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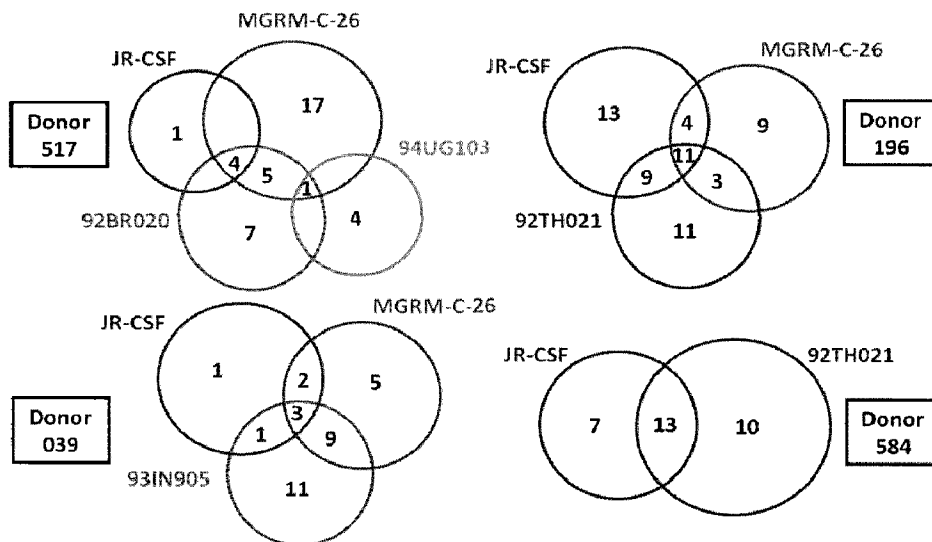
(72) Inventeurs/Inventors:
CHAN-HUI, PO-YING, US;
DOORES, KATHERINE, US;
HUBER, MICHAEL, CH;
...

(73) Propriétaires/Owners:
THERACLONE SCIENCES, INC., US;
THE SCRIPPS RESEARCH INSTITUTE, US;

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(54) Title: HUMAN IMMUNODEFICIENCY VIRUS (HIV)-NEUTRALIZING ANTIBODIES

Number of HIV-Neutralizing Hits Detected in Primary Screening



(57) Abrégé/Abstract:

The invention provides a method for obtaining a broadly neutralizing antibody (bNab), including screening memory B cell cultures from a donor PBMC sample for neutralization activity against a plurality of HIV-1 species, cloning a memory B cell that exhibits

(72) **Inventeurs(suite)/Inventors(continued)**: KAMINSKY, STEPHEN, US; FREY, STEVEN, US; OLSEN, OLE, US; MITCHAM, JENNIFER, US; MOYLE, MATTHEW, US; PHOGAT, SANJAY K., US; BURTON, DENNIS R., US; WALKER, LAURA MARJORIE, US; POIGNARD, PASCAL RAYMOND GEORGES, US; KOFF, WAYNE, US; SIMEK-LEMOIS, MELISSA DANIELLE DE JEAN DE ST. MARCEL, US

(73) **Propriétaires(suite)/Owners(continued)**: INTERNATIONAL AIDS VACCINE INITIATIVE, US

(74) **Agent**: MBM INTELLECTUAL PROPERTY LAW LLP

(57) **Abrégé(suite)/Abstract(continued)**:

broad neutralization activity; and rescuing a monoclonal antibody from that memory B cell culture. The resultant monoclonal antibodies may be characterized by their ability to selectively bind epitopes from the Env proteins in native or monomeric form, as well as to inhibit infection of HIV-1 species from a plurality of clades. Compositions containing human monoclonal anti-HIV antibodies used for prophylaxis, diagnosis and treatment of HIV infection are provided. Methods for generating such anti-bodies by immunization using epitopes from conserved regions within the variable loops of gp120 are provided. Immunogens for generating anti-HIV1 bNAbs are also provided. Furthermore, methods for vaccination using suitable epitopes are provided.

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- (71) **Applicants (for all designated States except US):** **THER-ACLONE SCIENCES, INC.** [US/US]; 1124 Columbia Street, Suite 300, Seattle, WA 98104 (US). **THE SCRIPPS RESEARCH INSTITUTE** [US/US]; 10550 North Torrey Pines Road, La Jolla, CA 92037 (US). **INTERNATIONAL AIDS VACCINE INITIATIVE** [US/US]; 125 Broad Street, 9th Floor, New York, NY 10004 (US).
- (72) **Inventors; and**
- (75) **Inventors/Applicants (for US only):** **CHAN-HUI, Po-ying** [US/US]; 2485 132nd Avenue Se, Bellevue, WA 98005 (US). **DOORES, Katherine** [GB/US]; 827 Agate Street, San Diego, CA 92109 (US). **HUBER, Michael**

[CH/CH]; Forchstrasse 50, CH-8008 Zurich (CH). **KAM-INSKY, Stephen** [US/US]; 5204 Delafield Avenue, Bronx, NY 10471 (US). **FREY, Steven** [US/US]; 7714 230th Avenue NE, Redmond, WA 98053 (US). **OLSEN, Ole** [CA/US]; 5309 117th Street SE, Everett, WA 98208 (US). **MITCHAM, Jennifer** [US/US]; 20330 NE 85th Street, Redmond, WA 98053 (US). **MOYLE, Matthew** [US/US]; 15737 NE 134th Street, Redmond, WA 98052 (US). **PHOGAT, Sanjay, K.** [IN/US]; 8027 Admiralty Place, Frederick, MD 21701 (US). **BURTON, Dennis, R.** [US/US]; 6044 Beaumont Avenue, La Jolla, CA 92037 (US). **WALKER, Laura, Marjorie** [US/US]; 4172 Carmino Ticino, San Diego, CA 92122 (US). **POIGNARD, Pascal Raymond, Georges** [FR/US]; 1435 Wilbur Avenue, San Diego, CA 92109 (US). **KOFF, Wayne** [US/US]; 7 Night Heron Drive, Stony Brook, NY 11790 (US). **SIMEK-LEMO, Melissa Danielle, De Jean De St. Marcel** [US/US]; 32 Woodhull Street, Apt. 1a, Brooklyn, NY 11231 (US).

(74) **Agents:** **KOWALSKI, Thomas, J.** et al.; Vedder Price P.C., 1633 Broadway, New York, NY 10019 (US).

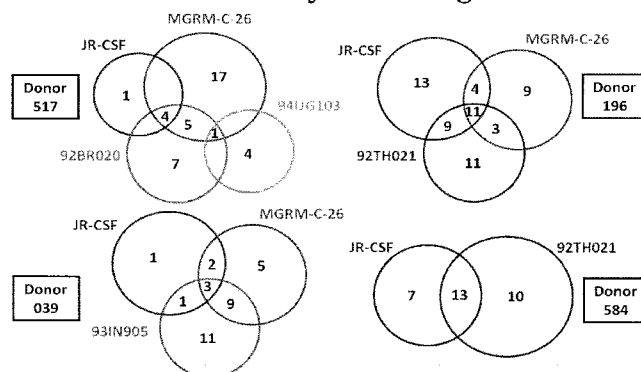
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[Continued on next page]

(54) **Title:** HUMAN IMMUNODEFICIENCY VIRUS (HIV)-NEUTRALIZING ANTIBODIES

FIGURE 22

Number of HIV-Neutralizing Hits Detected in Primary Screening



(57) **Abstract:** The invention provides a method for obtaining a broadly neutralizing antibody (bNab), including screening memory B cell cultures from a donor PBMC sample for neutralization activity against a plurality of HIV-1 species, cloning a memory B cell that exhibits broad neutralization activity; and rescuing a monoclonal antibody from that memory B cell culture. The resultant monoclonal antibodies may be characterized by their ability to selectively bind epitopes from the Env proteins in native or monomeric form, as well as to inhibit infection of HIV-1 species from a plurality of clades. Compositions containing human monoclonal anti-HIV antibodies used for prophylaxis, diagnosis and treatment of HIV infection are provided. Methods for generating such antibodies by immunization using epitopes from conserved regions within the variable loops of gp120 are provided. Immunogens for generating anti-HIV1 bNabs are also provided. Furthermore, methods for vaccination using suitable epitopes are provided.

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HUMAN IMMUNODEFICIENCY VIRUS (HIV)-NEUTRALIZING ANTIBODIES

[0001] DELETED

[0002] DELETED

FIELD OF THE INVENTION

[0003] The present invention relates generally to therapy, diagnosis and monitoring of human immunodeficiency virus (HIV) infection. The invention is more specifically related to human neutralizing monoclonal antibodies specific for HIV-1, such as broad and potent neutralizing monoclonal antibodies specific for HIV-1 and their manufacture and use. Broad neutralization suggests that the antibodies can neutralize HIV-1 isolates from different individuals. Such antibodies are useful in pharmaceutical compositions for the prevention and treatment of HIV, and for the diagnosis and monitoring of HIV infection and for design of HIV vaccine immunogens.

[0004] DELETED

BACKGROUND OF THE INVENTION

[0005] AIDS was first reported in the United States in 1981 and has since become a major worldwide epidemic. AIDS is caused by the human immunodeficiency virus, or HIV. By killing or damaging cells of the body's immune system, HIV progressively destroys the body's ability to fight infections and certain cancers. People diagnosed with AIDS may get life-threatening diseases called opportunistic infections. These infections are caused by microbes such as viruses or bacteria that usually do not make healthy people sick. HIV is spread most often through unprotected sex with an infected partner. HIV also is spread through contact with infected blood. The human immunodeficiency virus (HIV) is the cause of acquired immune deficiency syndrome (AIDS) (Barre-Sinoussi, F., et al., 1983, Science 220:868-870; Gallo, R., et al., 1984, Science 224:500-503). There are currently 1.25 million people in the US infected with HIV-induced acquired immunodeficiency syndrome according to a Center for Disease Control report. The epidemic is growing most rapidly among minority populations and is a leading killer of African-American males ages 25 to 44. According, AIDS affects nearly seven times more African Americans and three times more Hispanics than whites. In recent years, an increasing number of African-American women and children are being affected by HIV/AIDS. With over 40 million people infected worldwide, the current global HIV pandemic ranks among the greatest infectious disease scourges in human history.

[0006] There is therefore a need for the efficient identification and production of neutralizing antibodies effective against multiple clades and strains of HIV as well as the elucidation of the target and antigenic determinants to which such antibodies bind.

[0007] Citation or identification of any document in this application is not an admission that such document is available as prior art to the present invention.

SUMMARY OF THE INVENTION

[0008] The present invention provides a novel method for isolating potent, broadly neutralizing monoclonal antibodies against HIV. Peripheral Blood Mononuclear Cells (PBMCs) are obtained from an HIV-infected donor selected for HIV-1 neutralizing activity in the plasma, and memory B cells are isolated for culture in vitro. The B cell culture supernatants may then be screened by a primary neutralization assay in a high throughput format, and B cell cultures exhibiting neutralizing activity may be selected for rescue of monoclonal antibodies. It is

surprisingly observed that neutralizing antibodies obtained by this method do not always exhibit gp120 or gp41 binding at levels that correlate with neutralization activity. The method of the invention therefore allows identification of novel antibodies with cross-clade neutralization properties.

[0009] The present invention provides human monoclonal antibodies specifically directed against HIV. In certain embodiments, the invention provides human anti-HIV monoclonal antibodies including, but not limited to, 1443_C16 (PG16) (TCN-116), 1503 H05 (PG16) (TCN-119), 1456 A12 (PG16) (TCN-117), 1469 M23 (PG16) (TCN-118), 1489_I13 (PG16) (TCN-120), 1480_I08 (PG16), 1456_P20 (PG20), 1460_G14 (PGG14), 1495_C14 (PGC14), 1496_C09 (PG9) (TCN-109), 4838_L06 (PGT-121), 4873_E03 (PGT-121), 4877_D15 (PGT-122), 4858_P08 (PGT-123), 6123_A06 (PGT-125), 5141_B17 (PGT-126), 5145_B14 (PGT-127), 5114_A19 (PGT-128), 5147_N06 (PGT-130), 5136_H01 (PGT-131), 5343_B08 (PGT-135), 5344_E16 (PGT-135), 5329_C19 (PGT-136), 5366_P21 (PGT-136), 4964_G22 (PGT-141), 5345_I01 (PGT-137), 4993_K13 (PGT-141), 4995_E20 (PGT-142), 4980_N08 (PGT-143), 4970_K22 (PGT-144), 4995_P16 (PGT-145), 4835_F12 (PGT-124), 4869_K15 (PGT-133), 4876_M06 (PGT-134), 5131_A17 (PGT-132), 5138_G07 (PGT-138), 5120_N10 (PGT-139), 6831_A21 (PGT-151), 6889_I17 (PGT-152), 6891_F06 (PGT-153), 6843_G20 (PGT-154), 6892_D19 (PGT-155), 6808_B09 (PGT-156), 6892_C23 (PGT-157), and 6881_N05 (PGT-158) and sister clones thereof. For instance, an exemplary sister clone of the 1443_C16 (PG16) (TCN-116) antibody is the 1503 H05 (PG16) (TCN-119) antibody, the 1456 A12 (PG16) (TCN-117) antibody, the 1469 M23 (PG16) (TCN-118) antibody, the 1489_I13 (PG16) (TCN-120) antibody, or the 1480_I08 (PG16) antibody.

[0010] Specifically, the invention provides an isolated anti-HIV antibody, wherein said antibody may have heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of KYGMH (SEQ ID NO: 88), LISDDGMRKYHSDSMWG (SEQ ID NO: 89), and EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of NGTSSDVGGFDSVS (SEQ ID NO: 97), DVSHRPS (SEQ ID NO: 95), and SSLTDRSHRI (SEQ ID NO: 41).

[0011] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of GFTFHK (SEQ ID NO: 266), LISDDGMRKY (SEQ ID NO: 267), and EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of NGTSSDVGGFDSVS (SEQ ID NO: 97), DVSHRPS (SEQ ID NO: 95), and SSLTDRSHRI (SEQ ID NO: 41).

[0012] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of KYGMH (SEQ ID NO: 88), LISDDGMRKYHSDSMWG (SEQ ID NO: 89), and EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of NGTRSDVGGFDSVS (SEQ ID NO: 92), DVSHRPS (SEQ ID NO: 95), and SSLTDRSHRI (SEQ ID NO: 41).

[0013] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of GFTFHK (SEQ ID NO: 266), LISDDGMRKY (SEQ ID NO: 267), and EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of NGTRSDVGGFDSVS (SEQ ID NO: 92), DVSHRPS (SEQ ID NO: 95), and SSLTDRSHRI (SEQ ID NO: 41).

[0014] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of KYGMH (SEQ ID NO: 88), LISDDGMRKYHSDSMWG (SEQ ID NO: 89), and EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of NGTSRDVGGFDSVS (SEQ ID NO: 93), DVSHRPS (SEQ ID NO: 95), and SSLTDRSHRI (SEQ ID NO: 41).

[0015] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of GFTFHK (SEQ ID NO: 266), LISDDGMRKY (SEQ ID NO: 267), and EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of NGTSRDVGGFDSVS (SEQ ID NO: 93), DVSHRPS (SEQ ID NO: 95), and SSLTDRSHRI (SEQ ID NO: 41).

[0016] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of KYGMH (SEQ ID NO: 88), LISDDGMRKYHSNSMWG (SEQ ID NO: 98), and EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of NGTSSDVGGFDSVS (SEQ ID NO: 97), DVSHRPS (SEQ ID NO: 95), and SSLTDRSHRI (SEQ ID NO: 41).

[0017] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of SYAFT (SEQ ID NO: 104), MVTPIFGAEKYSQRFEG (SEQ ID NO: 105), and DRRAVPIATDNWLDP (SEQ ID NO: 9), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of RASQTINNYLN (SEQ ID NO: 107), GASNLQN (SEQ ID NO: 108), and QQSFSPTPT (SEQ ID NO: 42).

[0018] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of GGTFSS (SEQ ID NO: 268), MVTPIFGAEK (SEQ ID NO: 269), and DRRAVPIATDNWLDP (SEQ ID NO: 9), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of RASQTINNYLN (SEQ ID NO: 107), GASNLQN (SEQ ID NO: 108), and QQSFSPTPT (SEQ ID NO: 42).

[0019] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from

the group consisting of the amino acid sequences of SYAFS (SEQ ID NO: 110), MITPVFGETKYAPRFQG (SEQ ID NO: 111), and DRRVVPMTADNWLDP (SEQ ID NO: 8), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of RASQTIHTYLN (SEQ ID NO: 113), GASTLQS (SEQ ID NO: 114), and QQSYSTPRT (SEQ ID NO: 43).

[0020] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of GGAFSS (SEQ ID NO: 270), MITPVFGETK (SEQ ID NO: 271), DRRVVPMTADNWLDP (SEQ ID NO: 8), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of RASQTIHTYLN (SEQ ID NO: 113), GASTLQS (SEQ ID NO: 114), and QQSYSTPRT (SEQ ID NO: 43).

[0021] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of DYYLH (SEQ ID NO: 116), LIDPENGEARYAEKFQG (SEQ ID NO: 117), GAVGADSGSWFDP (SEQ ID NO: 10), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of SGSKLGDKYVS (SEQ ID NO: 120), ENDRRPS (SEQ ID NO: 121), QAWETTTTTFVF (SEQ ID NO: 44).

[0022] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of GYSFID (SEQ ID NO: 102), LIDPENGEAR (SEQ ID NO: 103), GAVGADSGSWFDP (SEQ ID NO: 10), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of SGSKLGDKYVS (SEQ ID NO: 120), ENDRRPS (SEQ ID NO: 121), QAWETTTTTFVF (SEQ ID NO: 44).

[0023] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of RQGMH (SEQ ID NO: 123), FIKYDGSEKYHADSVWG (SEQ ID NO: 124), and EAGGPDYRNGYNYDFYDGYNYHYMDV (SEQ ID NO: 7), and a light chain with three

CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of NGTSNDVGGYESVS (SEQ ID NO: 126), DVSKRPS (SEQ ID NO: 127), and KSLTSTRRRV (SEQ ID NO: 45).

[0024] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of GFDFSR (SEQ ID NO: 118), FIKYDGSEKY (SEQ ID NO: 272), and EAGGPDYRNGYNYDFYDGYNYHYMDV (SEQ ID NO: 7), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of NGTSNDVGGYESVS (SEQ ID NO: 126), DVSKRPS (SEQ ID NO: 127), and KSLTSTRRRV (SEQ ID NO: 45).

[0025] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs including an amino acid sequence selected from the group consisting of the amino acid sequences of DSYWS (SEQ ID NO: 90), YVHKSGDTNYSPLKS (SEQ ID NO: 265), TLHGRRYIGIVAFNEWFTYFYMDV (SEQ ID NO: 143), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of GEKSLGSRAVQ (SEQ ID NO: 150), NNQDRPS (SEQ ID NO: 151), HIWDSRVPTKWV (SEQ ID NO: 152).

[0026] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs including an amino acid sequence selected from the group consisting of the amino acid sequences of GASISD (SEQ ID NO: 144), YVHKSGDTN (SEQ ID NO: 145), TLHGRRYIGIVAFNEWFTYFYMDV (SEQ ID NO: 143), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of GEKSLGSRAVQ (SEQ ID NO: 150), NNQDRPS (SEQ ID NO: 151), HIWDSRVPTKWV (SEQ ID NO: 152).

[0027] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs including an amino acid sequence selected from the group consisting of the amino acid sequences of DNYWS (SEQ ID NO: 261), YVHDSGDTNYSPLKS (SEQ ID NO: 157), and TKHGRRYIGVAVFKEWFTYFYMDV (SEQ ID NO: 262), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of GEESLGSRSVI (SEQ ID NO: 162), NNNDRPS (SEQ ID NO: 163), and HIWDSRRPTNWV (SEQ ID NO: 164).

[0028] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs including an amino acid sequence selected from the group consisting of the amino acid sequences of GTLVRD (SEQ ID NO: 263), YVHDSGDTN (SEQ ID NO: 264), and TKHGRRYGVVAFKEWFTYFYMDV (SEQ ID NO: 262), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of GEESLGSRSVI (SEQ ID NO: 162), NNDRPS (SEQ ID NO: 163), and HIWDSRRPTNWV (SEQ ID NO: 164).

[0029] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs including an amino acid sequence selected from the group consisting of the amino acid sequences of DAYWS (SEQ ID NO: 169), YVHHSAGDTNYPNPSLKR (SEQ ID NO: 170), and ALHGKRIYGIVALGELFTYFYMDV (SEQ ID NO: 171), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of GKESIGSRAVQ (SEQ ID NO: 178), NNQDRPA (SEQ ID NO: 179), and HIYDARGGTNWV (SEQ ID NO: 180).

[0030] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs including an amino acid sequence selected from the group consisting of the amino acid sequences of GASIND (SEQ ID NO: 172), YVHHSAGDTN (SEQ ID NO: 173), and ALHGKRIYGIVALGELFTYFYMDV (SEQ ID NO: 171), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of GKESIGSRAVQ (SEQ ID NO: 178), NNQDRPA (SEQ ID NO: 179), and HIYDARGGTNWV (SEQ ID NO: 180).

[0031] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs including an amino acid sequence selected from the group consisting of the amino acid sequences of ACTYFWG (SEQ ID NO: 185), SLSHCQSFWSGSGWTFHNPSLKS (SEQ ID NO: 186), and FDGEVLVYNHWPKPAWVDL (SEQ ID NO: 187), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of NGTATNFVS (SEQ ID NO: 194), GVDKRPP (SEQ ID NO: 195), and GSLVGNWDVI (SEQ ID NO: 196).

[0032] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs including an amino acid sequence selected from the group consisting of the amino acid sequences of GESTGACT (SEQ ID NO: 188),

SLSHCQSFWGSGWTF (SEQ ID NO: 189), and FDGEVLVYNHWPKPAWVDL (SEQ ID NO: 187), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of NGTATNFVS (SEQ ID NO: 194), GVDKRPP (SEQ ID NO: 195), and GSLVGNWDVI (SEQ ID NO: 196).

[0033] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs including an amino acid sequence selected from the group consisting of the amino acid sequences of ACDYFWG (SEQ ID NO: 201), GLSHCAGYYNTGWTYHNPSLKS (SEQ ID NO: 202), and FDGEVLVYHDWPKPAWVDL (SEQ ID NO: 203), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of TGTSNRFVS (SEQ ID NO: 210), GVNKRPS (SEQ ID NO: 211), and SSLVGNWDVI (SEQ ID NO: 212).

[0034] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs including an amino acid sequence selected from the group consisting of the amino acid sequences of GDSTAACD (SEQ ID NO: 204), GLSHCAGYYNTGWTY (SEQ ID NO: 205), and FDGEVLVYHDWPKPAWVDL (SEQ ID NO: 203), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of TGTSNRFVS (SEQ ID NO: 210), GVNKRPS (SEQ ID NO: 211), and SSLVGNWDVI (SEQ ID NO: 212).

[0035] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs including an amino acid sequence selected from the group consisting of the amino acid sequences of TGHYYWG (SEQ ID NO: 217), HIHYTTAVLHNPSLKS (SEQ ID NO: 218), and SGGDILYYYEWQKPHWFSP (SEQ ID NO: 219), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of NGTSSDIGGWNFVS (SEQ ID NO: 226), EVNKRPS (SEQ ID NO: 227), and SSLFGRWDVV (SEQ ID NO: 228).

