection.

[0096] To examine the molecular basis for H015 binding, its Fab fragment was co-crystallized with the target peptide epitope PSSSSTKPSDGNSTS (SEQ ID NO: 24), where all cysteine residues that flank the recognition sequence were substituted with serine to avoid non-physiological cross-linking. The 1.78 Å structure (Figure 6B and 13B) revealed that the peptide is primarily bound to the immunoglobulin heavy chain (Figure 6B and 6C), interacting with residues from CDR1 (R31), CDR2 (W52, F53) and CDR3 (E99, P101, L103, L104) of IgH with only one contact with CDR3 (P95) of IgL. The peptide adopts a three-residue beta hairpin (class 3) of the 3:5 type involving residues K141 through G145 as only one hydrogen bond is seen, between K141 and G145 (Milner-White and Poet, 1986), and they are not part of a beta sheet. The peptide is further stabilized by a salt-bridge formed between K141 and D144 (Figure 6D and 13C). Interestingly, the distance between the Cαs of the two residues (C139 and C147) flanking the recognition residues is 6.4 Å and are poised to form a disulfide bond between C139 and C147 found in the native HBsAg structure (Ito et al., 2010). The H015 Fab appears to stabilize the conformation of the peptide via the Fab-peptide contacts (Figure 13D) including a large binding surface (866 Å²; antibody-antigen buried surface of 600-900 Å² (Braden and Poljak, 1995)) comprised primarily of a single salt-bridge (lysine to aspartate; 0.9± 0.3 Kcal/mol) (White et al., 2013) and five hydrogen bonds (1-2 Kcal/mol/bond) (Sheu et al., 2003). Moreover, the peptide further restricts loop through intra-peptide contacts (Figure 13D) even in the absence of the disulfides.

[0097] The residues that form the hairpin are important for anti-HBs antibody recognition as determined by alanine scanning (Figure 4B and 11). In addition, each of these residues has been identified as important for immune recognition during natural infection (Ma and Wang, 2012). G145R, the most common naturally occurring S-protein escape mutation substitutes a large positively charged residue for a small neutral residue (circled residue in Figure 6E) potentially altering the antigenic binding surface. G145 adopts a positive phi angle of 77.9 and by doing so introduces a kink in the beta-strand, a structure that would be disrupted with the substitution to arginine.

[0098] HBsAg can be glycosylated at N146 and this site is also strictly conserved. However, some studies have suggested that this glycosylation site is never fully occupied, resulting in a nearly 1:1 ratio of glycosylated and non-glycosylated isoforms on the surface of viral envelope (Julithe et al., 2014). The glycosylation may be either NAG-NAG-MAN or NAG-(FUC)-NAG-MAN (Hyakumura et al., 2015). We have modeled both fucosylated and non-fucosylated options by grafting a 7mer and 11mer glycan conjugated at N146 of peptide

in the presence of the Fab. We found that both glycosylation forms are tolerated at that location with only minimal torsional adaptations without clashes with the Fab, though the fucosylated (branched) glycan required some additional torsional angle changes to the Fab, as well.

5

Example 7

[0099] Protection and Therapy in Humanized Mice

[0100] HBV infection is limited to humans, chimpanzees, tree shrews, and human liver chimeric mice (Sun and Li, 2017). To determine whether our anti-HBs bNAbs prevent infection *in vivo* we produced human liver chimeric *Fah*^{-/-}*NODRag1*^{-/-}*IL2rg*^{null} (huFNRG) mice (de Jong et al., 2014) and injected them with control or H020 (Group-I) or H007 (Group-II) antibodies before infection with HBV (Figure 7A-7D). These two antibodies were chosen because they bind to non-overlapping sites, and have broad and potent neutralizing activity. Whereas all six control animals in two independent experiments were infected, pre-exposure prophylaxis with either H007 or H020 was fully protective (Figure 7B-7D). We conclude that single anti-HBs bNAbs targeting different epitopes on the major virus surface antigen can prevent infection *in vivo*.

[0101] To determine whether bNAbs can also control established infections, we infused control antibody or bNAbs H020 (Group-I) or H007 (Group-II) into huFNRG mice with HBV viral loads of 10⁶-10⁸ copies/ml of serum (Figure 7E-7H and Figure 14A). *Fah*^{-/-}*NODRag1*^{-/-}*IL2rg*^{null} mice are highly immunodeficient and unable to mount adaptive immune responses due to absence of T and B lymphocytes. In addition, the *IL2rg*^{null} mutation prevents cytokine signaling through multiple receptors, leading to a deficiency in innate immune function including antibody-dependent cellular cytotoxicity. Thus, elimination of viremia of 10⁶-10⁸ DNA copies/ml in huFNRG mice by antibody therapy alone would not be expected.

[0102] Animals that received the control antibodies further increased viremia to as high as ~10¹¹ DNA copies/ml (Figure 7F). In contrast, the 5 mice that received H020 maintained stable levels of viremia for around 30 days (Figure 7G), after which time 2 mice showed increased viremia (arrow-1/3 in Figure 7G). A similar result was observed in the 5 mice that received H007 (Figure 7H), where only one showed a slight increase viremia at around day 50 (arrow-5 in Figure 7H).

[0103] To determine whether the animals that showed increased HBV DNA levels during antibody monotherapy developed escape mutations, we sequenced the viral DNA recovered from mouse blood. All three mice that escaped H020 (Group-I) or H007 (Group-II)

monotherapy developed viruses that carried a G145R mutation in the S-protein (arrow-1/3 in Figure 7G, arrow-5 in Figure 7H, Figure 7I, and Figure 14). This mutation represents a major immune escape mutation in humans (Zanetti et al., 1988). Furthermore, mutations at the same position in the S-protein were also identified in mice that maintained low level viremia (arrow-2/4 in Figure 7G, arrow-6/7 in Figure 7H, Figure 7I, and Figure 14), but not in control animals (Figure 14). These results show that anti-HBs bNAb monotherapy leads to the emergence of escape mutations that are consistent with bNAb binding properties *in vitro* (Figure 4C).

[0104] To determine whether a combination of bNAbs targeting 2 separate epitopes would interfere with the emergence of resistant strains, we co-administered H006 + H007 (Group-I and -II, respectively) to 8 HBV-infected huFNRG mice (Figure 7J). H006 (Group-I) was chosen for this purpose because of its resistance to D144A and G145A mutation (Figure 4B). Similar to H007 monotherapy, there was only a slight increase in viremia in animals treated with the H006 + H007 anti-HBs bNAb combination during the 60-day observation period (Figure 7J and 14A). However, sequence analysis revealed that 3 of the mice developed resistance mutations including K122R/G145R, C137Y, and C137Y/D144V (arrow-8/9/10 in Figure 7J, Figure 7I, and Figure 14). These mutations confer loss of binding to both H006 (Group-I) and H007 (Group-II) (Figure 4C). Thus, the combination of 2 anti-HBs bNAbs targeting separate epitopes but susceptible to the same clinical escape variants is not sufficient to inhibit emergence of escape mutations.

[0105] To attempt to block the emergence of escape mutations, we combined H017 + H019 (Group-III and -I, respectively) bNAbs because they displayed complementary sensitivity to commonly occurring natural mutations (Figure 4C). None of 7 mice treated with the combination of showed increased viremia or escape mutations as assessed by sequence analysis (Figure 7K and 14A). Similar effects were also observed in the 9 animals treated with the H016, H017 and H019 (Group-II, -III, -I, respectively) triple antibody combination (Figure 7L and 14A). Moreover, both these combinations dramatically reduced the HBsAg levels in serum (Figure 14C and 14D). Altogether, these findings suggest that control of HBV infection by bNAbs requires a combination of antibodies targeting non-overlapping groups of common escape mutations.

[0106] RESOURCES TABLE

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Experimental Models: Cell Lines		

Human Hepatocytes, Cryopreserved, Plateable and Interaction Qualified	Lonza Bioscience	Cat#HUCPI
Hepatocyte Defined Medium	Corning	Cat#05449
HepG2-NTCP	(Michailidis et al., 2017)	N/A
HEK293-6E	National Research Council of Canada	NRC file 11565
HepDE19 cells	(Cai et al., 2012)	N/A
Huh-7.5	(Robbiani et al., 2017)	N/A
Experimental Models: Mouse Strains		
<i>Fah</i> ^{-/-} NODRag1 ^{-/-} IL2rg ^{-/-} mouse (huFNRG)	(de Jong et al., 2014)	N/A
Bacteria and Viruses		
Subcloning Efficiency™ DH5α™ Competent Cells	Thermo Fisher Scientific	Cat#18265017
HBV viruses	(Cai et al., 2012)	N
Antibodies		
Human recombinant 10-1074	(Mouquet et al., 2012)	N/A
Human recombinant ED38	(Wardemann et al., 2003)	N/A
Human recombinant mG053	(Yurasov et al., 2005)	N/A
Goat anti-Human IgG (H+L) Secondary Antibody, HRP	Thermo Fisher Scientific	Cat#31410
Alexa Fluor 488 Mouse anti-Human CD19	BD Biosciences	Cat#557697
BV421 Mouse Anti-Human CD19	BD Biosciences	Cat#562440
anti-CD20-PECy7	BD Biosciences	Cat#335811
Anti-CD27-PE	BD Biosciences	Cat#555441
APC Mouse Anti-Human IgG	BD Pharmingen	Cat#550931
Bv421 Mouse Anti-Human IgG	BD Biosciences	Cat#562581
Anti-Hepatitis B virus core antigen IgG	AUSTRAL Biologicals	Cat#HBP-023-9
Alexa Fluor® 488 AffiniPure Goat Anti-Human IgG, F(ab') ₂ fragment specific	Jackson ImmunoResearch	Cat#109-545-006
Goat anti-Rabbit IgG (H+L) Alexa Fluor 594	Thermo Fisher Scientific	Cat#A11037
Chemicals and Proteins		
Streptavidin HRP	BD Biosciences	Cat#554066
APC Streptavidin	BD Biosciences	Cat#554067
Strep-PE	eBioscience	Cat#12-4317-87
Streptavidin, Alexa Fluor™ 488	Thermo Fisher Scientific	Cat#S32354
Human BD Fc Block™	BD Biosciences	Cat#564220
Ovalbumin (257-264) chicken	Sigma-Aldrich	Cat#S7951
HBsAg adr CHO	ProSpec	Cat#HBS-875
HBsAg adw	ProSpec	Cat#HBS-872

HBsAg protein adr	Fitzgerald	Cat#30-AH37
HBsAg protein ay	Fitzgerald	Cat#30-1816
HBsAg protein ad	Fitzgerald	Cat#30-AH15
HBsAg protein ayw	Fitzgerald	Cat#30R-AH018
RNAasin Plus RNase inhibitor	Promega	Cat#N2615
Random Primers	Thermo Fisher Scientific	Cat#48190011
Lipopolysaccharides from <i>E. coli</i> O55:B5	Sigma-Aldrich	Cat#L2637
Insulin solution human	Sigma-Aldrich	Cat#I1927
Deoxyribonucleic acid from calf thymus	Sigma-Aldrich	Cat#4522
Hemocyanin from Megathura crenulata (keyhole limpet)	Sigma-Aldrich	Cat#H8283
Poly(ethylene glycol)	Sigma-Aldrich	Cat#81268
Normal Goat Serum	Jackson ImmunoResearch	Cat#005-000-121
DAPI, FluoroPure™ grade	Thermo Fisher Scientific	Cat#D21490
Paraformaldehyde 4% Aqueous Solution	Electron Microscopy Sciences	Cat#157-4
Phusion High-Fidelity DNA Polymerase	Thermo Fisher Scientific	Cat#F-530L
Commercial Assays		
ARCHITECT Anti-HBs	Abbott Laboratories	Cat#B7C180
ARCHITECT HBsAg Qualitative	Abbott Laboratories	Cat#B1P970
ARCHITECT Anti-HBc II	Abbott Laboratories	Cat#B8L440
HBsAg CLIA kit	Autobio Diagnostics Co.	Cat#CL0310-2
HBeAg CLIA kit	Autobio Diagnostics Co.	Cat#CL0312-2
Anti-HBs CLIA kit	Autobio Diagnostics Co.	Cat#CL0311-2
LS magnetic columns	Miltenyi Biotech	Cat#130-042-401
CD19 MicroBeads, human	Miltenyi Biotech	Cat#130-097-055
EZ-Link™ Micro NHS-PEG4-Biotinylation Kit	Thermo Fisher Scientific	Cat#21955
Superscript III Reverse Transcriptase	Thermo Fisher Scientific	Cat#18080044
QIAamp DNA blood mini kit	Qiagen	Cat#51104
TaqMan Universal PCR Master Mix	Applied Biosystems	Cat#4304437
Antinuclear antibodies (HEp-2) Kit	MBL International	Cat#ANK-120
Centricon Plus-70 Ultracel PL-100	Millipore Sigma	Cat#UFC710008
X-tremeGENE 9 DNA Transfection Reagent	Sigma-Aldrich	Cat#6365787001
Plasmids		
IGγ1 expression vector	(von Boehmer et al., 2016)	N/A
IGκ expression vector	(von Boehmer et al., 2016)	N/A
IGλ expression vector	(von Boehmer et al., 2016)	N/A
p1.3xHBV-WT	Laboratory of Charles M. Rice	N/A

Softwares and Websites		
PRISM	GraphPad	www.graphpad.com
IgBlast	(Ye et al., 2013)	www.ncbi.nlm.nih.gov/igblast/
IMGT/V-QUEST	(Lefranc et al., 2015)	www.imgt.org/IMGT_vquest/vquest
Geneious Prime	Geneious	www.geneious.com/

Example 8

[0107] This Example provides a description of materials, methods, and subjects used to obtain the foregoing results.

5 [0108] EXPERIMENTAL MODELS AND SUBJECTS

[0109] Human Subjects

[0110] Volunteer recruitment and blood draws were performed at the Rockefeller University Hospital under a protocol approved by the institutional review board (IRB QWA-0947). Study participants ranged in age from 22-65 with a mean of 43, the female:male ratio
10 was 81:78 (Figure 8D and 8E; Table S1).

[0111] Animals

[0112] *Fah^{-/-}NODRag1^{-/-}IL2rg^{null}* (FNRG) female mice were produced as reported (de Jong et al., 2014) and maintained in the AAALAC-certified facility of the Rockefeller University. Animal protocols were in accordance with NIH guidelines and approved by the
15 Rockefeller University Institutional Animal Care and Use Committee under protocol #18063. Female littermates were randomly assigned to experimental groups.

[0113] Cell Lines

[0114] HepG2-NTCP cells (Michailidis et al., 2017) and HepDE19 cells (Cai et al., 2012) were maintained in collagen-coated flasks in Dulbecco's Modified Eagle Medium
20 (DMEM) supplemented with 10% or 3% fetal bovine serum (FBS) and 0.1 mM non-essential amino acids (NEAA). Huh7.5-NTCP cells were maintained in DMEM supplemented with 10% FBS and 0.1 mM NEAA. All liver cell lines were cultured at 37°C in 5% CO₂. Human embryonic kidney HEK293-6E suspension cells were cultured at 37°C in 8% CO₂ with shaking at 120 rpm.

25 [0115] Viruses

[0116] HBV-containing supernatant from HepDE19 cells was collected and concentrated as previously described (Michailidis et al., 2017). The concentrated virus stock was aliquoted and stored at -80°C. For *in vivo* experiments one aliquot of mouse-passaged

genotype C HBV virus, originally launched from patient serum (Billerbeck et al., 2016), was stored at -80°C and thawed for mouse infection experiments. For protection and treatment experiments, animals were challenged intravenously using 1×10^4 DNA copies per mouse.

[0117] Bacteria

5 **[0118]** *E. coli* DH5-alpha were cultured at 37°C with shaking at 230 rpm.

[0119] METHODS

[0120] Collection of Human Samples

[0121] Samples of peripheral blood were collected from volunteers at the Rockefeller University Hospital. Serum was isolated by centrifugation of coagulated whole blood, and
10 aliquoted for storage at -80°C. PBMCs were isolated using a cell separation tube with frit barrier and cryopreserved in liquid nitrogen in 90% heat-inactivated FBS supplemented with 10% dimethylsulfoxide (DMSO).

[0122] HBV Stock

[0123] HepDE19 cells (Cai et al., 2012) were cultured in the absence of tetracycline
15 to induce HBV replication. After seven days, supernatant was collected every other day for two weeks and fresh medium was added. After each collection, medium was spun down to remove cell debris, passed through a 0.22 µm filter, and kept at 4°C. Collected medium was concentrated 100-fold via centrifugation using Centricon Plus-70 centrifugal filter devices (Millipore-Sigma, Billerica, MA). Mouse-passaged genotype C HBV virus (Billerbeck et al.,
20 2016) was used for *in vivo* mouse experiment.

[0124] *In Vitro* HBV Neutralization Assay

[0125] *In vitro* HBV infection was performed as previously described (Michailidis et al., 2017). Briefly, HepG2-NTCP cells were seeded in 96-well collagen-coated plates in DMEM supplemented with 10% FBS and 0.1 mM NEAA. The medium was changed to
25 DMEM with 3% FBS, 0.1 mM NEAA, and 2% DMSO the next day and cultured for an additional 24 hours before infection. The inoculation was in DMEM supplemented with 3% FBS and 0.1 mM NEAA 4% PEG and 2% DMSO. Antibodies or serum samples were incubated with the virus in the inoculation medium for one hour at 37°C before adding to cells. Serum neutralization capacity (y-axis in Figure 1A and 8B) was calculated as the
30 reciprocal of the relative percentage of infected HepG2-NTCP cells immunostained by rabbit anti-HBV core antibody (AUSTRAL Biologicals). For example, if the relative percentage of infected cells were 100% (no serum added or the sera from unexposed naïve control donors), the serum neutralization capacity would be calculated as 1; but if the relative percentage of

infected cells were 50% or 10%, the serum neutralization capacity would be 2 or 10. For the blocking neutralization assay, S-protein antigen at different concentration was incubated with purified polyclonal antibodies for one hour at 37°C before incubation with HBV virus. The cells were then spinoculated for one hour by centrifugation at 1,000 g at 37°C. After a 24-hour incubation, supernatant was removed, cells were washed five times with PBS, and 100 µl of fresh DMEM supplemented with 3% FBS, 0.1 mM NEAA, and 2% DMSO. Both supernatant and cells were harvested 7 days after infection for analysis. Neutralization assays in primary human hepatocytes were performed as above using hepatocytes from livers of highly humanized mice that were harvested and seeded on collagen-coated plates in hepatocyte defined medium (Corning) (Michailidis et al., 2020).

[0126] Chemiluminescence Immunoassay

[0127] For quantitative analysis of secreted antigen HBsAg or HBeAg, 50 µl of the collected supernatant was loaded into 96-well plates of a chemiluminescence immunoassay (CLIA) kit (Autobio Diagnostics Co., Zhengzhou, China) according to the manufacturer's instructions. Plates were read using a FLUOstar Omega luminometer (BMG Labtech). The absolute concentrations were measured and the relative values were calculated by normalizing to the virus-only control well in the same lane. For example, the absolute HBsAg/HBeAg level in virus-only control well (considered as reference) was 20 NCU/ml (national clinical units per milliliter), while adding one neutralizing serum sample might reduce this to 5 NCU/ml. Therefore, after normalization, the relative HBsAg/HBeAg level were calculated as 100% in control and 25% for this neutralizing serum. Since many factors (virus concentration, cell concentration, immunofluorescence reading, etc.) vary between different plates or different rounds of experiments, normalization is necessary for combining data for comparison.

[0128] Immunofluorescence

[0129] Cells were fixed in 4% paraformaldehyde for 20 minutes at room temperature, washed with PBS and permeabilized with 0.1% Triton X-100 in PBS. After blocking with 5% goat serum, the cells were incubated with rabbit anti-HBV core antibody (AUSTRAL Biologicals) overnight at 4°C and visualized with goat anti-rabbit Alexa Fluor 594 (Thermo Fisher Scientific). Nuclei were stained with DAPI. Cells were imaged using a Nikon Eclipse TE300 fluorescent microscope and processed with ImageJ. For high-content imaging analysis ImageXpress Micro XLS (Molecular Devices, Sunnyvale, CA) was used. The absolute HBC⁺ percentages were obtained and the relative percentage of HBC⁺ cells was calculated by

normalizing to the virus-only control well in the same lane. For example, the absolute HBc⁺ cell percentage in virus-only control well (considered as reference) was 40%, while adding one neutralizing serum sample might reduce this to 10%. Therefore, after normalization, the relative percentages of HBc⁺ cells were calculated as 100% in control well and 25% for this neutralizing serum sample. Since many factors (virus concentration, cell concentration, immunofluorescence reading, etc.) vary between different plates or different rounds of experiments, normalization is necessary for combining data for comparison.

[0130] ELISA Assays

[0131] Blood samples were submitted to Memorial Sloan Kettering Cancer Center for clinical testing. The presence of HBsAg protein and anti-HBc antibody, as well as anti-HBs titers, were determined by ELISA (Abbott Laboratories) as per the manufacturer's instructions.