[0036] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs including an amino acid sequence selected from the group consisting of the amino acid sequences of GESINTGH (SEQ ID NO: 220), HIHYTTAVL (SEQ ID NO: 221), and SGGDILYYYEWQKPHWFSP (SEQ ID NO: 219), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino

acid sequences of NGTSSDIGGWNFVS (SEQ ID NO: 226), EVNKRPS (SEQ ID NO: 227), and SSLFGRWDVV (SEQ ID NO: 228).

[0037] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs including an amino acid sequence selected from the group consisting of the amino acid sequences of GGEWGD KDYHWG (SEQ ID NO: 233), SIHWRGTTTHYKESLRR (SEQ ID NO: 234), and HRHHDVFMLVPIAGWFDV (SEQ ID NO: 235), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of RASQNINKNLA (SEQ ID NO: 243), ETYSKIA (SEQ ID NO: 244), and QQYEEWPRT (SEQ ID NO: 245).

[0038] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs including an amino acid sequence selected from the group consisting of the amino acid sequences of GDSIRGGEWGD KD (SEQ ID NO: 236), SIHWRGTTTH (SEQ ID NO: 237), and HRHHDVFMLVPIAGWFDV (SEQ ID NO: 235), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of RASQNINKNLA (SEQ ID NO: 243), ETYSKIA (SEQ ID NO: 244), and QQYEEWPRT (SEQ ID NO: 245).

[0039] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs including an amino acid sequence selected from the group consisting of the amino acid sequences of GTDWGENDFHYG (SEQ ID NO: 250), SIHWRGRTTHYKTSFRS (SEQ ID NO: 251), HKYHDIFRVVPVAGWFDP (SEQ ID NO: 252), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of RASQNVKNNLA (SEQ ID NO: 259), DASSRAG (SEQ ID NO: 260), QQYEEWPRT (SEQ ID NO: 245).

[0040] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs including an amino acid sequence selected from the group consisting of the amino acid sequences of GGSMRGTDWGEND (SEQ ID NO: 253), SIHWRGRTTH (SEQ ID NO: 254), HKYHDIFRVVPVAGWFDP (SEQ ID NO: 252), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of RASQNVKNNLA (SEQ ID NO: 259), DASSRAG (SEQ ID NO: 260), QQYEEWPRT (SEQ ID NO: 245).

[0041] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of KYDVH (SEQ ID NO: 277), WMSHEGDKTESAQRFKG (SEQ ID NO: 278), and GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (SEQ ID NO: 279), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of SSTQSLRHSNGANYLA (SEQ ID NO: 286), LGSQRAS (SEQ ID NO: 287), and MQGLNRPWT (SEQ ID NO: 288).

[0042] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of GNTFSK (SEQ ID NO: 280), WMSHEGDKTE (SEQ ID NO: 281), GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (SEQ ID NO: 279), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of SSTQSLRHSNGANYLA (SEQ ID NO: 286), LGSQRAS (SEQ ID NO: 287), and MQGLNRPWT (SEQ ID NO: 288).

[0043] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of KYDVH (SEQ ID NO: 277), WISHERDKTESAQRFKG (SEQ ID NO: 293), GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (SEQ ID NO: 279), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of SSTQSLRHSNGANYLA (SEQ ID NO: 286), LGSQRAS (SEQ ID NO: 287), and MQGLNRPWT (SEQ ID NO: 288).

[0044] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of GNTFSK (SEQ ID NO: 280), WISHERDKTE (SEQ ID NO: 294), GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (SEQ ID NO: 279), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of SSTQSLRHSNGANYLA (SEQ ID NO: 286), LGSQRAS (SEQ ID NO: 287), and MQGLNRPWT (SEQ ID NO: 288).

[0045] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of KYDVH (SEQ ID NO: 277), WMSHEGDKTESAQRFKG (SEQ ID NO: 278), and GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (SEQ ID NO: 279), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of TSTQSLRHSNGANYLA (SEQ ID NO: 303), LGSQRAS (SEQ ID NO: 287), and MQGLNRPWT (SEQ ID NO: 288).

[0046] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of GNTFSK (SEQ ID NO: 280), WMSHEGDKTE (SEQ ID NO: 281), GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (SEQ ID NO: 279), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of TSTQSLRHSNGANYLA (SEQ ID NO: 303), LGSQRAS (SEQ ID NO: 287), and MQGLNRPWT (SEQ ID NO: 288).

[0047] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of KYDVH (SEQ ID NO: 277), WMSHEGDKTESAQRFKG (SEQ ID NO: 278), GSKHRLRDYVLYDDYGLINQQEWNDYLEFLDV (SEQ ID NO: 308), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of TSTQSLRHSNGANYLA (SEQ ID NO: 303), LGSQRAS (SEQ ID NO: 287), and MQGLNRPWT (SEQ ID NO: 288).

[0048] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of GNTFRK (SEQ ID NO: 309), WMSHEGDKTE (SEQ ID NO: 281), and GSKHRLRDYVLYDDYGLINQQEWNDYLEFLDV (SEQ ID NO: 308), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of TSTQSLRHSNGANYLA (SEQ ID NO: 303), LGSQRAS (SEQ ID NO: 287), and MQGLNRPWT (SEQ ID NO: 288).

[0049] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of RCNYFWG (SEQ ID NO: 320), SLSHCRSYYNTDWTYHNPSLKS (SEQ ID NO: 321), and FGGEVLVYRDWPKPAWVDL (SEQ ID NO: 322), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of TGTSNNFVS (SEQ ID NO: 325), EVNKRPS (SEQ ID NO: 227), and SSLVGNWDVI (SEQ ID NO: 212).

[0050] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of GDSTGRCN (SEQ ID NO: 323), SLSHCRSYYNTDWTY (SEQ ID NO: 324), and FGGEVLVYRDWPKPAWVDL (SEQ ID NO: 322), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of TGTSNNFVS (SEQ ID NO: 325), EVNKRPS (SEQ ID NO: 227), and SSLVGNWDVI (SEQ ID NO: 212).

[0051] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of ACNSFWG (SEQ ID NO: 326), SLSHCASYWNRGWTYHNPSLKS (SEQ ID NO: 335), and FGGEVLRYTDWPKPAWVDL (SEQ ID NO: 336), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of TGTSNNFVS (SEQ ID NO: 325), (SEQ ID NO: 343), and (SEQ ID NO: 196).

[0052] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of GDSTAACN (SEQ ID NO: 337), SLSHCASYWNRGWTY (SEQ ID NO: 338), and FGGEVLRYTDWPKPAWVDL (SEQ ID NO: 336), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of TGTSNNFVS (SEQ ID NO: 325), DVNKRPS (SEQ ID NO: 343), and GSLVGNWDVI (SEQ ID NO: 196).

[0053] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of TGHHYWG (SEQ ID NO: 348),

HHYNTAVLHNPALKS (SEQ ID NO: 349), and SGGDILYYIEWQKPHWFYP (SEQ ID NO: 350), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of SGTGSDIGSWNFVS (SEQ ID NO: 357), EVNRRRS (SEQ ID NO: 358), and SSLSGRWDIV (SEQ ID NO: 359).

[0054] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of GDSINTGH (SEQ ID NO: 351), HHYNTAVL (SEQ ID NO: 352), and SGGDILYYIEWQKPHWFYP (SEQ ID NO: 350), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of SGTGSDIGSWNFVS (SEQ ID NO: 357), EVNRRRS (SEQ ID NO: 358), and SSLSGRWDIV (SEQ ID NO: 359).

[0055] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of GGEWGDSYHWG (SEQ ID NO: 364), SIHWRGTTTHYNAPFRG (SEQ ID NO: 365), and HKYHDIVMVVPIAGWFDP (SEQ ID NO: 366), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of RASQSVKNNLA (SEQ ID NO: 372), DTSSRAS (SEQ ID NO: 373), and QQYEEWPRT (SEQ ID NO: 245).

[0056] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of GGSIRGGEWGDS (SEQ ID NO: 367), SIHWRGTTTH (SEQ ID NO: 237), and HKYHDIVMVVPIAGWFDP (SEQ ID NO: 366), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of RASQSVKNNLA (SEQ ID NO: 372), DTSSRAS (SEQ ID NO: 373), and QQYEEWPRT (SEQ ID NO: 245).

[0057] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of NHDVH (SEQ ID NO: 378), WMSHEGDKTGLAQKFQG (SEQ ID NO: 379), and GSKHRLRDYFLYNEYGPNYEEWGDYLATLDV (SEQ ID NO: 380), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino

acid sequences of KCSHSLQHSTGANYLA (SEQ ID NO: 387), LATHRAS (SEQ ID NO: 388), and MQGLHSPWT (SEQ ID NO: 389).

[0058] The invention provides an isolated anti-HIV antibody, wherein said antibody may have a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of GNSFSN (SEQ ID NO: 381), WMSHEGDKTG (SEQ ID NO: 382), and GSKHRLRDYFLYNEYGPNYEEWGDYLATLDV (SEQ ID NO: 380), and a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of KCSHSLQHSTGANYLA (SEQ ID NO: 387), LATHRAS (SEQ ID NO: 388), and MQGLHSPWT (SEQ ID NO: 389).

[0059] The invention provides an isolated anti-HIV antibody, wherein said antibody may comprise a V_H CDR1 region which may comprise the amino acid sequence of NYWT (SEQ ID NO: 406); a V_H CDR2 region which may comprise the amino acid sequence of YISDRETTTYNPSLNS (SEQ ID NO: 407); a V_H CDR3 region which may comprise the amino acid sequence of ARRQRIYGVVSFGEFFYYYYMDV (SEQ ID NO: 408); a V_L CDR1 region which may comprise the amino acid sequence of GRQALGSRAVQ (SEQ ID NO: 415); a V_L CDR2 region which may comprise the amino acid sequence of NNQDRPS (SEQ ID NO: 151); and a V_L CDR3 region which may comprise the amino acid sequence of HMWDSRSGFSWS (SEQ ID NO: 416).

[0060] The invention provides an isolated anti-HIV antibody, wherein said antibody may comprise a V_H CDR1 region which may comprise the amino acid sequence of GRFWS (SEQ ID NO: 421); a V_H CDR2 region which may comprise the amino acid sequence of YFSDTDRSEYNPSLRS (SEQ ID NO: 422); a V_H CDR3 region which may comprise the amino acid sequence of AQQGKRIYGIVSFGEFFYYYYMDA (SEQ ID NO: 423); a V_L CDR1 region which may comprise the amino acid sequence of GERSRGSRAVQ (SEQ ID NO: 430); a V_L CDR2 region which may comprise the amino acid sequence of NNQDRPA (SEQ ID NO: 179); and a V_L CDR3 region which may comprise the amino acid sequence of HYWDSRSPISWI (SEQ ID NO: 431).

[0061] The invention provides an isolated anti-HIV antibody, wherein said antibody may comprise a V_H CDR1 region which may comprise the amino acid sequence of GRFWS (SEQ ID NO: 421); a V_H CDR2 region which may comprise the amino acid sequence of YFSDTDRSEYNPSLRS (SEQ ID NO: 422); a V_H CDR3 region which may comprise the amino

acid sequence of AQQGKRIYGIVSFGELFYYYMDA (SEQ ID NO: 436); a V_L CDR1 region which may comprise the amino acid sequence of GERSRGSRAVQ (SEQ ID NO: 430); a V_L CDR2 region which may comprise the amino acid sequence of NNQDRPA (SEQ ID NO: 179); and a V_L CDR3 region which may comprise the amino acid sequence of HYWDSRSPISWI (SEQ ID NO: 431).

[0062] The invention provides an isolated anti-HIV antibody, wherein said antibody may comprise a V_H CDR1 region which may comprise the amino acid sequence of TGHHYWG (SEQ ID NO: 348); a V_H CDR2 region which may comprise the amino acid sequence of HIIHNTAVLHNPAKLS (SEQ ID NO: 349); a V_H CDR3 region which may comprise the amino acid sequence of SGGDILYYNEWQKPHWFYP (SEQ ID NO: 445); a V_L CDR1 region which may comprise the amino acid sequence of SGTASDIGSWNFVS (SEQ ID NO: 450); a V_L CDR2 region which may comprise the amino acid sequence of EVNRRRS (SEQ ID NO: 358); and a V_L CDR3 region which may comprise the amino acid sequence of SSLSGRWDIV (SEQ ID NO: 359).

[0063] The invention provides an isolated anti-HIV antibody, wherein said antibody may comprise a V_H CDR1 region which may comprise the amino acid sequence of ACDYFWG (SEQ ID NO: 201); a V_H CDR2 region which may comprise the amino acid sequence of SLSHCAGYYNSGWTYHNPSLKS (SEQ ID NO: 455); a V_H CDR3 region which may comprise the amino acid sequence of FGGDVLVYHDWPKPAWVDL (SEQ ID NO: 456); a V_L CDR1 region which may comprise the amino acid sequence of TGNINNFVS (SEQ ID NO: 458); a V_L CDR2 region which may comprise the amino acid sequence of GVNKRPS (SEQ ID NO: 211); and a V_L CDR3 region which may comprise the amino acid sequence of GSLAGNWDVV (SEQ ID NO: 459).

[0064] The invention provides an isolated anti-HIV antibody, wherein said antibody may comprise a V_H CDR1 region which may comprise the amino acid sequence of GCDYFWG (SEQ ID NO: 464); a V_H CDR2 region which may comprise the amino acid sequence of GLSHCAGYYNTGWTYHNPSLKS (SEQ ID NO: 202); a V_H CDR3 region which may comprise the amino acid sequence of FDGEVLVYNDWPKPAWVDL (SEQ ID NO: 465); a V_L CDR1 region which may comprise the amino acid sequence of TGTSNNFVS (SEQ ID NO: 325); a V_L CDR2 region which may comprise the amino acid sequence of GVNKRPS (SEQ ID

NO: 211); and a V_L CDR3 region which may comprise the amino acid sequence of GSLVGNWDVI (SEQ ID NO: 196).

[0065] The invention provides an isolated anti-HIV antibody, wherein said antibody may comprise a V_H CDR1 region which may comprise the amino acid sequence of KYPMY (SEQ ID NO: 475); a V_H CDR2 region which may comprise the amino acid sequence of AISGDAWHVVYSNSVQG (SEQ ID NO: 476); a V_H CDR3 region which may comprise the amino acid sequence of MFQESGPPRLDRWSGRNYYYYSGMDV (SEQ ID NO: 477); a V_L CDR1 region which may comprise the amino acid sequence of KSSESRLRQSNGKTSLY (SEQ ID NO: 484); a V_L CDR2 region which may comprise the amino acid sequence of EVSNRFS (SEQ ID NO: 485); and a V_L CDR3 region which may comprise the amino acid sequence of MQSKDFPLT (SEQ ID NO: 486).

[0066] The invention provides an isolated anti-HIV antibody, wherein said antibody may comprise a V_H CDR1 region which may comprise the amino acid sequence of KYPMY (SEQ ID NO: 475); a V_H CDR2 region which may comprise the amino acid sequence of AISADAWHVVYSGSVQG (SEQ ID NO: 491); a V_H CDR3 region which may comprise the amino acid sequence of MFQESGPPRFDSWSGRNYYYYSGMDV (SEQ ID NO: 492); a V_L CDR1 region which may comprise the amino acid sequence of KSSQSLRQSNGKTSLY (SEQ ID NO: 498); a V_L CDR2 region which may comprise the amino acid sequence of EVSNRFS (SEQ ID NO: 485); and a V_L CDR3 region which may comprise the amino acid sequence of (MQSKDFPLT (SEQ ID NO: 486).

[0067] The invention provides an isolated anti-HIV antibody, wherein said antibody may comprise a V_H CDR1 region which may comprise the amino acid sequence of KRHMH (SEQ ID NO: 503); a V_H CDR2 region which may comprise the amino acid sequence of VISSDAIHVDYASSVRG (SEQ ID NO: 504); a V_H CDR3 region which may comprise the amino acid sequence of DRDGYGPPQIQTWSGRYLHLYSGIDA (SEQ ID NO: 505); a V_L CDR1 region which may comprise the amino acid sequence of KSSQSLRQSNGKTYLY (SEQ ID NO: 512); a V_L CDR2 region which may comprise the amino acid sequence of EVSIRFS (SEQ ID NO: 513); and a V_L CDR3 region which may comprise the amino acid sequence of MQSKDFPLT (SEQ ID NO: 486).

[0068] The invention provides an isolated anti-HIV antibody, wherein said antibody may comprise a V_H CDR1 region which may comprise the amino acid sequence of KYPMY (SEQ ID

NO: 475); a V_H CDR2 region which may comprise the amino acid sequence of AISADAWHVDYAASVKD (SEQ ID NO: 518); a V_H CDR3 region which may comprise the amino acid sequence of NIEEFSVPQFDSWSGRSYYHYFGMDV (SEQ ID NO: 519); a V_L CDR1 region which may comprise the amino acid sequence of SSSESLGRGDGRTYLH (SEQ ID NO: 526); a V_L CDR2 region which may comprise the amino acid sequence of EVSTRFS (SEQ ID NO: 527); and a V_L CDR3 region which may comprise the amino acid sequence of MQSRDFPIT (SEQ ID NO: 528).

[0069] The invention provides an isolated anti-HIV antibody, wherein said antibody may comprise a V_H CDR1 region which may comprise the amino acid sequence of EYPMY (SEQ ID NO: 533); a V_H CDR2 region which may comprise the amino acid sequence of AISADAWHVDYAGSVRG (SEQ ID NO: 534); a V_H CDR3 region which may comprise the amino acid sequence of DGEEHKVPQLHSWSGRNLYHYTGFDV (SEQ ID NO: 535); a V_L CDR1 region which may comprise the amino acid sequence of KSSQSVRQSDGKTFLY (SEQ ID NO: 541); a V_L CDR2 region which may comprise the amino acid sequence of EGSSRFS (SEQ ID NO: 542); and a V_L CDR3 region which may comprise the amino acid sequence of LQTKDFPLT (SEQ ID NO: 543).

[0070] The invention provides an isolated anti-HIV antibody, wherein said antibody may comprise a V_H CDR1 region which may comprise the amino acid sequence of QYPMY (SEQ ID NO: 548); a V_H CDR2 region which may comprise the amino acid sequence of AISADAWHVDYPGSVRG (SEQ ID NO: 549); a V_H CDR3 region which may comprise the amino acid sequence of DGEEHKVPQLHSWSGRNLYHYTGFDV (SEQ ID NO: 535); a V_L CDR1 region which may comprise the amino acid sequence of KSSQTVRQSDGKTFLY (SEQ ID NO: 555); a V_L CDR2 region which may comprise the amino acid sequence of EGSNRFS (SEQ ID NO: 556); and a V_L CDR3 region which may comprise the amino acid sequence of LQTKDFPLT (SEQ ID NO: 543).

[0071] The invention provides an isolated anti-HIV antibody, wherein said antibody may comprise a V_H CDR1 region which may comprise the amino acid sequence of QYPMY (SEQ ID NO: 548); a V_H CDR2 region which may comprise the amino acid sequence of AISADAWHVDYAGSVRG (SEQ ID NO: 534); a V_H CDR3 region which may comprise the amino acid sequence of DGEEHEVPQLHSWSGRNLYHYTGVDI (SEQ ID NO: 561); a V_L CDR1 region which may comprise the amino acid sequence of KSSQSLRQSDGKTFLY (SEQ

ID NO: 567); a V_L CDR2 region which may comprise the amino acid sequence of EASNRF (SEQ ID NO: 568); and a V_L CDR3 region which may comprise the amino acid sequence of MQTKDFPLT (SEQ ID NO: 569).

[0072] The invention provides an isolated anti-HIV antibody, wherein said antibody may comprise a V_H CDR1 region which may comprise the amino acid sequence of KYPMY (SEQ ID NO: 475); a V_H CDR2 region which may comprise the amino acid sequence of AISADAWHVDYPGSVRG (SEQ ID NO: 549); a V_H CDR3 region which may comprise the amino acid sequence of DGEEHEVPQLHSWSGRNLYHYTGVDV (SEQ ID NO: 574); a V_L CDR1 region which may comprise the amino acid sequence of KSSQSVRQSDGKTFLY (SEQ ID NO: 541); a V_L CDR2 region which may comprise the amino acid sequence of EASKRFS (SEQ ID NO: 580); and a V_L CDR3 region which may comprise the amino acid sequence of MQTKDFPLT (SEQ ID NO: 569).

[0073] The invention also provides an isolated anti-HIV antibody, wherein said antibody has a heavy chain with three CDRs including an amino acid sequence selected from the group consisting of the amino acid sequences of KYGMH (SEQ ID NO: 88), LISDDGMRKYHSDSMWG (SEQ ID NO: 89), EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6), SYAFT (SEQ ID NO: 104), MVTPIFGEAKYSQRFEG (SEQ ID NO: 105), DRRVPIATDNWLDP (SEQ ID NO: 9), SYAFS (SEQ ID NO: 110), MITPVFGETKYAPRFQG (SEQ ID NO: 111), DRRVPMATDNWLDP (SEQ ID NO: 8), DYVLH (SEQ ID NO: 116), LIDPENGEARYAEKFQG (SEQ ID NO: 117), GAVGADSGSWFDP (SEQ ID NO: 10), RQGMH (SEQ ID NO: 123), FIKYDGSEKYHADSVWG (SEQ ID NO: 124), EAGGPDYRNGYNYDFYDGYNYHYMDV (SEQ ID NO: 7), LISDDGMRKYHSNSMWG (SEQ ID NO: 98), DSYWS (SEQ ID NO: 90), YVHKSGDTNYSPLKS (SEQ ID NO: 265), TLHGRIYGIVAFNEWFTYFYMDV (SEQ ID NO: 143), DNYWS (SEQ ID NO: 261), YVHDSGDTNYPNPSLKS (SEQ ID NO: 157), TKHGRIYGVVAFKEWFTYFYMDV (SEQ ID NO: 262), DAYWS (SEQ ID NO: 169), YVHHSGDTNYPNPSLKR (SEQ ID NO: 170), ALHGKRIYGIVALGELFTYFYMDV (SEQ ID NO: 171), ACTYFWG (SEQ ID NO: 185), SLSHCQSFWSGWTGHNPSLKS (SEQ ID NO: 186), FDGEVLVYNHWPKEWVDL (SEQ ID NO: 187), ACDYFWG (SEQ ID NO: 201), GLSHCAGYYNTGWTYHNPSLKS (SEQ ID NO: 202), FDGEVLVYHWPKEWVDL

(SEQ ID NO: 203), TGHYYWG (SEQ ID NO: 217), HIIHYTTAVLHNPSLKS (SEQ ID NO: 218), SGGDILYYEYWQKPHWFSP (SEQ ID NO: 219), GGEWGDKDYHWG (SEQ ID NO: 233), SIHWRGTTTHYKESLRR (SEQ ID NO: 234), HRHHDVFMVLPIAGWFDV (SEQ ID NO: 235), GTDWGENDFHYG (SEQ ID NO: 250), SIHWRGRTTHYKTSFRS (SEQ ID NO: 251), HKYHDI FRVVPVAGWFDP (SEQ ID NO: 252), KYDVH (SEQ ID NO: 277), WMSHEGDKTESAQRFGK (SEQ ID NO: 278), GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (SEQ ID NO: 279), WISHERDKTESAQRFGK (SEQ ID NO: 293), and GSKHRLRDYVLYDDYGLINQQEWNDYLEFLDV (SEQ ID NO: 308), wherein said antibody binds to and neutralizes HIV-1. Optionally, this antibody has a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of NGTSSDVGGFDSVS (SEQ ID NO: 97), DVSHRPS (SEQ ID NO: 95), SSLTDRSHRI (SEQ ID NO: 41), RASQTINNYLN (SEQ ID NO: 107), GASNLQN (SEQ ID NO: 108), QQSFSTPRT (SEQ ID NO: 42), RASQTIHTYLN (SEQ ID NO: 113), GASTLQS (SEQ ID NO: 114), QQSYSTPRT (SEQ ID NO: 43), SGSKLGDKYVS (SEQ ID NO: 120), ENDRRPS (SEQ ID NO: 121), QAWETTTTTTFVF (SEQ ID NO: 44), NGTSNDVGGYESVS (SEQ ID NO: 126), DVSKRPS (SEQ ID NO: 127), KSLTSTRRRV (SEQ ID NO: 45), NGTRSDVGGFDSVS (SEQ ID NO: 92), NGTSRDVGGFDSVS (SEQ ID NO: 93), GEKSLGSRAVQ (SEQ ID NO: 150), NNQDRPS (SEQ ID NO: 151), HIWDSRVPTKWV (SEQ ID NO: 152), GEESLGSRSVI (SEQ ID NO: 162), NNDRPS (SEQ ID NO: 163), HIWDSRRPTNWV (SEQ ID NO: 164), GKESIGSRAVQ (SEQ ID NO: 178), NNQDRPA (SEQ ID NO: 179), HIYDARGGTNWV (SEQ ID NO: 180), NGTATNFVS (SEQ ID NO: 194), GVDKRPP (SEQ ID NO: 195), GSLVGNWDVI (SEQ ID NO: 196), TGTSNRFVS (SEQ ID NO: 210), GVNKRPS (SEQ ID NO: 211), SSLVGNWDVI (SEQ ID NO: 212), NGTSSDIGGWNFVS (SEQ ID NO: 226), EVNKRPS (SEQ ID NO: 227), SSLFGRWDVV (SEQ ID NO: 228), RASQNINKNLA (SEQ ID NO: 243), ETYSKIA (SEQ ID NO: 244), QQYEEWPRT (SEQ ID NO: 245), RASQNVKNNLA (SEQ ID NO: 259), DASSRAG (SEQ ID NO: 260), SSTQSLRHSNGANYLA (SEQ ID NO: 286), LGSQRAS (SEQ ID NO: 287), and MQGLNRPWT (SEQ ID NO: 288), and TSTQSLRHSNGANYLA (SEQ ID NO: 303).

[0074] The invention provides an isolated anti-HIV antibody, wherein said antibody has a light chain with three CDRs that include an amino acid sequence selected from the group

consisting of the amino acid sequences of NGTSSDVGGFDSVS (SEQ ID NO: 97), DVSHRPS (SEQ ID NO: 95), SSLTDRSHRI (SEQ ID NO: 41), RASQTINNYLN (SEQ ID NO: 107), GASNLQN (SEQ ID NO: 108), QQSFSPTPT (SEQ ID NO: 42), RASQTIHTYLN (SEQ ID NO: 113), GASTLQS (SEQ ID NO: 114), QQSYSTPTPT (SEQ ID NO: 43), SGSKLGDKYVS (SEQ ID NO: 120), ENDRRPS (SEQ ID NO: 121), QAWETTTTTTFVF (SEQ ID NO: 44), NGTSNDVGGYESVS (SEQ ID NO: 126), DVSKRPS (SEQ ID NO: 127), KSLTSTRRRV (SEQ ID NO: 45), NGTRSDVGGFDSVS (SEQ ID NO: 92), NGTSRDVGGFDSVS (SEQ ID NO: 93), GEKSLGSRAVQ (SEQ ID NO: 150), NNQDRPS (SEQ ID NO: 151), HIWDSRVPTKWV (SEQ ID NO: 152), GEESLGSRSVI (SEQ ID NO: 162), NNNDRPS (SEQ ID NO: 163), HIWDSRRPTNWV (SEQ ID NO: 164), GKESIGSRAVQ (SEQ ID NO: 178), NNQDRPA (SEQ ID NO: 179), HIYDARGGTNWV (SEQ ID NO: 180), NGTATNFVS (SEQ ID NO: 194), GVDKRPP (SEQ ID NO: 195), GSLVGNWDVI (SEQ ID NO: 196), TGTSNRFFVS (SEQ ID NO: 210), GVNKRPS (SEQ ID NO: 211), SSLVGNWDVI (SEQ ID NO: 212), NGTSSDIGGWNFVS (SEQ ID NO: 226), EVNKRPS (SEQ ID NO: 227), SSLFGRWDVV (SEQ ID NO: 228), RASQNINKNLA (SEQ ID NO: 243), ETYSKIA (SEQ ID NO: 244), QQYEEWPRT (SEQ ID NO: 245), RASQNVKNNLA (SEQ ID NO: 259), DASSRAG (SEQ ID NO: 260), SSTQSLRHSNGANYLA (SEQ ID NO: 286), LGSQRAS (SEQ ID NO: 287), and MQGLNRPWT (SEQ ID NO: 288), and TSTQSLRHSNGANYLA (SEQ ID NO: 303), wherein said antibody binds to and neutralizes HIV-1.

[0075] The invention provides an isolated anti-HIV antibody, wherein said antibody has a heavy chain with three CDRs which may comprise an amino acid sequence selected from the group consisting of the amino acid sequences of GFTFHK (SEQ ID NO: 266), LISDDGMRKY (SEQ ID NO: 267), and EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6), GGTFSS (SEQ ID NO: 268), MVTPIFGEAK (SEQ ID NO: 269), and DRAVPIATDNWLDP (SEQ ID NO: 9), GGAFSS (SEQ ID NO: 270), MITPVFGETK (SEQ ID NO: 271), DRRVVPMTDNWLDP (SEQ ID NO: 8), GYSFID (SEQ ID NO: 102), LIDPENGAR (SEQ ID NO: 103), GAVGADSGSWFDP (SEQ ID NO: 10), GFDFSR (SEQ ID NO: 118), FIKYDGSEKY (SEQ ID NO: 272), and EAGGPDYRNGYNYDFYDGYNYHYMDV (SEQ ID NO: 7), GASISD (SEQ ID NO: 144), YVHKSGDTN (SEQ ID NO: 145), TLHGRRYIVAFNEWFTYFYMDV (SEQ ID NO: 143), GTLVRD (SEQ ID NO: 263), YVHDSGDTN (SEQ ID NO: 264), TKHGRRYGVVAFKEWFTYFYMDV (SEQ ID NO:

262), GASIND (SEQ ID NO: 172), YVHHSGDTN (SEQ ID NO: 173), ALHGKRIYGIVALGELFTYFYMDV (SEQ ID NO: 171), GESTGACT (SEQ ID NO: 188), SLSHCQSFWSGSGWTF (SEQ ID NO: 189), FDGEVLVYNHWPKPAWVDL (SEQ ID NO: 187), GDSTAACD (SEQ ID NO: 204), GLSHCAGYYNTGWTY (SEQ ID NO: 205), FDGEVLVYHDPKPAWVDL (SEQ ID NO: 203), GESINTGH (SEQ ID NO: 220), HIIHTTAVL (SEQ ID NO: 221), SGGDILYYYEWQKPHWFSP (SEQ ID NO: 219), GDSIRGGEWGDKD (SEQ ID NO: 236), SIHWRGTTH (SEQ ID NO: 237), HRHHDVFMVPIAGWFDV (SEQ ID NO: 235), GGSMRGTDWGEND (SEQ ID NO: 253), SIHWRGRTH (SEQ ID NO: 254), HKYHDIFRVVPVAGWFDP (SEQ ID NO: 252), GNTFSK (SEQ ID NO: 280), WMSHEGDKTE (SEQ ID NO: 281), GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (SEQ ID NO: 279), WISHERDKTE (SEQ ID NO: 294), GNTFRK (SEQ ID NO: 309), and GSKHRLRDYVLYDDYGLINQQEWNDYLEFLDV (SEQ ID NO: 308), wherein said antibody binds to and neutralizes HIV-1. Optionally, this antibody has a light chain with three CDRs that include an amino acid sequence selected from the group consisting of the amino acid sequences of NGTSSDVGGFDSVS (SEQ ID NO: 97), DVSHRPS (SEQ ID NO: 95), SSLTDRSHRI (SEQ ID NO: 41), RASQTINNYLN (SEQ ID NO: 107), GASNLQN (SEQ ID NO: 108), QQSFSPTPT (SEQ ID NO: 42), RASQTIHTYLN (SEQ ID NO: 113), GASTLQS (SEQ ID NO: 114), QQSYSTPTPT (SEQ ID NO: 43), SGSKLGDKYVS (SEQ ID NO: 120), ENDRRPS (SEQ ID NO: 121), QAWETTTTTTFVF (SEQ ID NO: 44), NGTSNDVGGYESVS (SEQ ID NO: 126), DVSKRPS (SEQ ID NO: 127), KSLTSTRRRV (SEQ ID NO: 45), NGTRSDVGGFDSVS (SEQ ID NO: 92), NGTSRDVGGFDSVS (SEQ ID NO: 93), GEKSLGSRAVQ (SEQ ID NO: 150), NNQDRPS (SEQ ID NO: 151), HIWDSRVPTKWV (SEQ ID NO: 152), GEESLGSRSVI (SEQ ID NO: 162), NNNDRPS (SEQ ID NO: 163), HIWDSRRPTNWV (SEQ ID NO: 164), GKESIGSRAVQ (SEQ ID NO: 178), NNQDRPA (SEQ ID NO: 179), HIYDARGGTNWV (SEQ ID NO: 180), NGTATNFVS (SEQ ID NO: 194), GVDKRPP (SEQ ID NO: 195), GSLVGNWDVI (SEQ ID NO: 196), TGTSNRPFVS (SEQ ID NO: 210), GVNKRPS (SEQ ID NO: 211), SSLVGNWDVI (SEQ ID NO: 212), NGTSSDIGGWNFVS (SEQ ID NO: 226), EVNKRPS (SEQ ID NO: 227), SSLFGRWDVV (SEQ ID NO: 228), RASQNINKNLA (SEQ ID NO: 243), ETYSKIA (SEQ ID NO: 244), QQYEEWPRT (SEQ ID NO: 245), RASQNVKNNLA (SEQ ID NO: 259), DASSRAG (SEQ ID NO: 260),

SSTQSLRHSNGANYLA (SEQ ID NO: 286), LGSQRAS (SEQ ID NO: 287), and MQGLNRPWT (SEQ ID NO: 288), and TSTQSLRHSNGANYLA (SEQ ID NO: 303).

[0076] Moreover, the invention provides an isolated anti-HIV antibody or fragment thereof, wherein said antibody includes: (a) a V_H CDR1 region including the amino acid sequence of SEQ ID NO: 88, 104, 110, 116, 123, 90, 261, 169, 185, 201, 217, 233, 250, or 277; (b) a V_H CDR2 region including the amino acid sequence of SEQ ID NO: 98, 89, 105, 111, 117, 124, 265, 157, 170, 186, 202, 218, 234, 251, 278, or 293; and (c) a V_H CDR3 region including the amino acid sequence of SEQ ID NO: 6, 9, 8, 10, 7, 143, 262, 171, 187, 203, 219, 235, 252, 279, or 308; wherein said antibody binds to and neutralizes HIV-1. This antibody may further include: (a) a V_L CDR1 region including the amino acid sequence of SEQ ID NO: 93, 92, 97, 94, 107, 113, 120, 126, 150, 162, 178, 194, 210, 226, 243, 259, 286 or 303; (b) a V_L CDR2 region including the amino acid sequence of SEQ ID NO: 95, 108, 114, 121, 127, 151, 163, 179, 195, 211, 227, 244, 260, or 287; and (c) a V_L CDR3 region including the amino acid sequence of SEQ ID NO: 41, 42, 43, 44, 45, 152, 164, 180, 196, 212, 228, 245, or 288.

[0077] Alternatively, the invention provides an isolated anti-HIV antibody or fragment thereof, wherein said antibody includes: (a) a V_H CDR1 region including the amino acid sequence of SEQ ID NO: 266, 268, 270, 201, 118, 144, 263, 172, 188, 204, 220, 236, 253, 280 or 309; (b) a V_H CDR2 region including the amino acid sequence of SEQ ID NO: 267, 269, 271, 103, 272, 145, 264, 173, 189, 205, 221, 237, 254, 281, or 294; and (c) a V_H CDR3 region including the amino acid sequence of SEQ ID NO: 6, 9, 8, 10, 7, 143, 262, 171, 187, 203, 219, 235, 252, 279, or 308; wherein said antibody binds to and neutralizes HIV-1. This antibody may further include: (a) a V_L CDR1 region including the amino acid sequence of SEQ ID NO: 93, 92, 97, 94, 107, 113, 120, 126, 150, 162, 178, 194, 210, 226, 243, 259, 286 or 303; (b) a V_L CDR2 region including the amino acid sequence of SEQ ID NO: 95, 108, 114, 121, 127, 151, 163, 179, 195, 211, 227, 244, 260, or 287; and (c) a V_L CDR3 region including the amino acid sequence of SEQ ID NO: 41, 42, 43, 44, 45, 152, 164, 180, 196, 212, 228, 245, or 288.

[0078] The invention provides an isolated fully human monoclonal anti-HIV antibody including: a) a heavy chain sequence including the amino acid sequence of SEQ ID NO: 31 and a light chain sequence including amino acid sequence SEQ ID NO: 32, or b) a heavy chain sequence including the amino acid sequence of SEQ ID NO: 33 and a light chain sequence including amino acid sequence SEQ ID NO: 34, or c) a heavy chain sequence including the

amino acid sequence of SEQ ID NO: 35 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 36, or d) a heavy chain sequence including the amino acid sequence of SEQ ID NO: 37 and a light chain sequence including amino acid sequence SEQ ID NO: 38, or e) a heavy chain sequence including the amino acid sequence of SEQ ID NO: 39 and a light chain sequence including amino acid sequence SEQ ID NO: 40, or f) a heavy chain sequence including the amino acid sequence of SEQ ID NO: 140 and a light chain sequence including amino acid sequence SEQ ID NO: 96, or g) a heavy chain sequence including the amino acid sequence of SEQ ID NO: 48 and a light chain sequence including amino acid sequence SEQ ID NO: 51, or h) a heavy chain sequence including the amino acid sequence of SEQ ID NO: 54 and a light chain sequence including amino acid sequence SEQ ID NO: 57, or i) a heavy chain sequence including the amino acid sequence of SEQ ID NO: 60 and a light chain sequence including amino acid sequence SEQ ID NO: 32, or j) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 79 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 149, or k) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 156 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 161, or l) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 168 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 177, or m) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 184 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 193, or n) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 200 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 209, or o) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 216 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 225, or p) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 232 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 242 or q) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 249 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 258 or r) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 276 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 285 or s) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 292 and a light chain sequence which may

comprise amino acid sequence SEQ ID NO: 285 or t) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 298 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 302 or u) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 307 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 313 or v) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 319 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 330 or w) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 334 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 393 or x) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 347 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 356 or y) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 363 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 397 or z) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 401 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 386, or aa) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 405 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 414, or ab) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 420 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 429, or ac) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 435 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 440, or ad) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 444 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 449, or ae) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 454 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 584, or af) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 463 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 470, or ag) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 474 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 483, or ah) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 490 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 497, or ai) a heavy chain sequence which may

comprise the amino acid sequence of SEQ ID NO: 502 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 511, or aj) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 517 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 525, or ak) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 532 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 540, or al) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 547 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 554, or am) a heavy chain sequence which may comprise the amino acid sequence of SEQ ID NO: 560 and a light chain sequence which may comprise amino acid sequence SEQ ID NO: 566.

[0079] The invention provides a composition including any one of the isolated anti-HIV antibodies described herein.

[0080] Optionally, an anti-HIV human monoclonal antibody of the invention is isolated from a B-cell from an HIV-1-infected human donor. In some embodiments, the antibody is effective in neutralizing a plurality of different clades of HIV. In some embodiments, the antibody is effective in neutralizing a plurality of different strain within the same clade of HIV-1. In some embodiments, the neutralizing antibody binds to the HIV envelope proteins gp120, or gp41 or envelope protein on HIV-1 pseudovirions or expressed on transfected or infected cell surfaces. In some embodiments, the neutralizing antibody does not bind to recombinant or monomeric envelope proteins gp120, or gp41 or envelope protein on HIV-1 pseudovirions or expressed on transfected or infected cell surfaces but binds to natural trimeric forms of the HIV-1 Env proteins.

[0081] The present invention provides human monoclonal antibodies wherein the antibodies are potent, broadly neutralizing antibody (bNAb). In some embodiments, a broadly neutralizing antibody is defined as a bNAb that neutralizes HIV-1 species belonging to two or more different clades. In some embodiments the different clades are selected from the group consisting of clades A, B, C, D, E, AE, AG, G or F. In some embodiments the HIV-1 strains from two or more clades comprise virus from non-B clades.

[0082] In some embodiments, a broadly neutralizing antibody is defined as a bNAb that neutralizes at least 60% of the HIV-1 strains listed in Tables 18A-18F. In some embodiments, at

least 70%, or at least 80%, or at least 90% of the HIV-1 strains listed in Tables 18A-18F are neutralized.

[0083] In some embodiments, a potent, broadly neutralizing antibody is defined as a bNAb that displays a potency of neutralization of at least a plurality of HIV-1 species with an IC₅₀ value of less than 0.2 µg/mL. In some embodiments the potency of neutralization of the HIV-1 species has an IC₅₀ value of less than 0.15 µg/mL, or less than 0.10 µg/mL, or less than 0.05 µg/mL. A potent, broadly neutralizing antibody is also defined as a bNAb that displays a potency of neutralization of at least a plurality of HIV-1 species with an IC₉₀ value of less than 2.0 µg/mL. In some embodiments the potency of neutralization of the HIV-1 species has an IC₉₀ value of less than 1.0 µg/mL, or less than 0.5 µg/mL.

[0084] Exemplary monoclonal antibodies that neutralize HIV-1 include 1443_C16 (PG16) (TCN-116), 1503 H05 (PG16) (TCN-119), 1456 A12 (PG16) (TCN-117), 1469 M23 (PG16) (TCN-118), 1489_I13 (PG16) (TCN-120), 1480_I08 (PG16), 1456_P20 (PG20), 1460_G14 (PGG14), 1495_C14 (PGC14), 1496_C09 (PG9) (TCN-109), 4838_L06 (PGT-121), 4873_E03 (PGT-121), 4877_D15 (PGT-122), 4858_P08 (PGT-123), 6123_A06 (PGT-125), 5141_B17 (PGT-126), 5145_B14 (PGT-127), 5114_A19 (PGT-128), 5147_N06 (PGT-130), 5136_H01 (PGT-131), 5343_B08 (PGT-135), 5344_E16 (PGT-135), 5329_C19 (PGT-136), 5366_P21 (PGT-136), 4964_G22 (PGT-141), 5345_I01 (PGT-137), 4993_K13 (PGT-141), 4995_E20 (PGT-142), 4980_N08 (PGT-143), 4970_K22 (PGT-144), 4995_P16 (PGT-145), 4835_F12 (PGT-124), 4869_K15 (PGT-133), 4876_M06 (PGT-134), 5131_A17 (PGT-132), 5138_G07 (PGT-138), 5120_N10 (PGT-139), 6831_A21 (PGT-151), 6889_I17 (PGT-152), 6891_F06 (PGT-153), 6843_G20 (PGT-154), 6892_D19 (PGT-155), 6808_B09 (PGT-156), 6892_C23 (PGT-157), and 6881_N05 (PGT-158) described herein. Alternatively, the monoclonal antibody is an antibody that binds to the same epitope as 1443_C16 (PG16) (TCN-116), 1503 H05 (PG16) (TCN-119), 1456 A12 (PG16) (TCN-117), 1469 M23 (PG16) (TCN-118), 1489_I13 (PG16) (TCN-120), 1480_I08 (PG16), 1456_P20 (PG20), 1460_G14 (PGG14), 1495_C14 (PGC14), 1496_C09 (PG9) (TCN-109), 4838_L06 (PGT-121), 4873_E03 (PGT-121), 4877_D15 (PGT-122), 4858_P08 (PGT-123), 6123_A06 (PGT-125), 5141_B17 (PGT-126), 5145_B14 (PGT-127), 5114_A19 (PGT-128), 5147_N06 (PGT-130), 5136_H01 (PGT-131), 5343_B08 (PGT-135), 5344_E16 (PGT-135), 5329_C19 (PGT-136), 5366_P21 (PGT-136), 4964_G22 (PGT-141), 5345_I01 (PGT-137), 4993_K13 (PGT-141), 4995_E20 (PGT-142), 4980_N08 (PGT-

143), 4970_K22 (PGT-144), 4995_P16 (PGT-145), 4835_F12 (PGT-124), 4869-K15 (PGT-133), 4876_M06 (PGT-134), 5131_A17 (PGT-132), 5138_G07 (PGT-138), 5120_N10 (PGT-139), 6831_A21 (PGT-151), 6889_I17 (PGT-152), 6891_F06 (PGT-153), 6843_G20 (PGT-154), 6892_D19 (PGT-155), 6808_B09 (PGT-156), 6892_C23 (PGT-157), or 6881_N05 (PGT-158). Specifically, monoclonal antibodies PG9 and PG16 are broad and potent neutralizing antibodies. The antibodies are respectively referred to herein as HIV antibodies.

[0085] The invention provides a number of isolated human monoclonal antibodies, wherein each said monoclonal antibody binds to HIV-1 infected or transfected cells; and binds to HIV-1 virus. A neutralizing antibody having potency in neutralizing HIV-1, or a fragment thereof is provided. In some embodiments a neutralizing antibody of the invention exhibits higher neutralization index and/or a higher affinity for binding to the envelope proteins gp120, or gp41 than anti-HIV mAbs known in the art, such as the mAb b12. (Burton DR et al., Science Vol. 266. no. 5187, pp. 1024 – 1027). Exemplary monoclonal antibodies 1496_C09 (PG9), 1443_C16 (PG16), 1456_P20 (PG20), 1460_G14 (PGG14), and 1495_C14 (PGC14) exhibit binding to the envelope glycoprotein gp120, but not gp41, in an ELISA assay, however gp120 binding does not always correlate with neutralization activity against specific strains of HIV-1. In some embodiments, monoclonal antibodies, for example 1443_C16 (PG16) and 1496_C09 (PG9), display none or weak gp120 binding activity against a particular strain but bind to HIV-1 trimer on transfected or infected cell surface and/or virion and exhibit broad and potent neutralization activity against that strain of HIV-1.