[0132] The binding of serum or recombinant IgG antibodies to HBsAg proteins (see KEY RESOURCES TABLE) was measured by coating ELISA plates with 10 µg/ml of antigen in PBS. Plates were blocked with 2% BSA in PBS and incubated with antibody for one hour at room temperature. Visualization was with HRP-conjugated goat anti-human IgG (Thermo Fisher Scientific). The 50% effective concentration (EC₅₀) needed for maximal binding was determined by non-linear regression analysis in software PRISM.

[0133] For competition ELISAs plates were coated with 0.12 µg/ml HBsAg (*adr* CHO) and incubated with 16.7 µg/ml primary antibody for two hours, followed by directly adding 0.25 µg/ml biotinylated secondary antibody and incubation for 30 minutes all at room temperature. Detection was with streptavidin-HRP (BD Biosciences).

[0134] Autoreactivity and Polyreactivity

[0135] Autoreactivity and polyreactivity assays were performed as described (Gitlin et al., 2016; Mayer et al., 2017; Robbiani et al., 2017). For the autoreactivity assays, monoclonal antibodies were tested with the Antinuclear antibodies (HEp-2) Kit (MBL International). Antibodies were incubated at 100 µg/ml and were detected with Alexa Fluor 488 AffiniPure F(ab')₂ Fragment Goat Anti-Human IgG (H+L) (Jackson ImmunoResearch) at 10 µg/ml. Fluorescence images were taken with a wide-field fluorescence microscope (Axioplan 2, Zeiss), a 40x dry objective and a Hamamatsu Orca ER B/W digital camera. Images were analyzed with Image J. Human serum containing antinuclear antibodies (MBL International) was used as a positive control. For the polyreactivity ELISA assays, antibody binding to five different antigens, double-stranded DNA (dsDNA), insulin, keyhole limpet

hemocyanin (KLH), lipopolysaccharides (LPS), and single-stranded DNA (ssDNA), were measured. ED38 (Wardemann et al., 2003) and mG053 (Yurasov et al., 2005) antibodies were used as positive and negative controls, respectively.

[0136] Synthetic Peptides

5 **[0137]** Eighteen peptides spanning the antigenic loop region of S-protein antigen were synthesized at the Proteomics Resource Center of The Rockefeller University. For peptide ELISAs plates were coated with 10 µg/ml peptide in PBS.

[0138] HBsAg-Binding Memory B cells

[0139] S-protein (*adr* serotype) expressed and purified from Chinese hamster ovary
10 (CHO) cells (ProSpec) and ovalbumin (Sigma-Aldrich) were biotinylated using EZ-Link™ Micro NHS-PEG4-Biotinylation kit (Thermo Fisher Scientific). S-protein-PE and S-protein-APC were prepared by incubating 2-3 µg of biotin-S-protein with streptavidin-PE (eBioscience) or streptavidin-APC (BD Biosciences) in PBS respectively overnight at 4°C in the dark. Ovalbumin-Alexa Fluor 488 was generated by incubating biotin-ovalbumin
15 with streptavidin-Alexa Fluor 488 (Thermo Fisher Scientific).

[0140] B cell purification, labeling, and sorting were as previously described (Escolano et al., 2019; Robbiani et al., 2017; Tiller et al., 2008; von Boehmer et al., 2016). Briefly, PBMCs were thawed and washed with RPMI medium at 37°C. B lymphocytes were positively selected using CD19 MicroBeads (Miltenyi Biotec) followed by incubation
20 with human Fc block (BD Biosciences) and anti-CD20-PECy7 (BD Biosciences), anti-IgG-Bv421 (BD Biosciences), S-protein-PE at 10 µg/ml, S-protein-APC at 10 µg/ml, and ovalbumin-Alexa Fluor 488 at 10 µg/ml at 4°C for 20 minutes. Single CD20⁺ IgG⁺ S-protein-PE⁺ S-protein-APC⁺ Ova-Alexa Fluor 488⁻ memory B cells were sorted into 96-well plates using a FACSAriaII (Becton Dickinson) and stored at -80°C.

25 **[0141] Antibody Cloning, Sequencing and Production**

[0142] Antibody cloning, sequencing and production were done as previously reported (Robbiani et al., 2017; Tiller et al., 2008; von Boehmer et al., 2016). Primers are listed in Table S3. Unmutated common ancestor (UCA) antibody sequences of H006, H019 and H020 were synthesized by gBlock IDT (Table S3) and were inserted into antibody
30 vectors for expression. V(D)J gene segment and CDR3 sequences were determined by IgBlast (Ye et al., 2013) and/or IMGT/V-QUEST (Brochet et al., 2008).

[0143] S-protein Mutagenesis

[0144] Oligonucleotides fragments with the target point mutations were synthesized by gBlock IDT (Table S3), and were substituted into the antigenic loop region in plasmid p1.3xHBV-WT by Sequence and Ligation-Independent Cloning (SLIC) (Jeong et al., 2012). Mutant plasmids were transfected into Huh-7.5-NTCP cells using X-tremeGENE 9 DNA Transfection Reagent (Sigma-Aldrich) and the culture medium was changed to serum-free DMEM after 24 hours. Supernatants were collected 2 days later and stored at -80°C. Serum-free medium (50 µl) was directly used to coat ELISA plates.

[0145] **Crystallization, X-ray Data Collection, Structure Determination and Refinement**

10 [0146] Antibody Fab (25 mg/ml) in 50 mM Tris 8.0, 50 mM NaCl was mixed with peptide (5 mg/ml) in the same buffer at 5:1 v/v. Molar ratio of Fab:peptide is around 1:2. Crystals were obtained upon substitution of all peptide-11 cysteine residues with serine in the peptide synthesis (Proteomics Resource Center, RU). The crystallization condition for Fab15/peptide-11Ser was identified from a commercial screen (Morpheus by Molecular Dimensions) by the sitting-drop vapor-diffusion method at room temperature. The crystal used for data collection was obtained directly from the initial setup (position E1) in a precipitant solution consisting of 0.12 M Ethylene glycols (Di, Tri, Tetra and Penta-ethylene glycol), 0.1 M Buffer Mix 1 (Imidazole/MES) at pH 6.5 and 30% Precipitant Mix 1 (20% v/v PEG 500* MME; 10 % w/v PEG 20000). The crystals were flash-cooled in liquid nitrogen directly from the mother liquor without additional cryoprotectant. X-ray diffraction data were collected from a single crystal on the Advanced Photon Source (APS) beamline 24-ID-E to 1.78 Å resolution. The data were integrated and scaled with the program XDS (Kabsch, 2010a, b) and other data processing utilities from the CCP4 suite (Collaborative Computational Project, 1994) using RAPD, the software available at the beam-line. Initial phase estimates and electron-density maps were obtained by molecular replacement with Phaser (McCoy et al., 2007) using a single FAB molecule from (PDB: 5GGU) as an initial search model in Phenix (Adams et al., 2010). Iterative model building and structural refinement were manually performed using COOT (Emsley et al., 2010) and Phenix, respectively. The peptide density was well defined, and refined to 90% occupancy, for residues STKPSDGNST (SEQ ID NO: 25). All other residues were not visible and the area where they would be is fully solvent, with no crystal contacts involving any of the peptide atoms. The quality of the final model was good as noted in a Ramachandran of 96% of the observed residues within the allowable region. Data-collection and refinement statistics are

summarized (Figure 13B). All molecular graphics were prepared with PyMOL (Version 2.0 Schrödinger, LLC). Atomic coordinates and experimental structure factors have been deposited in the PDB under accession code 6VJT.

[0147] Humanized Mice and *In Vivo* Studies

- 5 **[0148]** Six to eight week old *Fah*^{-/-}NOD*Rag1*^{-/-}*IL2rg*^{null} (FNRG) female mice were transplanted with one million human hepatocytes from a pediatric female donor HUM4188 (Lonza Bioscience) as previously described (de Jong et al., 2014). Briefly, during isoflurane anesthesia mice underwent skin and peritoneal incision, exposing the spleen. One million hepatocytes were injected in the spleen using a 28-gauge needle. The peritoneum was then
- 10 approximated using 4.0 VICRYL sutures (Johnson & Johnson), and skin was closed using MikRon Autoclip surgical clips (Becton Dickinson). Mice were cycled off the drug nitisinone (Yecuris) on the basis of weight loss and overall health. Humanization was monitored by human albumin quantification in mouse serum using a human-specific ELISA (Bethyl Labs). Humanized FNRG mice with human albumin values greater than 1 mg/ml were used for
- 15 infection experiments. The human liver chimeric (huFNRG) mice are extremely immunodeficient. The *Rag1*^{-/-} renders the mice B and T cell deficient and the *IL2rg*^{null} mutation prevents cytokine signaling through multiple receptors, leading to a deficiency in functional NK cells. Moreover, the genetic background is NOD background, with suboptimal antigen presentation, defects in T and NK cell function, reduced macrophage cytokine
- 20 production, suppressed wound healing, and C5 complement deficiency. Thus the mice would be unable to produce antibody-dependent effector functions, including antibody-dependent cell-mediated cytotoxicity (ADCC), or passive antibody-enhanced adaptive immunity.
- [0149]** Mice were challenged intravenously with 1x10⁴ genome equivalent (GE) of mouse-passaged genotype C HBV viruses diluted in PBS. For prophylaxis experiments, 500
- 25 µg of monoclonal antibody was administered intraperitoneally at 20 and again at 6 hours before infection. For therapy experiments, huFNRG mice with established HBV infections (<10⁸ DNA copies/ml of serum) were injected with 500 µg of each monoclonal antibody intraperitoneally 3 times per week.
- [0150]** DNA in mouse serum collected weekly was extracted using a QIAamp DNA
- 30 Blood Mini Kit (Qiagen). Total HBV DNA was determined by quantitative PCR (Michailidis et al., 2017). PCR was performed using a TaqMan Universal PCR Master Mix (Applied Biosystems), primers and probe (Table S3).

[0151] To obtain HBV DNA from serum for sequence analysis the S domain was amplified using primers (Table S3), and Phusion DNA polymerase (Thermo Fisher Scientific). Initial denaturation was at 98°C for 30 s, followed by 40 amplification cycles (98°C for 10 s, 60°C for 30 s, and 72°C for 30 s), followed by one cycle at 72°C for 5 min. A
 5 ~700 bp fragment was gel extracted for Sanger sequencing. Sequence alignments were performed using MacVector.

[0152] QUANTIFICATION AND STATISTICAL ANALYSIS

[0153] The detailed information of statistical analysis could be found in the Result and Figure Legends. Correlation was evaluated by Spearman's rank correlation method
 10 (Figure 1A and 2B). Statistical significance was calculated by Dunn's Kruskal-Wallis multiple comparisons with p values corrected with the Benjamini-Hochberg procedure (Figure 8C). The 50% effective concentration (EC₅₀) values by ELISA assays (Figure 3A and 3C) and 50% inhibitory concentration (IC₅₀) values by neutralization assays (Figure 5C) were calculated by nonlinear regression analysis in PRISM software.

15 [0154] Discussion of Examples

[0155] Previous studies have identified several anti-HBs neutralizing antibodies from a small number of otherwise unselected spontaneously recovered or vaccinated individuals (Cerino et al., 2015; Colucci et al., 1986; Eren et al., 1998; Heijtkink et al., 2002; Heijtkink et al., 1995; Jin et al., 2009; Kim and Park, 2002; Li et al., 2017; Sa'adu et al., 1992; Sankhyan
 20 et al., 2016; Tajiri et al., 2007; Tokimitsu et al., 2007; Wang et al., 2016). In contrast, in the present disclosure, sera from 144 exposed volunteers was screened to identify elite neutralizers. Serologic activity varied greatly among the donors with a small number of individuals demonstrating high levels of neutralizing activity. To understand this activity, we isolated 244 anti-HBs antibodies from single B cells obtained from the top donors. Each of
 25 the elite donors tested showed expanded clones of memory B cells expressing bNAbs that targeted 3 non-overlapping sites on the S-protein. Moreover, the amino acid sequence of several of the bNAbs was highly similar in different individuals. These closely related antibodies target the same epitope.

[0156] The near identity of clones of HBV bNAbs in unrelated elite individuals is
 30 akin to reports for elite responders to HIV-1 (Scheid et al., 2011; West et al., 2012), influenza (Laursen and Wilson, 2013; Pappas et al., 2014; Wrammert et al., 2011), Zika (Robbiani et al., 2017), and malaria (Tan et al., 2018). However, none of the elite anti-HBs bNAbs shares both IgH and IgL with previously reported HBV neutralizing antibodies, the best of which have been tested in the clinic but are less potent than some of the bNAbs of this disclosure

(libivirumab IC₅₀: 35 ng/ml, tuvirumab IC₅₀: ~100 ng/ml) (Galun et al., 2002; Heijntink et al., 2001; van Nunen et al., 2001).

[0157] The described alanine scanning and competition binding analyses are consistent with the existence of at least 3 domains that can be recognized concomitantly by bNAbs (Gao et al., 2017; Tajiri et al., 2010; Zhang et al., 2016). However, the domains do not appear to be limited to either of two previously defined circular peptide epitopes, 123-137 and 139-148 (Tajiri et al., 2010; Zhang et al., 2016). Instead, residues spanning most of the external domain can contribute to binding by both Group-I and -II antibodies. For example, alanine scanning indicates that Group-I H020 binding is dependent on I110, K141, D144, G145 and T148, while Group-II H016 binding depends on T123, D144, and G145. Thus, despite having non-overlapping binding sites some of the essential residues are shared by Group-I and II suggesting that the epitopes are conformational. Moreover, the antibody epitopes on S-protein identified using mouse and human antibodies may be distinct (Chen et al., 1996; Ijaz et al., 2003; Paulij et al., 1999; Zhang et al., 2019; Zhang et al., 2016). Finally, G145, a residue that is frequently mutated in infected humans (Ma and Wang, 2012; Tong et al., 2013), is believed to be essential for binding by all the Group-II but not all Group-I or -III antibodies tested.

[0158] Crystallization of the Group-II bNAb H015 and its linear epitope revealed a loop that includes P142, S/T143, D144, and G145, all of which are frequently mutated during natural infection to produce well-documented immune escape variants (Hsu et al., 2015; Ijaz et al., 2012; Ma and Wang, 2012; Salpini et al., 2015). In addition to immune escape, the residues that form this structure are also essential for infectivity, possibly by facilitating virus interactions with cell surface glycosaminoglycans (Sureau and Salisse, 2013). Mutations in K141, P142 as well as C139 and C147, all of which contribute to the stability of the structure, decrease viral infectivity (Salisse and Sureau, 2009). Without intending to be bound by any particular theory, it is considered that drugs that destabilize the newly elucidated H015-peptide loop structure may also interfere with infectivity.

[0159] The G145R mutation, which is among the most frequent immune escape variants, replaces a small neutral residue with a bulky charged residue that would likely interfere with antigenicity by destroying the salt bridge between K141 and D144 that anchors the peptide loop. However, this drastic structural change does not alter infectivity (Salisse and Sureau, 2009), possibly because the additional charge compensates for otherwise altered interactions between HBV and cell surface glycosaminoglycans (Sureau and Salisse, 2013).

Thus, the additional charge may allow G145R to function as a dominant immune escape variant while preserving infectivity.

[0160] The present disclosure describes antibodies directed at S-protein antigen in part because this is the antigen used in the currently FDA-approved vaccines, and because
5 purified S-protein blocked nearly all of the neutralizing activity in the serum of the elite neutralizers irrespective of whether they were vaccinated or spontaneously recovered. Nevertheless, individuals who recover from infection also produce antibodies to the PreS1 domain of HBsAg (Li et al., 2017; Sankhyan et al., 2016). The PreS1 domain is essential for the virus to interact with the entry factor NCTP on hepatocytes and potent neutralizing
10 antibodies to PreS1 have been described (Li et al., 2017). However, these are not naturally occurring antibodies but rather randomly paired IgH and IgL chains derived from phage libraries obtained from unexposed or vaccinated healthy donors (Li et al., 2017). Moreover, the phage antibodies required further engineering to enhance their neutralizing activity (Li et al., 2017). Thus, whether the human immune system also produces potent anti-PreS1 bNAbs
15 has not been determined.

[0161] Chronic HBV infection remains a major global public health problem in need of an effective curative strategy (Graber-Stiehl, 2018; Lazarus et al., 2018; Revill et al., 2016). Chronically infected individuals produce an overwhelming amount of HBsAg that is postulated to incapacitate the immune system. Consequently, immune cells, which might
20 normally clear the virus, are unable to react to antigen, a phenomenon referred to as exhaustion or anergy (Ye et al., 2015). The appearance of anti-HBs antibodies is associated with spontaneous recovery from the disease, perhaps because they can clear the antigen and facilitate the emergence of a productive immune response (Celis and Chang, 1984; Zhang et al., 2016; Zhu et al., 2016). These findings led to the hypothesis that passively administered
25 antibodies might be used in conjunction with antiviral drugs to further decrease the antigenic burden while enhancing immune responses that maintain long-term control of the disease. The presently described results in huFNRG mice infected with HBV indicate that antibody monotherapy with a potent bNAb can lead to the emergence of the very same escape mutations commonly found in chronically infected individuals. Moreover, not all bNAb
30 combinations are effective in preventing escape by mutation. Combinations that target separate epitopes but have overlapping sensitivity to commonly occurring escape mutations such as H006 and H007 are ineffective. In contrast, combinations with complementary sensitivity to common escape mutations prevent the emergence of escape mutations in huFNRG mice infected with HBV. Thus, as described above, the present disclosure provides

immunotherapy for HBV infection with combinations of antibodies with complementary activity to avert this potential problem.

[0162] The following reference listing is not an indication that any particular reference(s) is material to patentability.

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5

[0163] Supplemental Table S1. Detailed information of donors, Related to Figure 1.

[0164] The anti-HBs ELISA titer (x-axis in Figure 1A and 8B) and relative infection rate (y-axis in Figure 1A and 8B) of each donor's serum sample were determined by ELISA assay and *in vitro* neutralization assay, respectively.

10

DONOR ID	ANTI-HBs ELISA TITER	STATUS	BIG BLOOD DRAW	INFECTION RATE (1:5 SERUM) PERCENTAGE OF HBcAg+ CELLS			AVE RAGE	NEUTRALIZING CAPACITY	INFECTION RATE (1:50 SERUM) PERCENTAGE OF HBcAg+ CELLS			AVE RAGE	NEUTRALIZING CAPACITY
QWA-0947-001	9.08	Vaccinated		11.4	12.7	13.6	124.92	0.80	11.6	12.8	12.9	123.05	0.81
QWA-0947-002	516.12	Vaccinated		65.28	77.58	75.13	72.66	1.38	13.0	13.6	13.4	134.03	0.75
QWA-0947-003	0	Vaccinated		10.9	11.8	11.3	115.14	0.87	13.1	13.5	13.2	133.89	0.75
QWA-0947-004	267.1	Vaccinated		11.3	12.9	12.6	118.99	0.84	14.9	14.6	15.3	147.54	0.68
QWA-0947-005	113.01	Vaccinated		82.9	87.48	95.39	88.59	1.13	14.4	14.8	14.6	148.12	0.68
QWA-0947-006	325.77	Vaccinated		81.19	85.97	96.43	87.86	1.14	11.8	11.3	11.4	118.02	0.85
QWA-0947-007	63.54	Vaccinated		10.3	10.5	11.3	105.54	0.95	13.1	13.5	13.1	135.92	0.74
QWA-0947-008	21.8	Vaccinated		40.86	35.60	42.82	39.76	2.52	78.64	84.09	84.79	82.51	1.21
QWA-0947-009	>1000	Vaccinated	BIG BLOOD DRAW	12.84	14.39	17.20	14.81	6.75	34.66	38.81	33.48	35.65	2.81
QWA-0947-010	0.33	Vaccinated		93.33	93.42	10.9	97.22	1.03	10.1	11.5	11.8	112.57	0.89
QWA-0947-011	1.29	Vaccinated	BIG BLOOD DRAW	10.0	11.3	94.7	105.79	0.95	95.79	93.25	81.95	90.33	1.11