[0086] In one aspect the antibody is a monoclonal antibody which may comprise one or more polypeptides selected from the group consisting of 1443_C16 (PG16) (TCN-116), 1503_H05 (PG16) (TCN-119), 1456_A12 (PG16) (TCN-117), 1469_M23 (PG16) (TCN-118), 1489_I13 (PG16) (TCN-120), 1480_I08 (PG16), 1456_P20 (PG20), 1460_G14 (PGG14), 1495_C14 (PGC14), 1496_C09 (PG9) (TCN-109), 4838_L06 (PGT-121), 4873_E03 (PGT-121), 4877_D15 (PGT-122), 4858_P08 (PGT-123), 6123_A06 (PGT-125), 5141_B17 (PGT-126), 5145_B14 (PGT-127), 5114_A19 (PGT-128), 5147_N06 (PGT-130), 5136_H01 (PGT-131), 5343_B08 (PGT-135), 5344_E16 (PGT-135), 5329_C19 (PGT-136), 5366_P21 (PGT-136), 4964_G22 (PGT-141), 5345_I01 (PGT-137), 4993_K13 (PGT-141), 4995_E20 (PGT-142), 4980_N08 (PGT-143), 4970_K22 (PGT-144), 4995_P16 (PGT-145), 4835_F12 (PGT-124), 4869-K15 (PGT-133), 4876_M06 (PGT-134), 5131_A17 (PGT-132), 5138_G07 (PGT-138), 5120_N10

(PGT-139), 6831_A21 (PGT-151), 6889_I17 (PGT-152), 6891_F06 (PGT-153), 6843_G20 (PGT-154), 6892_D19 (PGT-155), 6808_B09 (PGT-156), 6892_C23 (PGT-157), and 6881_N05 (PGT-158); which may comprise a heavy chain selected from the group consisting of the heavy chain of 1443_C16 (PG16) (TCN-116), 1503_H05 (PG16) (TCN-119), 1456_A12 (PG16) (TCN-117), 1469_M23 (PG16) (TCN-118), 1489_I13 (PG16) (TCN-120), 1480_I08 (PG16), 1456_P20 (PG20), 1460_G14 (PGG14), 1495_C14 (PGC14), 1496_C09 (PG9) (TCN-109), 4838_L06 (PGT-121), 4873_E03 (PGT-121), 4877_D15 (PGT-122), 4858_P08 (PGT-123), 6123_A06 (PGT-125), 5141_B17 (PGT-126), 5145_B14 (PGT-127), 5114_A19 (PGT-128), 5147_N06 (PGT-130), 5136_H01 (PGT-131), 5343_B08 (PGT-135), 5344_E16 (PGT-135), 5329_C19 (PGT-136), 5366_P21 (PGT-136), 4964_G22 (PGT-141), 5345_I01 (PGT-137), 4993_K13 (PGT-141), 4995_E20 (PGT-142), 4980_N08 (PGT-143), 4970_K22 (PGT-144), 4995_P16 (PGT-145), 4835_F12 (PGT-124), 4869_K15 (PGT-133), 4876_M06 (PGT-134), 5131_A17 (PGT-132), 5138_G07 (PGT-138), 5120_N10 (PGT-139), 6831_A21 (PGT-151), 6889_I17 (PGT-152), 6891_F06 (PGT-153), 6843_G20 (PGT-154), 6892_D19 (PGT-155), 6808_B09 (PGT-156), 6892_C23 (PGT-157), and 6881_N05 (PGT-158); which may comprise a heavy chain which may comprise a CDR selected from the group consisting of the CDRs of the heavy chain of 1443_C16 (PG16) (TCN-116), 1503_H05 (PG16) (TCN-119), 1456_A12 (PG16) (TCN-117), 1469_M23 (PG16) (TCN-118), 1489_I13 (PG16) (TCN-120), 1480_I08 (PG16), 1456_P20 (PG20), 1460_G14 (PGG14), 1495_C14 (PGC14), 1496_C09 (PG9) (TCN-109), 4838_L06 (PGT-121), 4873_E03 (PGT-121), 4877_D15 (PGT-122), 4858_P08 (PGT-123), 6123_A06 (PGT-125), 5141_B17 (PGT-126), 5145_B14 (PGT-127), 5114_A19 (PGT-128), 5147_N06 (PGT-130), 5136_H01 (PGT-131), 5343_B08 (PGT-135), 5344_E16 (PGT-135), 5329_C19 (PGT-136), 5366_P21 (PGT-136), 4964_G22 (PGT-141), 5345_I01 (PGT-137), 4993_K13 (PGT-141), 4995_E20 (PGT-142), 4980_N08 (PGT-143), 4970_K22 (PGT-144), 4995_P16 (PGT-145), 4835_F12 (PGT-124), 4869_K15 (PGT-133), 4876_M06 (PGT-134), 5131_A17 (PGT-132), 5138_G07 (PGT-138), 5120_N10 (PGT-139), 6831_A21 (PGT-151), 6889_I17 (PGT-152), 6891_F06 (PGT-153), 6843_G20 (PGT-154), 6892_D19 (PGT-155), 6808_B09 (PGT-156), 6892_C23 (PGT-157), and 6881_N05 (PGT-158); which may comprise a light chain selected from the group consisting of the light chain of 1443_C16 (PG16) (TCN-116), 1503_H05 (PG16) (TCN-119), 1456_A12 (PG16) (TCN-117), 1469_M23 (PG16) (TCN-118), 1489_I13 (PG16) (TCN-120), 1480_I08 (PG16), 1456_P20 (PG20), 1460_G14 (PGG14),

1495_C14 (PGC14), 1496_C09 (PG9) (TCN-109), 4838_L06 (PGT-121), 4873_E03 (PGT-121), 4877_D15 (PGT-122), 4858_P08 (PGT-123), 6123_A06 (PGT-125), 5141_B17 (PGT-126), 5145_B14 (PGT-127), 5114_A19 (PGT-128), 5147_N06 (PGT-130), 5136_H01 (PGT-131), 5343_B08 (PGT-135), 5344_E16 (PGT-135), 5329_C19 (PGT-136), 5366_P21 (PGT-136), 4964_G22 (PGT-141), 5345_I01 (PGT-137), 4993_K13 (PGT-141), 4995_E20 (PGT-142), 4980_N08 (PGT-143), 4970_K22 (PGT-144), 4995_P16 (PGT-145), 4835_F12 (PGT-124), 4869_K15 (PGT-133), 4876_M06 (PGT-134), 5131_A17 (PGT-132), 5138_G07 (PGT-138), 5120_N10 (PGT-139), 6831_A21 (PGT-151), 6889_I17 (PGT-152), 6891_F06 (PGT-153), 6843_G20 (PGT-154), 6892_D19 (PGT-155), 6808_B09 (PGT-156), 6892_C23 (PGT-157), and 6881_N05 (PGT-158); which may comprise a light chain which may comprise a CDR selected from the group consisting of the CDRs of the light chain of 1443_C16 (PG16) (TCN-116), 1503_H05 (PG16) (TCN-119), 1456_A12 (PG16) (TCN-117), 1469_M23 (PG16) (TCN-118), 1489_I13 (PG16) (TCN-120), 1480_I08 (PG16), 1456_P20 (PG20), 1460_G14 (PGG14), 1495_C14 (PGC14), 1496_C09 (PG9) (TCN-109), 4838_L06 (PGT-121), 4873_E03 (PGT-121), 4877_D15 (PGT-122), 4858_P08 (PGT-123), 6123_A06 (PGT-125), 5141_B17 (PGT-126), 5145_B14 (PGT-127), 5114_A19 (PGT-128), 5147_N06 (PGT-130), 5136_H01 (PGT-131), 5343_B08 (PGT-135), 5344_E16 (PGT-135), 5329_C19 (PGT-136), 5366_P21 (PGT-136), 4964_G22 (PGT-141), 5345_I01 (PGT-137), 4993_K13 (PGT-141), 4995_E20 (PGT-142), 4980_N08 (PGT-143), 4970_K22 (PGT-144), 4995_P16 (PGT-145), 4835_F12 (PGT-124), 4869_K15 (PGT-133), 4876_M06 (PGT-134), 5131_A17 (PGT-132), 5138_G07 (PGT-138), 5120_N10 (PGT-139), 6831_A21 (PGT-151), 6889_I17 (PGT-152), 6891_F06 (PGT-153), 6843_G20 (PGT-154), 6892_D19 (PGT-155), 6808_B09 (PGT-156), 6892_C23 (PGT-157), and 6881_N05 (PGT-158).

[0087] The invention relates to an antibody or a fragment thereof, such as Fab, Fab', F(ab')₂ and Fv fragments that binds to an epitope or immunogenic polypeptide capable of binding to an antibody selected from 1443_C16 (PG16) (TCN-116), 1503_H05 (PG16) (TCN-119), 1456_A12 (PG16) (TCN-117), 1469_M23 (PG16) (TCN-118), 1489_I13 (PG16) (TCN-120), 1480_I08 (PG16), 1456_P20 (PG20), 1460_G14 (PGG14), 1495_C14 (PGC14), 1496_C09 (PG9) (TCN-109), 4838_L06 (PGT-121), 4873_E03 (PGT-121), 4877_D15 (PGT-122), 4858_P08 (PGT-123), 6123_A06 (PGT-125), 5141_B17 (PGT-126), 5145_B14 (PGT-127), 5114_A19 (PGT-128), 5147_N06 (PGT-130), 5136_H01 (PGT-131), 5343_B08 (PGT-135), 5344_E16 (PGT-

135), 5329_C19 (PGT-136), 5366_P21 (PGT-136), 4964_G22 (PGT-141), 5345_I01 (PGT-137), 4993_K13 (PGT-141), 4995_E20 (PGT-142), 4980_N08 (PGT-143), 4970_K22 (PGT-144), 4995_P16 (PGT-145), 4835_F12 (PGT-124), 4869_K15 (PGT-133), 4876_M06 (PGT-134), 5131_A17 (PGT-132), 5138_G07 (PGT-138), 5120_N10 (PGT-139), 6831_A21 (PGT-151), 6889_I17 (PGT-152), 6891_F06 (PGT-153), 6843_G20 (PGT-154), 6892_D19 (PGT-155), 6808_B09 (PGT-156), 6892_C23 (PGT-157), and 6881_N05 (PGT-158).

[0088] The invention also relates to immunogenic polypeptides encoding such epitopes.

[0089] Nucleic acid molecules encoding such antibodies, and vectors and cells carrying such nucleic acids are also provided.

[0090] The invention relates to a pharmaceutical composition which may comprise at least one antibody or fragment as recited herein, together with a pharmaceutically acceptable carrier.

[0091] The invention relates to a method of immunizing, preventing or inhibiting HIV infection or an HIV-related disease which may comprise the steps of identifying a patient in need of such treatment and administering to said patient a therapeutically effective amount of at least one monoclonal antibody as recited herein.

[0092] In a further aspect the HIV antibodies according to the invention are linked to a therapeutic agent or a detectable label.

[0093] Additionally, the invention provides methods for stimulating an immune response, treating, preventing or alleviating a symptom of an HIV viral infection by administering an HIV antibody to a subject

[0094] In another aspect, the invention provides methods of administering the HIV antibody of the invention to a subject prior to, and/or after exposure to an HIV virus. For example, the HIV antibody of the invention is used to treat or prevent HIV infection. The HIV antibody is administered at a dose sufficient to promote viral clearance or eliminate HIV infected cells.

[0095] Also included in the invention is a method for determining the presence of an HIV virus infection in a patient, by contacting a biological sample obtained from the patient with an HIV antibody; detecting an amount of the antibody that binds to the biological sample; and comparing the amount of antibody that binds to the biological sample to a control value.

[0096] The invention further provides a diagnostic kit which may comprise an HIV monoclonal antibody.

[0097] The invention relates to a broadly neutralizing antibody (bNAb) wherein the antibody neutralizes at least one member of each clade with a potency greater than that of the bNAbs b12, 2G12, 2F5 and 4E10 respectively.

[0098] The invention relates to a broadly neutralizing antibody (bNAb) wherein the antibody binds or does not bind monomeric gp120 or gp41 proteins of the HIV-1 env gene. The antibody binds with higher affinity to trimeric forms of the HIV-1 Env expressed on a cell surface than to the monomeric gp120 or artificially trimerized gp140. In some aspects, the antibody binds with high affinity to uncleaved HIV-1 gp160 trimers on a cell surface.

[0099] The invention relates to a broadly neutralizing antibody (bNAb) wherein the antibody binds an epitope within the variable loop of gp120, wherein the epitope may comprise the conserved regions of V2 and V3 loops of gp120, wherein the epitope may comprise N-glycosylation site at residue Asn-160 within the V2 loop of gp120, wherein the antibody binds an epitope presented by a trimeric spike of gp120 on a cell surface, wherein the epitope is not presented when gp120 is artificially trimerized. In some embodiments, the antibody does not neutralize the HIV-1 in the absence of N-glycosylation site at residue Asn-160 within the V2 loop of gp120.

[00100] The invention relates to a broadly neutralizing antibody (bNAb) selected from the group consisting of PG16 and PG9. Moreover, the invention relates to a broadly neutralizing antibody (bNAb) selected from the group consisting of 1443_C16 (PG16) (TCN-116), 1503_H05 (PG16) (TCN-119), 1456_A12 (PG16) (TCN-117), 1469_M23 (PG16) (TCN-118), 1489_I13 (PG16) (TCN-120), 1480_I08 (PG16), 1456_P20 (PG20), 1460_G14 (PGG14), 1495_C14 (PGC14), 1496_C09 (PG9) (TCN-109), 4838_L06 (PGT-121), 4873_E03 (PGT-121), 4877_D15 (PGT-122), 4858_P08 (PGT-123), 6123_A06 (PGT-125), 5141_B17 (PGT-126), 5145_B14 (PGT-127), 5114_A19 (PGT-128), 5147_N06 (PGT-130), 5136_H01 (PGT-131), 5343_B08 (PGT-135), 5344_E16 (PGT-135), 5329_C19 (PGT-136), 5366_P21 (PGT-136), 4964_G22 (PGT-141), 5345_I01 (PGT-137), 4993_K13 (PGT-141), 4995_E20 (PGT-142), 4980_N08 (PGT-143), 4970_K22 (PGT-144), 4995_P16 (PGT-145), 4835_F12 (PGT-124), 4869_K15 (PGT-133), 4876_M06 (PGT-134), 5131_A17 (PGT-132), 5138_G07 (PGT-138), 5120_N10 (PGT-139), 6831_A21 (PGT-151), 6889_I17 (PGT-152), 6891_F06 (PGT-153), 6843_G20 (PGT-154), 6892_D19 (PGT-155), 6808_B09 (PGT-156), 6892_C23 (PGT-157), and 6881_N05 (PGT-158).

[00101] The invention relates to an antigen or an immunogenic polypeptide, or a vaccine which may comprise such antigen or immunogenic polypeptide, for producing a broadly neutralizing antibody (bNAbs) by an immune response, the antigen which may comprise an epitope within the variable loop of gp120 according to the invention.

[00102] The invention relates to method for passive or active immunization of an individual against a plurality of HIV-1 species across one or more clades, the method which may comprise: providing a broadly neutralizing antibody (bNAbs) wherein the bNAbs neutralizes HIV-1 species belonging to two or more clades, and further wherein the potency of neutralization of at least one member of each clade is determined by an IC₅₀ value of less than 0.005 µg/mL. In some embodiments, the antibody is selected from the group consisting of PG9 and PG16. Alternatively, or in addition, the antibody is selected from the group consisting of 1443_C16 (PG16) (TCN-116), 1503_H05 (PG16) (TCN-119), 1456_A12 (PG16) (TCN-117), 1469_M23 (PG16) (TCN-118), 1489_I13 (PG16) (TCN-120), 1480_I08 (PG16), 1456_P20 (PG20), 1460_G14 (PGG14), 1495_C14 (PGC14), 1496_C09 (PG9) (TCN-109), 4838_L06 (PGT-121), 4873_E03 (PGT-121), 4877_D15 (PGT-122), 4858_P08 (PGT-123), 6123_A06 (PGT-125), 5141_B17 (PGT-126), 5145_B14 (PGT-127), 5114_A19 (PGT-128), 5147_N06 (PGT-130), 5136_H01 (PGT-131), 5343_B08 (PGT-135), 5344_E16 (PGT-135), 5329_C19 (PGT-136), 5366_P21 (PGT-136), 4964_G22 (PGT-141), 5345_I01 (PGT-137), 4993_K13 (PGT-141), 4995_E20 (PGT-142), 4980_N08 (PGT-143), 4970_K22 (PGT-144), 4995_P16 (PGT-145), 4835_F12 (PGT-124), 4869_K15 (PGT-133), 4876_M06 (PGT-134), 5131_A17 (PGT-132), 5138_G07 (PGT-138), 5120_N10 (PGT-139), 6831_A21 (PGT-151), 6889_I17 (PGT-152), 6891_F06 (PGT-153), 6843_G20 (PGT-154), 6892_D19 (PGT-155), 6808_B09 (PGT-156), 6892_C23 (PGT-157), and 6881_N05 (PGT-158).

[0100] In some embodiments, the antibody is produced by active immunization with an antigen which may comprise an epitope within the variable loop of gp120, wherein the epitope may comprise the conserved regions of V2 and V3 loops of gp120 or, wherein the epitope may comprise an N-glycosylation site at residue Asn-160 within the V2 loop of gp120. In some aspects, the epitope is presented by a trimeric spike of gp120 on a cell surface, and the epitope is not presented when gp120 is monomeric or artificially trimerized.

[0101] The invention provides a method for obtaining a broadly neutralizing human monoclonal antibody, the method including: (a) screening memory B cell cultures from a donor

PBMC sample for a broad neutralization activity against a plurality of HIV-1 species; (b) cloning a memory B cell that exhibits broad neutralization activity; and then (c) rescuing the monoclonal antibody from the clonal memory B cell culture that exhibits broad neutralization activity. In one embodiment the method, the screening step includes screening polyclonal transfectants for neutralization activity prior to the cloning step of monoclonal transfection. In this embodiment, the screening step is optionally repeated following monoclonal transfection. Finally, in this embodiment, the DNA sequence of the monoclonal antibody is determined as part of the rescue step. Exemplary antibodies that are generated using this embodiment include, but are not limited to, 1443_C16 (PG16) (TCN-116), 1503 H05 (PG16) (TCN-119), 1456 A12 (PG16) (TCN-117), 1469 M23 (PG16) (TCN-118), 1489_I13 (PG16) (TCN-120), 1480_I08 (PG16), 1456_P20 (PG20), 1460_G14 (PGG14), 1495_C14 (PGC14), 1496_C09 (PG9) (TCN-109), 4838_L06 (PGT-121), 4873_E03 (PGT-121), 4877_D15 (PGT-122), 4858_P08 (PGT-123), 6123_A06 (PGT-125), 5141_B17 (PGT-126), 5145_B14 (PGT-127), 5114_A19 (PGT-128), 5147_N06 (PGT-130), 5136_H01 (PGT-131), 5343_B08 (PGT-135), 5344_E16 (PGT-135), 5329_C19 (PGT-136), 5366_P21 (PGT-136), 4964_G22 (PGT-141), 5345_I01 (PGT-137), 4993_K13 (PGT-141), 4995_E20 (PGT-142), 4980_N08 (PGT-143), 4970_K22 (PGT-144), 4995_P16 (PGT-145), 4835_F12 (PGT-124), 4869_K15 (PGT-133), 4876_M06 (PGT-134), 5131_A17 (PGT-132), 5138_G07 (PGT-138), 5120_N10 (PGT-139), 6831_A21 (PGT-151), 6889_I17 (PGT-152), 6891_F06 (PGT-153), 6843_G20 (PGT-154), 6892_D19 (PGT-155), 6808_B09 (PGT-156), 6892_C23 (PGT-157), and 6881_N05 (PGT-158).

[0102] Alternatively, or in addition, the screening step includes determining variable gene sequences from selected B cell wells by deep sequencing, which is optionally followed by sequence alignment to cluster related antibodies. In this alternative embodiment, following the screening step, a monoclonal transfection is performed as part of the cloning step. Subsequently, in this alternative embodiment, monoclonal transfectants are screened for neutralization activity against an HIV virus from one or more clades. Exemplary antibodies that are generated using this embodiment include, but are not limited to, 1443_C16 (PG16) (TCN-116), 1503 H05 (PG16) (TCN-119), 1456 A12 (PG16) (TCN-117), 1469 M23 (PG16) (TCN-118), 1489_I13 (PG16) (TCN-120), 1480_I08 (PG16), 1456_P20 (PG20), 1460_G14 (PGG14), 1495_C14 (PGC14), 1496_C09 (PG9) (TCN-109), 4838_L06 (PGT-121), 4873_E03 (PGT-121), 4877_D15 (PGT-122), 4858_P08 (PGT-123), 6123_A06 (PGT-125), 5141_B17 (PGT-126), 5145_B14

(PGT-127), 5114_A19 (PGT-128), 5147_N06 (PGT-130), 5136_H01 (PGT-131), 5343_B08 (PGT-135), 5344_E16 (PGT-135), 5329_C19 (PGT-136), 5366_P21 (PGT-136), 4964_G22 (PGT-141), 5345_I01 (PGT-137), 4993_K13 (PGT-141), 4995_E20 (PGT-142), 4980_N08 (PGT-143), 4970_K22 (PGT-144), 4995_P16 (PGT-145), 4835_F12 (PGT-124), 4869_K15 (PGT-133), 4876_M06 (PGT-134), 5131_A17 (PGT-132), 5138_G07 (PGT-138), 5120_N10 (PGT-139), 6831_A21 (PGT-151), 6889_I17 (PGT-152), 6891_F06 (PGT-153), 6843_G20 (PGT-154), 6892_D19 (PGT-155), 6808_B09 (PGT-156), 6892_C23 (PGT-157), and 6881_N05 (PGT-158).

[00103] DELETED

[00104] It is noted that in this disclosure and particularly in the claims and/or paragraphs, terms such as “comprises”, “comprised”, “comprising” and the like can have the meaning attributed to it in U.S. Patent law; e.g., they can mean “includes”, “included”, “including”, and the like; and that terms such as “consisting essentially of” and “consists essentially of” have the meaning ascribed to them in U.S. Patent law, e.g., they allow for elements not explicitly recited, but exclude elements that are found in the prior art or that affect a basic or novel characteristic of the invention.

[00105] These and other embodiments are disclosed or are obvious from and encompassed by, the following Detailed Description.

BRIEF DESCRIPTION OF THE DRAWINGS

[0100] Figure 1A is a schematic tree diagram of Clustal W-aligned variable region sequences of heavy chains of the monoclonal antibodies.

[0101] Figure 1B is a schematic tree diagram of Clustal W-aligned variable region sequences of light chains of the monoclonal antibodies.

[0102] Figure 2 is a flow chart of the process for isolation of monoclonal antibodies according to the invention.

[0103] Figure 3A is a schematic diagram that summarizes the screening results for neutralization and HIV-env protein (gp120 and gp41) binding assays from which B cell cultures were selected for antibody rescue and the monoclonal antibodies 1496_C09 (PG9), 1443_C16 (PG16), 1456_P20 (PG20), 1460_G14 (PGG14), and 1495_C14 (PGC14) were derived. A neutralization index value of 1.5 was used as a cut-off.

[0104] Figure 3B is a schematic diagram that summarizes the neutralizing activity and HIV-env protein (gp120 and gp41) binding activities of the monoclonal antibodies 1496_C09 (PG9), 1443_C16 (PG16), 1456_P20 (PG20), 1460_G14 (PGG14), and 1495_C14 (PGC14) as determined by ELISA assays among the B cell supernatants using a neutralization index cut-off value of 2.0. The neutralization index was expressed as the ratio of normalized relative luminescence units (RLU) of SIVmac239 to that of test viral strain derived from the same test B cell culture supernatant. The cut-off values used to distinguish neutralizing hits were determined by the neutralization index of a large number of negative control wells containing B cell culture supernatants derived from healthy donors.

[0105] Figure 4 is a series of graphs depicting the neutralization activity of monoclonal antibodies 1443_C16 (PG16) and 1496_C09 (PG9) to additional pseudoviruses not included in Tables 17A and 17B.