QWA-0947-012	12.87	Vaccinated		10.204	10.294	10.881	104.60	0.96		14.295	13.795	12.512	135.34	0.74
QWA-0947-013	>1000	Vaccinated	BIG BLOOD DRAW	9.24	8.31	8.33	8.63	11.59		19.95	20.81	17.29	19.35	5.17
QWA-0947-014	248.31	Vaccinated		80.90	80.65	79.88	80.48	1.24		11.758	12.017	11.537	117.71	0.85
QWA-0947-015	76.1	Vaccinated		97.26	91.48	86.95	91.90	1.09		11.279	10.982	10.119	107.93	0.93
QWA-0947-016	0.36	Non-Vaccinated		10.022	96.77	95.84	97.61	1.02		11.804	12.005	11.734	118.48	0.84
QWA-0947-017	0.63	Vaccinated		10.030	10.298	10.155	101.61	0.98		12.227	11.942	11.093	117.54	0.85
QWA-0947-018	3.24	Vaccinated		10.165	11.338	96.98	104.00	0.96		11.818	12.126	10.705	115.50	0.87
QWA-0947-019	>1000	Vaccinated		47.62	43.35	40.11	43.69	2.29		10.586	10.046	89.54	98.62	1.01
QWA-0947-020	1.21	Non-Vaccinated		77.13	75.25	60.04	70.81	1.41		11.628	11.372	10.865	112.88	0.89
QWA-0947-021	15.81	Vaccinated		33.85	41.39	34.98	36.74	2.72		89.74	89.87	88.60	89.40	1.12
QWA-0947-022	2.17	Vaccinated		83.52	94.22	93.88	90.54	1.10		10.008	11.988	11.019	110.05	0.91
QWA-0947-023	183.37	Vaccinated		93.15	11.957	11.608	109.60	0.91		11.343	11.791	10.345	111.60	0.90
QWA-0947-024	256.85	Vaccinated		55.70	60.03	49.13	54.95	1.82		10.468	11.621	10.517	108.69	0.92
QWA-0947-025	709.29	Vaccinated		76.18	77.38	75.01	76.19	1.31		10.058	10.557	11.682	107.66	0.93
QWA-0947-026	0.49	Non-Vaccinated		83.02	10.242	96.98	94.14	1.06		10.424	11.709	10.573	109.02	0.92
QWA-0947-027	0.3	Non-Vaccinated	BIG BLOOD DRAW	10.351	12.879	11.482	115.71	0.86		10.591	12.668	11.703	116.54	0.86
QWA-0947-028	6.51	Non-Vaccinated		84.03	90.88	87.77	87.56	1.14		10.723	11.789	10.821	111.11	0.90
QWA-0947-029	1.67	Non-Vaccinated		10.372	98.68	83.74	95.38	1.05		96.06	10.225	10.020	99.50	1.00
QWA-0947-030	0.09	Vaccinated	BIG BLOOD DRAW	86.06	84.44	91.73	87.41	1.14		11.174	11.573	10.226	109.91	0.91

QWA-0947-031	488.3	Core Ab +		71.30	66.21	56.71	64.74	1.54		94.99	102.87	94.27	97.38	1.03
QWA-0947-032	>1000	Vaccinated		71.12	67.87	56.53	65.17	1.53		97.45	107.81	106.59	103.95	0.96
QWA-0947-033	330.93	Vaccinated		99.61	93.60	87.25	93.49	1.07		106.28	116.65	108.45	110.46	0.91
QWA-0947-034	588.26	Core Ab +		40.92	41.19	35.30	39.14	2.56		99.54	111.6	105.28	105.32	0.95
QWA-0947-035	365.7	Vaccinated		101.52	113.83	94.76	103.37	0.97		129.77	131.60	121.19	127.52	0.78
QWA-0947-036	108.83	Vaccinated		87.55	85.69	77.65	83.63	1.20		122.8	122.03	107.69	117.33	0.85
QWA-0947-037	>1000	Vaccinated		23.79	21.09	18.46	21.11	4.74		66.02	59.97	52.64	59.54	1.68
QWA-0947-038	11.76	Vaccinated		94.89	95.53	96.87	95.76	1.04		119.79	125.09	115.27	120.05	0.83
QWA-0947-039	230.99	Vaccinated		102.08	99.23	91.54	97.62	1.02		113.01	115.04	98.95	109.00	0.92
QWA-0947-040	0.26	Vaccinated		54.12	57.38	45.32	52.27	1.91		102.43	107.89	95.37	101.90	0.98
QWA-0947-041	0.42	Non-Vaccinated		77.09	78.29	84.91	80.09	1.25		87.59	101.25	101.19	96.68	1.03
QWA-0947-042	128.75	Core Ab +		97.03	106.51	110.26	104.60	0.96		114.07	149.01	121.98	128.35	0.78
QWA-0947-043	229.75	Core Ab +		78.56	94.35	95.71	89.54	1.12		95.18	144.23	123.82	121.08	0.83
QWA-0947-044	222.48	Core Ab +		45.85	56.61	65.34	55.93	1.79		94.00	133.96	109.86	112.60	0.89
QWA-0947-045	>1000	Core Ab +		51.82	66.02	61.55	59.80	1.67		104.36	122.03	120.96	115.78	0.86
QWA-0947-046	350.93	Vaccinated		89.57	99.40	111.55	100.17	1.00		100.98	129.50	111.79	114.09	0.88
QWA-0947-047	0.33	Vaccinated		126.88	138.30	142.37	135.85	0.74		112.35	156.77	127.72	132.28	0.76
QWA-0947-048	>1000	Vaccinated	BIG BLOOD DRAW	35.94	44.44	46.02	42.14	2.37		83.08	109.89	94.60	95.86	1.04
QWA-0947-049	>1000	Core Ab +	BIG BLOOD DRAW	94.21	120.65	119.57	111.48	0.90		113.33	139.10	126.42	126.28	0.79

QWA-0947-050	6.2	Vaccinated		93.10	11.4.26	11.3.58	106.98	0.93		93.34	12.1.07	11.2.91	109.10	0.92
QWA-0947-051	228.35	Vaccinated		11.1.78	11.2.69	11.5.97	113.48	0.88		10.4.71	10.2.64	83.60	96.98	1.03
QWA-0947-052	2.77	Vaccinated		11.6.53	11.5.59	11.0.83	114.32	0.87		11.3.48	11.4.25	12.5.60	117.78	0.85
QWA-0947-053	48.25	Vaccinated		11.4.90	11.2.78	98.40	108.69	0.92		10.5.04	11.6.61	11.9.01	113.55	0.88
QWA-0947-054	24.06	Vaccinated		12.1.56	12.5.13	11.1.71	119.47	0.84		99.64	11.8.99	12.2.11	113.58	0.88
QWA-0947-055	772.43	Core Ab +	BIG BLOOD DRAW	8.79	9.33	5.78	7.97	12.55		82.33	95.93	87.80	88.69	1.13
QWA-0947-056	441.12	Vaccinated		86.57	86.67	79.10	84.12	1.19		98.81	12.0.31	11.6.13	111.75	0.89
QWA-0947-057	91.37	Vaccinated		12.0.46	11.3.18	11.0.80	114.82	0.87		11.1.45	10.7.08	11.6.80	111.78	0.89
QWA-0947-058	>1000	Vaccinated		27.66	27.74	26.37	27.26	3.67		82.86	83.73	74.74	80.44	1.24
QWA-0947-059	83.28	Vaccinated		11.0.69	10.9.95	99.34	106.66	0.94		11.5.21	11.5.69	99.96	110.29	0.91
QWA-0947-060	>1000	Vaccinated	BIG BLOOD DRAW	5.68	6.72	5.17	5.86	17.08		25.39	26.65	24.93	25.66	3.90
QWA-0947-061	104.78	Vaccinated		10.9.98	12.0.25	13.1.62	120.61	0.83		10.7.59	13.4.01	12.4.63	122.08	0.82
QWA-0947-062	2.56	Vaccinated		11.3.16	14.0.19	14.3.78	132.38	0.76		12.0.58	13.9.98	13.5.32	131.96	0.76
QWA-0947-063	246.16	Vaccinated		10.1.93	11.2.01	14.1.39	118.44	0.84		11.4.71	13.4.13	14.3.18	130.67	0.77
QWA-0947-064	Not Available	Vaccinated		12.8.17	11.4.29	14.7.09	129.85	0.77		13.3.50	13.3.31	13.3.23	133.35	0.75
QWA-0947-065	0.28	Core Ab +		11.2.39	13.3.12	15.5.43	133.65	0.75		13.1.76	13.4.78	15.0.74	139.09	0.72
QWA-0947-066	265.6	Vaccinated		50.87	68.37	86.59	68.61	1.46		12.9.24	13.3.43	11.9.16	127.28	0.79
QWA-0947-067	0	Vaccinated		10.6.36	12.0.57	15.0.56	125.83	0.79		12.2.57	14.2.42	13.9.51	134.84	0.74
QWA-0947-068	0.25	Vaccinated		58.26	87.26	10.5.25	83.59	1.20		12.3.65	12.8.77	12.4.58	125.67	0.80

QWA-0947-069	>1000	Vaccinated	BIG BLOOD DRAW	11.42	27.20	22.32	20.31	4.92		50.80	55.44	64.27	56.84	1.76
QWA-0947-070	7.01	Vaccinated		107.39	113.96	138.16	119.84	0.83		118.06	116.97	118.95	117.99	0.85
QWA-0947-071	638.24	Vaccinated		56.39	48.55	55.42	53.45	1.87		94.83	111.19	117.23	107.75	0.93
QWA-0947-072	15.55	Vaccinated		128.74	135.08	126.34	130.05	0.77		137.00	132.93	122.94	130.96	0.76
QWA-0947-073	225.34	Vaccinated		131.87	122.33	137.50	130.57	0.77		137.43	128.35	124.59	130.12	0.77
QWA-0947-074	159.52	Core Ab +		120.51	119.04	128.75	122.76	0.81		140.98	130.18	124.00	131.72	0.76
QWA-0947-075	0.37	Vaccinated		131.78	125.05	159.51	138.78	0.72		133.08	135.29	117.74	128.70	0.78
QWA-0947-076	27.37	Vaccinated		137.32	145.89		141.60	0.71		132.06			132.06	0.76
QWA-0947-077	52.77	Vaccinated		112.72	121.48		117.10	0.85		137.12			137.12	0.73
QWA-0947-078	181.6	Vaccinated		116.16	107.29		111.72	0.90		138.30	131.27		134.79	0.74
QWA-0947-079	>1000	Vaccinated		54.73	59.28	71.14	61.72	1.62		130.53	128.66	118.32	125.84	0.79
QWA-0947-080	>1000	Vaccinated		62.38	53.55	69.34	61.76	1.62		122.37	106.42		114.40	0.87
QWA-0947-081	7.23	Vaccinated		113.81	111.55	142.59	122.65	0.82		109.38	105.63	116.78	110.60	0.90
QWA-0947-082	24.98	Vaccinated		120.69	124.58	118.10	121.12	0.83		106.45	118.55	117.79	114.26	0.88
QWA-0947-083	90.5	Vaccinated		84.79	87.62	99.65	90.69	1.10		91.86	99.93	105.67	99.15	1.01
QWA-0947-084	880.92	Core Ab +		112.81	125.10	114.29	117.40	0.85		106.78	117.78	147.46	124.01	0.81
QWA-0947-085	82.25	Vaccinated		120.45	148.83	159.96	143.08	0.70		114.14	114.33	136.45	121.64	0.82
QWA-0947-086	19.16	Vaccinated		147.29	173.59	166.75	162.55	0.62		110.03	128.28	120.46	119.59	0.84
QWA-0947-087	88.6	Vaccinated		126.58	146.46	145.74	139.59	0.72		105.86	119.12	119.22	114.74	0.87

QWA-0947-088	288.42	Core Ab +		108.25	120.39	140.09	122.91	0.81		90.55	101.28	115.15	102.33	0.98
QWA-0947-089	15.74	Vaccinated		101.12	94.87	98.43	98.14	1.02		75.70	96.65	111.21	94.52	1.06
QWA-0947-090	>1000	Vaccinated		54.59	47.73	53.63	51.99	1.92		71.09	87.31	99.22	85.87	1.16
QWA-0947-091	>1000	Vaccinated		18.28	23.05	19.85	20.39	4.90		48.17	59.50	53.15	53.61	1.87
QWA-0947-093	2.64	Vaccinated		155.82	147.87	143.25	148.98	0.67		126.83	113.67	124.04	121.51	0.82
QWA-0947-094	127.58	Vaccinated		160.76	145.63	119.61	142.00	0.70		105.84	110.91	114.14	110.30	0.91
QWA-0947-095	23.74	Vaccinated		176.74	160.65	159.27	165.55	0.60		110.83	103.36	112.17	108.78	0.92
QWA-0947-096	>1000	Vaccinated		51.24	50.60	36.36	46.07	2.17		109.95	99.89	100.76	103.54	0.97
QWA-0947-097	25.97	Vaccinated		151.86	144.37	127.26	141.16	0.71		109.63	109.86	98.50	106.00	0.94
QWA-0947-098	>1000	Vaccinated		73.82	83.70	70.82	76.11	1.31		88.55	95.98	100.28	94.94	1.05
QWA-0947-099	688.28	Vaccinated	BIG BLOOD DRAW	110.48	112.47	90.05	104.33	0.96		100.29	103.59	94.65	99.51	1.00
QWA-0947-100	366.05	Vaccinated		85.68	99.38	86.23	90.43	1.11		97.85	101.09	85.62	94.85	1.05
QWA-0947-101	1.22	Vaccinated		88.54	96.48	92.77	92.60	1.08		107.51	104.47	106.69	106.22	0.94
QWA-0947-102	0.65	Vaccinated		96.90	94.97	99.88	97.25	1.03		109.63	101.73	102.43	104.60	0.96
QWA-0947-103	45.53	Core Ab +		100.38	104.13	93.37	99.29	1.01		103.40	95.77	93.83	97.67	1.02
QWA-0947-104	95.76	Vaccinated		95.99	87.67	79.38	87.68	1.14		111.24	105.95	113.01	110.07	0.91
QWA-0947-105	1.48	Vaccinated		42.47	43.05	47.61	44.38	2.25		102.15	99.45	98.24	99.95	1.00
QWA-0947-106	>1000	Vaccinated		16.40	16.66	16.15	16.40	6.10		64.77	68.47	66.59	66.61	1.50
QWA-0947-107	32.84	Vaccinated		148.16	141.65	127.35	139.05	0.72		123.79	119.06	104.81	115.89	0.86

QWA-0947-108	352.99	Vaccinated		78.23	81.50	84.50	81.41	1.23		109.31	116.46	103.38	109.72	0.91
QWA-0947-109	15.04	Vaccinated		112.45	103.15	97.70	104.43	0.96		110.85	121.08	117.28	116.40	0.86
QWA-0947-110	26.27	Vaccinated		86.31	102.24	99.68	96.08	1.04		115.57	130.13	116.61	120.77	0.83
QWA-0947-111	40.79	Vaccinated		81.44	86.98	87.80	85.40	1.17		109.93	98.54	91.77	100.08	1.00
QWA-0947-112	260.82	Core Ab +		35.62	36.63	32.67	34.97	2.86		69.44	65.66	65.06	66.72	1.50
QWA-0947-113	1.97	Vaccinated		93.25	98.77	81.76	91.26	1.10		101.75	104.27	100.12	102.05	0.98
QWA-0947-114	>1000	Vaccinated		32.49	27.64	25.33	28.49	3.51		80.93	61.56	71.59	71.36	1.40
QWA-0947-115	798.12	Core Ab +		13.86	14.67	15.02	14.52	6.89		45.62	46.82	42.16	44.87	2.23
QWA-0947-116	459.84	Vaccinated		99.96	93.67	81.32	91.65	1.09		107.55	108.08	109.31	108.31	0.92
QWA-0947-117	0.46	Vaccinated		98.06	92.72	95.42	95.40	1.05		106.12	104.66	111.74	107.51	0.93
QWA-0947-118	20.87	Vaccinated		15.182	146.04	144.65	147.50	0.68		112.36	109.15	112.429	115.26	0.87
QWA-0947-119	91.47	Vaccinated		114.36	109.63	108.87	110.96	0.90		108.91	112.79	104.89	108.86	0.92
QWA-0947-120	13	Core Ab +		44.97	45.06	40.30	43.44	2.30		102.35	110.61	97.70	103.55	0.97
QWA-0947-121	175.21	Vaccinated		91.44	91.91	96.95	93.43	1.07		166.31	164.27	144.97	158.52	0.63
QWA-0947-122	51.51	Vaccinated		95.47	92.45	100.97	96.30	1.04		180.79	174.92	143.73	166.48	0.60
QWA-0947-123	36.81	Vaccinated		145.77	156.75	146.88	149.80	0.67		180.84	176.71	135.18	164.24	0.61
QWA-0947-124	1.3	Vaccinated		147.11	133.31	131.87	137.43	0.73		170.89	169.84	127.57	156.10	0.64
QWA-0947-125	1.44	Vaccinated		110.99	111.85	118.19	113.68	0.88		178.09	178.48	149.45	168.67	0.59
QWA-0947-126	359.06	Core Ab +		79.16	76.31	85.67	80.38	1.24		167.98	161.85	154.57	161.47	0.62

QWA-0947-127	1.23	Non-Vaccinated		12.8.75	12.5.40	14.3.54	132.56	0.75		16.2.01	15.7.22	13.9.08	152.77	0.65
QWA-0947-128	>1000	Vaccinated		30.63	25.86	36.31	30.94	3.23		69.73	82.09	84.44	78.76	1.27
QWA-0947-129	0.17	Non-Vaccinated		16.6.56	15.6.86	15.7.89	160.44	0.62		16.2.24	16.8.18	15.4.52	161.65	0.62
QWA-0947-131	11.81	Vaccinated		14.3.14	12.9.67	11.4.98	129.26	0.77		15.6.94	14.4.37	11.9.26	140.19	0.71
QWA-0947-132	0	Non-Vaccinated		14.3.37	14.8.51	13.4.41	142.09	0.70		17.0.72	14.6.03	12.6.56	147.77	0.68
QWA-0947-133	731.27	Core Ab +		86.48	85.37	78.16	83.34	1.20		15.7.64	13.7.87	13.1.07	142.20	0.70
QWA-0947-134	>1000	Vaccinated		31.62	30.52	27.60	29.92	3.34		14.4.36	13.7.82	11.5.14	132.44	0.76
QWA-0947-135	796.93	Core Ab +		81.56	81.84	88.25	83.88	1.19		15.7.58	14.2.42	11.6.84	138.95	0.72
QWA-0947-136	0	Non-Vaccinated		12.8.19	13.2.95	13.9.91	133.68	0.75		16.5.85	14.0.56	13.7.58	148.00	0.68
QWA-0947-137	1.56	Non-Vaccinated		15.5.09	15.1.93	13.7.05	148.02	0.68		17.5.51	15.5.22	12.8.75	153.16	0.65
QWA-0947-138	0.74	Non-Vaccinated		16.0.76	15.9.87	13.5.61	152.08	0.66		16.5.30	13.7.96	11.9.52	140.93	0.71
QWA-0947-139	0	Non-Vaccinated		14.3.96	14.5.71	12.3.98	137.88	0.73		14.3.82	12.5.60	11.4.22	127.88	0.78
QWA-0947-140	609.46	Core Ab +		93.61	96.21	89.99	93.27	1.07		12.5.42	13.5.92	10.6.58	122.64	0.82
QWA-0947-141	>1000	Vaccinated		35.14	37.74	36.31	36.40	2.75		90.32	87.71	83.80	87.28	1.15
QWA-0947-142	0.01	Non-Vaccinated		72.39	72.79	69.24	71.47	1.40		85.86	89.49	80.98	85.44	1.17
QWA-0947-143	51.9	Vaccinated		83.85	74.96	78.42	79.07	1.26		89.70	83.02	81.24	84.65	1.18
QWA-0947-144	192.41	Vaccinated		99.03	10.3.75	10.4.69	102.49	0.98		88.00	80.96	10.0.21	89.73	1.11
QWA-0947-145	>1000	Vaccinated		35.23	36.75	36.99	36.32	2.75		91.40	83.04	84.37	86.27	1.16
QWA-0947-146	>1000	Vaccinated	BIG BLOOD DRAW	3.21	3.17	3.47	3.28	30.45		4.66	4.45	3.82	4.31	23.18

QWA-0947-147	>1000	Vaccinated		74.42	79.63	70.02	74.69	1.34		96.43	89.82	90.93	92.39	1.08
QWA-0947-149	>1000	Vaccinated		48.09	53.38	53.47	51.65	1.94		85.58	89.74	84.49	86.60	1.15
QWA-0947-150	>1000	Vaccinated		45.84	50.91	49.78	48.84	2.05		97.27	93.55	92.90	94.57	1.06
QWA-0947-151	24.03	Vaccinated		76.16	78.93	83.53	79.54	1.26		104.49	103.12	97.68	101.76	0.98
QWA-0947-152	32.89	Vaccinated		76.50	74.31	58.42	69.75	1.43		80.82	81.72	78.43	80.33	1.24
QWA-0947-153	0.36	Vaccinated		92.38	95.06	83.56	90.33	1.11		81.13	82.29	70.79	78.07	1.28
QWA-0947-154	8.02	Vaccinated		81.20	78.04	61.49	73.58	1.36		89.89	80.29	72.54	80.90	1.24
QWA-0947-155	271.68	Vaccinated		83.98	86.99	69.06	80.01	1.25		79.14	80.93	74.47	78.18	1.28
QWA-0947-156	>1000	Vaccinated		23.65	20.82	15.97	20.15	4.96		78.25	75.10	58.66	70.67	1.42
QWA-0947-157	93.05	Vaccinated		93.75	95.02	83.23	90.67	1.10		77.02	80.62	70.27	75.97	1.32
QWA-0947-158	261.09	Vaccinated		78.75	78.50	64.50	73.92	1.35		88.22	86.79	71.09	82.03	1.22
QWA-0947-159	61.12	Vaccinated		87.14	91.02	76.00	84.72	1.18		80.77	86.19	74.40	80.45	1.24
QWA-0947-160	381.69	Vaccinated		72.70	68.79	62.46	67.98	1.47		81.13	74.64	66.11	73.96	1.35
QWA-0947-161	3.62	Vaccinated		91.93	85.42	72.87	83.40	1.20		85.76	80.35	74.62	80.24	1.25
QWA-0947-162	198.58	Vaccinated		91.35	92.25	79.20	87.60	1.14		112.63	106.14	95.29	104.69	0.96

[0165] Supplemental Table S2. Detailed information about cloned antibodies with paired heavy and light chains, Related to Figure 2.

[0166] Variable (V), diversity (D) and joining (J) genes, mutation on the variable gene (V MUT), and CDR3 amino acid sequences of cloned immunoglobulin heavy, kappa light and lambda light chains are listed. These antibodies are grouped by their IGHV genes, with our selected H001-H020 antibodies indicated. H021 antibody used for sequence alignment in Figure 2D is also indicated. The amino acid length of IGH CDR3 was between 5 and 27 amino acids, with the highest peak at 16 amino acids and the average around 15 amino acids. There are 16 of IGH CDR3 containing cysteines.

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN								
DO NO R ID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:		V	J	CDR 1	SEQ ID NO:	CD R3	SEQ ID NO:		V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
9	IG H V1							ARN																	
	- 18 *0							GYS SSW HGG THY YYY ALD																	
	1	IGH D6-13* 01	IGHJ 6*0 2	GYT FTT YG	26	ISTY NRN T	27	F	28		IGH V1-5*0 3	IGKJ 1*0 1	QSI TN W	29	KAS T	30									
55	IG H V1							ARD SVS WW NLL FKS LEK LTL DY																	
	- 18 *0							ARD SVS WW NLL FKS LEK LTL DY																	
	1	IGH D2-15* 01	IGHJ 4*0 2	GYS FNT YG	31	ISTY NGK T	32	T	33																
55	IG H V1							ARD SVS WW NLL FKS																	
	- 18 *0							ARD SVS WW NLL FKS																	
	1	IGH D2-15* 01	IGHJ 4*0 2	GYS FNT YG	36	ISTY NGK T	37	T	38		IGH V3-20* 01	IGKJ 4*0 1	QSV SNS Y	39	GAS LT	40									

		HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN					
DO NO RID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
	*0 1							LEK LTL DY															
55	IG H V1							ARD SVS WW NLL FKS															
	- 18 *0 1	IGH D2- 15* 01	IGHJ 4*0 2	GYS FNT YG	43	ISTY NGK T	44	LEK LTL DY	45	IGK V3- 11* 01	IGKJ 1*0 1	QSV SSY	46	QH RS NS WT	47								
55	IG H V1							ARD PDF GDY															
	- 18 *0 1	IGH D4- 17* 01	IGHJ 4*0 2	GYT FSS YG	48	ISA HSG NT	49	GSD IVD Y	50							IGL V3- 25* 02	IG LJ 3* 02	ALP VQF	51	KD S	QSA DST ATY WV	52	
99	IG H V1							AR WG VGM															
	- 18 *0 1	IGH D3- 16* 01	IGHJ 6*0 3	GYS FSS YG	53	ISAY NGD T	54	TFS YHY HYM DV	55							IGL V3- 19* 01	IG LJ 3* 02	SLR TTY	56	GK N	GSR DNS GYS	57	
99	IG H V1							ARG RGD SST															
	- 18 *0 1	IGH D6- 13* 01	IGHJ 4*0 2	GYT FGS FG	58	ISGY SGK T	59	WYS LY	60	IGK V3- 11* 01	IGKJ 4*0 1	QSV GSY	61	QQ YN DW LT	62								
14 6	IG H V1	IGH D1- 01	IGHJ 1*0 1	DYR SINS G	63	ISPF NGN T	64	AGD TTS	65	IGK V4- 01	IGKJ 3*0 1	ESV FFS	66	QQ YY	67								

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN							
DO NO RID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CDR 2	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
	- 18 *0 1	1*0 1				SAA LTF				1*0 1		PHN RNY			TT PS									
14 6	IG H V1	IGH D1- 26* 01	IGHJ 6*0 2	GYN FISY A	68	ISPY NGK K	69	ARF FGG ATM TVY FYG LDV		IGK V1- 5*0 1	IGKJ 1*0 1	QSI KT W	71	DAS T	QQ YN SYS GW T	72								
14 6	IG H V1	IGH D6- 19* 01	IGHJ 4*0 2	GYK FTN YG	73	INA YNG HT	74	TRS EQ WRS RGE Y									IGL V1- 44* 01	IG LJ 3* 02	NSN VG NN V	76	AN S	ASW DDS LSG SWV	77	
14 6	IG H V1	IGH D1- 26* 01	IGHJ 5*0 2	GYT FSN YG	78	ISAS SGN T	79	GRD DSG SYP MSP		IGK V3- 20* 01	IGKJ 4*0 1	QSV SGS Y	81	GAS LA	QQ YX SSP LA	82								
14 6	IG H V1	IGH D1- 20* 01	IGHJ 4*0 2	GYT FRN YG	83	INA HNG DT	84	VRD INF1 FDY									IGL V7- 43* 01	IG LJ 3* 02	TGA VTS SYV	86	RT N	LLY XWS SSA LG	87	
69	IG H V1	IGH D3- 01	IGHJ 6*0 3	GYS FTS YG	88	INV YNA NT	89	ARE GWF GEF		IGK V3- 01	IGKJ 1*0 1	LSV SSN	91	DAS EW	QQ YH	92								

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN								
	DO NO RID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CDR 2	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
		- 18 *0 4	10* 01						RRN YNY NYV MD V		15* 01					PR T									
	49	IG H V1	IGH D4- 11* 01	IGHJ 3*0 1	GYT LTE LS	93	FDP DEG EV	94	TLV TRV DAF DV	95	IGK V1- 39* 01	IGKJ 2*0 1	QSV RTY	96	AAS	QQ SYF AP YT	97								
	49	IG H V1	IGH D4- 11* 01	IGHJ 3*0 1	GYS HTE LP	98	FDP DEG ET	99	TLV TRV DAF EV	100	IGK V1- 39* 01	IGKJ 2*0 1	QNI RNY	101	AAS	QQ SYF AP YT	102								
	49	IG H V1	IGH D2- 21* 02	IGHJ 3*0 1	GYT LTE LP	10	FDP DEG ET	10	TLV TGV DAF AV	105	IGK V1- 39* 01	IGKJ 2*0 1	QNI RTY	106	TAS	QQ SYF AP YT	107								
	49	IG H V1	IGH D3- 16* 01	IGHJ 3*0 1	GYIF SEL S	10	FDP DEG ET	10	TSVI KAD AFE V	110	IGK V1- 39* 01	IGKJ 2*0 1	QNI RTY	111	VAS	QQ SYF AP YT	112								

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN								
DO NO RID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CDR 2	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
13	IG H V1 - 3* 01	IGH D2- 21* 01	IGHJ 6*0 2	GYT FTH YA	11 3	LNG GND DR	11 4	ARG GWI IQN GGA RYY HG MD V	115 115	IGK V3- 20* 01	IGKJ 4*0 1	QSV SSS Q	116 116	GAS VA	117 117	QH YN NP	IGL V3- 21* 02	IG LJ 2* 01	NIR NK N	118 118	AD S	QV WD GGS YHV I	119 119		
	IG H V1 - 3* 01	IGH D3- 10* 01	IGHJ 4*0 2	GYT FTR YP	12 0	INA ANG DT	12 1	ARK DYY GSG SYE FDN	122 122								IGL V2- 11* 01	IG LJ 2* 01	SSD VGG YNY	123 123	DV N	CSY AGN YILV	124 124		
69	IG H V1 - 3* 01	IGH D2- 2*0 1	IGHJ 3*0 1	GYN FQR SA	12 5	GNG NT	12 6	AKG RSS HDL YDP FDF	127 127	IGK V1- 5*0 3	IGKJ 2*0 1	ENI GG W	128 128	KAS T	129 129	QQ YN SYS RY									
99	IG H V1 - 3* 01	IGH D3- 10* 01	IGHJ 4*0 2	GYT FTS YP	13 0	INP ANG DT	13 1	ARK NYV ASG SYH FDL	132 132								IGL V2- 11* 01	IG LJ 3* 02	NSD VGG YNY	133 133	DV T	SSY AGK YTL V	134 134		
14 6	IG H V1 - 3* 01	IGH D1- 1*0 1	IGHJ 3*0 2	GYT LTS YA	13 5	INA GSG LT	13 6	ARV GIPL RGA GGS PFD I	137 137	IGK V1- 39* 01	IGKJ 4*0 1	QSV STY	138 138	TAS LT	139 139	QQ SSS VP									
14 6 H 0	IG H V1	IGH D3-	IGHJ 3*0 2	GYT FTT YA	14 0	INA GNG IT	14 1	ARV GIL VRG	142 142	IGK V1-	IGKJ 4*0 1	QSV QSV	143 143	SAS SYS	144 144	QQ SYS									

	HEAVY CHAIN												KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN					
DO NO RID	V	D	J	CDR 1	SEQ ID NO:	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
01	- 3* 01	16* 01							AGG SPF DI		39* 01					TP LT								
146	IG H V1	IGH D3- 16* 01	IGHJ 3*0 2	GYT FTT YA	14 5	INA GNG IT	14 6		VRG AGG SPF DI	IGK V1- 39* 01	IGK V1- 39* 01	IGKJ 4*0 1	QSYS TY	148	TAS	QQ SYS TP LT								
146	IG H V1	IGH D4- 11* 01	IGHJ 3*0 1	GYT FSR HA	15 0	INIG NGN T	15 1		ARE DYT GNY YDA FDF	IGK V1- 5*0 3	IGK V1- 5*0 3	IGKJ 4*0 1	QSV STW	153	KAS	QL YN SYS GT T								
146	IG H V1	IGH D6- 13* 01	IGHJ 6*0 2	GYS FSN YA	15 5	INA AYG NT	15 6		ARD GVK EQL VYY YFG MD V								IGL V1- 40* 01	IG LJ 2* 01	SSN IGK NY D	158 T	GD T	QSY DSN LSG SVV	159	
146	IG H V1	IGH D3- 10* 01	IGHJ 4*0 2	TYV FTA YA	16 0	INA GNG DT	16 1		ARG ALL WF RDD FDF	IGK V1- 27* 01	IGK V1- 27* 01	IGKJ 3*0 1	QGI SNY	163	AAS	QK YD SA PY T	IGL V1- 51* 01	IG LJ 1* 01	SSN IGK TY	165 N	DN N	GSW DSS LYS FYV	166	
99	IG H V1	IGH D2- 2*0 1	IGHJ 1*0 1	GYT FSN YH	16 7	INPS GDS T	16 8		ASR LDA IPF QV	IGK V3- 20* 01	IGK V3- 20* 01	IGKJ 2*0 1	PNA NSG S	170	GAS	QQ YG GL PF T								171

	HEAVY CHAIN												KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN					
DO NO RID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:	
99	IG H V1	IGH	IGHJ 6*0 4	GYI VTS YR	17 2	IDPS DTY T	17 3	ARK GNY GSR YD WYF DV	174							IGL V2- 14* 01	IG LJ 3* 02	SSD VG DYS Y	175	DV N		SSY TSS STG V	176	
	IG H V1	IGH	IGHJ 3*0 1	GYT FTN FN	17 7	INP GAG TT	17 8	TRD PILR YFD WQS RDA FDV	179	IGK V1- 17* 01	IGKJ 3*0 1	QGI RND	180	LQ HN GY PIT	181									
	IG H V1	IGH	IGHJ 6*0 1	GGT FSS YS	18 2	IVPI FGIP	18 3	ARA SFG DL WSG YPN QFF DH	191	IGK V1- 17* 03	IGKJ 1*0 1	QGI SNS	192	LQ HN TY PW T	193									
	IG H V2	IGH	IGHJ 5*0 2	GFS FST GGV G	19 4	DGD E	19 5	AHR LLT AYY DH	196	IGK V1- 5*0 3	IGKJ 1*0 1	QGIS RW	197	QQ YN SYS WA	198									
14 6	IG H V1	IGH	IGHJ 4*0 2	GGK FIAY G	18 9	TIPI YGT A	19 0																	
	IG H V2	IGH	IGHJ 5*0 2	GFS FST GGV G	19 4	DGD E	19 5																	
13	IG H V2	IGH	IGHJ 5*0 2	GFS FST GGV G	19 4	DGD E	19 5																	
	IG H V2	IGH	IGHJ 5*0 2	GFS FST GGV G	19 4	DGD E	19 5																	

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN						
DO NO R ID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
55	IG H V2 - 5* 02	IGH D6- 13* 01	IGHJ 5*0 2	GFS LST FGV G	19 9	DDD K	20 0	AHT VAA AAT FWF DP	201							IGL V1- 44* 01	IG LJ 2* 01	SSN IGS NT	202 N	ST		AT WD DSL NGL V	203
69	IG H V2 - 5* 02	IGH D2- 21* 02	IGHJ 3*0 2	GFS LST TAV G	20 4	DDD K	20 5	AHS SYF DCG GDC SDV AFD I	206							IGL V3- 10* 01	IG LJ 3* 02	ALP RKY	207 N	ED		YST DSS GDP V	208
14 6	IG H V2 - 5* 02	IGH D2- 15* 01	IGHJ 3*0 1	GFS LTT NG MG	20 9	DDD K	21 0	ARS YCR GGN CYS TAF NV	211							IGL V2- 11* 01	IG LJ 2* 01	SSD VGG YDY	212 N	GV		CSY AGA YTY VA	213
14 6	IG H V2 - 70 D* 04	IGH D7- 27* 01	IGHJ 4*0 2	GFS LST NT MR	21 4	DDE K	21 5	ARS NH WGS HFD Y	216							IGL V3- 21* 02	IG LJ 1* 01	NIG GKT	217 S	DN		QV WD TSG DHL YV	218
55	IG H V3 - 11* 01	IGH D2- 21* 01	IGHJ 3*0 1	GFT FSD YY	21 9	HSS V	22 0	ARD LPG DEY LDA FDL	221	IGK V4- 1*0 1	IGKJ 4*0 1	QSL SNN KNY	222	QQ FY TA PL T									

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN								
DO NO RID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CDR 2	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
60	IG H V3	IGH D6- 13* 01	IGHJ 6*0 2	GLT	22 4	ISH DGS TI	22 5	ASG AAV PYF YYG VDV	226										IGL V3- 1*0 1	IG LJ 2* 01	KLK DAY	227	QD T	QA WGS SPA KV	228
	IGL V3- 1*0 1			IGL V1- 44* 01	SSN IGS NT	232 N																			
99	IG H V3	IGH D3- 22* 01	IGHJ 4*0 2	GFT	22 9	IGA ATD T	23 0	ARA VHY YDS SGH YSG YYF DY	231										IGL V1- 44* 01	IG LJ 2* 01	SSN IGS NT	232 N	SN N	AT WD ASL KGV V	233
	IGL V3- 21* 01			IGL V3- 21* 01	NIG SKS	237 S																			
55	IG H V3	IGH D1- 1*0 1	IGHJ 4*0 2	GFT	23 4	IRSK TDG GTA	23 5	TTQ NAF ES	236										IGL V3- 21* 01	IG LJ 1* 01	NIG SKS	237 S	YD S	QV WD SSS DHY V	238
	IGL V3- 20* 01			IGKJ 4*0 1	QSV TSN Y	242 GAS	QQ YIN SPL T	243																	
55	IG H V3	IGH D2/ OR1 5- 2a*0 1	IGHJ 6*0 2	GFT	23 9	IKSI TDG GTI	24 0	HTL STT HYY GM DV	241										IGK V3- 20* 01	IGKJ 2*0 1	QSV TSN Y	242 GAS	QQ YIN SPL T	243	
	IGL V3- 21* 01			IGKJ 2*0 1	QSV TSN Y	242 GAS	QQ YIN SPL T	243																	
14 6	IG H V3	IGH D6- 25* 01	IGHJ 4*0 2	GFT	24 4	IQR KTD A	24 5	AAH NRA AY	246										IGK V1- 5*0 1	IGKJ 2*0 1	QSV TSN Y	242 GAS	QQ YIN SPL T	243	
	IGL V3- 21* 01			IGKJ 2*0 1	QSV TSN Y	242 GAS	QQ YIN SPL T	243																	

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN									
DO NO R ID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
9	IG H V3																									
	- 21 D3- 3*0 1 2	IGH	IGHJ 4*0 2	GLT FST HS	24 9	ISGS SDYI 25 0	ARA RPP GTA FGF DH 251													IGL V1- 40* 01	IG LJ 2* 01	SSN IGA GYD 252	DN N	QSY DSS LSG AL 253		
13	IG H V3																									
	- 21 D3- 16* 1 01	IGH	IGHJ 4*0 2	GFT FSS YV	25 4	VSS SSYS 25 1	VRT FYF DY 256				IGK V3- 15* 01	IGKJ 1*0 1	QSV RTN 257	SAS	QQ YDI WP PR T 258											
55	IG H V3																									
	- 21 D4- 17* 1 01	IGH	IGHJ 1*0 1	GFT FSS FS	25 9	ISSS SRYI 26 0	VRD MTT VTT CXX QH 261												IGL V1- 44* 01	IG LJ 2* 01	SSN IGS HT 262	TN S	AA WD DSL NGL V 263			
55	IG H V3																									
	- 21 D4- 17* 1 01	IGH	IGHJ 1*0 1	GFT FSS FS	26 4	ISSS SRYI 26 5	VRD MTT VTT CYL QH 266												IGL V1- 44* 01	IG LJ 2* 01	SSN IGS HT 267	TN S	AA WD DSL NGL V 268			
14 6	IG H V3																									
	- 21 D4- 17* 1 01	IGH	IGHJ 4*0 2	GFS FSIY S	26 9	IGN RGN PK 27 0	ARG RTY GDS N 271				IGK V3- 15* 01	IGKJ 1*0 1	RSIS SN 272	RAS	QQ YD NW HT 273											

	HEAVY CHAIN												KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN					
DO NO RID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:	
14 6	IG H V3	IGH D3- 3*0 1	IGHJ 4*0 2	GFS FNA YS	27 4	ISSS SSYI	27 5	ARV PILL AQG VPT FDL	276 276	IGK V3- 15* 01	IGKJ 2*0 1	QSV NSN	277 277	QQ YS DW PR YT	278 278									
9	IG H V3	IGH D2- 2*0 2	IGHJ 6*0 3	GFT FTR YT	27 9	VSG SGS ST	28 0	AKA AIL GNY NYY MD V	281 281							IGL V3- 21* 02	IG LJ 2* 01	NIA SKS	282 282	DD N		QV WD SSA DHL VV	283 283	
13	IG H V3	IGH D1- 1*0 1	IGHJ 4*0 1	EFR FGS YA	28 4	IIAT GAK T	28 5	WKD AIY MSN WP WYF DY	286 286							IGL V3- 21* 02	IG LJ 2* 01	NIG SKS	287 287	DD N				
13	IG H V3	IGH D6- 13* 01	IGHJ 4*0 2	GFT FTN YA	28 8	ISGS GGS T	28 9	AKD PIYS SSW PYY FDY	290 290							IGL V3- 21* 02	IG LJ 2* 01	NIG SRG	291 291	ED S		QV WD SSS DHP EVV	292 292	
H 0 2 1	IG H V3	IGH D6- 13* 01	IGHJ 4*0 2	GFR FSS YA	29 3	ISGS GGS T	29 4	AKD PIYT SRW PYY FDY	295 295	IGK V1- 39* 01	IGKJ 2*0 3	QSSS SY	296 296	QQ SYS LYS	297 297	IGL V3- 21* 02	IG LJ 2* 01	NIG SKS	298 298	DD S		QV WH SSS DHS EVI	299 299	

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	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN																	
DO NO RID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	ARP	DAL	HCS	SITS	CSL	YGL	AYY	YGM	DV	330	V	J	CDR 1	SEQ ID NO:	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:	
55	IG	H	V3																															
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	HEAVY CHAIN												KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN					
DO NO R ID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:	
H 0 0 3	60	- 23 *0 1	IGH D2- 21* 01	IGHJ 2*0 1	GFT FSS YA	35 3	LTA TGG NT	35 4	AKD AIR NSN HA WYF DV	355							IGL V3- 21* 02	IG LJ 2* 01	NIG SKS	356 N	DD N	QV WD PTS DQV	357	
		IG H V3																						
		- 23 *0 1	IGH D2- 8*0 1	IGHJ 4*0 2	GFT FSS YG	35 8	ISGR GDE T	35 9	AKS RVT NSG SID H	360	IGK V1- 39* 01	IGKJ 5*0 1	QTI GTJ	361	AAS	362								
60	IG H V3	IGH D4/ OR1															IGL V3- 21* 02	IG LJ 3* 02	NIG TNS	368 S	ED S	QV WD SSS DHP KVV	369	
	- 23 *0 1	IGH D2- 5- 4a*0 1	IGHJ 2*0 1	GFR FNN YA	36 3	ISGG DGY T	36 4	AKD AILS ANH PWY FDF	365	IGK V4- 1*0 1	IGKJ 4*0 1	QSV LYS SNN KNY	366	WAS	367		IGL V3- 21* 02	IG LJ 2* 01	NIG SES	373 S	DD S	QV WD GSS DHP KVL	374	
	IG H V3																IGL V3- 21* 02	IG LJ 2* 01	NIG SES	373 S	DD S	QV WD RSS DQS KVV	379	
60	IG H V3	IGH D4/ OR1	IGHJ 2*0 1	GFR FNN YA	37 5	ITG GEG YT	37 6	AKD AILS ANH PWY FDF	372								IGL V3- 21* 02	IG LJ 3* 02	NIG TNS	378 S	ED S	QV WD RSS DQS KVV	379	
	- 23 *0 1	IGH D2- 21* 01	IGHJ 2*0 1	GFT FSS YA	37 0	IVN SGG ST	37 1	AKD AIRS SNH PWY FHV	372								IGL V3- 21* 02	IG LJ 2* 01	NIG SES	373 S	DD S	QV WD GSS DHP KVL	374	
	IG H V3																IGL V3- 21* 02	IG LJ 2* 01	NIG SES	373 S	DD S	QV WD RSS DQS KVV	379	