[0106] Figure 5 is a graph depicting the dose response curves of 1456_P20 (PG20), 1495_C14 (PGC14) and 1460_G14 (PGG14) binding to recombinant gp120 in ELISA as compared to control anti-gp120 (b12). Data is presented as average OD values of triplicate ELISA wells obtained on the same plate.

[0107] Figure 6 is a series of graphs depicting the results from ELISA binding assays of monoclonal antibodies 1443_C16 (PG16) and 1496_C09 (PG9) to HIV-1 YU2 gp140, JR-CSFgp120, membrane-proximal external regions (MPER) peptide of gp41 and V3 polypeptide.

[0108] Figure 7 is a graph depicting the results of a binding assay using monoclonal antibodies 1443_C16 (PG16) and 1496_C09 (PG9) to HIV-1 YU2 gp160 expressed on the cell surface in the presence and absence of soluble CD4 (sCD4).

[0109] Figure 8 is a graph depicting the results of a binding assay using monoclonal antibodies 1443_C16 (PG16) and 1496_C09 (PG9) to HIV-1 gp160 transfected cells.

[0110] Figure 9 is a series of graphs depicting the results of a capture assay. The data describe capturing of entry-competent JRCSF pseudovirus by neutralizing monoclonal antibodies 1443_C16 (PG16) and 1496_C09 (PG9) in a dose-dependent manner.

[0111] Figure 10A is a graph depicting the results of a competitive binding assay using monoclonal antibodies sCD4, PG16 and PG9, wherein the claimed antibodies compete for the binding of monoclonal antibody 1443_C16 (PG16) to pseudovirus but control antibodies b12, 2G12, 2F5 and 4E10 do not competitively bind to the pseudovirus.

[0112] Figure 10B is a graph depicting the results of a competitive binding assay using monoclonal antibodies sCD4, PG16 and PG9, wherein the claimed antibodies compete for the binding of monoclonal antibody 1496_C09 (PG9) to pseudovirus but control antibodies b12, 2G12, 2F5 and 4E10 do not competitively bind to the pseudovirus.

[0113] Figure 11A is a series of graphs depicting the results of a binding assay using PG9 and PG16. The data show that PG9 and PG16 bind to monomeric gp120 and artificially trimerized gp140 constructs as determined by ELISA. IgG b12 was used as a control for ELISA assays.

[0114] Figure 11B is a series of graphs depicting the results of a binding assay using PG9 and PG16. The data show that PG9 and PG16 bind to Env expressed on the surface of 293T cells as determined by flow cytometry. The bNAb b12 and the non-neutralizing antibody b6 are included in the cell surface binding assays to show the expected percentages of cleaved and uncleaved Env expressed on the cell surface.

[0115] Figure 12 is a series of graphs depicting the results of a binding assay using PG9 and PG16 and cleavage-defective HIV-1YU2 trimers. PG9 and PG16 bind with high affinity to cleavage-defective HIV-1YU2 trimers as determined by flow cytometry. Binding curves were generated by plotting the MFI of antigen binding as a function of antibody concentration.

[0116] Figure 13A-E is a series of graphs depicting the mapping the PG9 and PG16 epitopes. Competitor antibody is indicated at the top of each graph. 2G12 is included to control for cell surface Env expression. A: PG9 and PG16 compete with each other for cell surface Env binding and neither antibody competes with the CD4bs antibody b12 for Env binding. B: Ligation of cell surface Env with sCD4 diminishes binding of PG9 and PG16. 2G12 is included to control for CD4-induced shedding of gp120. C: sCD4 inhibits binding of PG9 to artificially trimerized gp140YU-2 as determined by ELISA. D: PG9 competes with 10/76b (anti-V2), F425/b4e8 (anti-

V3) and X5 (CD4i) for gp120 binding in competition ELISA assays. E: PG9 and PG16 fail to bind variable loop deleted HIV-1JR-CSF variants expressed on the surface of 293T cells.

[0117] Figure 14 is a series of graphs depicting the results of competition ELISA assays using the monoclonal antibody PG9.

[0118] Figure 15 is a graph depicting monoclonal antibody binding, PG9 or PG16, to HIV-1JR-FLΔCT E168K Env expressed on the surface of 293T cells as determined by flow cytometry.

[0119] Figure 16 is a graph depicting monoclonal antibody PG9 binding to deglycosylated gp120.

[0120] Figure 17 is a series of graphs depicting the neutralization activity of PG9 and PG16 against HIV-1SF162 and HIV-1SF162 K160N, which was determined using a single-round replication luciferase reporter assay of pseudotyped virus.

[0121] Figure 18 is a series of graphs depicting the binding of PG9 and PG16 to mixed trimers. Alanine substitutions at positions 160 and 299 were introduced into HIV-1YU2 Env to abolish binding of PG9 and PG16. An alanine substitution at position 295 was also introduced into the same construct to abrogate binding of 2G12. Co-transfection of 293T cells with WT and mutant plasmids in a 1:2 ratio resulted in the expression of 29% mutant homotrimers, 44% heterotrimers with two mutant subunits, 23% heterotrimers with one mutant subunit, and 4% wild-type homotrimers.

[0122] Figure 19 is a series of graphical depictions of the number of nucleotide or amino acid differences in the heavy chain sequences of sister clones of 1443 C16 (PG16) among each other. Note that the single nucleotide difference of 1408 I08 translates into an identical protein sequence of 1443 C16. The nucleotide sequence of the 1408 I08 light chain is identical to the nucleotide sequence of the light chain of 1443 C16.

[0123] Figure 20A is a tree diagram illustrating the correlation of the heavy chain of 1443 C16 sister clones to the heavy chain of 1496 C09 at the nucleotide level.

[0124] Figure 20B is a tree diagram illustrating the correlation of the light chain of 1443 C16 sister clones to the light chain of 1496 C09 at the nucleotide level.

[0125] Figure 21A is a tree diagram illustrating the correlation of the heavy chain of 1443 C16 sister clones to the heavy chain of 1496 C09 at the protein level.

[0126] Figure 21B is a tree diagram illustrating the correlation of the light chain of 1443 C16 sister clones to the light chain of 1496 C09 at the protein level.

[0127] Figure 22 is a Venn diagram depicting the viruses used in primary HIV-neutralization screening (JR-CSF, MGRM-C-26, 92BR020, 94UG103, 93IN905, 92TH021) and the number of neutralizing antibodies identified using these viruses alone, or in the demonstrated combinations. The results of screening antibodies isolated from B-cell cultures established from four human donors (#517, 039, 196, and 584) are shown.

[0128] Figure 23 is a tree diagram illustrating the relationships between the heavy chain variable gene sequences of antibodies PGT-121, PGT-122, PGT-123, PGT-125, PGT-126, PGT-130, PGT-135, and PGT-136. Scale bar = 0.03. A value of zero demonstrates that an identical antibody was produced by two separate B-cell clones. Antibodies are less closely-related as the provided values increase.

[0129] Figure 24 is a tree diagram illustrating the relationships between the light chain variable gene sequences of antibodies PGT-121, PGT-122, PGT-123, PGT-125, PGT-126, PGT-130, PGT-135, and PGT-136. Scale bar = 0.04. A value of zero demonstrates that an identical antibody was produced by two separate B-cell clones. Antibodies are less closely-related as the provided values increase.

[0130] Figure 25 is a tree diagram illustrating the relationships between the heavy chain variable gene sequences of antibodies PGT-141, PGT-142, and PGT-143. Scale bar = 0.04. A value of zero demonstrates that an identical antibody was produced by two separate B-cell clones. Antibodies are less closely-related as the provided values increase.

[0131] Figure 26 is a tree diagram illustrating the relationships between the light chain variable gene sequences of antibodies PGT-141, PGT-142, and PGT-143. Scale bar = 0.04. A value of zero demonstrates that an identical antibody was produced by two separate B-cell clones. Antibodies are less closely-related as the provided values increase.

[0132] Figure 27 is a pie chart showing that a limited number of antibody specificities mediate broad and potent serum neutralization in elite neutralizers (Walker LM, et al. PLOS Pathogen, 2010).

[0133] Figure 28 is a schematic diagram depicting the I-Star™ Human bNAbs (broadly Neutralizing Antibody) Discovery Platform developed by Theraclone Sciences.

[0134] Figure 29 is a schematic diagram depicting the method of bNMab (broadly Neutralizing Monoclonal Antibody) isolation from IgG-positive (IgG⁺) Memory B Cells developed by Theraclone Sciences.

[0135] Figure 30 is a computer-generated three-dimensional depiction of trimer-specific PG9 and PG16 antibodies in close proximity of conserved regions of V2 and V3, where they bind.

[0136] Figure 31 is a computer-generated three-dimensional depiction of highly conserved epitopes on the HIV spike, including the V1/V2 and V3 loops to which PG9 and PG16 bind and the epitopes to which PGT-121, PGT-122, PGT-123, PGT-125, PGT-126, PGT-130, PGT-135, PGT-136, PGT-141, PGT-142, PGT-143, and PGT-144.

[0137] Figure 32 is a graph depicting the potency of monoclonal anti-HIV antibodies PGT-121, PGT-122, PGT-123, PGT-125, PGT-126, PGT-127, PGT-128, PGT-130, PGT-131, PGT-135, PGT-136, PGT-137, PGT-141, PGT-142, PGT-143, PGT-144, PGT-145, and PG9, expressed as the half-maximal inhibitory concentration, or IC₅₀ (μg/ml). The bar for each antibody represents the median IC₅₀ value.

[0138] Figure 33A-D is a series of graphs depicting the newly identified PGT antibodies redefine broad and potent neutralisation of HIV. A, Key MAbs fully recapitulate serum neutralization by the corresponding donor serum. Serum breadth was correlated with the breadth of the broadest MAb for each donor (% viruses neutralized at NT₅₀ > 100 or IC₅₀ < 50 μg/ml, respectively). Of note, MAbs isolated from donor 39 could not completely recapitulate the serum neutralization breadth. B-D. Certain antibodies or antibody combinations are able to cover a broad range of HIV isolates at low, vaccine achievable, concentrations. B, Cumulative frequency distribution of IC₅₀ values of broadly neutralizing MAbs tested against a 162-virus panel. The y-axis shows the cumulative frequency of IC₅₀ values up to the concentration shown on the x-axis and can therefore also be interpreted as the breadth at a specific IC₅₀ cut-off. C-D, Percent viruses covered by single MAbs (solid lines) or by at least one of the MAbs in dual combinations (dashed black lines) dependent on individual concentrations. The grey area in both panels is the coverage of 26 MAbs tested on the 162-virus panel (PGT121-123, PGT125-128, PGT130-131, PGT135-137, PGT141-145, PG9, PG16, PGC14, VRC01, PGV04, b12, 2G12, 4E10, 2F5) and depicts the theoretical maximal achievable coverage known to date.

[0139] Figure 34A is a table depicting the competition of PGT MAbs with sCD4 (soluble CD4), b12 (anti-CD4bs), 2G12 (anti-glycan), F425/b4e8 (anti-V3), X5 (CD4i), PG9 (anti-V1/V2

and V3, quaternary) and each other. Competition assays were performed by ELISA using gp120_{Bal} or gp120_{JR-FL}, except for the PG9 competition assay, which was performed on the surface of JR-FL_{E168K} or JR-CSF transfected cells. Boxes are color coded as follows: red, 75-100% competition; orange, 50-75% competition; yellow, 25-50% competition; gray, <25% competition. Experiments were performed in duplicate, and data represent an average of at least two independent experiments.

[0140] Figure 34B-D is a series of graphs depicting the epitope mapping of PGT antibodies. b, Glycan microarray analysis (Consortium for Functional Glycomics, CFG, v 5.0) reveals that PGT MAbs 125, 126, 127, 128, and 130 contact Man₈ (313), Man₈GlcNAc₂ (193), Man₉ (314) and Man₉GlcNAc₂ (194) glycans directly. Only glycans structures with RFU (relative fluorescent units) > 3000 are shown. PGT-131 showed no detectable binding to the CFG glycan array but bound to Man₉-oligodendrons³⁰ (data not shown). Error bars represent standard deviation. c, d, Binding of PGT MAbs 125, 126, 127, 128 and 130 to gp120 is competed by Man₉ oligodendrons but not Man₄ oligodendrons. Binding of 131 to immobilized gp120 was too low to measure any competition.

[0141] Figure 35 is a series of graphs depicting the lack of polyreactivity of PGT monoclonal antibodies (mAbs) in ELISA assay. PGT mAbs were tested for ELISA reactivity against a panel of antigens. The bNAbs b12 and 4E10 were also included for comparison. d.s, double-stranded; s.s, single-stranded.

[0142] Figure 36 is a series of graphs depicting the results of an analysis of neutralization activity by virus clades. Cumulative frequency distribution of IC₅₀ values of broadly neutralizing MAbs tested against a 162 virus panel separated by clades A, B, C, D, F, G, AE and AG. VRC01 was tested on a different virus panel (n = 190, ref 6).

[0143] Figure 37A-D is a series of graphs showing that MAb neutralization correlates strongly with serum neutralization. Correlation of IC₅₀s of the MAbs and serum NT₅₀s of the corresponding donors 17 (a), 36 (b), 39 (c) and 84 (d) is shown. Spearman correlation was used for statistical analyses. Only viruses neutralized by either the MAb (IC₅₀ < 50 µg/ml) or the serum (NT₅₀ > 100) were included.

[0144] Figure 38A-B is a series of graphs showing that PGT 141-145 bind preferentially to cell-surface expressed trimers. A) Binding of PGTs 141-145 to monomeric gp120 and artificially trimerized gp140 constructs as determined by ELISA. The bNAbs b12 and PG9 are included for

comparison. OD, optical density (absorbance at 450 nm). B) Binding of PGTs 141-145 to Env expressed on the surface of 293T cells as determined by flow cytometry. The bNAbs 2G12 and PG9 are included for comparison.

[0145] Figure 39A-B is a series of graphs showing that PGT mAbs 141-145 bind to epitopes overlapping those of PG9 and PG16. A) PGTs 141-145 are sensitive to the N160K mutation and PGTs 141-144 fail to neutralize pseudoviruses produced in the presence of kifunensine. The bNAb 2G12 was also included for comparison. B) PG9 competes with PGTs 141-145 for binding to cell-surface trimers. The bNAb 2G12 was included as a negative control.

[0146] Figure 40A-B is a series of graphs showing PGTs 121, 122 and 123 in competition with oligodendrons. Unlike PGTs 125, 126, 127, 128 and 130, the binding of PGTs 121, 122 and 123 to gp120 could not be competed by A) Man₄ or B) Man₉ dendrons.

[0147] Figure 41 is a series of graphs showing the neutralization activity of Fab fragments. Fab fragments of PGTs-125, 126, 127, 128, 130 and 131 were generated by Lys-C digestion and the neutralizing activity tested against HIV-1_{JR-CSF} using a single round of replication pseudovirus assay.

[0148] Figure 42A-B is a series of graphs showing that the combination of two or three antibody specificities is sufficient to cover a broad range of HIV isolates at vaccine achievable concentration. Cumulative frequency distribution of IC₅₀ values of double (**a**) and triple (**b**) combinations of neutralization activities (overall lowest IC₅₀ against each isolate). The grey area depicts the theoretical maximal achievable neutralization activity known to date.

[0149] Figure 43A-C is a series of graphs showing that combinations of two or three antibody specificities are sufficient to cover a broad range of HIV isolates at vaccine achievable concentrations. A-C Cumulative frequency distribution of IC₅₀ values of single MAb (solid lines) and combined neutralisation activity (overall lowest IC₅₀ against each isolate) of two or three MABs (dashed lines). The grey area is the combined neutralisation activity of 25 MABs tested on the 162-virus panel (b12, 2G12, 4E10, 2F5, PG9, PG16, PGC14, PGV04, PGTs 121-123, PGTs 125-128, PGTs 130-131, PGTs 135-137, PGTs 141-145) and depicts the theoretical maximal achievable neutralisation activity known to date. VRC01 and PGV04 in panel c are measured on a different virus panel (n = 97).

[0150] Figure 44A-M is a series of graphs depicting the percent of viruses covered by single MABs (solid lines) or by at least one of the MABs in dual combinations (dashed black lines)

dependent on individual concentrations. The grey area in all panels is the coverage of 26 MAbs tested on the 162-virus panel (PGT121-123, PGT125-128, PGT130-131, PGT135-137, PGT141-145, PG9, PG16, PGC14, VRC01, PGV04, b12, 2G12, 4E10, 2F5) and depicts the theoretical maximal achievable coverage known to date.

DETAILED DESCRIPTION OF THE INVENTION

[0151] In the sera of human immunodeficiency virus type 1 (HIV-1) infected patients, anti-virus antibodies can be detected over a certain period after infection without any clinical manifestations of the acquired immunodeficiency syndrome (AIDS). At this state of active immune response, high numbers of antigen-specific B-cells are expected in the circulation. These B-cells are used as fusion partners for the generation of human monoclonal anti-HIV antibodies. One major drawback to finding a vaccine composition suitable for more reliable prevention of human individuals from HIV-1 infection and/or for more successful therapeutic treatment of infected patients is the ability of the HIV-1 virus to escape antibody capture by genetic variation, which very often renders the remarkable efforts of the researchers almost useless. Such escape mutants may be characterized by a change of only one or several of the amino acids within one of the targeted antigenic determinants and may occur, for example, as a result of spontaneous or induced mutation. In addition to genetic variation, certain other properties of the HIV-1 envelope glycoprotein makes it difficult to elicit neutralizing antibodies making generation of undesirable non-neutralizing antibodies a major concern (see, Phogat SK and Wyatt RT, Curr Pharm Design 2007;13(2):213-227).

[0152] HIV-1 is among the most genetically diverse viral pathogens. Of the three main branches of the HIV-1 phylogenetic tree, the M (main), N (new), and O (outlier) groups, group M viruses are the most widespread, accounting for over 99% of global infections. This group is presently divided into nine distinct genetic subtypes, or clades (A through K), based on full-length sequences. Env is the most variable HIV-1 gene, with up to 35% sequence diversity between clades, 20% sequence diversity within clades, and up to 10% sequence diversity in a single infected person (Shankarappa, R. et al. 1999. J. Virol. 73:10489-10502). Clade B is dominant in Europe, the Americas, and Australia. Clade C is common in southern Africa, China, and India and presently infects more people worldwide than any other clade (McCutchan, FE. 2000. Understanding the genetic diversity of HIV-1. AIDS 14(Suppl. 3):S31-S44). Clades A and D are prominent in central and eastern Africa.

[0153] Neutralizing antibodies (NAbs) against viral envelope proteins (Env) provide adaptive immune defense against human immunodeficiency virus type 1 (HIV-1) exposure by blocking the infection of susceptible cells (Kwong PD et al., 2002. *Nature* 420: 678–682). The efficacy of vaccines against several viruses has been attributed to their ability to elicit NAbs. However, despite enormous efforts, there has been limited progress toward an effective immunogen for HIV-1. (Burton, D. R. 2002. *Nat. Rev. Immunol.* 2:706-713).

[0154] HIV-1 has evolved with an extensive array of strategies to evade antibody-mediated neutralization. (Barouch, D.H. *Nature* 455, 613-619 (2008); Kwong, P.D. & Wilson, I.A. *Nat Immunol* 10, 573-578 (2009); Karlsson Hedestam, G.B., et al. *Nat Rev Microbiol* 6, 143-155 (2008)). However, broadly neutralizing antibodies (bNAbs) develop over time in a proportion of HIV-1 infected individuals. (Leonidas Stamatatos, L.M., Dennis R Burton, and John Mascola. *Nature Medicine* (E-Pub: Jun. 14, 2009); PMID: 19525964.) A handful of broadly neutralizing monoclonal antibodies have been isolated from clade B infected donors. (Burton, D.R., et al. *Science* 266, 1024-1027 (1994); Trkola, A., et al. *J Virol* 69, 6609-6617 (1995); Stiegler, G., et al. *AIDS Res Hum Retroviruses* 17, 1757-1765 (2001)). These antibodies tend to display less breadth and potency against non-clade B viruses, and they recognize epitopes on the virus that have so far failed to elicit broadly neutralizing responses when incorporated into a diverse range of immunogens. (Phogat, S. & Wyatt, R. *Curr Pharm Design* 13, 213-227 (2007); Montero, M., van Houten, N.E., Wang, X. & Scott, J.K. *Microbiol Mol Biol Rev* 72, 54-84, table of contents (2008); Scanlan, C.N., Offer, J., Zitzmann, N. & Dwek, R.A. *Nature* 446, 1038-1045 (2007)). Despite the enormous diversity of the human immunodeficiency virus (HIV), all HIV viruses known to date interact with the same cellular receptors (CD4 and/or a co-receptor, CCR5 or CXCR4). Most neutralizing antibodies bind to functional regions involved in receptor interactions and cell membrane fusion. However, the vast majority of neutralizing antibodies isolated to date do not recognize more than one clade, therefore exhibiting limited protective efficacy in vitro or in vivo. (See Binley JM et al., 2004. *J. Virol.* 78(23):13232-13252). The rare broadly neutralizing human monoclonal antibodies (mAbs) that have been isolated from HIV+ clade B-infected human donors bind to products of the env gene of HIV-1, gp120 and the transmembrane protein gp41. (Parren, PW et al. 1999. *AIDS* 13:S137-S162). However, a well-known characteristic of the HIV-1 envelope glycoprotein is its extreme variability. It has been recognized that even relatively conserved epitopes on HIV-1, such as the CD4 binding site, show

some variability between different isolates (Poignard, P., et al., *Ann. Rev. Immunol.* (2001) 19:253–274). Even an antibody targeted to one of these conserved sites can be expected to suffer from a reduced breadth of reactivity across multiple different isolates.

[0155] The few cross-clade reactive monoclonal antibodies known to date have been isolated by processes involving generation of panels of specific viral antibodies from peripheral blood lymphocytes (PBLs) of HIV-infected individuals, either via phage display, or via conventional immortalization techniques such as hybridoma or Epstein Barr virus transformation, electrofusion and the like. These are selected based on reactivity in vitro to HIV-1 proteins, followed by testing for HIV neutralization activity.

[0156] An antibody phage surface expression system was used to isolate the cross-clade neutralizing Fab (fragment, antigen binding) b12 occurring in a combinatorial library. The Fab b12 was screened by panning for envelope glycoprotein gp120 binding activity and neutralizing activity against the HIV-1 (HXBc2) isolate was observed. (Roben P et al., *J. Virol.* 68(8): 4821-4828(1994); Barbas CF et al., *Proc. Natl. Acad. Sci. USA* Vol. 89, pp. 9339-9343, (1992); Burton DP et al., *Proc. Natl. Acad. Sci. USA* Vol. 88, pp. 10134-10137 (1991)).

[0157] Human B cell immortalization was used to isolate the cross-clade neutralizing monoclonal antibodies 2G12, 2F5, and 4E10 from HIV-infected individuals. The monoclonal antibody 2G12 binds to a glycotope on the gp120 surface glycoprotein of HIV-1 and had been shown to display broad neutralizing patterns. (Trkola A., et al., *J. Virol.* 70(2):1100-1108 (1996), Buchacher, A., et al., 1994. *AIDS Res. Hum. Retroviruses* 10:359–369). The monoclonal antibody 2F5 which had been shown to bind a sequence within the external domain of the gp41 envelope glycoprotein of HIV-1 was found to have broad neutralization properties. (Conley AJ *Proc. Natl. Acad. Sci. USA* Vol. 91, pp. 3348-3352 (1994); Muster T et al., *J. Virol.* 67(11):6642-6647 (1993); Buchacher A et al., 1992, *Vaccines* 92:191-195). The monoclonal antibody 4E10, which binds to a novel epitope C terminal of the ELDKWA sequence in gp41 recognized by 2F5, has also been found to have potent cross-clade neutralization activity. (Buchacher, A., et al., 1994. *AIDS Res. Hum. Retroviruses* 10:359–369; Stiegler, G., et al., 2001. *AIDS Res. Hum. Retroviruses* 17(18):1757-1765)).