	HEAVY CHAIN												KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN					
DO NO RID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CDR 2	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
	*0 1	4a*0 1																						
14 6	IG H V3	IGH D3/ OR1																						
	23 *0 1	5- 3a*0 1	IGHJ 4*0 2	GFT FST HA	38 0	ISGG SEW S	38 1	AKG YGL FDF	382	IGK V3- 15* 01	IGKJ 1*0 1	QSV SSN	383	GPS	384	QQ YIN RP PW T								
9	IG H V3																							
	23 *0 3	IGH D1- 1*0 1	IGHJ 4*0 2	GFT FSN YA	38 5	IYT GGS KT	38 6	AKV LLG GW NGV FDH	387	IGK V3- 11* 01	IGKJ 4*0 1	QSV DSY	388	DAS	389	QQ RS TW PP S								
14 6	IG H V3																							
	23 *0 4	IGH D3- 10* 01	IGHJ 6*0 2	GFR FNN YG	39 0	FSG SGS NI	39 1	AKD GYF GSG SLY GID V	392								IGL V3- 21* 02	IG LJ 2* 01	NIG SKS	393	ED S	QV WD SNH DHP GVV	394	
14 6	IG H V3																							
	23 *0 4	IGH D3- 10* 01	IGHJ 6*0 2	GFT FTS YA	39 5	ISGS GGS T	39 6	AKD GYG GSG SLY GM DV	397								IGL V3- 21* 02	IG LJ 2* 01	NIG SKS	398	DD S	QV WD STS DHP GVV	399	
14 6	IG H V3	IGH D3- 9*0 1	IGHJ 6*0 2	GFT FSS YA	40 0	FSG SGS ST	40 1	AKV IQY PRG FWF	402								IGL V1- 51* 01	IG LJ 3* 02	SSN IGN NY	403	DN N	GT WD SSL NNC V	404	

		HEAVY CHAIN						KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN											
DO NO R ID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	YGM DV	SEQ ID NO:	CDR 3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
	*0 4																								
	IG H V3																								
	- 30	IGH	IGHJ 6*0 2	GFT FTS YA	40 5	ISVD GST H	40 6	ARD PGV PYY HYA MD V																	
60	3* 01	D3- 10* 01																							
	IG H V3																								
	- 30	IGH	IGHJ 4*0 2	EFT FST YA	41 0	ISA DGN NR	41 1	VRD ETD WEI GVV VAT PEF DY																	
14 6	3* 01	D3- 3*0 1																							
	IG H V3																								
	- 30	IGH	IGHJ 4*0 2	GFP FSS HA	41 7	LSF NGD YI	41 8	VTG IRA RDY GGS TFD L																	
	3* 02	D4- 23* 01																							
	IG H V3																								
	- 30	IGH	IGHJ 3*0 1	GFR FTN YG	42 2	IRY DGS KK	42 3	AKD GR WFG ESG GFD V																	
9	30 *0 2	D3- 10* 01																							

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN					
DO NO RID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	CDR 1	SEQ ID NO:	CDR 2	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
9	IG H V3							ARD YCS RTN														
	- 30 *0 3	IGH D2- 2*0 1	IGHJ 2*0 1	GFT FTS YS	42 7	MSY DGS YE	42 8	CIN WIF DL	429 434	IGK V3- 20* 01	IGKJ 4*0 1	PSV SSSY	430 435	QQ YG SSP LT	431							
60	IG H V3							AKD GYL SAA														
	- 30 *0 3	IGH D2- 8*0 2	IGHJ 6*0 2	GFR FTG YG	43 2	ISN DGS KK	43 3	RGY GM DV	434							IGL V3- 21* 02	IG LJ 2* 01	NIG GKS	DD R	435 440	QV WE TTS DQL V	436
14 6	IG H V3																					
	- 30 *0 3	IGH D4- 17* 01	IGHJ 4*0 2	GFT FSN YD	43 7	ISYD GSN K	43 8	ARD TFG DYY FDY	439							IGL V1- 40* 01	IG LJ 1* 01	NSN IGA GYD	GN H	440 444	QSY DSR LSV PYV	441
9	IG H V3							ARG GGY TYG														
	- 30 *0 4	IGH D5- 18* 01	IGHJ 6*0 2	KFT FSK YA	44 2	TSY NGG SK	44 3	SY YSM DV	444	IGK V4- 1*0 1	IGKJ 3*0 1	QSV LYS SNN KNY	445	QQ YY ST PF T	446							
9	IG H V3							ARG GGY TYG														
	- 30 *0 4	IGH D5- 18* 01	IGHJ 6*0 2	RFT FSK YA	44 7	ISYD GSS K	44 8	SY YAM DV	449	IGK V4- 1*0 1	IGKJ 3*0 1	QSL LYS SNN KNY	450	QQ YY ST PF T	451							

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN							
DO NO R ID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
55	IG H V3							ARA LLS VVG																
	- 30 D1- *0 4	IGH D1- 26*	IGHJ 4*0 2	GFT FSS YS	45 2	MSN TGS TK	45 3	SKS YYF DF	454	IGK V3- 11*	IGKJ 1*0 1	QSV SSY	455	QSV SSY	455	QSV SSY	455	QSV SSY	455	QSV SSY	455	QSV SSY	455	QSV SSY
55	IG H V3							ARA LLS VVG																
	- 30 D1- *0 4	IGH D1- 26*	IGHJ 4*0 2	GFT FSS YS	45 7	MSN TGS TK	45 8	SKS YYF DF	459	IGK V3- 11*	IGKJ 1*0 1	QSV SSY	460	QSV SSY	460	QSV SSY	460	QSV SSY	460	QSV SSY	460	QSV SSY	460	QSV SSY
55	IG H V3							ARD EKY SGL YSG RTG																
	- 30 D1- *0 4	IGH D1- 26*	IGHJ 6*0 2	GFN FNV YA	46 2	ISYD GSK K	46 3	DYY YGM DV	464	IGL V1- 51*	IG LJ 2* 01	NSN IGN NF	465	NSN IGN NF	465	NSN IGN NF	465	NSN IGN NF	465	NSN IGN NF	465	NSN IGN NF	465	NSN IGN NF
55	IG H V3							ARD GKL GRT YHD																
	- 30 D3- *0 4	IGH D3- 22*	IGHJ 6*0 2	GFT FSA YS	46 7	ISYD GSN R	46 8	SRQ SYF YIM DV	469	IGL V2- 14*	IG LJ 2* 01	SSD VGG YNY	470	SSD VGG YNY	470	SSD VGG YNY	470	SSD VGG YNY	470	SSD VGG YNY	470	SSD VGG YNY	470	SSD VGG YNY
13	IG H V3							AKD AAY FAS																
	- 30 D3- *0 13	IGH D3- 10*	IGHJ 6*0 2	GFR FSS YG	47 2	TSF DGS KT	47 3	AYY EAS GSF	474	IGL V3- 21*	IG LJ 2* 01	NIG SKS	475	NIG SKS	475	NIG SKS	475	NIG SKS	475	NIG SKS	475	NIG SKS	475	NIG SKS

		HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN					
DO NO RID	V	D	J	CDR 1	SEQ ID NO:	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 1	SEQ ID NO:	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:			
	*1 8																						
13	IG H V3																						
	- 30 *1 8	IGH D3- 10*	IGHJ 6*0	GFT FSR YG	47 7	ISYD GSN K	47 8	AKD AYY YGS GYG MD V	479 480	IGK V1- 5*0 3	IGKJ 4*0 1	QSI VW	480 481	IGL V1- 47*	IG LJ 1*	SSN IGS DY	RN N	AA WD DRL SGY V	483				
	IG H V3																						
	- 30 *1 8	IGH D3- 10*	IGHJ 6*0	GFT FRS YG	48 4	ISSD GSK K	48 5	AKD GYV VSG SGY GM DV	486					IGL V3- 21*	IG LJ 2*	NIG SKS	DD S	QV WD SSS DHV V	488				
H 0 0 9	IG H V3																						
	- 30 *1 8	IGH D1- 26*	IGHJ 6*0	RFS FNT YG	48 9	ISYD GSH E	49 0	AKT DIK WG ATN YGM DV	491					IGL V3- 21*	IG LJ 2*	NIG RKS	DD N	QV WD GTR DHL VV	493				
	IG H V3																						
	- 30 *1 8	IGH D5- 12*	IGHJ 4*0	GFT FSN YA	49 4	TLY DGS HS	49 5	AKD SAG YGL HY	496 497	IGK V1- 17* 01	IGKJ 1*0 1	QGI RTD	AAS T	IGL V3- 19*	IG LJ 2*	SLR SFY	NK D	NSR DSI GNH VV	500				
60	IG H V3																						
	- 30	IGH D3- 22*	IGHJ 6*0	GFR FTG YG	50 1	ISN DGS KK	50 2	AKD GYL SAA RGY	503					IGL V3- 21*	IG LJ 2*	NV GSK S	DD S	QV WD TTT DQL V	505				

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN					
DO NO RID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:		
	*1 8							GM DV														
60	IG H V3							AKD GYL SAA											QV WD TTS DQL V			
	- 30 *1 8	IGH D3- 22* 01	IGHJ 6*0 2	GFR FTG YG	50 6	ISN DGS KT	50 7	GM DV	508									DD S	509 S	510		
60	IG H V3							AKD GYL SAA											QV WD TSS DQL V			
	- 30 *1 8	IGH D3- 22* 01	IGHJ 6*0 2	GFR FTG YG	51 1	ISN DGS KK	51 2	GM DV	513									DD N	514 N	515		
H 0 0 5	IG H V3							AKD AYL SAA											QV WD TAS DQL V			
	- 30 *1 8	IGH D3- 16* 01	IGHJ 6*0 2	GFR FTG YG	51 6	ISN DGS KK	51 7	GM HV	518									DD S	519 S	520		
60	IG H V3							AKD GYL SAA											QV WD TTS DQL V			
	- 30 *1 8	IGH D3- 22* 01	IGHJ 6*0 2	GFR FTG YG	52 1	ISN DGS KK	52 2	GM DV	523									DD R	524 R	525		
60	IG H V3							AKD GYL SAA											QV WD TTS DQL V			
	- 30 *1 8	IGH D3- 22* 01	IGHJ 6*0 2	GFR FTG YG	52 6	ISN DGS KK	52 7	GM RGY	528									DD T	529 T	530		

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN							
DO NO R ID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R3	SEQ ID NO:			CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
	*1 8							GM DV																
60	IG H V3							AKD GYL SAA RGY GM DV																
	- 30 *1 8	IGH D3-22* 01	IGHJ 6*0 2	GFR FTG YG	53 1	ISN DGS KK	53 2			533														
60	IG H V3							AKT DIR WG ATN YGM DV																
	- 30 *1 8	IGH D1-26* 01	IGHJ 6*0 2	GFT FNT YA	53 6	ISYD GSN K	53 7			538														
H 0 1 0	IG H V3							AKG PLF GLF SFD Q																
	- 30 *1 8	IGH D3-3*0 1	IGHJ 4*0 2	GFS FST YG	54 1	ISYD GMI K	54 2			543														
60	IG H V3							AKD GYL SAA RGY GM DV																
	- 30 *1 8	IGH D3-22* 01	IGHJ 6*0 2	GFR FTG YG	54 6	ISN DGS KK	54 7			548														
60	IG H V3							AKD GYL SAA RGY																
	- 30 *1 8	IGH D3-22* 01	IGHJ 6*0 2	GFR FTG YS	55 1	ISN DGS KR	55 2			553	IGK V2-30* 01	IGKJ 1*0 1	QSL VYS DGN TY	554	KVS	TQ VT LW PP WT								

	DO NO R ID	HEAVY CHAIN						KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN					
		V	D		J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
		*1 8								GM DV									
		IG H V3								AKD GYL SAA								QV WD TTS DQL V	560
H 0 0 6	60	- 30 *1 8	IGH D3- 22* 01	IGHJ 6*0 2	GFR FTG YG	55 6	55 6	ISN DGS KK	55 7	RGY GM DV	558	IGL V3- 21* 02	IG LJ 2* 01	NIG GKS	559	DD N			
	60	IG H V3								AKD GYL SAA		IGL V2- 18* 02	IG LJ 2* 01	SSD VGS YN R	564	EV S		SSY TSS STL V	565
		- 30 *1 8	IGH D2- 21* 02	IGHJ 4*0 2	GFT FRS YG	56 6	56 6	ISSD GSK K	56 7	AKD PIK VSA NG WGF DY	568	IGL V3- 21* 03	IG LJ 2* 01	NIG SKS	569	DD T		QV WD SNS DHL V	570
	60	IG H V3								AKD GYL SAA		IGL V3- 21* 02	IG LJ 2* 01	NIG GKS	574	DD S		QV WD TTS DQL V	575
		- 30 *1 8	IGH D3- 22* 01	IGHJ 6*0 2	GFR FTG YG	57 1	57 1	ISN DGS RK	57 2	RGF GM DV	573	IGL V3- 21* 02	IG LJ 2* 01	NIG GKS	579	DD N		QV WD DSR DHL VI	580
	60	IG H V3								AKT DIM WR AVN	578	IGL V3- 21* 02	IG LJ 2* 01	NIG SKS	579	DD N			

DO NO R ID	HEAVY CHAIN						KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN					
	V	D	J	CDR 1	SEQ ID NO:	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
	*1 8								YGM DV									
60	IG H V3								AKT DIM WR								QV WD DSR DHL VI	
	- 30 *1 8	IGH D2- 15* 01	IGHJ 6*0 2	RFS FST YG	58 1	ISYD GSE K	58 2		AVN YGM DV	583	IGL V3- 21* 02	IG LJ 2* 01	NIG SKS	584	DD N			585
60	IG H V3								AKT DIM WQ								QV WD DSR DHL VI	
	- 30 *1 8	IGH D2- 21* 01	IGHJ 6*0 2	GFS FST YG	58 6	ISYD GSS K	58 7		AVN YGM DV	588	IGL V3- 21* 02	IG LJ 2* 01	NIG SKS	589	DD N			590
60	IG H V3								AKD GYL SAA								QV WD TTS DQL V	
	- 30 *1 8	IGH D3- 22* 01	IGHJ 6*0 2	GFR FTG YG	59 1	ISN DGS KK	59 2		RGY GM DV	593	IGL V3- 21* 02	IG LJ 2* 01	NIG GKS	594	DD R			595
60	IG H V3								AKT DIM WR								QV WD ESR DHL VI	
	- 30 *1 8	IGH D2- 15* 01	IGHJ 6*0 2	RFS FST YG	59 6	ISYD GSE K	59 7		AVN YGM DV	598	IGL V3- 21* 02	IG LJ 2* 01	NIG SKS	599	DD N			600
60	IG H V3								AKD GYL SAA								QV WD TTS DQL V	
	- 30 *1 8	IGH D3- 22* 01	IGHJ 6*0 2	GFR FTG YG	60 1	ISN DGS KK	60 2		RGY SAA RGY	603	IGL V3- 21* 02	IG LJ 2* 01	NIG GKS	604	DD R			605

[illegible]

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN									
DO NO R ID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:		V	J	CDR 1	SEQ ID NO:	CDR 2	CD R3	SEQ ID NO:		V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
	IG H V3 - 30 D1- 26* *1 8	IGH D1- 26* 01	IGHJ 6*0 2	GFR FTK YG	62 6	ISFD GST Q	62 7	AKD GIL GAR RGX YGI DV	628										IGL V3- 21* 02	IG LJ 2* 01	NIR SKN	629 N	DD N		QV WD SYS DHV V	630
	IG H V3 - 30 D3- 3*0 *1 8	IGH D3- 3*0 1	IGHJ 6*0 2	GFT FSN YA	63 1	ISFD GSN K	63 2	AKG IGG FDF RSG KQR SY YVG VDV	633	IGK V3- 20* 01	IGKJ 2*0 1	QTV YNT Y	634	GAS	QQ YG NS PP GY T	635										
	IG H V3 - 30 D3- 10* *1 8	IGH D3- 10* 01	IGHJ 4*0 2	GFR FTIY G	63 6	VSY DGS KQ	63 7	AKD AYY YGS GSH NNP DY	638									IGL V3- 21* 02	IG LJ 3* 02	NIG SQS	639 S	DD S		QV WD SSS MGV	640	
	IG H V3 - 30 D3- 16* *1 8	IGH D3- 16* 02	IGHJ 4*0 2	GFT FSN YG	64 1	ISYD GRD K	64 2	AKG YDY IWG TYR PRP DLD S	643								IGL V1- 44* 01	IG LJ 3* 02	NSN VG NN V	644 S	AN S		ASW DDS LSG SWV	645		
	IG H V3 - 30 D6- 13* *1 30	IGH D6- 13* 01	IGHJ 4*0 2	GFT FSD YG	64 6	VSY DGT SE	64 7	AKD PVQ RSN WYY FDY	648								IGL V3- 21* 02	IG LJ 2* 01	NIG SKT	649 R	DD R		QV WH STT EPV V	650		

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN						
DO NO RID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
	*1 8																						
14 6	IG H V3							AKD PVH RSN WFY FDH	653								IGL V3- 21* 02	IG LJ 2* 01	YIG SKT	654 R		QV WYS NSE PVV	655
	- 30 *1 8	IGH D1- 20* 01	IGHJ 4*0 2	GFT FSN YG	65 1	TSY DGI NK	65 2																
14 6	IG H V3							AKG SPII RFL MM DV	658								IGL V3- 21* 02	IG LJ 3* 02	NIG SKN	661 N		QV WD NNS DHV V	662
	- 30 *1 8	IGH D3- 3*0 1	IGHJ 6*0 2	GTS FST SG	65 6	ISPN AFD K	65 7					QSI DT W	659 W	KAS ST									
13	IG H V3							ARE AGI AAP ASL DF	665								IGL V3- 21* 02	IG LJ 2* 01	NIR GKS	666 S		QV WD SSS DHV V	667
	- 33 *0 1	IGH D6- 13* 01	IGHJ 4*0 2	GFT FSS YG	66 3	IWS DGS NK	66 4																
13	IG H V3							TRE AGI AAP AAL DY	670								IGL V3- 21* 02	IG LJ 2* 01	NIG NK N	671 N		QV WD SSSY HVV	672
	- 33 *0 1	IGH D6- 13* 01	IGHJ 4*0 2	GFT FSN YG	66 8	IWS DGT NK	66 9																
H 0 1 1	IG H V3	IGH D1- 7*0 1	IGHJ 3*0 1	GFT FSN YG	67 3	VW YDG SYK	67 4	VRD NW SYN AFD V	675 V	IGK V3- 11* 01	IGKJ 2*0 3	QSSS SY	676 S	GTS S	QH RN SW PY S								

	HEAVY CHAIN												KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN					
DO NO RID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	IGK V1- 17*	IGKJ 4*0 1	CDR 1	SEQ ID NO:	CDR 2	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
	*0 1																							
	IG H V3																							
	- 33 *0 1	IGH D6- 19* 01	IGHJ 4*0 2	GFIF SDY G	67 8	IWK DGS NK	67 9	VRE NSG WYY FDY	680	IGK V1- 17*	IGKJ 4*0 1	QGI RNN	681	TAS	LQ HD SY PF T	682								
	IG H V3																							
	- 33 *0 1	IGH D6- 13* 01	IGHJ 4*0 2	GFA FRS YG	68 3	IWH DGS NK	68 4	ARE GAI AAP ASL DV	685								IGL V3- 21* 02	IG LJ 2* 01	NIR SRN	686	AD S		QV WD SGT DHV I	687
	IG H V3																							
	- 33 *0 1	IGH D6- 13* 01	IGHJ 4*0 2	GFT FSS FG	68 8	IWS DGS NQ	68 9	ARE GGI AAP AAL DF	690								IGL V3- 21* 02	IG LJ 2* 01	NIR NK N	691	AD S		QV WD GGS YHV I	692
	IG H V3																							
	- 33 *0 1		IGHJ 4*0 2	GVT FNS YG	69 3	IWY DGT NK	69 4	ARE SKA YPY YFD Y	695	IGK V1- 39*	IGKJ 2*0 3	QNI SIF	696	DAS	QH SSF PP QD S	697								
	IG H V3																							
	- 33 *0 1	IGH D1- 1*0 1	IGHJ 4*0 2	GFT FSN YA	69 8	IWY DGT YK	69 9	ARE SNG FGS DF	700	IGK V1- 17*	IGKJ 1*0 1	QGI RNN	701	AAS	LQ HN SFP RT	702								
	IG H V3																							

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN								
DO NO RID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:		V	J	CDR 1	SEQ ID NO:	CD R3	SEQ ID NO:		V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
13	*0 1																								
	IG H V3																								
	- 33 *0 1	IGH D3- 10* 01	IGHJ 3*0 2	GFV FSS YG	70 3	VW YDG SYK	70 4	VRD NW SYN AFD I	705	IGK V3- 11* 01	IGKJ 2*0 3	QSV SY	706	ATS	QH RN SW PY S	707									
	IG H V3	IGH D1- 20* 01	IGHJ 3*0 2	GFT FSN YG	70 8	IWY DGS YK	70 9	ARD NW KYN AFD I	710	IGK V3- 11* 01	IGKJ 2*0 3	QSV SSY	711	DAS	QH RS NW PY S	712									
13	IG H V3																								
	- 33 *0 1	IGH D6- 19* 01	IGHJ 4*0 2	GFT FSR YG	71 3	IWS DGS NQ	71 4	ARE SSG WYY FDY	715																
	IG H V3	IGH D6- 13* 01	IGHJ 5*0 2	GFT FSS FG	71 8	IWY DGS NE	71 9	ARE ERI AAP ASL DL	720	IGL V3- 21* 02	IG LJ 2* 01														
	IG H V3	IGH D6- 25* 01	IGHJ 4*0 2	GFT FSS YG	72 3	IWH DGT NQ	72 4	ARE LRI AAP AAL DY	725	IGL V3- 21* 02	IG LJ 2* 01														

	HEAVY CHAIN												KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN					
DO NO RID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:	
	*0 1																							
	IG H V3																							
	-	IGH D3- 16*	IGHJ 4*0 2	GFT FSS FN	72 8	IWY DGS HK	72 9	ARQ MFT GHF DY	730	IGK V3- 15* 01	IGKJ 1*0 1	QGV SSN	731	DAS	QH YN NW PR T	732								
49	IG H V3																							
	-	IGH D2- 2*0	IGHJ 6*0 2	GFT FSG YG	73 3	IWN DGS FK	73 4	ARE GRG QLL FHG MD V	735	IGK V3- 20* 01	IGKJ 3*0 1	QSV SSSY	736	GAS	QQ YG RS QG FT	737								
60	IG H V3																							
	-	IGH D2- 21*	IGHJ 4*0 2	GFT FSG HG	73 8	IWS SGS KT	73 9	ARD GHC DGG CYS ALY DY	740							IGL V2- 23* 01	IG SSD LJ VG NY NL	741	EG T	CSF AGS RW V	742			
H 0 1 1 5	IG H V3																							
	-	IGH D6- 6*0	IGHJ 4*0 2	GFS FSR HG	74 3	IWF DGT ND	74 4	ARE DPH LLIA TLD L	745	IGK V1- 39* 01	IGKJ 4*0 1	QGL TSF	746	SAS	QQ SY GT PA LA	747								
60	IG H V3																							
	-	IGH D4- 11*	IGHJ 2*0 1	GFT FRS YG	74 8	IWA DGT KQ	74 9	ARE TTIF NW YFD L	750	IGK V1- 39* 01	IGKJ 4*0 1	QSI NKY	751	TAS	QQ SFS IPP T	752								
60	IG H V3																							
	-	IGH D4- 11*	IGHJ 2*0 1	GFT FRS YG	74 8	IWA DGT KQ	74 9	ARE TTIF NW YFD L	750	IGK V1- 39* 01	IGKJ 4*0 1	QSI NKY	751	TAS	QQ SFS IPP T	752								

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN							
DO NO RID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CDR 2	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
	*0 1																							
	IG H V3																							
	- 33 *0 1	IGH D5- 18* 01	IGHJ 4*0 2	GFT FSD YG	75 3	IWS DGS NK	75 4	ARE RRG FSY GLD DN	755								IGL V2- 11* 01	IG LJ 2* 01	SSD VGG YNS	756 S	DV S		CSY AGR YTF VV	757
60	IG H V3																							
	- 33 *0 1	IGH D6- 19* 01	IGHJ 3*0 1	GFT FSR YG	75 8	IWK DGT ND	75 9	ARE QAE IAV ASF DF	760	IGK V1- 39* 01	IGKJ 4*0 1	QRI GDF	761	AAS	QQ AY NA PP LT	762								
60	IG H V3																							
	- 33 *0 1	IGH D6- 19* 01	IGHJ 4*0 2	GFT FSN YG	76 3	IWK DGT NK	76 4	ARE SHY SAW YVL DY	765								IGL V1- 51* 01	IG LJ 3* 02	RSN IGS NY	766 D	GN D		GSW DGS LSV GV	767
60	IG H V3																							
	- 33 *0 1	IGH D2- 8*0 1	IGHJ 4*0 2	GFT FSR HG	76 8	IWK DGS NK	76 9	ARE DPN VFI ATL DL	770	IGK V1- 39* 01	IGKJ 4*0 1	QTI TRS	771	ATS	QQ SD ST PA LA	772								
60	IG H V3																							
	- 33 *0 1	IGH D3- 16* 01	IGHJ 4*0 2	GFT FSR YG	77 3	IWN DGS TK	77 4	ARE DPY VFM ATL DS	775								IGL V2- 11* 01	IG LJ 3* 02	SSD VGG YNY	776 S	DV S		CSY AGS YT WV	777

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN							
	DO NO RID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
		*0 1																						
60		IG H V3																						
	- 33 *0 1	IGH D2- 21*	IGHJ 2*0 1	GFT FRN YG	77 8	IWA DGT NQ	77 9	ARE TTIF QW YFD L	780 780	IGK V1- 39*	IGKJ 4*0 1	QSI NNY	781 781	GAS T	QQ SFS IPP	782 782								
		IG H V3																						
69		- 33 *0 1	IGH D2- 15*	IGHJ 6*0 2	GFT FSS YG	78 3	IWY DGS LK	78 4	ARE TTIF GRF CSG GSC YSD YYY GM DV	785 785	IGK V2- 24*	IGKJ 1*0 1	QSL VHS DGN TY	786 786	MQ AA QF PW T	787 787								
		IG H V3																						
69		- 33 *0 1	IGH D6- 13*	IGHJ 4*0 2	GFV FSN YG	78 8	IWA DGT NS	78 9	ARE GGI VAA DK	790 790														
		IG H V3																						
H 0 1 4		- 33 *0 1	IGH D4/ OR1 5- 4a*0	IGHJ 4*0 2	GFS FSD YG	79 2	IWR DGS NS	79 3	ARE ARV AAP ASY DY	794 794														
		IG H V3																						
14 1 4		- 33 *0 1	IGH D6- 13*	IGHJ 4*0 2	FSS CG	79 7	IWA DGT NK	79 8	ARE ALI AAP	799 799														
		IG H V3																						

HEAVY CHAIN										KAPPA LIGHT CHAIN							LAMBDALIGHT CHAIN						
DO NO R ID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:
H 0 1 3	14 6	- 33 01 1	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804	ATF DY																
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	
H 0 1 3	14 6	IGH D6- 13* 01	IGHJ 5*0 2	GFT FRN 80 2 YG	IWA DGS 80 3 NK	ARE GHI AAP AAL DL 804																	

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN							
DO NO RID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CDR 2	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
14 6	-	33 01 *0 1						GCL DY										48* 02 01					AM W	
	IG H V3	IGH D6- 13* 01	IGHJ 4*0 2	GFT FSS HG	82 8	IWY DGS TK	82 9	ARE ALJ AAP ATF DY		IGK V1- 5*0 3	IGKJ 1*0 1	QSI DT W	831	KAS	QY YS VY ST	832	IGL V3- 21* 02	IG LJ 3* 02	NIG SKN	833	DD N		QV WD NNS DHV V	834
	IG H V3	IGH D5- 12* 01	IGHJ 6*0 2	GFS FSR YG	83 5	IWY DGS TR	83 6	AGG GYS SRG YVN YGL DV		IGK V1- 33* 01	IGKJ 4*0 1	QDI SNY	838	DAS	QQ YD NL PP LT	839	IGL V3- 10* 01	IG LJ 2* 01			ED N		YST DRS GDQ RV	840
	IG H V3	IGH D2- 15* 01	IGHJ 4*0 2	GFT FSR YG	84 1	IWS DGS NK	84 2	AKA TCG DGS CGL YYF DY									IGL V1- 40* 01	IG LJ 3* 02	SSN IGA GYD	844	GN S		QSY DSN LSG WV	845
55	IG H V3	IGH D2- 21* 01	IGHJ 5*0 2			ING NGR DT	84 6	AKD IWI FDG RR WIA GSP DA		IGK V2- 30* 01	IGKJ 1*0 1	QSL VYS DGN TY	848	KVS	MQ QT HW PW A	849								
	IG H V3	IGH D1-	IGHJ 6*0 2	GFS FSS YS	85 0	ITS NSA TI	85 1	ARA GPP SPP		IGK V4-	IGKJ 4*0 1	QSL LYR	853	WAS	QQ YY TA	854								
49	IG H V3	IGH D1-	IGHJ 6*0 2	GFS FSS YS	85 0	ITS NSA TI	85 1	ARA GPP SPP		IGK V4-	IGKJ 4*0 1	QSL LYR	853	WAS	QQ YY TA	854								

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN							
DO NO R ID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CDR 2	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
H 0 1 6	-	1*0 1						NYG MD V		1*0 1		SNN KNY				PL L								
	H	IGH						ASV GLD SKIS		IGK V3- 15*	IGKJ 4*0 1	QSI5 SN	858		QQ YD HW PL T	859								
	-	5- 3a*0	IGHJ 2*0 1	GFT FPS HT	85 5	ISTT SEAI	85 6	GY WYF DL																
	48 *0 2	1	1																					
69	IG	IGH						ARV GLA LTIS		IGK V3- 15*	IGKJ 4*0 1	QSV SSN	863	GAS	PL T	864								
	H	IGH																						
	-	5- 3a*0	IGHJ 2*0 1	GFT FST YT	86 0	ISS GDT	86 1	GY WYF DL																
	48 *0 2	1	1																					
14 6	IG	IGH						ARA KLG SGS		IGK V3- 15*	IGKJ 4*0 1	QSV GSN	868	AAS	PL T	869								
	H	IGH																						
	-	D7- 27*	IGHJ 2*0 1	GFT FSSS V	86 5	ISTT SAAI	86 6	YWY FDL																
	48 *0 2	01	1																					
13	IG	IGH						ARD TGI WN																
	H	IGH																						
	-	D1- 1*0	IGHJ 3*0 2	GIT LRT YK	87 0	ISSD DKT	87 1	GAY DAF DI									IGL V5- 45* 02	IG LJ 1* 01	SGI NV GTY R	873	YR SD SD M	87 4	MIW HST AYV	875
	48 *0 3	1	2																					
13	IG	IGH						VGF DH		IGK V4-	IGKJ 5*0 1	RSL LYT	879	WAS	QQ YY	880								
	H	IGH																						
	-	D1- 1*0	IGHJ 3*0 2	GFT YE	87 6	ISNS GNT	87 1	FST YE																
	48 *0 3	1	2																					

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN								
DO NO RID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CDR 2	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
	-	48									1*0			SVN			SP								
	48										1			KNH			PIT								
	3																								
55	IG	H																							
	V3																								
	-	IGH																							
	48	D2-																							
	3	2*0																							
	3	2	2	IGHJ	GFT	ISSS	88	AGH	883																
	IG	H																							
	V3																								
	-	IGH																							
	49	D3-																							
	3	22*																							
69	3	01	2	IGHJ	GFT	IKP	88	ARD	888																
	IG	H																							
	V3																								
	-	IGH																							
	49	D6-																							
	14	13*																							
	6	01	2	IGHJ	GFT	IRSK	89	ARV	893																
	3	01	2	IGHJ	GFT	GYG	89	PYS																	
	IG	H																							
	V3																								
	-	IGH																							
	49	D3-																							
	4	10*																							
	IG	H																							
	V3																								
	-	IGH																							
	49	D3-																							
	4	01	2	IGHJ	GFT	IRR	89	TRG	898																
	IG	H																							
	V3																								
	-	IGH																							
	49	D3-																							
	4	10*																							
	IG	H																							
	V3																								
	-	IGH																							
	49	D6-																							
	69	3	2	IGHJ	GFT	IYSG	90	ARV	903																
	IG	H																							
	V3																								
	-	IGH																							
	49	D6-																							
	69	3	2	IGHJ	GFT	VNT	90	IAV	903																
	IG	H																							
	V3																								
	-	IGH																							

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN									
DO NO R ID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:		V	J	CDR 1	SEQ ID NO:	CDR 2	CD R3	SEQ ID NO:		V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
	-	19* 53 *0 1																	43* 01	3* 02 Y	AN Y					
9	IG H V3 - 7* 01	IGH D3- 3*0 1	IGHJ 4*0 2	GLT FSR YW	90 6	INE EGS HS	90 7												IGL V1- 51* 01	IG LJ 3* 02	SSN VGK NY		DS Y		GT WD SSL KVV V	910
9	IG H V3 - 7* 01	IGH D1- 26* 01	IGHJ 4*0 2	GFT FTN FK	91 1	IKQ DGS EK	91 2	TRD TW VDS			IGK V1- 17* 03	IGKJ 3*0 1	QGI SKY	914	ASS		LQ HQ SY PF T	915								
13	IG H V3 - 7* 01	IGH D2- 21* 01	IGHJ 4*0 2	GFS FSN YW	91 6	IKE DGS EK	91 7												IGL V1 0- 54* 01	IG LJ 3* 02	NK NV GN KG	919	RH N		SAW DFS LRA WV	920
55	IG H V3 - 7* 03	IGH D6- 13* 01	IGHJ 5*0 2	GFIF SSS W	92 1	IKQ DGS DK	92 2				IGK V3- 11* 01	IGKJ 2*0 1	QSV SSY	924	DAS	QH RS K	925									
55	IG H V3 - 7* 01	IGH D6- 13* 01	IGHJ 5*0 1	SFT FST SW	92 6	INQ DGS ER	92 7				IGK V3- 11* 01	IGKJ 2*0 1	QNI NSQ	929	DAS	HH RI N	930									

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN								
DO NO R ID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
	7*							WID																	
	03							S																	
55	IG							ARL																	
	H							DRG																	
	V3	IGH	IGHJ	GFT	93	INQ	93	TGE																AA	
	-	D3-16*	3*0	FSD	DGS	DGS	93	SGY																WD	
	7*							RSS																DSL	
	03	02	1	YW	1	EY	2	DV	933															NGV	
	IG							ARS																	935
55	H							HVA																	
	V3	IGH	IGHJ	GFIF	93	INQ	93	ASG																	
	-	D1-7*0	5*0	SSN	DGS	DGS	93	TR																	
	7*	03	2	W	6	DI	7	WF	938																
	03	1	2					DP																	
	IG							ARD																	
55	H							GYD																	
	V3	IGH	IGHJ	GFT	94	TRN	94	ILN																	
	-	D3-9*0	4*0	FSD	94	KAN	94	HFV																	
	72	IGH	IGHJ	GFT	94	SYT	94	RFD	943																
	*0	1	2	HF	1	T	2	F																	
	IG																								
60	H							ARE																	
	V3	IGH	IGHJ	GFT	94	IRN	94	GLG																	
	-	D3-16*	3*0	FSD	94	KAK	94	SPT																	
	72	IGH	IGHJ	GFT	94	SYT	94	SDA	948																
	*0	1	2	HY	6	T	7	FDI																	
	1	01	2																						
	IG																								
60	H							TSQ																	
	V3	IGH	IGHJ	GFT	95	IRSK	95	YGD																	
	-	D4-17*	6*0	LSG	95	ANN	95	GYY																	
	73	IGH	IGHJ	GFT	95	ANN	95	YAM																	
	*0	2	2	SA	1	YAT	2	DV	953																
	2	01	2																						
	IG																								
	H																								
	V3	IGH	IGHJ	GFT	95	IRSK	95	YAM																	
	-	D4-17*	6*0	LSG	95	ANN	95	YAM																	
	73	IGH	IGHJ	GFT	95	ANN	95	YAM																	
	*0	2	2	SA	1	YAT	2	DV	953																
	2	01	2																						
	IG																								
	H																								
	V3	IGH	IGHJ	GFT	95	IRSK	95	YAM																	
	-	D4-17*	6*0	LSG	95	ANN	95	YAM																	
	73	IGH	IGHJ	GFT	95	ANN	95	YAM																	
	*0	2	2	SA	1	YAT	2	DV	953																
	2	01	2																						
	IG																								
	H																								
	V3	IGH	IGHJ	GFT	95	IRSK	95	YAM																	
	-	D4-17*	6*0	LSG	95	ANN	95	YAM																	
	73	IGH	IGHJ	GFT	95	ANN	95	YAM																	
	*0	2	2	SA	1	YAT	2	DV	953																
	2	01	2																						
	IG																								
	H																								
	V3	IGH	IGHJ	GFT	95	IRSK	95	YAM																	
	-	D4-17*	6*0	LSG	95	ANN	95	YAM																	
	73	IGH	IGHJ	GFT	95	ANN	95	YAM																	
	*0	2	2	SA	1	YAT	2	DV	953																
	2	01	2																						
	IG																								
	H																								
	V3	IGH	IGHJ	GFT	95	IRSK	95	YAM																	
	-	D4-17*	6*0	LSG	95	ANN	95	YAM																	
	73	IGH	IGHJ	GFT	95	ANN	95	YAM																	
	*0	2	2	SA	1	YAT	2	DV	953																
	2	01	2																						
	IG																								
	H																								
	V3	IGH	IGHJ	GFT	95	IRSK	95	YAM																	
	-	D4-17*	6*0	LSG	95	ANN	95	YAM																	
	73	IGH	IGHJ	GFT	95	ANN	95	YAM																	
	*0	2	2	SA	1	YAT	2	DV	953																
	2	01	2																						
	IG																								
	H																								
	V3	IGH	IGHJ	GFT	95	IRSK	95	YAM																	
	-	D4-17*	6*0	LSG	95	ANN	95	YAM																	
	73	IGH	IGHJ	GFT	95	ANN	95	YAM																	
	*0	2	2	SA	1	YAT	2	DV	953																
	2	01	2																						
	IG																								
	H																								
	V3	IGH	IGHJ	GFT	95	IRSK	95	YAM																	
	-	D4-17*	6*0	LSG	95	ANN	95	YAM																	
	73	IGH	IGHJ	GFT	95	ANN	95	YAM																	
	*0	2	2	SA	1	YAT	2	DV	953																
	2	01	2																						
	IG																								
	H																								
	V3	IGH	IGHJ	GFT	95	IRSK	95	YAM																	
	-	D4-17*	6*0	LSG	95	ANN	95	YAM																	
	73	IGH	IGHJ	GFT	95	ANN	95	YAM																	
	*0	2	2	SA	1	YAT	2	DV	953																
	2	01	2																						
	IG																								
	H																								
	V3	IGH	IGHJ	GFT	95	IRSK	95	YAM																	

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN										
	DO NO RID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:		V	J	CDR 1	SEQ ID NO:	CDR 2	CD R3	SEQ ID NO:		V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
H 0 1 7	9	IG H V3	- 74 *0 1	IGHJ 6*0 2			VRG LNH AM DV	957																			
		IG H V3	- 74 *0 1	IGHJ 6*0 2			ISD DER ST	95 6																			
H 0 1 7	13	IG H V3	- 74 *0 1	IGH D3- 22* 01	IGHJ 4*0 2	GFT FST YR	96 0 ST	96 1	IKY DGS FRH FDS	962																	
		IG H V3	- 74 *0 1	IGH D3- 10* 01	IGHJ 4*0 2	GFT FSN YW	96 5 T	96 6	ISTD GSS VDY	967																	
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 74 *0 1	IGHJ 4*0 2			ARG STY YFG SGS VDY	967																			
		IG H V3	- 74 *0 1	IGHJ 4*0 2			IESD GSG SLD F	97 1																			
H 0 1 7	55	IG H V3	- 7																								

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN									
DO NO R ID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	SEQ ID NO:	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
99	IG H V3	IGH D4/OR1	IGHJ 4*0 2	GFT FSN YW	98 0	INS DGT NT	98 1	ACL RVP DRN	982				IGL V7-46* 01	IG LJ 2* 01	TGA VTS GH Y	983 S	DA S								LLS YSG A QV	984
	IG H V3	IGH D2-2* 01		IGHJ 4*0 2	GFIF DDY S	98 5	ISW NSE FM	98 6	VKA NVK KGS TSC FDY	987	IGK V3-20* 01	IGKJ 1*0 1	QSV SSSY	988 DAS												
60	IG H V3	IGH D6-19* 01	IGHJ 4*0 1	GFN FNM YA	99 0	ISYN GGA R	99 1	VKD KSQ GIP VAG LEY	992				IGL V1-51* 01	IG LJ 2* 01	NSN IGN NY	993 S	DD S								GT WD SSLS AA	994
	IG H V3	IGH D6-19* 01	IGHJ 4*0 2	GFT FNM YA	99 5	ISFN GGA R	99 6	VKD KSQ GIPL AGL EY	997				IGL V1-51* 01	IG LJ 2* 01	SSN IGN NY	998 S	DD S								AT WD SSL TAA	999
H 0 1 1 8	IG H V3	IGH D6-19* 01	IGHJ 4*0 1	GFN FNM YA	10 00	ISYN GGA R	10 01	VKD KSQ GIP VAG LEY	100 2				IGL V1-51* 01	IG LJ 2* 01	NSN IGN NF	100 3	DD S								GT WD SSLS AA	100 4
	IG H V4	IGH D2-2* 03	IGHJ 3*0 2	GGSI TTG DYY	10 05	IYYS GST	10 06	AIY MDE AW AFEI	100 7	IGK V1-39* 01	IGKJ 2*0 1	QSI GNY	1008 AVS													