[0158] Other studies on antibody neutralization of HIV-1 (Nara, P. L., et al. (1991) *FASEB J.* 5:2437-2455.) focused on a single linear epitope in the third hypervariable region of the viral envelope glycoprotein gp120 known as the V3 loop. Antibodies to this loop are suggested to

neutralize by inhibiting fusion of viral and cell membranes. However there is sequence variability within the loop and neutralizing antibodies are sensitive to sequence variations outside the loop (Albert J. et al., (1990) AIDS 4, 107-112). Hence anti-V3 loop antibodies are often strain-specific and mutations in the loop in vivo may provide a mechanism for viral escape from antibody neutralization. There is some indication that not all neutralizing antibodies act by blocking the attachment of virus, since a number of mouse monoclonal antibodies inhibiting CD4 binding to gp120 are either non-neutralizing (Lasky LA, et al., (1987) Cell 50:975-985.) or only weakly neutralizing (Sun N., et al., (1989) J. Virol. 63, 3579-3585).

[0159] It is widely accepted that such a vaccine will require both T-cell mediated immunity as well as the elicitation of a broadly neutralizing antibody (bNAb) response. (Barouch, D.H. Nature 455, 613-619 (2008); Walker, B.D. & Burton, D.R. Science 320, 760-764 (2008); Johnston, M.I. & Fauci, A.S. N Engl J Med 356, 2073-2081 (2007)). All of the known bNAbs provide protection in the best available primate models (Veazey, R.S., et al. Nat Med 9, 343-346 (2003); Hessel, A.J., et al. PLoS Pathog 5, e1000433 (2009); Parren, P.W., et al. J Virol 75, 8340-8347 (2001); Mascola, J.R. Vaccine 20, 1922-1925 (2002); Mascola, J.R., et al. Nat Med 6, 207-210 (2000); Mascola, J.R., et al. J Virol 73, 4009-4018 (1999)). Therefore, broadly neutralizing antibodies (bNAbs) are considered to be the types of antibodies that should be elicited by a vaccine. Unfortunately, existing immunogens, often designed based on these bNAbs, have failed to elicit NAb responses of the required breadth and potency. Therefore, it is of high priority to identify new bNAbs that bind to epitopes that may be more amenable to incorporation into immunogens for elicitation of NAb responses.

[0160] The present invention provides a novel method for isolating novel broad and potent neutralizing monoclonal antibodies against HIV. The method involves selection of a PBMC donor with high neutralization titer of antibodies in the plasma. B cells are screened for neutralization activity prior to rescue of antibodies. Novel broadly neutralizing antibodies are obtained by emphasizing neutralization as the initial screen.

[0161] The invention relates to potent, broadly neutralizing antibody (bNAb) wherein the antibody neutralizes HIV-1 species belonging to two or more clades, and further wherein the potency of neutralization of at least one member of each clade is determined by an IC₅₀ value of less than 0.2 µg/mL. In some aspects, the clades are selected from Clade A, Clade B, Clade C, Clade D and Clade AE. In some aspects, the HIV-1 belonging two or more clades are non-Clade

B viruses. In some aspects, the broadly neutralizing antibody neutralizes at least 60% of the HIV-1 strains listed in Tables 18A-18F. In some embodiments, at least 70%, or at least 80%, or at least 90% of the HIV-1 strains listed in Tables 18A-18F are neutralized.

[0162] The invention relates to potent, broadly neutralizing antibody (bNAb) wherein the antibody neutralizes HIV-1 species with a potency of neutralization of at least a plurality of HIV-1 species with an IC₅₀ value of less than 0.2 µg/mL. In some embodiments the potency of neutralization of the HIV-1 species has an IC₅₀ value of less than 0.15 µg/mL, or less than 0.10 µg/mL, or less than 0.05 µg/mL. In some aspects, a potent, broadly neutralizing antibody is defined as a bNAb that displays a potency of neutralization of at least a plurality of HIV-1 species with an IC₉₀ value of less than 2.0 µg/mL. In some embodiments the potency of neutralization of the HIV-1 species has an IC₉₀ value of less than 1.0 µg/mL, or less than 0.5 µg/mL.

[0163] An exemplary method is illustrated in the schematic shown in Figure 4. Peripheral Blood Mononuclear Cells (PBMCs) were obtained from an HIV-infected donor selected for HIV-1 neutralizing activity in the plasma. Memory B cells were isolated and B cell culture supernatants were subjected to a primary screen of neutralization assay in a high throughput format. Optionally, HIV antigen binding assays using ELISA or like methods were also used as a screen. B cell lysates corresponding to supernatants exhibiting neutralizing activity were selected for rescue of monoclonal antibodies by standard recombinant methods.

[0164] In one embodiment, the recombinant rescue of the monoclonal antibodies involves use of a B cell culture system as described in Weitzcamp J-H et al., *J. Immunol.* 171:4680-4688 (2003). Any other method for rescue of single B cells clones known in the art also may be employed such as EBV immortalization of B cells (Traggiai E., et al., *Nat. Med.* 10(8):871-875 (2004)), electrofusion (Buchacher, A., et al., 1994. *AIDS Res. Hum. Retroviruses* 10:359-369), and B cell hybridoma (Karpas A. et al., *Proc. Natl. Acad. Sci. USA* 98:1799-1804 (2001)).

[0165] In some embodiments, monoclonal antibodies were rescued from the B cell cultures using variable chain gene-specific RT-PCR, and transfectant with combinations of H and L chain clones were screened again for neutralization and HIV antigen binding activities. mAbs with neutralization properties were selected for further characterization.

[0166] A novel high-throughput strategy was used to screen IgG-containing culture screening supernatants from approximately 30,000 activated memory B cells from a clade A

infected donor for recombinant, monomeric gp120JR-CSF and gp41HxB2 (Env) binding as well as neutralization activity against HIV-1JR-CSF and HIV-1SF162 (See Table 1).

Table 1: Memory B cell Screening.

Total number of wells screened	23,328
Number of sIgG ⁺ memory B cells screened	30,300
gp120 ELISA hits	411 (1.36%)
gp41 ELISA hits	167 (0.55%)
SF162 neutralization hits	401 (1.32%)
JR-CSF neutralization hits	401 (1.32%)

[0167] Unexpectedly, a large proportion of the B cell supernatants that neutralized HIV-1JR-CSF did not bind monomeric gp120JR-CSF or gp41HxB2, and there were only a limited number of cultures that neutralized both viruses (Fig. 3B). Antibody genes were rescued from five B cell cultures selected for differing functional profiles; one bound to gp120 and only neutralized HIV-1SF162, two bound to gp120 and weakly neutralized both viruses, and two potently neutralized HIV-1JR-CSF, failed to neutralize HIV-1SF162, and did not bind to monomeric gp120 or gp41. Five antibodies identified according to these methods are disclosed herein. The antibodies were isolated from a human sample obtained through International AIDS Vaccine Initiative's (IAVI's) Protocol G, and are produced by the B cell cultures referred to as 1443_C16 (PG16) (TCN-116), 1503_H05 (PG16) (TCN-119), 1456_A12 (PG16) (TCN-117), 1469_M23 (PG16) (TCN-118), 1489_I13 (PG16) (TCN-120), 1480_I08 (PG16), 1456_P20 (PG20), 1460_G14 (PGG14), 1495_C14 (PGC14), 1496_C09 (PG9) (TCN-109), 4838_L06 (PGT-121), 4873_E03 (PGT-121), 4877_D15 (PGT-122), 4858_P08 (PGT-123), 6123_A06 (PGT-125), 5141_B17 (PGT-126), 5145_B14 (PGT-127), 5114_A19 (PGT-128), 5147_N06 (PGT-130), 5136_H01 (PGT-131), 5343_B08 (PGT-135), 5344_E16 (PGT-135), 5329_C19 (PGT-136), 5366_P21 (PGT-136), 4964_G22 (PGT-141), 5345_I01 (PGT-137), 4993_K13 (PGT-141), 4995_E20 (PGT-142), 4980_N08 (PGT-143), 4970_K22 (PGT-144), 4995_P16 (PGT-145), 4835_F12 (PGT-124), 4869_K15 (PGT-133), 4876_M06 (PGT-134), 5131_A17 (PGT-132), 5138_G07 (PGT-138), 5120_N10 (PGT-139), 6831_A21 (PGT-151), 6889_I17 (PGT-152), 6891_F06 (PGT-153), 6843_G20 (PGT-154), 6892_D19 (PGT-155), 6808_B09 (PGT-156), 6892_C23 (PGT-157), and 6881_N05 (PGT-158). Antibodies referred to as 1443_C16 (PG16) (TCN-116), 1503_H05 (PG16) (TCN-119), 1456_A12 (PG16) (TCN-117), 1469_M23 (PG16) (TCN-118), 1489_I13 (PG16) (TCN-120), 1480_I08 (PG16), 1456_P20 (PG20), 1460_G14 (PGG14), 1495_C14

(PGC14), 1496_C09 (PG9) (TCN-109), 4838_L06 (PGT-121), 4873_E03 (PGT-121), 4877_D15 (PGT-122), 4858_P08 (PGT-123), 6123_A06 (PGT-125), 5141_B17 (PGT-126), 5145_B14 (PGT-127), 5114_A19 (PGT-128), 5147_N06 (PGT-130), 5136_H01 (PGT-131), 5343_B08 (PGT-135), 5344_E16 (PGT-135), 5329_C19 (PGT-136), 5366_P21 (PGT-136), 4964_G22 (PGT-141), 5345_I01 (PGT-137), 4993_K13 (PGT-141), 4995_E20 (PGT-142), 4980_N08 (PGT-143), 4970_K22 (PGT-144), 4995_P16 (PGT-145), 4835_F12 (PGT-124), 4869_K15 (PGT-133), 4876_M06 (PGT-134), 5131_A17 (PGT-132), 5138_G07 (PGT-138), 5120_N10 (PGT-139), 6831_A21 (PGT-151), 6889_I17 (PGT-152), 6891_F06 (PGT-153), 6843_G20 (PGT-154), 6892_D19 (PGT-155), 6808_B09 (PGT-156), 6892_C23 (PGT-157), and 6881_N05 (PGT-158), were isolated from the corresponding B cell cultures. These antibodies have been shown to neutralize HIV in vitro.

[0168] Analysis of the antibody variable genes revealed that two antibody pairs were related by somatic hypermutation and that two of the somatic variants contained unusually long CDRH3 loops (Table 2). Long CDRH3 loops have previously been associated with polyreactivity. (Ichiyoshi, Y. & Casali, P. J Exp Med 180, 885-895 (1994)). The antibodies were tested against a panel of antigens and the antibodies were confirmed to be not polyreactive.

Table 2: Sequence Analysis of mAb Variable Genes

Clone	Germline IGVL ^a	Germline IGVH ^a	CDRL 3 ^b	SEQ ID NO:	CDRH3 ^b	SEQ ID NO:
PG16	VL2- 14*01	VH3- 33*05	SSLTD RSHR IF	1	EAGGPIWHDDVKY YDFNDGYNYHY MDV	6
PG9	VL2- 14*01	VH3- 33*05	KSLT STRR RVF	2	EAGGPDYRNGYNY YDFYDGYNYHY MDV	7
PGG1 4	VK1- 39*01	VH1- 69*12	SYSTP RTF	3	DRRVVPMATDNW LDP	8
PG20	VK2- 14*01	VH1- 69*12	SFSTP RTF	4	DRRAVPIATDNWL DP	9
PGC1 4	VL3-1*01	VH1- 24*01	AWET TTTTF VFF	5	GAVGADSGSWFDP	10

^a Germ line gene sequences were determined using the IMGT database, which is publicly available at imgt.cines.fr. "L" and "K" refer to lambda and kappa chains, respectively,

^b Bolded amino acids denote differences between somatic variants.

Table 3A. Heavy Chain Gene Usage Summary

mAb ID	mAb Specificity	V-Gene & allele	V-Gene identity	J-Gene & allele	J-Gene identity	CDR3
1443_C16	ELISA-negative	IGHV3-33*05	85.07% (245/288 nt)	IGHJ6*03	85.48% (53/62 nt)	AREAGGPIWHDDVK YYDFNDGYNYHYM DV (SEQ ID NO: 46)
1456_P20	gp120	IGHV1-69*11 or IGHV1-69*12	85.07% (245/288 nt)	IGHJ5*02	88.24% (45/51 nt)	ARDRRAVPIATDNWL DP (SEQ ID NO: 47)
1460_G14	gp120	IGHV1-69*11 or IGHV1-69*12	86.11% (248/288 nt)	IGHJ5*02	86.27% (44/51 nt)	TRDRRVVPMATDNW LDP (SEQ ID NO: 48)
1495_C14	gp120	IGHV1-f*01	88.89% (256/288 nt)	IGHJ5*02	84.31% (43/51 nt)	AAGAVGADSGSWFD P (SEQ ID NO: 49)
1496_C09	ELISA-negative	IGHV3-33*05	85.07% (245/288 nt)	IGHJ6*03	83.87% (52/62 nt)	VREAGGPDYRNGYN YYDFYDGYNYHYM DV (SEQ ID NO: 50)

Table 3B. Light Chain Gene Usage Summary

mAb ID	mAb Specificity	V-Gene and allele	V-gene identity	J-GENE and allele	J-Gene identity	CDR3	SEQ ID NO:
1443_C16	ELISA-negative	IGLV2-14*01	88.19% (254/288 nt)	IGLJ2*01 or IGLJ3*01 or IGLJ3*02	83.33% (30/36 nt)	SSLTDRSHRI	41
1456_P20	gp120	IGKV1-39*01, or IGKV1D-39*01	92.11% (257/279 nt)	IGKJ5*01	92.11% (35/38 nt)	QQSFSTPRT	42
1460_G14	gp120	IGKV1-39*01, or IGKV1D-39*01	92.11% (257/279 nt)	IGKJ5*01	89.47% (34/38 nt)	QQSYSTPRT	43
1495_C14	gp120	IGLV3-1*01	88.89% (248/279 nt)	IGLJ2*01 or IGLJ3*01	86.84% (33/38 nt)	QAWETTTTT FVF	44
1496_C09	ELISA-negative	IGLV2-14*01	91.32% (263/288 nt)	IGLJ3*02	86.11% (31/36 nt)	KSLTSTRRRV	45

[0169] The broadly neutralizing antibodies from 1443_C16 (PG16) and 1496_C09 (PG9) clones obtained by this method did not exhibit soluble gp120 or gp41 binding at levels that correlate with neutralization activity. The method of the invention therefore allows identification of novel antibodies with broad cross-clade neutralization properties regardless of binding activities in an ELISA screen. Further characterization of PG16 and PG9 is disclosed herein.

[0170] All five antibodies were first tested for neutralization activity against a multi-clade 16-pseudovirus panel (Table 4). Two of the antibodies that bound to monomeric gp120 in the initial screen (PGG14 and PG20) did not show substantial neutralization breadth or potency against any of the viruses tested, and the third antibody that bound to gp120 (PGC14) neutralized 4/16 viruses with varying degrees of potency. In contrast, the two antibodies that failed to bind recombinant Env in the initial screen (PG9 and PG16) neutralized a large proportion of the viruses at sub-microgram per ml concentrations. PG9 and PG16 neutralized non-clade B viruses with greater breadth than three out of the four existing bNAbs. This is significant considering that the majority of HIV-1 infected individuals worldwide are infected with non-clade B viruses.

Table 4: Neutralization Profiles of Rescued mAbs

	Isolate	IC50 (µg/mL)				
		PGC14	PG9	PG16	PGG14	P20
Clade A	94UG163	>50	0.17	0.000	>50	>50
	92RW028	>50	0.06	0.004*	>50	>50
	93UG077	>50	>50	>50	>50	>50
Clade B	92BR026	0.04	>50	>50	>50	>50
	APV-13	>50	>50	>50	>50	>50
	JRC8F	>50	<0.0025	<0.0025	>50	>50
	APV-17	>50	26.45	>50	>50	>50
	APV-6	7.41	0.09	0.002	>50	25.770
Clade C	93IN905	>50	N/A	0.10*	>50	>50
	IAVL-C18	>50	0.05	0.007	>50	>50
	IAVL-C22	>50	N/A	0.009*	>50	>50
	IAVL-C3	9.50	12.94	14.00	>50	>50
Clade D	92UG024	>50	10.96	>50	>50	>50
	92UG005	>50	>50	>50	>50	>50
CRF01_AE	92TH021	>50	0.11	0.13*	>50	>50
	CMU02	>50	>50	>50	>50	>50
negative control	aMLV	>50	>50	>50	>50	>50

* Plateau observed in curve.

[0171] Table 17A shows neutralization profiles (IC50 values) of monoclonal antibodies 1443_C16 (PG16), 1456_P20 (PG20), 1460_G14 (PGG14), 1495_C14 (PGC14) and 1496_C09 (PG9) and the known cross-clade neutralizing antibodies b12, 2G12, 2F5 and 4E10 on a diverse panel of 16 HIV pseudoviruses from different clades. 1443_C16 (PG16) and 1496_C09 (PG9)

neutralize HIV-1 species from Clades A, B, C, D and CRF01_AE with better potency for most viral strains tested than known and generally accepted broad and potent neutralizing antibodies. However, neutralization profiles of individual species of HIV-1 belonging to these clades vary between 1443_C16 (PG16) and 1496_C09 (PG9) and the known cross-clade neutralizing antibodies b12, 2G12, 2F5 and 4E10. 1495_C14 (PGC14) neutralizes fewer HIV-1 species from Clades A, B and C comparable to other neutralizing antibodies. Table 17B shows IC90 values of the monoclonal antibodies 1443_C16 (PG16) and 1496_C09 (PG9) and the known cross-clade neutralizing antibodies b12, 2G12, 2F5 and 4E10 on the same panel of pseudoviruses. Figure 4 shows neutralization activities of monoclonal antibodies 1443_C16 (PG16) and 1496_C09 (PG9) to six other HIV pseudoviruses (YU2, Bal, ADA, DU172, DU422, and ZM197) for clades B and C not included in Tables 17A and 17B.

[0172] PG9, PG16, and PGC14 were next evaluated on a large multi-clade pseudovirus panel consisting of 162 viruses to further assess the neutralization breadth and potency of these three antibodies (Tables 5A-5B, Tables 18A-18F and Tables 19A-19B). The bNAbs b12, 2G12, 2F5, and 4E10, as well as the donor's serum, were also included in the panel for comparison. Overall, PG9 neutralized 127 out of 162 and PG16 neutralized 119 out of 162 viruses with a potency that frequently considerably exceeded that noted for the four control bNAbs.

[0173] The median IC50 and IC90 values for neutralized viruses across all clades were an order of magnitude lower for PG9 and PG16 than any of the four existing bNAbs (Table 5A, Tables 18A-18F and Tables 19A-19B). Both mAbs showed overall greater neutralization breadth than b12, 2G12, and 2F5 (Table 5B, Tables 18A-18F and Tables 19A-19B). At low antibody concentrations, PG9 and PG16 also demonstrated greater neutralization breadth than 4E10 (Table 5B). Furthermore, both mAbs potently neutralized one virus (IAVI-C18) that exhibits resistance to all four existing bNAbs (Tables 18A-18F). The mAb neutralization curves reveal that, whereas the PG9 neutralization curves usually exhibit sharp slopes, the neutralization curves for PG16 sometimes exhibit gradual slopes or plateaus at less than 100% neutralization. Although neutralization curves with similar profiles have been reported previously (W. J. Honnen et al., J Virol 81, 1424 (Feb, 2007), A. Pinter et al., J Virol 79, 6909 (Jun, 2005)), the mechanism for this is not well understood.

[0174] Comparison of the neutralization profile of the serum with the neutralization profile of PG9, PG16 and PGC14 revealed that these three antibodies could recapitulate the breadth of

the serum neutralization in most cases (Tables 18A-18F). For example, almost all of the viruses that were neutralized by the serum with an IC₅₀ > 1:500 were neutralized by PG9 and/or PG16 at <0.05 µg/mL. The one case where this did not occur was against HIV-1SF162, but this virus was potentially neutralized by PGC14. Despite the fact that PG9 and PG16 are somatic variants, they exhibited different degrees of potency against a number of the viruses tested. For instance, PG9 neutralized HIV-16535.30 approximately 185 times more potently than PG16, and PG16 neutralized HIV-1MGRM-AG-001 approximately 440 times more potently than PG9. In some cases, the two antibodies also differed in neutralization breadth; PG9 neutralized nine viruses that were not affected by PG16, and PG16 neutralized two viruses that were not affected by PG9. Based on these results, it is postulated that broad serum neutralization might be mediated by somatic antibody variants that recognize slightly different epitopes and display varying degrees of neutralization breadth and potency against any given virus. In the face of an evolving viral response, it seems reasonable that the immune system might select for these types of antibodies.

[0175] Comparison of the neutralization profile of the serum with the neutralization profile of PG9, PG16 and PGC14 revealed that these three antibodies could recapitulate the breadth of the serum neutralization in most cases. For example, almost all of the viruses that were neutralized by the serum with an IC₅₀ > 1:1000 were neutralized by PG9 and/or PG16 at <0.005 µg/mL. The one case where this did not occur was against HIV-1SF162, but this virus was potentially neutralized by PGC14. Tables 5(a) and 5(b) show the neutralization activities—breadth and potency, respectively -- of PG9, PG16, and PGC14 as well as four control bNAbs as measured by IC₅₀ values. Tables 19A-19B show results of the same analysis using IC₉₀ values.

Table 5(A). Neutralization Potency of mAbs

		Median IC ₅₀ (µg/mL) against viruses neutralized with an IC ₅₀ <50 µg/mL						
Clade ^a	# viruses	b12	2G12	2F5	4E10	PG9	PG16	PGC14
A	27	6.98	17.10	5.70	6.20	0.16	0.11	41.59
B	31	0.80	0.82	2.41	5.22	0.43	0.70	21.88
C	27	6.46	2.93	31.51	2.97	0.22	0.25	11.97
D	25	1.47	7.71	3.17	4.60	0.10	0.02	38.57
CRF01_AE	10	21.53	>50	0.26	0.51	0.08	0.03	>50
CRF_AG	10	10.40	0.95	0.64	1.42	0.80	0.03	45.10
G	15	3.07	31.03	1.24	1.44	0.29	1.21	>50

		Median IC ₅₀ (µg/mL) against viruses neutralized with an IC ₅₀ <50 µg/mL						
Clade ^a	# viruses	b12	2G12	2F5	4E10	PG9	PG16	PGC14
F	15	>50	9.23	1.78	2.30	0.09	0.05	25.71
Total	162	2.82	2.43	2.30	3.24	0.22	0.15	25.99

Boxes are color coded as follows: white, median potency >50 µg/mL; light grey, median potency between 2 and 20 µg/mL; medium grey, median potency between 0.2 and 2 µg/mL; dark grey, median potency <0.2 µg/mL.

^a CRF_07BC and CRF_08BC viruses are not included in the clade analysis because there was only one virus tested from each of these clades.

Table 5(B). Neutralization Breadth of mAbs

		% viruses neutralized with an IC ₅₀ <50 µg/mL						
Clade ^a	# viruses	b12	2G12	2F5	4E10	PG9	PG16	PGC14
A	27	30	37	74	96	85	85	11
B	31	58	71	68	97	74	74	29
C	27	33	11	7	96	78	78	19
D	25	48	24	56	96	76	60	8
CRF01_AE	10	30	0	89	100	100	100	0
CRF_A								
G	10	30	50	80	100	80	60	10
G	15	13	20	80	100	87	73	7
F	15	0	21	87	100	67	64	13
Total	162	35	32	60	98	79	73	15
		% viruses neutralized with an IC ₅₀ <1.0 µg/mL						
Clade	# viruses	b12	2G12	2F5	4E10	PG9	PG16	PGC14
A	27	0	4	4	0	70	63	0
B	31	32	39	23	0	45	42	3
C	27	7	0	0	11	56	48	0
D	25	12	8	12	8	48	44	0
CRF01_AE	10	11	0	88	80	70	70	0
CRF_AG	10	10	30	60	30	40	50	0
G	15	0	0	27	0	60	33	0
F	15	0	14	13	28	80	79	0
Total	162	11	12	19	12	57	51	1

Boxes are color coded as follows: white, no viruses neutralized; black, 1 to 30% of viruses neutralized; light grey, 30 to 60% of viruses neutralized; medium grey, 60 to 90% of viruses neutralized; dark grey, 90 to 100% of viruses neutralized.

^a CRF_07BC and CRF_08BC viruses are not included in the clade analysis because there was only one virus tested from each of these clades.

[0176] Despite the fact that PG9 and PG16 are somatic variants, they exhibited different degrees of potency against a number of the viruses tested. For instance, PG9 neutralized the virus 6535.30 about 100 times more potently than PG16, and PG16 neutralized the virus MGRM-AG-001 about 3000 times more potently than PG9. In some cases, the two antibodies also differed in neutralization breadth; PG9 neutralized seven viruses that were not neutralized by PG16, and PG16 neutralized three viruses that were not neutralized by PG9. Without being bound by theory, it appears that broad serum neutralization might be mediated by somatic variants that recognize slightly different epitopes and display varying degrees of neutralization breadth and potency against any given virus. In the face of an evolving viral response, the immune system likely selects for these types of antibodies.

[0177] The antibodies were also tested for ability to bind soluble recombinant HIV envelope proteins. Figure 5 shows dose response curves of 1456_P20 (PG20), 1495_C14 (PGC14) and 1460_G14 (PGG14) binding to recombinant gp120 in ELISA as compared to control anti-gp120 (b12). Figure 6 shows ELISA binding assays of monoclonal antibodies 1443_C16 (PG16) and 1496_C09 (PG9) to HIV-1 strain YU2 gp140 and JR-CSF gp120, the membrane proximal region (MPER) of HIV-1 envelope glycoprotein gp41, and the V3 polypeptide. PG-9 binds to YU2 gp140 (IC_{50} ~20-40 nM), YU2 gp120 and weakly binds to JR-CSF gp120. However, PG16 weakly binds Yu2 gp120, but not the soluble form of HIV-1 envelope glycoprotein, gp120 JR-CSF. Neither mAb binds to JR-FL gp120, JR-FL gp140, MPER peptide of gp41 or V3 peptide.

[0178] Figure 7 shows binding of monoclonal antibodies 1443_C16 (PG16) and 1496_C09 (PG9) to HIV-1 YU2 gp160 expressed on the cell surface in the presence and absence of sCD4. Competitive inhibition of the binding by sCD4 indicates that the binding of monoclonal antibody 1496_C09 to HIV-1 envelope protein gp160 expressed on the cell surface is presumably affected due to the conformational changes induced by sCD4. The data further suggest that 1443_C16 (PG16) and 1496_C09 (PG9) exhibit relatively stronger binding to trimeric forms of the HIV-1 Env (gp160 and gp140) than to the monomeric gp120.

[0179] Figure 8 shows binding of monoclonal antibodies 1443_C16 (PG16) and 1496_C09 (PG9) to HIV-1 transfected cells. PG9 and PG16 do not bind untransfected cells. PG9 and PG16 bind JR-CSF, ADA, and YU2 gp160 transfected cells. PG9 and PG16 do not bind JR-FL gp160

transfected cells (cleaved or uncleaved). PG9 and PG16 do not bind ADA $\Delta V1/\Delta V2$ transfected cells. PG9 and PG16 binding to JR-CSF gp160 transfected cells is inhibited by sCD4.

[0180] Figure 9 shows the capturing of entry-competent JR-CSF pseudovirus by neutralizing monoclonal antibodies 1443_C16 (PG16) and 1496_C09 (PG9) in a dose-dependent manner. The ability of both antibodies to capture JR-CSF pseudovirus is higher than IgG b12 but comparable to IgG 2G12. It is postulated that the capture may be mediated by the binding of the mAbs to the HIV-1 Env on the virions.

[0181] Figure 10A shows that sCD4, PG16 and PG9 compete for the binding of monoclonal antibody 1443_C16 (PG16) to JR-CSF pseudovirus but b12, 2G12, 2F5 and 4E10 do not. Figure 10B shows sCD4, PG16 and PG9 compete for the binding of monoclonal antibody 1496_C09 (PG9) to JR-CSF pseudovirus but b12, 2G12, 2F5 and 4E10 do not. This suggests that the PG16 and PG9 mAbs bind gp120 at a site different from those bound by b12 and 2G12. PG9 and PG16 binding to HIV-1 envelope protein is competitively inhibited by sCD4. Given that the MAbs are not inhibited by the CD4 binding site MAb b12, this suggests that PG9 and PG16 are binding to an epitope that is unavailable for sCD4 binding to gp120 as a result of conformational changes. The inability of PG9 and PG16 to bind monomeric gp120JR-CSF or gp41HxB2 in the initial screen while potently neutralizing HIV-1JR-CSF suggests that the epitope targeted by these antibodies is preferentially expressed on trimeric HIV envelope protein. The ability of PG9 and PG16 to bind monomeric gp120 from several different strains, artificially trimerized gp140 constructs, and trimeric Env expressed on the surface of transfected cells respectively, was compared. Although both antibodies bound with high affinity to cell surface Env, PG16 did not bind to any of the soluble gp120 or gp140 constructs and PG9 bound only weakly to monomeric gp120 and trimerized gp140 from certain strains (Fig. 11). It has been previously shown that a substantial fraction of cell surface Env is comprised of uncleaved gp160 molecules. (Pancera, M. & Wyatt, R. *Virology* 332, 145-156 (2005)). That PG9 and PG16 do not exhibit exclusive specificity for native HIV-1 trimers was confirmed by the fact that both antibodies bound with high affinity to cleavage-defective HIV-1YU2 trimers expressed on the surface of transfected cells (Figure 12).

[0182] The epitopes recognized by PG9 and PG16 were investigated. Since the PG9 and PG16 antibodies are somatic variants, they recognize the same or overlapping epitopes. Both antibodies cross-competed for binding to HIV-1JR-CSF transfected cells (Fig. 13A). Ligation of

monomeric gp120 or cell surface Env with soluble CD4 diminished binding of both PG9 and PG16, although neither antibody competed with CD4-binding site antibodies for trimer binding (Fig. 13A-13C). This result suggests that CD4-induced conformational changes cause a loss of the epitope targeted by the antibodies.

[0183] Since PG9 bound well enough to gp120 from certain isolates to generate ELISA binding curves, competition ELISAs were performed with PG9 using a panel of neutralizing and non-neutralizing antibodies. These data revealed that PG9 cross-competed with anti-V2, anti-V3, and to a lesser extent, CD4i antibodies for gp120. (Figures 13D and 14).

[0184] Neither PG9 nor PG16 bound to V1/V2 or V3 deleted HIV-1JR-CSF variants expressed on the surface of transfected cells, further suggesting contributions of variable loops in forming their epitopes (Fig. 13E).

[0185] To dissect the fine specificity of PG9 and PG16, alanine scanning was performed using a large panel of HIV-1JR-CSF Env alanine mutants that have been described previously (Pantophlet, R., et al. J Virol 77, 642-658 (2003); Pantophlet, R., et al. J Virol 83, 1649-1659 (2009); Darbha, R., et al. Biochemistry 43, 1410-1417 (2004); Scanlan, C.N., et al. J Virol 76, 7306-7321 (2002)) as well as several new alanine mutants. Pseudoviruses incorporating single Env alanine mutations were generated, and PG9 and PG16 were tested for neutralization activity against each mutant pseudovirus. Mutations that resulted in viral escape from PG9 and PG16 neutralization were considered important for formation of the PG9 and PG16 epitopes (Tables 12 and 13).

[0186] Based on these criteria, and consistent with the competition experiments, residues that form the epitopes recognized by PG9 and PG16 appear to be located in conserved regions of the V2 and V3 loops of gp120. Certain co-receptor binding site mutations also had an effect on PG9 and PG16 neutralization, albeit to a lesser extent. Generally, PG9 and PG16 were dependent on the same residues, although PG16 was more sensitive to mutations located in the tip of the V3 loop than PG9. Interestingly, although neither antibody bound to wild-type HIV-1JR-FL transfected cells, a D to K mutation at position 168 in the V2 loop of HIV-1JR-FL generated high-affinity PG9 and PG16 recognition (Tables 18A-18F). N156 and N160, sites of V2 N-glycosylation, also appear to be critical in forming the epitope since substitutions at these positions resulted in escape from PG9 and PG16 neutralization. Deglycosylation of gp120

abolished binding of PG9 (Fig. 16), confirming that certain glycans may be important in forming the epitope.

[0187] HIV-1 SF162 contains a rare N to K polymorphism at position 160, and mutation of this residue to an Asn renders this isolate sensitive to PG9 and PG16 (Fig. 17).

[0188] The preferential binding of PG9 and PG16 to native trimers could either be a consequence of gp120 subunit cross-linking or recognition of a preferred oligomeric gp120 conformation. To address this question, the binding profiles of PG9 and PG16 to mixed HIV-1YU2 trimers were examined, in which two gp120 subunits containing point mutations abolished binding of the two antibodies. A third substitution that abrogates binding of 2G12, which binds with high affinity to both monomeric gp120 and trimeric Env, was also introduced into the same construct as an internal control. Cell surface binding analysis revealed that all three antibodies bound to the mixed trimers with similar apparent affinity as to wild-type trimers and all saturated at a similar lower level (Fig. 18). This result suggests that the preference of PG9 and PG16 for trimeric Env is due to gp120 subunit presentation in the context of the trimeric spike rather than gp120 cross-linking.

[0189] It has been shown that NAb that bind to epitopes encompassing parts of the V2 or both the V2 and V3 domains can exhibit potency comparable to that of PG9 and PG16, although these antibodies have thus far displayed strong strain-specificity. (Honnen, W.J., *et al. J Virol* 81, 1424-1432 (2007); Gorny, M.K., *et al. J Virol* 79, 5232-5237 (2005)). Importantly, the epitopes recognized by these antibodies have been shown to differ from that of the clade B consensus sequence only by single amino acid substitutions, which suggested the existence of a relatively conserved structure within the V2 domain. (Honnen, W.J., *et al. J Virol* 81, 1424-1432 (2007)). The results observed with PG9 and PG16 confirm that this region serves as a potent neutralization target and demonstrates that antibodies that recognize conserved parts of V2 and V3 can possess broad reactivity.

[0190] The invention is based on novel monoclonal antibodies and antibody fragments that broadly and potently neutralize HIV infection. In some embodiments, these monoclonal antibodies and antibody fragments have a particularly high potency in neutralizing HIV infection *in vitro* across multiple clades or across a large number of different HIV species. Such antibodies are desirable, as only low concentrations are required to neutralize a given amount of virus. This facilitates higher levels of protection while administering lower amounts of antibody. Human

monoclonal antibodies and the immortalized B cell clones that secrete such antibodies are included within the scope of the invention.

[0191] The invention provides methods for using high throughput functional screening to select neutralizing antibodies with unprecedented breadth and potency. The invention relates to other potent and broadly neutralizing antibodies that can be developed using the same methods. In particular, the invention relates to potent, broadly neutralizing antibodies against different strains of HIV, wherein the bNAbs bind poorly to recombinant forms of Env. The invention provides two neutralizing antibodies, PG9 and PG16, with broad neutralizing activities particularly against non-clade B isolates. The invention provides vaccine-induced antibodies of high specificity that provide protection against a diverse range of the most prevalent isolates of HIV circulating worldwide. The invention provides antibodies with very high and broad neutralization potency, such as that exhibited by PG9 and PG16 *in vitro*, which provides protection at relatively modest serum concentrations, and are generated by vaccination unlike the broad NAbs known in the art. The invention provides immunogens that can be designed that focus the immune response on conserved regions of variable loops in the context of the trimeric spike of the gp120 subunit of the Env protein.

[0192] The invention also relates to the characterization of the epitope to which the antibodies bind and the use of that epitope in raising an immune response.

[0193] The invention also relates to various methods and uses involving the antibodies of the invention and the epitopes to which they bind. For example, monoclonal antibodies according to the invention can be used as therapeutics. In some aspects, the monoclonal antibodies are used for adjuvant therapy. Adjuvant therapy refers to treatment with the therapeutic monoclonal antibodies, wherein the adjuvant therapy is administered after the primary treatment to increase the chances of a cure or reduce the statistical risk of relapse.

[0194] The invention provides novel monoclonal or recombinant antibodies having particularly high potency in neutralizing HIV. The invention also provides fragments of these recombinant or monoclonal antibodies, particularly fragments that retain the antigen-binding activity of the antibodies, for example which retain at least one complementarity determining region (CDR) specific for HIV proteins. In this specification, by “high potency in neutralizing HIV” is meant that an antibody molecule of the invention neutralizes HIV in a standard assay at a concentration lower than antibodies known in the art.

[0195] Preferably, the antibody molecule of the present invention can neutralize at a concentration of 0.16 µg/ml or lower (i.e. 0.15, 0.125, 0.1, 0.075, 0.05, 0.025, 0.02, 0.016, 0.015, 0.0125, 0.01, 0.0075, 0.005, 0.004 or lower), preferably 0.016 µg/ml or lower (an antibody concentration of 10^{-8} or lower, preferably 10^{-9} M or lower, preferably 10^{-10} M or lower, i.e. 10^{-11} M, 10^{-12} M, 10^{-13} M or lower). This means that only very low concentrations of antibody are required for 50% neutralization of a clinical isolate of HIV in vitro. Potency can be measured using a standard neutralization assay as described in the art.

[0196] The antibodies of the invention are able to neutralize HIV. Monoclonal antibodies can be produced by known procedures, e.g., as described by R. Kennet et al. in “Monoclonal Antibodies and Functional Cell Lines; Progress and Applications”. Plenum Press (New York), 1984. Further materials and methods applied are based on known procedures, e.g., such as described in J. Virol. 67:6642-6647, 1993.

[0197] These antibodies can be used as prophylactic or therapeutic agents upon appropriate formulation, or as a diagnostic tool.

[0198] A “neutralizing antibody” is one that can neutralize the ability of that pathogen to initiate and/or perpetuate an infection in a host and/or in target cells *in vitro*. The invention provides a neutralizing monoclonal human antibody, wherein the antibody recognizes an antigen from HIV.

[0199] Preferably an antibody according to the invention is a novel monoclonal antibody referred to herein as 1443_C16 (PG16) (TCN-116), 1503_H05 (PG16) (TCN-119), 1456_A12 (PG16) (TCN-117), 1469_M23 (PG16) (TCN-118), 1489_I13 (PG16) (TCN-120), 1480_I08 (PG16), 1456_P20 (PG20), 1460_G14 (PGG14), 1495_C14 (PGC14), 1496_C09 (PG9) (TCN-109), 4838_L06 (PGT-121), 4873_E03 (PGT-121), 4877_D15 (PGT-122), 4858_P08 (PGT-123), 6123_A06 (PGT-125), 5141_B17 (PGT-126), 5145_B14 (PGT-127), 5114_A19 (PGT-128), 5147_N06 (PGT-130), 5136_H01 (PGT-131), 5343_B08 (PGT-135), 5344_E16 (PGT-135), 5329_C19 (PGT-136), 5366_P21 (PGT-136), 4964_G22 (PGT-141), 5345_I01 (PGT-137), 4993_K13 (PGT-141), 4995_E20 (PGT-142), 4980_N08 (PGT-143), 4970_K22 (PGT-144), 4995_P16 (PGT-145), 4835_F12 (PGT-124), 4869_K15 (PGT-133), 4876_M06 (PGT-134), 5131_A17 (PGT-132), 5138_G07 (PGT-138), 5120_N10 (PGT-139), 6831_A21 (PGT-151), 6889_I17 (PGT-152), 6891_F06 (PGT-153), 6843_G20 (PGT-154), 6892_D19 (PGT-155), 6808_B09 (PGT-156), 6892_C23 (PGT-157), and 6881_N05 (PGT-158). These antibodies were

initially isolated from human samples and are produced by the B cell cultures referred to as 1443_C16 (PG16) (TCN-116), 1503 H05 (PG16) (TCN-119), 1456 A12 (PG16) (TCN-117), 1469 M23 (PG16) (TCN-118), 1489 _I13 (PG16) (TCN-120), 1480_I08 (PG16), 1456_P20 (PG20), 1460_G14 (PGG14), 1495_C14 (PGC14), 1496_C09 (PG9) (TCN-109), 4838_L06 (PGT-121), 4873_E03 (PGT-121), 4877_D15 (PGT-122), 4858_P08 (PGT-123), 6123_A06 (PGT-125), 5141_B17 (PGT-126), 5145_B14 (PGT-127), 5114_A19 (PGT-128), 5147_N06 (PGT-130), 5136_H01 (PGT-131), 5343_B08 (PGT-135), 5344_E16 (PGT-135), 5329_C19 (PGT-136), 5366_P21 (PGT-136), 4964_G22 (PGT-141), 5345_I01 (PGT-137), 4993_K13 (PGT-141), 4995_E20 (PGT-142), 4980_N08 (PGT-143), 4970_K22 (PGT-144), 4995_P16 (PGT-145), 4835_F12 (PGT-124), 4869-K15 (PGT-133), 4876_M06 (PGT-134), 5131_A17 (PGT-132), 5138_G07 (PGT-138), 5120_N10 (PGT-139), 6831_A21 (PGT-151), 6889_I17 (PGT-152), 6891_F06 (PGT-153), 6843_G20 (PGT-154), 6892_D19 (PGT-155), 6808_B09 (PGT-156), 6892_C23 (PGT-157), and 6881_N05 (PGT-158). These antibodies have been shown to neutralize HIV *in vitro*. 1443_C16 (PG16) (TCN-116), 1503 H05 (PG16) (TCN-119), 1456 A12 (PG16) (TCN-117), 1469 M23 (PG16) (TCN-118), 1489 _I13 (PG16) (TCN-120), 1480_I08 (PG16), 1456_P20 (PG20), 1460_G14 (PGG14), 1495_C14 (PGC14), 1496_C09 (PG9) (TCN-109), 4838_L06 (PGT-121), 4873_E03 (PGT-121), 4877_D15 (PGT-122), 4858_P08 (PGT-123), 6123_A06 (PGT-125), 5141_B17 (PGT-126), 5145_B14 (PGT-127), 5114_A19 (PGT-128), 5147_N06 (PGT-130), 5136_H01 (PGT-131), 5343_B08 (PGT-135), 5344_E16 (PGT-135), 5329_C19 (PGT-136), 5366_P21 (PGT-136), 4964_G22 (PGT-141), 5345_I01 (PGT-137), 4993_K13 (PGT-141), 4995_E20 (PGT-142), 4980_N08 (PGT-143), 4970_K22 (PGT-144), 4995_P16 (PGT-145), 4835_F12 (PGT-124), 4869-K15 (PGT-133), 4876_M06 (PGT-134), 5131_A17 (PGT-132), 5138_G07 (PGT-138), 5120_N10 (PGT-139), 6831_A21 (PGT-151), 6889_I17 (PGT-152), 6891_F06 (PGT-153), 6843_G20 (PGT-154), 6892_D19 (PGT-155), 6808_B09 (PGT-156), 6892_C23 (PGT-157), and 6881_N05 (PGT-158) have been shown to have broad, potent HIV neutralizing activity.

[0200] The CDRs of the antibody heavy chains are referred to as CDRH1, CDRH2 and CDRH3, respectively. Similarly, the CDRs of the antibody light chains are referred to as CDRL1, CDRL2 and CDRL3, respectively. The position of the CDR amino acids is defined according to the IMGT numbering system as: CDR1--IMGT positions 27 to 38, CDR2--IMGT positions 56 to 65 and CDR3--IMGT positions 105 to 117. (Lefranc, M P. et al. 2003 IMGT

unique numbering for immunoglobulin and T cell receptor variable regions and Ig superfamily V-like domains. Dev Comp Immunol. 27(1):55-77; Lefranc, M P. 1997. Unique database numbering system for immunogenetic analysis. Immunology Today, 18:509; Lefranc, M P. 1999. The IMGT unique numbering for Immunoglobulins, T cell receptors and Ig-like domains. The Immunologist, 7:132-136.)

[0201] The amino acid sequences of the CDR3 regions of the light and heavy chains of the antibodies are shown in Tables 3A and 3B.

[0202] A phylogram is a branching diagram (tree) assumed to be an estimate of phylogeny, branch lengths are proportional to the amount of inferred evolutionary change. Tree diagrams of the five heavy chains and the five light chains were prepared using ClustalW (Larkin M.A., Blackshields G., Brown N.P., Chenna R., McGettigan P.A., McWilliam H., Valentin F., Wallace I.M., Wilm A., Lopez R., Thompson J.D., Gibson T.J. and Higgins D.G. *Bioinformatics* 23(21): 2947-2948 (2007); Higgins DG *et al.* Nucleic Acids Research 22: 4673-4680. (1994)) and are shown in Figures 1A and 1B respectively.

[0203] The sequences of the antibodies were determined, including the sequences of the variable regions of the Gamma heavy and Kappa or Lambda light chains of the antibodies designated 1496_C09 (PG9), 1443_C16 (PG16), 1456_P20 (PG20), 1460_G14 (PGG14), and 1495_C14 (PGC14). In addition, the sequence of each of the polynucleotides encoding the antibody sequences was determined. Shown below are the polypeptide and polynucleotide sequences of the gamma heavy chains and kappa light chains, with the signal peptides at the N-terminus (or 5' end) and the constant regions at the C-terminus (or 3' end) of the variable regions, which are shown in bolded text.