[illegible]

	HEAVY CHAIN												KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN						
DO NO RID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	CDR 1	SEQ ID NO:	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 1	SEQ ID NO:	CDR 3	SEQ ID NO:		
13	IG H V4																								
	- 31 *0 3	IGH D3- 22* 01	IGHJ 4*0 2	GGSI SSG GY	10 30 31	IYYS DTT YYS GST	10 31	ARV VSS GHR HYY FDY	103 2	IGK V1- 27* 01	IGKJ 1*0 1	QGI SNY	1033	SAS					QK YW T	103 4					
	IG H V4																								
60	- 31 *0 3	IGH D1- 1*0 1	IGHJ 5*0 2	RGS VG WG ENF	10 35 36	ILN TGI D	10 36	AQS RRL VGP FVS	103 7	IGK V3- 15* 01	IGKJ 2*0 3	SINI N	1038	DAS					QQ YD KW PR S	103 9	IGL V6- 57* 01	IG LJ 3* 02	QSY DSS NHG V	104 1	
	IG H V4																								
	- 31 *0 3	IGH D2- 8*0 2	IGHJ 4*0 2	GGSI SSG GY	10 42 43	ISVS GST	10 43	ARG VLV	104 4	IGK V3- 20* 01	IGKJ 2*0 1	QSV SRA Y	1045	GAS					QQ YD SSP YT	104 6					
14 6	IG H V4																								
	- 31 *0 3	IGH D3- 10* 01	IGHJ 3*0 1	GGSI NSD DYY	10 47 48	IYY DGS A	10 48	ARV VHA SAN AFD V	104 9	IGK V1- 6*0 1	IGKJ 4*0 1	QGI RND	1050	AAS					LQ DY NY PL T	105 1	IGL V1- 51* 01	IG LJ 3* 02	GT WD SSL NG WV	105 3	
	IG H V4																								
14 6	- 31 *0 3	IGH D3- 10* 01	IGHJ 3*0 1	GGSI SND NYY	10 54 55	IYY DGS A	10 55	ARV VHA SAN AFD V	105 6	IGK V1- 39* 01	IGKJ 5*0 1	QSI NKF	1057	DAS					QQ TY ST PT	105 8					

	HEAVY CHAIN												KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN					
DO NO RID	V	D	J	CDR 1	SEQ ID NO:	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	CDR 1	SEQ ID NO:	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:		
14 6	IG H V4					ARV																		
	- 31 *0 3	IGH D4- 11* 01	IGHJ 3*0 2	GVP INN AGF Y	10 59	IHA SGA T	10 60	106 1	IGK V3- 15* 01	IGKJ 4*0 1	QSV SSD	1062 GAS	QQ YK NW PP LT	106 3										
9	IG H V4					AGG RFT NDF VW																		
	- 34 *0 1	IGH D3- 16* 02	IGHJ 5*0 2	RGS FSD YY	10 64	INH SGS T	10 65	106 6	IGK V2- 28* 01	IGKJ 4*0 1	QSL LHS NGY NY	1067 LGS	MQ AL- QT LLL T	106 8										
60	IG H V4					VRG GYS SAP																		
	- 34 *0 1	IGH D6- 19* 01	IGHJ 4*0 2	GGS FIG HY	10 69	ISHS GSA	10 70	107 1							IGL V1- 44* 01	IG LJ 3* 02	SSN IGS NT	107 2	SN N	AA WD DSL NG WV	107 3			
69	IG H V4					ARG RDG YNY																		
	- 34 *0 1	IGH D5- 24* 01	IGHJ 6*0 3	GGS FSG DF	10 74	INQ SGS T	10 75	107 6	IGK V3- 11* 01	IGKJ 1*0 1	QSV TNY	1077 DGS	QQ RS NW QW T	107 8										
14 6	IG H V4					ARG IFEV VIIP																		
	- 34 *0 1	IGH D3- 3*0 1	IGHJ 6*0 2	GGT FSG YY	10 79	IDH SGG T	10 80	108 1	IGK V3- 15* 01	IGKJ 3*0 1	QTI SNN	1082 GAS	QQ YN NW PP FT	108 3	IGL V3- 19* 01	IG LJ 2* 01	SLR SY	108 4	GR N	SSR SGN RLV	108 5			

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN					
DO NO RID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	CDR 1	SEQ ID NO:	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:	
9	IG H V4	IGH D6- 13* 01	IGHJ 5*0 2	GGP FSG YY	10 86	INH SGS T	10 87	GRG LGR EYS SSW YGG RRF DP	108 8					IGL V2- 14* 01	IG LJ 3* 02	SRQ DG RYX	108 9	EV N	RSYI SNN XXW V	109 0		
9	IG H V4	IGH D3- 22* 01	IGHJ 3*0 2	GYSI RNR YY	10 91	MYH SGS T	10 92	ARD RSG YVF FYD AFD I	109 3	IGK V3- 20* 01	IGKJ 4*0 1	QSV SSSY	1094 GAS				QQ YG SSP LT	109 5				
14 6	IG H V4	IGH D2- 21* 02	IGHJ 4*0 2	GYSI SRD YY	10 96	FSH SGT T	10 97	GGG VTR ADY	109 8					IGL V1- 47* 02	IG LJ 3* 02	SSN IGK NY	109 9	TN D	AV WD DNL SAW E	110 0		
60	IG H V4	IGH D2- 8*0 1	IGHJ 4*0 2	GGSI SSSS YY	11 01	IDY YGS T	11 02	ARR IQL MVF DF	110 3	IGK V1- 5*0 3	IGKJ 1*0 1	QSI SW	1104 KAS				HQ YN TY PW T	110 5				
60	IG H V4	IGH D3- 3*0 1	IGHJ 2*0 1	GGSI SNS NYY	11 06	IYYS GST	11 07	ARRH PY NF WY	110 8					IGL V1- 44* 01	IG LJ 2* 01	SST IGS NT	110 9	LN N	ASW DDS LNG LVV	111 0		

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN									
DO NO RID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	WYF DL	V	J	CDR 1	SEQ ID NO:	CDR 2	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:	
99	*0 1																									
	IG H V4																									
	- 39 *0 1	IGH D3- 10* 01	IGHJ 3*0 1		VSS 11 KGK T			WSQ 111 SPF LAV										IGL V1- 44* 01	IG LJ 3* 02	SSN IGV NT	111 4	AN N		AV WD DSL NT WV	111 5	
	IG H V4							AKG RYS GYN											IGL V1- 47* 02	IG LJ 3* 02				AA WD DSP EWL G	111 9	
14 6	IG H V4							TRP ASG AHD YVS																		
	- 39 *0 1	IGH D3- 10* 01	IGHJ 3*0 1		IYYS 11 GTT			YPG 112 QGA FGV			IGK V3- 20* 01	IGKJ 5*0 1	QSV SSSY	1123 GAS			QQ YG SSS IT									
	IG H V4							ARL LGI AAT										IGL V1 0- 54* 01	IG LJ 3* 02	SNN IDN QG	112 8	RN N		STW DSS LST WL	112 9	
	- 39 *0 1	IGH D6- 13* 01	IGHJ 4*0 2		LYY 11 TGI T			GHF DS																		
14 6	IG H V4							TRP ASG AHD YAS																		
	- 39 *0 1	IGH D3- 10* 01	IGHJ 3*0 2		IYYS 11 GTP			SSIS 31 YY			IGK V3- 20* 01	IGKJ 5*0 1	QSV STT Y	1133 GAS			QQ YG SSS TT									
	IG H V4							TRP ASG AHD YAS																		
	- 14 6	IGH D3- 10* 01	IGHJ 3*0 2		IYYS 11 GTP			SSIS 31 YY																		

DO NO R ID	HEAVY CHAIN						KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN					
	V	D	J	CDR 1	SEQ ID NO:	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
	39 *0 1					RSY YPG LGA FGI												
14 6	IG H V4					ARP LLN PMT LYG												
	- 39 *0 1	IGH D3- 3*0 1	IGHJ 3*0 2	GCSI TSL SYW	11 35	IYYS GTT	11 36	113 7	IGK V3- 20* 01	IGKJ 4*0 1	QSV SSK C	1138	GAS	NS LS	113 9			
14 6	IG H V4					AAH RVS SSY PAD Y												
	- 39 *0 1	IGH D6- 6*0 1	IGHJ 4*0 2	GDS MSR NSF Y	11 40	INY NGI T	11 41	114 2	IGK V1- 39* 01	IGKJ 1*0 1	QNI DDY	1143	AAS	QQ SY NT PT	114 4			
14 6	IG H V4					ARP LLN PSTI YGV TPG												
	- 39 *0 1	IGH D3- 3*0 1	IGHJ 3*0 2	GCSI SSL YY	11 45	IYYS GTA	11 46	114 7	IGK V3D - 15* 01	IGKJ 1*0 1	QSI RSN	1148	GAS	QQ YIN WP PW T	114 9			
14 6	IG H V4					ARG NYD YV WGS YRS												
	- 4* 02	IGH D3- 16* 02	IGHJ 6*0 2	GYS VST SN W	11 50	IYHI GST	11 51	115 2	IGK V1- 39* 01	IGKJ 2*0 1	QSI DNY	1153	LAS	QR SYS TP YT	115 4			

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN									
DO NO R ID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:		V	J	CDR 1	SEQ ID NO:	CDR 2	CD R3	SEQ ID NO:		V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
49	IG							ARE																		
	H							GGS																		
	V4	IGH	IGHJ	GASI				SYV												IGL	IG	SSD			SSY	
	- 4* 07	D6- 13* 01	6*0 3	RSH Y	11 55	VHS SGG T	11 56	YYY YMD V	115 7											V2- 8*0 1	LJ 2* 01	VGS YNY	115 8	DV T	AGI NSY VI	115 9
13	IG																									
	H																									
	V4	IGH	IGHJ	GCSI																						
	- 59 *0 1	D2- 2*0 1	5*0 2	STY F	11 60	IYY NGG T	11 61	KNQ LLL FDP	116 2		IGK V3- 15* 01	IGKJ 4*0 1	QSV GSD	1163	GAS		QQ YN DW PP LT	116 4								
13	IG																									
	H																									
	V4	IGH	IGHJ	GDS																						
	- 59 *0 1	D4- 23* 01	5*0 1	IGT YF	11 65	VYH TGG T	11 66	KNQ LLL FEF	116 7		IGK V1- 33* 01	IGKJ 4*0 1	QDI SNY	1168	DAS		QQ YD NL PL T	116 9								
55	IG																									
	H																									
	V4	IGH	IGHJ	GASI																IGL	IG	NN			SAW	
	- 59 *0 1	D7- 27* 01	3*0 1	SSN Y	11 70	MYS SGS V	11 71	AYD PFN V	117 2		IGK V1- 5*0 3	IGKJ 1*0 1	QNI NS W	1173	KAS		QQ YY SVS T	117 4	IGL V1- 36* 01	LJ 2* 01	NIG RSA	117 5	ED	DFS LSV QV	117 6	
60	IG																									
	H																									
	V4	IGH	IGHJ	GCSI																						
	- 59 *0 1	D2- 15* 01	6*0 2	SSY Y	11 77	IYDS GST	11 78	MD V	117 9		IGK V1- 5*0 3	IGKJ 4*0 1	QSI RW	1180	KAS		QQ YN SYF PL T	118 1								

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN							
DO NO R ID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	CDR 1	SEQ ID NO:	CD R3	SEQ ID NO:	V	IGL V1- 44*	IG LJ 2*	IGD NN	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 1	SEQ ID NO:	CDR 3	SEQ ID NO:
60	IG H V4				VRD																			
	- 59 *0 1	IGH D2- 8*0 2	IGHJ 6*0 2	GGSI SGS Y	11 82	IYDS GNT	11 83	MD V	118 4	IGK V1- 5*0 3	IGKJ 1*0 1	QSI SW	1185	KAS	RT	SY 118 6								
	IG H V4							ARL RRR GLT	118 9															
	- 59 *0 1	IGH D2- 8*0 2	IGHJ 4*0 2	GGSI SNY F	11 87	VYS SGT T	11 88	GTD FDY	118 9															
69	IG H V4				ARS YYY DSS GYR PSF YYY YMD V																			
	- 59 *0 1	IGH D3- 22* 01	IGHJ 6*0 3	GGSI RSY Y	11 92	IYYS GST	11 93	YMD V	119 4															
	IG H V4				ARG ILGS TW YYY YGL DV																			
	- 59 *0 1	IGH D1- 26* 01	IGHJ 6*0 2	GGSI SGY Y	11 97	IYYS GTT	11 98	YYY YGL DV	119 9	IGK V1- 39* 01	IGKJ 2*0 1	QSI SY	1200	ATS	HQ SYS SP YT	120 1								
55	IG H V4				ARH LYR YGY RNY FDY																			
	- 59	IGH D5- 18* 01	IGHJ 4*0 2	GGSI SND Y	12 02	KGD T	12 03	IHS KGD	120 4	IGK V1- 12* 01	IGKJ 4*0 1	QGI SSG	1205	AAS	QQ AN SFP LT	120 6								

	HEAVY CHAIN												KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN					
DO NO RID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CDR 2	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:
	*0 8																							
H 0 2 0	IG H V4																							
	- 59 *0 8	IGH D5- 18* 01	IGHJ 4*0 2	GGSI SND Y	12 07	IHS KGD T	12 08	ARH LYR YGY RNY FDY	120 9	IGK V1- 12* 01	IGKJ 4*0 1	QGI SSG	1210	AAS	QQ AN SFP LT	121 1								
	IG H V4																							
69	- 61 *0 8	IGH D6- 13* 01	IGHJ 3*0 2	GGV VRS TGY F	12 12	IYT GGA T	12 13	ARM TSF KQS GG WY	121 4	IGK V1- 5*0 1	IGKJ 2*0 1	QTI GTI	1215	EAS	QE YN SYS YT	121 6								
	IG H V4																							
69	- 61 *0 8	IGH D6- 19* 01	IGHJ 3*0 2	RGS VSN GGY Y	12 17	VYV TGS S	12 18	WY RGR HDA FDI	121 9	IGK V1- 5*0 1	IGKJ 2*0 1	QSI TL	1220	DGS	QE YSS YS YT	122 1								
	IG H V5																							
9	- 51 *0 1	IGH D3- 22* 01	IGHJ 4*0 2	GYS FTS YW	12 22	IQS GDY NT	12 23	ARR ARN VGN YGT SDF YPY FDH	122 4															
	IG H V5																							
60	IG H V5	IGH D1-	IGHJ 3*0 2	GYT FAS YW	12 27	INP PNS DT	12 28	ARR RVS VTG	122 9															

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN										
DO NO R ID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:	
60	-	51	14*01					TDA FDI											8*01		2*01						
	IG H V5																										
	-	51	IGH D1-14*01	IGHJ 3*02	GYT FAS YW	1232	INP PNS DT	1233	ARR RVS VTG TDA FDI	1234									IGL V2-8*01	IG LJ 2*01	SSD VGG YNY	1235	EV N		SSY AGT NTF VV	1236	
	IG H V5																										
69	-	51	IGH D1-1*01	IGHJ 4*02	GDT FGN YW	1237	ILLS DSD T	1238	ARA TPG NYV FDS	1239									IGL V2-14*01	IG LJ 1*01	SSD VGA YNY	1240	DV T		SSY TDS SPN CV	1241	
	IG H V5																										
	-	51	IGH D2-2*01	IGHJ 1*01	GYS FSN FW	1242	IYPG DSD T	1243	STS EYF HY	1244	IGK V3-20*01	IGKJ 4*01	QSV SSR S	1245	GAS		QQ YA NS PL T	1246									
	IG H V5																										
99	IG H V6																										
	-	1*	IGH D1-1*01	IGHJ 4*02	GDS VSN NTA V	1247	TYV RSK WF N	1248	AVG HH WH FKY	1249									IGL V2-8*01	IG LJ 1*01	SSD VGG YSH	1250	EV S		SSH AGS NYG V	1251	
	IG H V6																										
	-	1*	IGH D1-1*01	IGHJ 4*02	GDS VSN	1252	TYV RSK	1253	AVG HH	1254									IGL V2-8*01	IG LJ 1*01	SSD VGG YSH	1255	EV S		SSH AGS	1256	

	HEAVY CHAIN										KAPPA LIGHT CHAIN						LAMBDA LIGHT CHAIN							
DO NO R ID	V	D	J	CDR 1	SEQ ID NO:	CDR 2	SEQ ID NO:	CDR 3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R3	SEQ ID NO:	V	J	CDR 1	SEQ ID NO:	CD R2	SEQ ID NO:	CDR 3	SEQ ID NO:	
	- 1* 01	IGH D3- 10* 01	IGHJ 4*0 2	GSSI FTN SAG	12 57	TYV RSK WY N	12 58	ARD TYV YTS ASY YNV DY	125 9	IGH V1- 39* 01	IGHJ 5*0 1	ESIR SN	1260	AAS	QQ SY RT PIT	126 1	8*0 1	1* 01					NYG V	
55	IG H V7							ARD TYV YTS ASY YNV DY	125 9															
55	- 4- 1* 02	IGH D1- 7*0 1	IGHJ 4*0 2	GYT FTS YG	12 62	INT DTG NP	12 63	ARL GEY SW NSI GYF DY	126 4								IGL V1- 40* 01	IG LJ 2* 01	SSN IGA GYD	126 5	GN N	QSY DRS LJLV V	126 6	
99	- 4- 1* 02	IGH D3- 10* 01	IGHJ 4*0 2	GYV FTN YA	12 67	INT NTG NP	12 68	ARS YAY GDF	126 9	IGH V1- 39* 01	IGHJ 1*0 1	QNI AIR	1270	EAS	QQ SD TL PW T	127 1								
99	IG H V7							ARG ARS YYD SSG YYS WS DY		IGH V4- 1*0 1	IGHJ 1*0 1	QSV LYR SNN KNY	1275	WAS	QQ YY NT LT WA	127 6								

[0167] Table S3. Primers and synthesized nucleotide sequences.

Single-Cell Antibody Cloning Primers		SEQ ID NO:
A2		
F1-HC	5'-ACAGGTGCCCCACTCCCAGGTGCAG	1277
F2-HC	5'-AAGGTGTCCAGTGTGARGTGCAG	1278
F3-HC	5'-CCCAGATGGGTCTGTCCCAGGTGCAG	1279
F4-HC	5'-CAAGGAGTCTGTTCCGAGGTGCAG	1280
R-1st-HC	5'-GGAAGGTGTGCACGCCGCTGGTC	1281
R-2nd-HC	5'-GTTTCGGGGAAGTAGTCCCTTGAC	1282
F1-Kappa	5'-ATGAGGSTCCCYGCTCAGCTGCTGG	1283
F2-Kappa	5'-CTCTTCCTCCTGCTACTCTGGCTCCCAG	1284
F3-Kappa	5'-ATTTCTCTGTTGCTCTGGATCTCTG	1285
F4-Kappa	5'-ATGACCCAGWCTCCABYCWCCCTG	1286
R-1st-Kappa	5'-GTTTCTCGTAGTCTGCTTTGCTCA	1287
R-2nd-Kappa	5'-GTGCTGTCTTGCTGTCTGCTGCT	1288
F1-Lambda	5'-GGTCCTGGGCCCAGTCTGTGCTG	1289
F2-Lambda	5'-GGTCCTGGGCCCAGTCTGCCCTG	1290
F3-Lambda	5'-GCTCTGTGACCTCCTATGAGCTG	1291
F4-Lambda	5'-GGTCTCTCTCSCAGCYTGTGCTG	1292
F5-Lambda	5'-GTTCTTGGGCCAATTTTATGCTG	1293
F6-Lambda	5'-GGTCCAATTCYCAGGCTGTGGTG	1294
F7-Lambda	5'-GAGTGGATTCTCAGACTGTGGTG	1295
R-1st-Lambda	5'-CACCAGTGTGGCCTTGTTGGCTTG	1296
R-2nd-Lambda	5'-CTCCTCACTCGAGGGYGGGAACAGAGTG	1297
F-Vector Seq Primer	5'-GCTTCGTTAGAACGCGGCTAC	1298
Antibody Cloning Primers for Each Antibody		
F-H001-HC	5'-CTAGTAGCAACTGCAACCGGTGTACATTCT CAGGTCCAGCTTGTGCAGTCTGG	1299
R-H001-HC	5'-CCGATGGGCCCTTGGTCGACGC TGAAGAGACGGTGACCATTGTCCCTT	1300
F-H001-Kappa	5'- CTAGTAGCAACTGCAACCGGTGTACATTCT GACATCCAGATGA CCCAGTCTCCA	1301
R-H001-Kappa	5'- GAAGACAGATGGTGCAGCCACCGTACG TTTGATCTCCACCTTG GTCCCTCC	1302
F-H002-HC	5'-CTAGTAGCAACTGCAACCGGTGTACATTCT CAGGTCACCTTGAAGGAGTCTGG	1303

Single-Cell Antibody Cloning Primers A2		SEQ ID NO:
R-H002-HC	5'-CCGATGGGCCCTTGGTCGACGC TGAGGAGACGGTGACCAGGGTG	1304
F-H002-Lambda	5'- CTAGTAGCAACTGCAACCGGTTCTGGGCC TCCTATGTGCTGA CCCAGGCGC	1305
F-H003-HC	5'-CTAGTAGCAACTGCAACCGGTGTACATTCT GAGATGCAGCTGCTGGAGTCTGG	1306
R-H003-HC	5'-CCGATGGGCCCTTGGTCGACGC TGAGGAGACAGTGACCAGGGTGC	1307
F-H003-Lambda	5'- CTAGTAGCAACTGCAACCGGTTCTGGGCC TCCTATATGCTGA CTCAGGCACCC	1308
F-H004-HC	5'-CTAGTAGCAACTGCAACCGGTGTACATTCT GAGATGCAACTGGTGGAGTCTGG	1309
R-H004-HC	5'-CCGATGGGCCCTTGGTCGACGC TGAGGAGACGATGACCGTGGTCC	1310
F-H004-Lambda	5'- CTAGTAGCAACTGCAACCGGTTCTGGGCC TCCTATGTGCTGA CTCAGCCACC	1311
F-H005-HC	5'-CTAGTAGCAACTGCAACCGGTGTACATTCT CAGATGCGTCTGGTGGAAATCTGG	1312
R-H005-HC	5'-CCGATGGGCCCTTGGTCGACGC TGAGGAGACGGTGACCGGGGT	1313
F-H005-Lambda	5'- CTAGTAGCAACTGCAACCGGTTCTGGGCC TCCTATGTGCTGA CTCAGCCACC	1314
F-H006-HC	5'-CTAGTAGCAACTGCAACCGGTGTACATTCT CAGATGCGTCTGGTGGAAATCGGG	1315
R-H006-HC	5'-CCGATGGGCCCTTGGTCGACGC TGAGGAGACGGTGACCGGGATC	1316
F-H006-Lambda	5'- CTAGTAGCAACTGCAACCGGTTCTGGGCC TCCTATGTGCTGA CTCAGCCACC	1317
F-H007-HC	5'-CTAGTAGCAACTGCAACCGGTGTACATTCT CAGGTGCACCTGGTGGAGTCTG	1318
R-H007-HC	5'-CCGATGGGCCCTTGGTCGACGC TGAGGAGACGGTGACCGTGGTC	1319
F-H007-Kappa	5'- CTAGTAGCAACTGCAACCGGTGTACATTCT GAAATTGTGTTG ACGCAGTCTCCAG	1320
R-H007-Kappa	5'- GAAGACAGATGGTGCAGCCACCGTACG TTTGATCTCCAATTG GTCCCCCTGG	1321
F-H008-HC	5'-CTAGTAGCAACTGCAACCGGTGTACATTCT CAGATGCACCTATTGGAGTCTGGG	1322

Single-Cell Antibody Cloning Primers A2		SEQ ID NO:
R-H008-HC	5'-CCGATGGGCCCTTGGTCGACGC TGACGAGACGGTGACCCTGGTC	1323
F-H008-Lambda	5'- CTAGTAGCAACTGCAACCGGTTCTGGGCC TCCTATGTGCTGA CTCAGCCACC	1324
F-H009-HC	5'-CTAGTAGCAACTGCAACCGGTGTACATTCT CAGATGAAGTTGGTGGAGTCTGGG	1325
R-H009-HC	5'-CCGATGGGCCCTTGGTCGACGC TGAGGAGACGGTGACCCTGGTC	1326
F-H009-Lambda	5'- CTAGTAGCAACTGCAACCGGTTCTGGGCC TCCTATGTGCTGA CTCAGCCACC	1327
F-H010-HC	5'-CTAGTAGCAACTGCAACCGGTGTACATTCT CAGGTGCAGCTGGTGGAGTCTG	1328
R-H010-HC	5'-CCGATGGGCCCTTGGTCGACGC TGAGGAGACGGTGACCAGGGTT	1329
F-H010-Lambda	5'- CTAGTAGCAACTGCAACCGGTTCTGGGCC TCCTATGTGCTGA CTCAGCCACC	1330
F-H011-HC	5'-CTAGTAGCAACTGCAACCGGTGTACATTCT CAGGTTCACTTGGCGGAGTCTGG	1331
R-H011-HC	5'-CCGATGGGCCCTTGGTCGACGC TGAAGAGACGGTGACCAATGTCCC	1332
F-H011-Kappa	5'- CTAGTAGCAACTGCAACCGGTGTACATTCT GAAGTTGTGTTGA CACAGTCTCCAGC	1333
R-H011-Kappa	5'- GAAGACAGATGGTGCAGCCACCGTACG TTTGATCTCCAGCTTG GTCCCTG	1334
F-H012-HC	5'-CTAGTAGCAACTGCAACCGGTGTACATTCT CAGCTGCAGCTGGTGGAGTCTG	1335
R-H012-HC	5'-CCGATGGGCCCTTGGTCGACGC TGAGGAGACGGTGACCAGGGTTC	1336
F-H012-Lambda	5'- CTAGTAGCAACTGCAACCGGTTCTGGGCC TCCTATGTGCTGA CTCAGCCACC	1337
F-H013-HC	5'-CTAGTAGCAACTGCAACCGGTGTACATTCT CAGGTGCAGCTGGTGGAGTCTG	1338
R-H013-HC	5'-CCGATGGGCCCTTGGTCGACGC TGAGGAGACGGTGACCAGGGCT	1339
F-H013-Lambda	5'- CTAGTAGCAACTGCAACCGGTTCTGGGCC TCCTATGTGCTGA CTCAGCCACC	1340
F-H014-HC	5'-CTAGTAGCAACTGCAACCGGTGTACATTCT CAGGTACAACCTGATGGAGTCTGGG	1341

Single-Cell Antibody Cloning Primers A2		SEQ ID NO:
R-H014-HC	5'-CCGATGGGCCCTTGGTCGACGC TGAGGAGACGGTGACCAGGGCT	1342
F-H014-Lambda	5'- CTAGTAGCAACTGCAACCGGTTCTGGGCC TCCTATGTGCTGA CTCAGACACCC	1343
F-H015-HC	5'-CTAGTAGCAACTGCAACCGGTGTACATTCT CAGGTGCAGCTGGTGGAGTCTG	1344
R-H015-HC	5'-CCGATGGGCCCTTGGTCGACGC TGAGGAGACGGTGACCAGGGTTC	1345
F-H015-Kappa	5'- CTAGTAGCAACTGCAACCGGTGTACATTCT GACATCCAGGTGA CCCAGTCAC	1346
R-H015-Kappa	5'- GAAGACAGATGGTGCAGCCACCGTACG TTTGATGTCCACCTTG GTCCCTCC	1347
F-H016-HC	5'-CTAGTAGCAACTGCAACCGGTGTACATTCT GAGATGCACCTGGTGGAGTCTGG	1348
R-H016-HC	5'-CCGATGGGCCCTTGGTCGACGC TGAGGAGACAGTGACCAGGGTGC	1349
F-H016-Kappa	5'- CTAGTAGCAACTGCAACCGGTGTACATTCT GAAATACTGCTGA CGCAGTCTCCAG	1350
R-H016-Kappa	5'- GAAGACAGATGGTGCAGCCACCGTACG TTTGATCTCCACCTTG GTCCCTCC	1351
F-H017-HC	5'-CTAGTAGCAACTGCAACCGGTGTACATTCT GAGGTGCAGCTGGTGGAGTCC	1352
R-H017-HC	5'-CCGATGGGCCCTTGGTCGACGC TGAGGAGACGGTGACCAGGGTTC	1353
F-H017-Lambda	5'- CTAGTAGCAACTGCAACCGGTTCTGGGCC CAGTCTGCCCTGA CTCAGCCTG	1354
F-H018-HC	5'-CTAGTAGCAACTGCAACCGGTGTACATTCT GAAGGACAGCTGGTGGAGTCTGG	1355
R-H018-HC	5'-CCGATGGGCCCTTGGTCGACGC TGAGGAGACGGTGACCAGGGTTC	1356
F-H018-Lambda	5'- CTAGTAGCAACTGCAACCGGTTCTGGGCC CAGTCTGTGTTGA CGCAGCCGC	1357
F-H019-HC	5'-CTAGTAGCAACTGCAACCGGTGTACATTCT CAGGTGGTGCTGCAGGAGTCG	1358
R-H019-HC	5'-CCGATGGGCCCTTGGTCGACGC TGAAGAGACGGCGACCAGTGTCC	1359
F-H019-Kappa	5'- CTAGTAGCAACTGCAACCGGTGTACATTCT GACATCCAGATGA CCCAGTCTCCG	1360

Single-Cell Antibody Cloning Primers A2		SEQ ID NO:
R-H019-Kappa	5'- GAAGACAGATGGTGCAGCCACCGTACG TTTGATCTCCAGCTTG GTCCCCTG	1361
F-H020-HC	5'-CTAGTAGCAACTGCAACCGGTGTACATTCT CAGGTGCAGCTGCAGGAGTCG	1362
R-H020-HC	5'-CCGATGGGCCCTTGGTCGACGC TGAGGAGACGGTGACCAGGTTTCC	1363
F-H020-Kappa	5'- CTAGTAGCAACTGCAACCGGTGTACATTCT GACATCCAGATGA CCCAGTCTCCA	1364
R-H020-Kappa	5'- GAAGACAGATGGTGCAGCCACCGTACG TTTGAACTCCACCTTG GTCCCCTCC	1365
R-Lambda	5'-GGCTTGAAGCTCCTCACTCGAGGGYGGGAACAGAGTG	1366
gBlock Synthesis for Alanine Mutations		
101Q	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATGCAGGTATGTTGCCGTTTGTCTCT AATTCCAGGATCAACAACAACAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCCTGGGCTTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTC AGTGGTTTCGTAGGG	1367
102G	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGCAATGTTGCCGTTTGTCTCT AATTCCAGGATCAACAACAACAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCCTGGGCTTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTC AGTGGTTTCGTAGGG	1368

Single-Cell Antibody Cloning Primers A2		SEQ ID NO:
103M	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTGCATTGCCCCGTTTGTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1369
104L	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGGCACCCGTTTGTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1370
105P	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGGCAGTTTGTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1371

Single-Cell Antibody Cloning Primers A2		SEQ ID NO:
106V	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCCTTCTGGATTATCAAGGTATGTTGCCCCGATGTCCCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1372
108P	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCCTTCTGGATTATCAAGGTATGTTGCCCCGTTTGTGCACT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1373
109L	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCCTTCTGGATTATCAAGGTATGTTGCCCCGTTTGTCCCTGC AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1374

Single-Cell Antibody Cloning Primers A2		SEQ ID NO:
110I	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCCTTCTGGATTATCAAGGTATGTTGCCCCGTTTGTCCCTCT AGCACCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1375
111P	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCCTTCTGGATTATCAAGGTATGTTGCCCCGTTTGTCCCTCT AATTGCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1376
112G	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCCTTCTGGATTATCAAGGTATGTTGCCCCGTTTGTCCCTCT AATTCAGCATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1377

Single-Cell Antibody Cloning Primers A2		SEQ ID NO:
113S	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCT AATTCCAGGAGCAACAACAACCAAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1378
114T	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCT AATTCCAGGATCAGCAACAACCAAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1379
115T	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCT AATTCCAGGATCAACAGCAACCAAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1380

Single-Cell Antibody Cloning Primers A2		SEQ ID NO:
116T	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCGTTTGTCCCTCT AATTCCAGGATCAACAACAGCAAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1381
117S	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCGTTTGTCCCTCT AATTCCAGGATCAACAACAACCGCAACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1382
118T	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCGTTTGTCCCTCT AATTCCAGGATCAACAACAACAGTGCAGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1383

Single-Cell Antibody Cloning Primers A2		SEQ ID NO:
119G	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCGTTTGTCTCT AATTCCAGGATCAACAACAACCAGTACGGCACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1384
120P	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCGTTTGTCTCT AATTCCAGGATCAACAACAACCAGTACGGGAGCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1385
122K	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCGTTTGTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCGCAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1386

Single-Cell Antibody Cloning Primers A2		SEQ ID NO:
123T	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCT AATTCCAGGATCAACAACAACCAAGTACGGGACCATGCAAAGCA TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1387
125T	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCT AATTCCAGGATCAACAACAACCAAGTACGGGACCATGCAAACC TGCAGCAACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1388
126T	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCT AATTCCAGGATCAACAACAACCAAGTACGGGACCATGCAAACC TGCACGGCACCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1389

Single-Cell Antibody Cloning Primers A2		SEQ ID NO:
127P	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCGTTTGTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTGCAGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1390
129Q	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCGTTTGTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTGCAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1391
130G	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCGTTTGTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGCAAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1392

Single-Cell Antibody Cloning Primers A2		SEQ ID NO:
131N	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCT AATTCCAGGATCAACAACAACCAAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCGCATCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1393
132S	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCT AATTCCAGGATCAACAACAACCAAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACGCAATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1394
133M	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCT AATTCCAGGATCAACAACAACCAAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTGCATTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1395

Single-Cell Antibody Cloning Primers A2		SEQ ID NO:
134F	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGGCACCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1396
135P	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTGCATCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1397
136S	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCGCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1398

Single-Cell Antibody Cloning Primers A2		SEQ ID NO:
140T	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTGCAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1399
141K	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAGCACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1400
142P	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAAGCAACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1401

Single-Cell Antibody Cloning Primers A2		SEQ ID NO:
143T	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCTCT AATTCCAGGATCAACAACAACCAAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTGCAGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1402
144D	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCTCT AATTCCAGGATCAACAACAACCAAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGCAGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1403
145G	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCTCT AATTCCAGGATCAACAACAACCAAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGCAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1404

Single-Cell Antibody Cloning Primers A2		SEQ ID NO:
146N	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAGCATGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1405
148T	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCGCATGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1406
150I	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTGCACCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1407

Single-Cell Antibody Cloning Primers A2		SEQ ID NO:
151P	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCGTTTGTCCCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTGCAAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1408
152I	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCGTTTGTCCCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCGC ACCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1409
153P	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCGTTTGTCCCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CGCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1410

Single-Cell Antibody Cloning Primers A2		SEQ ID NO:
154S	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCAGCATCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1411
155S	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGGCATGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1412
156W	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCGCAGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1413

Single-Cell Antibody Cloning Primers A2		SEQ ID NO:
158F	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCGTTTGTCCCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTGCAGCAAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1414
160K	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCGTTTGTCCCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAGCATACTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1415
161Y	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCGTTTGTCCCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAAGCACTATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1416

Single-Cell Antibody Cloning Primers A2		SEQ ID NO:
162L	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACGCATGGGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1417
163W	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTAGCAGAGTGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1418
164E	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGCATGGGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1419

Single-Cell Antibody Cloning Primers A2		SEQ ID NO:
165W	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCGTTTGTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGGCAGCC TCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1420
167S	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCGTTTGTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC GCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1421
168V	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCGTTTGTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGCACGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1422

Single-Cell Antibody Cloning Primers A2		SEQ ID NO:
169R	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCGCATTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1423
170F	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTGCATCTTGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1424
171S	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCTTGTCTCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCGCATGGCTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1425

Single-Cell Antibody Cloning Primers A2		SEQ ID NO:
172W	5'- ACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGGA CTTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCA AAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTC CTCCAATTTGTCTGCTGTTATCGCTGGATGTGTCTGCGGCGTTT TATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTAT TGGTTCTTCTGGATTATCAAGGTATGTTGCCCCGTTTGTCCCTCT AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACC TGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT GCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCAT CCCATCGTCCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCC TCAGTCCGTTTCTCTGCACTCAGTTTACTAGTGCCATTTGTTT AGTGGTTCGTAGGG	1426
gBlock Synthesis for Germline Antibodies		
H006- HC_GL	5'- CTAGTAGCAACTGCAACCGGTGTACATTCTCAGGTGCAGCTGG TGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAG ACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGG TGGCAGTTATATCATATGATGGAAGTAATAAATACTATGCAG ACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAA GAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGAC ACGGCTGTGTATTACTGTGCGAAAGATGCTTATCTTTCTGCAG CGAGAGGATACGGTATGGACGTCTGGGGCCAAGGGACCACGGT CACCGTCTCCTCAGCGTCGACCAAGGGCCCATCGG	1427
H006- Lambda_GL	5'- CTAGTAGCAACTGCAACCGGTTCTGGGCCTCCTATGTGCTGA CTCAGCCACCCTCGGTGTCAGTGGCCCCAGGACAGACGGCCAG GATTACCTGTGGGGGAAACAACATTGGAAGTAAAAGTGTGCAC TGGTACCAGCAGAAGCCAGGCCAGGCCCTGTGCTGGTCTGTCT ATGATGATAGCGACCGGCCCTCAGGGATCCCTGAGCGATTCTC TGGCTCCAACCTCTGGGAACACGGCCACCCTGACCATCAGCAGG GTCGAAGCCGGGGATGAGGCCGACTATTACTGTCAGGTGTGGG ATAGTAGTAGTGATCATGTGGTATTTCGGCGGAGGGACCAAGCT GACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGT TCCCACCCTCGAGTGAGGAGCTTCAAGCC	1428

Single-Cell Antibody Cloning Primers A2		SEQ ID NO:
H019- HC_GL	5'- CTAGTAGCAACTGCAACCGGTGTACATTCTCAGGTGCAGCTGC AGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCCTGTC CCTCACCTGCACTGTCTCTGGTGGCTCCATCAGCAGTGGTGAT TACTACTGGAGTTGGATCCGCCAGCCCCAGGGAAGGGCCTGG AGTGGATTGGGTACATCTATTACAGTGGGAGCACCTACTACAA CCCGTCCCTCAAGAGTCGAGTTACCATATCAGTAGACACGTCC AAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGCCGCAG ACACGGCCGTGTATTACTGTGCCATCTACATGGATGAGGCCTG GGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCT TCAGCGTCGACCAAGGGCCCATCGG	1429
H019- Kappa_GL	5'- CTAGTAGCAACTGCAACCGGTGTACATTCTGACATCCAGATGA CCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTC ACCATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGAT CTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTT AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCA GTCTGCAACCTGAAGATTTTGCAACTTACTACTGTCAACAGAG TTACAGTATTTCTTATTCACTTTTGGCCAGGGGACCAAGCTG GAGATCAAACGTACGGTGGCTGCACCATCTGTCTTC	1430
H020- HC_GL	5'- CTAGTAGCAACTGCAACCGGTGTACATTCTCAGGTGCAGCTGC AGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTC CCTCACCTGCACTGTCTCTGGTGGCTCCATCAGTAGTTACTACT GGAGCTGGATCCGGCAGCCCCAGGGAAGGGACTGGAGTGGAT TGGGTATATCTATTACAGTGGGAGCACCAACTACAACCCCTCC CTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACC AGTTCTCCCTGAAGCTGAGCTCTGTGACCGCCGCAGACACGGC CGTGATTACTGTGCGAGACACCTTTATCGCTATGGTTATAGG AACTACTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCAGCGTCGACCAAGGGCCCATCGG	1431
H020- Kappa_GL	5'- CTAGTAGCAACTGCAACCGGTGTACATTCTGACATCCAGATGA CCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGT CACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTA GCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGA TCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT CAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGC AGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGG CTAACAGTTTCCCGCTCACTTTTCGGCGGAGGGACCAAGGTGGA GATCAAACGTACGGTGGCTGCACCATCTGTCTTC	1432
HBV TaqMan PCR		
F-sense	5'-CCGTCTGTGCCTTCTCATCTG	1433

Single-Cell Antibody Cloning Primers A2		SEQ ID NO:
R-anti-sense	5'-AGTCCAAGAGTCCTCTTATGTAAGACCTT	1434
Probe	5-/56 FAM/ CCGTGTGCA/ZEN/CTTCGCTTC ACCTCT GC/3IABkFQ/-3	1435
S-protein PCR		
F-S-protein	5'-CCCTGCGCTGAACATGGAGAACA	1436
R-S-protein	5'-AAATGTATACCCAAAGACAAAAGAAAA	1437

[0168] It will be recognized from the foregoing that the present disclosure describes screening individuals who were either vaccinated or had spontaneously recovered from HBV infection. Antibody cloning from memory B cells revealed that all 5 of the top individuals produced clones of broadly neutralizing antibodies (bNAbs) that targeted 3 non-overlapping epitopes on the HBV S antigen (HBsAg). Clones with the same immunoglobulin variable, diversity and joining heavy and light chain genes were shared among elite neutralizers. Single bNAbs protected humanized mice against infection, but selected for resistance mutations in mice with established infection. In contrast, infection was controlled in the absence of detectable escape mutations by a combination of bNAbs targeting non-overlapping epitopes with complementary sensitivity to mutations that commonly emerge during human infection. The co-crystal structure of one of the bNAbs with a peptide epitope containing residues frequently mutated in human immune escape variants revealed a loop anchored by oppositely charged residues. The structure provides a molecular explanation for why immunotherapy for chronic HBV infection may require combinations of complementary bNAbs, as described herein.

[0169] While the disclosure has been described through specific embodiments, routine modifications will be apparent to those skilled in the art and such modifications are intended to be within the scope of the present disclosure.