[0204] 1443_C16 (PG16) (TCN-116) gamma heavy chain nucleotide sequence: 1443 C16 γ3 coding sequence (variable region in bold)

ATGGAGTTTGGGCTGAGCTGGGTTTTCTCGCAACTCTGTAAAGAGTTGTG
AAGTGTCAGGAACA**ACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCC**
GGGGGGGTCCCTGAGACTCTCCTGTTTAGCGTCTGGATTACAGTTTC
ACAAATATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGCCTG
GAGTGGGTGGCACTCATCTCAGATGACGGAATGAGGAAATATCATTC
AGACTCCATGTGGGGCCGAGTCACCATCTCCAGAGACAATTCCAAGA
ACACTCTTTATCTGCAATTCAGCAGCCTGAAAGTCGAAGACACGGCT
ATGTTCTTCTGTGCGAGAGAGGCTGGTGGGCCAATCTGGCATGACGA
CGTCAAATATTACGATTTTAATGACGGCTACTACA**ACTACCACTACAT**
GGACGTCTGGGGCAAGGGGACCACGGTCACCGTCTCGAGCGCCTCCA

CCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCT
 GGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACC
 GGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGCACACCT
 TCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGA
 CCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
 CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTT
 GTGACAAAACCTCACACATGCCCACCGTGCCAGCACCTGAACTCCTGGGG
 GGACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGAT
 CTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAG
 ACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT
 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
 TCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
 AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT
 CTCCAAGGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCC
 CCATCCCGGGAGGAGATGACCAAGAACCAGGTACGCTGACCTGCCTGGT
 CAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG
 CAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG
 GCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA
 CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:
 11)

[0205] 1443_C16 (PG16) (TCN-116) gamma heavy chain variable region nucleotide sequence:

CAGGAACAACCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCGGGGGGGT
 CCCTGAGACTCTCCTGTTTAGCGTCTGGATTACGTTTCACAAATATGGCA
 TGCCTGGGTCCGCCAGGCTCCAGGCAAGGGCCTGGAGTGGGTGGCACTC
 ATCTCAGATGACGGAATGAGGAAATATCATTCAGACTCCATGTGGGGCCG
 AGTCACCATCTCCAGAGACAATTCCAAGAACACTCTTTATCTGCAATTCA
 GCAGCCTGAAAGTCGAAGACACGGCTATGTTCTTCTGTGCGAGAGAGGCT
 GGTGGGGCCAATCTGGCATGACGACGTCAAATATTACGATTTTAATGACGG
 CTACTACAACCTACCACTACATGGACGTCTGGGGCAAGGGGACCACGGTCA
 CCGTCTCGAGC (SEQ ID NO: 99)

[0206] 1443_C16 (PG16) (TCN-116) gamma heavy chain amino acid sequence: expressed protein with variable region in bold.

QEQLVESGGGVVQPGGSLRLSCLASGFTFHKYGMHWVRQAPGKGLEW
VALISDDGMRKYHSDSMWGRVTISRDN SKNTLYLQFSSLKVEDTAMFFC
AREAGGPIWHDDVKYYDFNDGYNYHYMDVWGKGTTVTVSSASTKGPS
 VFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP
 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGV
 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
 KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG

QPENNYKTTTPVLDSGSEFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY
TQKSLSLSPGK (SEQ ID NO: 12)

[0207] 1443_C16 (PG16) (TCN-116) gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

QEQLVESGGGVVQPGGSLRLSCLAS***GFTFHKYGMH***WVRQAPGKGLEWVA***L***
ISDDGMRKYHSDSMWGRVITISRDNSKNTLYLQFSSLKVEDTAMFFCARE***EAG***
GPIWHDDVKYYDFNDGYNYHYMDVWGKGTTTVTVSS (SEQ ID NO: 31)

[0208] 1443_C16 (PG16) (TCN-116) gamma heavy chain Kabat CDRs:

CDR 1: KYGMH (SEQ ID NO: 88)

CDR 2: LISDDGMRKYHSDSMWG (SEQ ID NO: 89)

CDR 3: EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6)

[0209] 1443_C16 (PG16) (TCN-116) gamma heavy chain Chothia CDRs:

CDR 1: GFTFHK (SEQ ID NO: 266)

CDR 2: LISDDGMRKY (SEQ ID NO: 267)

CDR 3: EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6)

[0210] 1443_C16 (PG16) (TCN-116) lambda light chain nucleotide sequence: 1443_C16 λ 2 coding sequence (variable region in bold)

ATGGCCTGGGCTCTGCTATTCCTCACCCCTCTTCACTCAGGGCACAGGGTCC
TGGGGCCAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCT
GGACAGACGATCACCATCTCCTGCAATGGAACCAGCAGTGACGTTGG
TGGATTTGACTCTGTCTCCTGGTACCAACAATCCCCAGGGAAAGCCC
CCAAAGTCATGGTTTTTGATGTCAGTCATCGGCCCTCAGGTATCTCTA
ATCGCTTCTCTGGCTCCAAGTCCGGCAACACGGCCTCCCTGACCATC
TCTGGGCTCCACATTGAGGACGAGGGCGATTATTTCTGCTCTTCACT
GACAGACAGAAGCCATCGCATATTCGGCGGCGGGACCAAGGTGACC
GTTCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTC
CTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTG
ACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCC
GTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACA
AGTACGCGGCCAGCAGCTACCTGAGCCTGACGCC

TGAGCAGTGGAAGTCCCACAAAAGCTACAGCTGCCAGGTCACGCATGAA
GGGAGCACCCTGGAGAAGACAGTGGCCCCCTACAGAATGTTTCATAG (SEQ
ID NO: 13)

[0211] 1443_C16 (PG16) (TCN-116) lambda light chain variable region nucleotide sequence:

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGACG
 ATCACCATCTCCTGCAATGGAACCAGCAGTGACGTTGGTGGATTGACTC
 TGTCTCCTGGTACCAACAATCCCCAGGGAAAGCCCCCAAAGTCATGGTTT
 TTGATGTCACTCATCGGCCCTCAGGTATCTCTAATCGCTTCTCTGGCTCCA
 AGTCCGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCACATTGAGGAC
 GAGGGCGATTATTTCTGCTCTTCACTGACAGACAGAAGCCATCGCATATT
 CGGCGGCGGGACCAAGGTGACCGTTCTA (SEQ ID NO: 100)

[0212] 1443_C16 (PG16) (TCN-116) lambda light chain amino acid sequence: expressed protein with variable region in bold.

QSALTQPASVSGSPGQTITISCNGTSSDVGGFDSVSWYQQSPGKAPKVMV
FDVSHRPSGISNRFSGSKSGNTASLTISGLHIEDEGDYFCSSLTDRSHRIFG
GGTKVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWK
 ADSSPVKAGVETTPSKQSNKYAASSYLSLTPEQWKSHKSYSCQVTHEGST
 VEKTVAPTECS (SEQ ID NO: 14)

[0213] 1443_C16 (PG16) (TCN-116) lambda light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

QSALTQPASVSGSPGQTITISC*NGTSSDVGGFDSVS*WYQQSPGKAPKVMV*FD*
*VSHRPS*GISNRFSGSKSGNTASLTISGLHIEDEGDYFC*SSLTDRSHRI*FGGGTK
 VTVL (SEQ ID NO: 32)

[0214] 1443_C16 (PG16) (TCN-116) lambda light chain Kabat CDRs:

CDR 1: NGTSSDVGGFDSVS (SEQ ID NO: 97)

CDR 2: DVSHRPS (SEQ ID NO: 95)

CDR 3: SSLTDRSHRI (SEQ ID NO: 41)

[0215] 1443_C16 (PG16) (TCN-116) lambda light chain Chothia CDRs:

CDR 1: NGTSSDVGGFDSVS (SEQ ID NO: 97)

CDR 2: DVSHRPS (SEQ ID NO: 95)

CDR 3: SSLTDRSHRI (SEQ ID NO: 41)

[0216] 1456_P20 (PG20) gamma heavy chain nucleotide sequence: 1456_P20 γ 1 coding sequence (variable region in bold)

ATGGACTGGATTTGGAGGTTCTCTTTGTGGTGGCAGCAGCTACAGGTGT
 CCAGTCCCAGGTCCGCCTGGTACAGTCTGGGCCTGAGGTGAAGAAGC
 CTGGGTCTCGGTGACGGTCTCCTGCCAGGCTTCTGGAGGCACCTTC
AGCAGTTATGCTTTCACCTGGGTGCGCCAGGCCCCCGGACAAGGTCT
TGAGTGGTTGGGCATGGTCACCCCAATCTTTGGTGAGGCCAAGTACT
CACAAAGATTTCGAGGGCAGAGTCACCATCACCGCGGACGAATCCACG
AGCACAACCTCCATAGAATTGAGAGGCCTGACATCCGAAGACACGGC
CATTTATTACTGTGCGCGAGATCGGCGCGCGGTTCCAATTGCCACGG

ACAACTGGTTAGACCCCTGGGGCCAGGGGACCCTGGTCAACCGTCTCG
AGCGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAA
 GAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACT
 TCCCCGAACCGGTGACGGTGTCGTGGA^{ACTCAGGCGCCCTGACCAGCGGC}
 GTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGC
 AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG
 CAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAG
 CCCAAATCTTGTGACAAA^{ACTCACACATGCCACCGTGCCAGCACCTGA}
 ACTCCTGGGGGGACCGTCAGTCTTCTTCCCCCAAAACCCAAGGACA
 CCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG
 AGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
 AGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAC
 GTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG
 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC^{ATC}
 GAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
 ACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTACGCCT
 GACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
 AGAGCAATGGGCAGCCGGAGAACA^{ACTACAAGACCACGCCTCCCCTGCT}
 GGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGA
 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT
 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATG
 A (SEQ ID NO: 15)

[0217] 1456_P20 (PG20) gamma heavy chain variable region nucleotide sequence:

CAGGTCCGCCTGGTACAGTCTGGGCCTGAGGTGAAGAAGCCTGGGTCTCTC
 GGTGACGGTCTCCTGCCAGGCTTCTGGAGGCACCTTCAGCAGTTATGCTTT
 CACCTGGGTGCGCCAGGCCCCCGGACAAGGTCTTGAGTGGTTGGGCATGG
 TCACCCCAATCTTTGGTGAGGCCAAGTACTCACAAAGATTCGAGGGGCAGA
 GTCACCATCACCGCGGACGAATCCACGAGCACAACTCCATAGAATTGAG
 AGGCCTGACATCCGAAGACACGGCCATTTATTACTGTGCGCGAGATCGGC
 GCGCGGTTCCAATTGCCACGGACA^{ACTGGTTAGACCCCTGGGGCCAGGGG}
 ACCCTGGTCAACCGTCTCGAGC (SEQ ID NO: 101)

[0218] 1456_P20 (PG20) gamma heavy chain amino acid sequence: expressed protein with variable region in bold.

QVRLVQSGPEVKKPGSSVTVSCQASGGTFSSYAFTWVRQAPGQGLEWL
GMVTPIFGEAKYSQRFEGRVTITADESTTTSIELRGLTSEDTAIYYCARD
RRAVPIATDNWLDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALG
 CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQ
 TYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKD
 TLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSF
 FLYSKLTVDKSRWQQGNVFC^{SV}MHEALHNHYTQKSLSLSPGK (SEQ ID
 NO: 16)

[0219] 1456_P20 (PG20) gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

QVRLVQSGPEVKKPGSSVTVSCQASGGTFSSYAFTWVRQAPGQGLEWLG***MTPIFGEAKYSQRFEG***RVTTITADESTTTSIELRGLTSEDTAIYYCARD***DRRAVPIATDNWLDP***WGQGTLLTVSS (SEQ ID NO: 33)

[0220] 1456_P20 (PG20) gamma heavy chain Kabat CDRs:

CDR 1: SYAFT (SEQ ID NO: 104)

CDR 2: MVTPIFGEAKYSQRFEG (SEQ ID NO: 105)

CDR 3: DRRAVPIATDNWLDP (SEQ ID NO: 9)

[0221] 1456_P20 (PG20) gamma heavy chain Chothia CDRs:

CDR 1: GGTFSS (SEQ ID NO: 268)

CDR 2: MVTPIFGEAK (SEQ ID NO: 269)

CDR 3: DRRAVPIATDNWLDP (SEQ ID NO: 9)

[0222] 1456_P20 (PG20) kappa light chain nucleotide sequence: 1456_P20 1 coding sequence (variable region in bold)

ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTACTCTGGCT
CCGAGGTGCCAGATGT**GACATCCAGTTGACCCAGTCTCCATCCTCCCT**
GTCTGCATCTGTTGGCGACAGAGTCTCCATCACTTGCCGGGCGAGTC
AGACCATTAACAACTACTTAAATTGGTATCAACAGACACCCGGGAAA
GCCCTAACTCCTGATCTATGGTGCCTCCAATTTGCAAAATGGGGT
CCCATCAAGGTT**CAGCGGCAGTGGCTCTGGGACAGACTTCACTCTCA**
CCATCAGCAGTCTGCAACCTGAGGATTTTGCAACTTACTACTGTCAAC
AGAGTTTCAGTACTCCGAGGACCTTCGGCCAAGGGACACGACTGGAT
ATTAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGAT
GAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTC
TATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAAT
CGGGTAACTCCCAGGAGAGTGT**CACAGAGCAGGACAGCAAGGACAGCAC**
CTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAA
CACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGT
CACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO: 17)

[0223] 1456_P20 (PG20) kappa light chain variable region nucleotide sequence:

GACATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTTGGCGAC
AGAGTCTCCATCACTTGCCGGGCGAGTCAGACCATTAACA**ACTACTTAAA**
TTGGTATCAACAGACACCCGGGAAAGCCCCTAACTCCTGATCTATGGTG
CCTCCAATTTGCAAAATGGGGTCCCATCAAGGTTCAAGCGGCAGTGGCTCT
GGGACAGACTTCACTCTACCATCAGCAGTCTGCAACCTGAGGATTTTGC
AACTTACTACTGTCAACAGAGTTTCACTACTCCGAGGACCTTCGGCCAAG
GGACACGACTGGATATTTAAA (SEQ ID NO: 106)

[0224] 1456_P20 (PG20) kappa light chain amino acid sequence: expressed protein with variable region in bold.

DIQLTQSPSSLSASVGDRVSITCRASQTINNYLNWYQQTPGKAPKLLIYGA
SNLQNGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSFSTPRTFGQGT
RLDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSSTLSSTLTLSKADYEKHKVYACEVTHQGLSSPVT
KSFNRGEC (SEQ ID NO: 18)

[0225] 1456_P20 (PG20) kappa light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

DIQLTQSPSSLSASVGDRVSITCRASQTINNYLNWYQQTPGKAPKLLIYGASNL
QNGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSFSTPRTFGQGT
(SEQ ID NO: 34)

[0226] 1456_P20 (PG20) kappa light chain Kabat CDRs:

CDR 1: RASQTINNYLN (SEQ ID NO: 107)

CDR 2: GASNLQN (SEQ ID NO: 108)

CDR 3: QQSFSTPRT (SEQ ID NO: 42)

[0227] 1456_P20 (PG20) kappa light chain Chothia CDRs:

CDR 1: RASQTINNYLN (SEQ ID NO: 107)

CDR 2: GASNLQN (SEQ ID NO: 108)

CDR 3: QQSFSTPRT (SEQ ID NO: 42)

[0228] 1460_G14 (PGG14) gamma heavy chain nucleotide sequence: 1460_G14 γ 1 coding sequence (variable region in bold)

ATGGACTGGATTTGGAGGTTCTCTTGGTGGTGGCAGCAGCTACAGGTGT
CCAGTCCCAGGTCCTGCTGGTGCAGTCTGGGACTGAGGTGAAGAAGC
CTGGGTCCTCGGTGAAGGTCTCCTGTCAGGCTTCTGGAGGCGCCTTC
AGTAGTTATGCTTTCAGCTGGGTGCGACAGGCCCTGGACAGGGGCT
TGAATGGATGGGCATGATCACCCCTGTCTTTGGTGAGACTAAATATG
CACCGAGGTTCCAGGGCAGACTCACACTTACCGCGGAAGAATCCTTG
AGCACCACTACATGGAATTGAGAAGCCTGACATCTGATGACACGGC
CTTTTATTATTGTACGAGAGATCGGCGCGTAGTTCCAATGGCCACAG
ACAACCTGGTTAGACCCCTGGGGCCAGGGGACGCTGGTCACCGTCTCG
AGCGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCAA
GAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACT
TCCCCGAACCGGTGACGGTGTCGTGGAACCTCAGGCGCCCTGACCAGCGGC
GTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG
CAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAG
CCCAAATCTTGTGACAAACTCACACATGCCACCGTGCCAGCACCTGA

ACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCAAACCCAAGGACA
 CCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTG
 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
 AGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAC
 GTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG
 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATC
 GAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
 ACACCCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTACGCCT
 GACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
 AGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCT
 GGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGA
 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT
 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATG
 A (SEQ ID NO: 19)

[0229] 1460_G14 (PGG14) gamma heavy chain variable region nucleotide sequence:

CAGGTCCTGCTGGTGCAGTCTGGGACTGAGGTGAAGAAGCCTGGGTCCTC
 GGTGAAGGTCTCCTGTCAGGCTTCTGGAGGCGCCTTCAGTAGTTATGCTTT
 CAGCTGGGTGCGACAGGCCCCCTGGACAGGGGCTTGAATGGATGGGCATG
 ATCACCCCTGTCTTTGGTGAGACTAAATATGCACCGAGGTTCCAGGGCAG
 ACTCACACTTACCGCGGAAGAATCCTTGAGCACCACCTACATGGAATTGA
 GAAGCCTGACATCTGATGACACGGCCTTTTATTATTGTACGAGAGATCGG
 CGCGTAGTTCCAATGGCCACAGACAACCTGGTTAGACCCCTGGGGCCAGGG
 GACGCTGGTCACCGTCTCGAGC (SEQ ID NO: 109)

[0230] 1460_G14 gamma heavy chain amino acid sequence: expressed protein with variable region in bold.

QVLLVQSGTEVKKPGSSVKVSCQASGGAFSSYAFSWVRQAPGQGLEWM
GMITPVFGETKYAPRFQGRLLTAEESLSTTYMELRSLTSDDTAFFYYCTR
DRRVVPMATDNWLDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA
 LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLG
 TQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP
 KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
 LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDG
 SFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG (SEQ ID
 NO: 20)

[0231] 1460_G14 gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

QVLLVQSGTEVKKPGSSVKVSCQASGGAFSSYAFSWVRQAPGQGLEWMGM
ITPVFGETKYAPRFQGRLLTAEESLSTTYMELRSLTSDDTAFFYYCTR***DRRVV***
PMATDNWLDPWGQGTLVTVSS (SEQ ID NO: 35)

[0232] 1460_G14 gamma heavy chain Kabat CDRs:

CDR 1: SYAFS (SEQ ID NO: 110)

CDR 2: MITPVFGETKYAPRFQG (SEQ ID NO: 111)

CDR 3: DRRVVPMATDNWLDP (SEQ ID NO: 8)

[0233] 1460_G14 gamma heavy chain Chothia CDRs:

CDR 1: GGAFFS (SEQ ID NO: 270)

CDR 2: MITPVFGETK (SEQ ID NO: 271)

CDR 3: DRRVVPMATDNWLDP (SEQ ID NO: 8)

[0234] 1460_G14 (PGG14) kappa light chain nucleotide sequence: 1460_G14 1 coding sequence (variable region in bold)

ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTCCTCTGGCTC
CGAGGTGCCACATGTGACATCCAGTTGACCCAGTCTCCATCCTCCCTG
TCTGCATCTGTAGGAGACAGGGTCACCGTCACTTGCCGGGCGAGTCA
GACCATACACACCTATTTAAATTGGTATCAGCAAATTCCAGGAAAAGC
CCCTAAGCTCCTGATCTATGGTGCCTCCACCTTGCAAAGTGGGGTCC
CGTCAAGGTTCACTGGCAGTGGATCTGGGACAGATTTCACTCTCACC
ATCAACAGTCTCCAACCTGAGGACTTTGCAACTTACTACTGTCAACAG
AGTTACAGTACCCCAAGGACCTTCGGCCAAGGGACACGACTGGATAT
TAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGA
GCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTA
TCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCG
GGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCT
ACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACA
CAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCA
CAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO: 21)

[0235] 1460_G14 (PGG14) kappa light chain variable region nucleotide sequence:

GACATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGAC
AGGGTCACCGTCACTTGCCGGGCGAGTCAGACCATACACACCTATTTAAA
TTGGTATCAGCAAATTCCAGGAAAAGCCCCTAAGCTCCTGATCTATGGTG
CCTCCACCTTGCAAAGTGGGGTCCCGTCAAGGTTCACTGGCAGTGGATCT
GGGACAGATTTCACTCTCACCATCAACAGTCTCCAACCTGAGGACTTTGC
AACTTACTACTGTCAACAGAGTTACAGTACCCCAAGGACCTTCGGCCAAG
GGACACGACTGGATATTAAA (SEQ ID NO: 112)

[0236] 1460_G14 kappa light chain amino acid sequence: expressed protein with variable region in bold.

DIQLTQSPSSLSASVGDRVTVTCRASQTIHTYLNWYQQIPGKAPKLLIYG
ASTLQSGVPSRFSGSGSGTDFTLTINSLQPEDFATYYCQQSYSTPRTEFGQG

TRLDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPV
TKSFNRGEC (SEQ ID NO: 22)

[0237] 1460_G14 kappa light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

DIQLTQSPSSLSASVGDRVTVTC***RASQTIHTYLN***NWYQQIPGKAPKLLIY***GASTL***
QSGVPSRFSSGSGTDFLTINS***LQPEDFATYYC******QOSYSTPRT***FGQGTRLDIK
 (SEQ ID NO: 36)

[0238] 1460_G14 kappa light chain Kabat CDRs:

CDR 1: RASQTIHTYLN (SEQ ID NO: 113)

CDR 2: GASTLQS (SEQ ID NO: 114)

CDR 3: QOSYSTPRT (SEQ ID NO: 43)

[0239] 1460_G14 kappa light chain Chothia CDRs:

CDR 1: RASQTIHTYLN (SEQ ID NO: 113)

CDR 2: GASTLQS (SEQ ID NO: 114)

CDR 3: QOSYSTPRT (SEQ ID NO: 43)

[0240] 1495_C14 (PGC14) gamma heavy chain nucleotide sequence: 1495_C14 γ 1 coding sequence (variable region in bold)

ATGGACTGGATTGGAGGATCCTCCTCTGGTGGCAGCAGCTACAGGCAC
 CCTCGCCGACGGCCACCTGGTTCACTCTGGGGTTGAGGTGAAGAAGA
 CTGGGGCTACAGTCAAAATCTCCTGCAAGGTTTCTGGATAACAGCTTC
 ATCGACTACTACCTTCATTGGGTGCAACGGGCCCCTGGAAAAGGCCT
 TGAGTGGGTGGGACTTATTGATCCTGAAAATGGTGAGGCTCGATATG
 CAGAGAAGTTCCAGGGCAGAGTCACCATAATCGCGGACACGTCTATA
 GATACAGGCTACATGGAAATGAGGAGCCTGAAATCTGAGGACACGGC
 CGTGTATTTCTGTGCAGCAGGTGCCGTGGGGGCTGATTCCGGGAGCT
 GGTTCGACCCCTGGGGCCAGGGAACCTCTGGTCACCGTCTCGAGCGCC
 TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCAAGAGCAC
 CTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG
 AACCGGTGACGGTGTCGTGGAATCAGGCGCCCTGACCAGCGGCGTGAC
 ACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTG
 GTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGT
 GAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAA
 TCTTGTGACAAACTCACACATGCCACCGTGCCAGCACCTGAACTCCT
 GGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCTCA
 TGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCAC
 GAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGAGGTGC
 ATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCG
 TGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGG

AGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA
 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCC
 TGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGC
 CTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAA
 TGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTGGACTCCG
 ACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGG
 CAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA
 CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID
 NO: 23)

[0241] 1495_C14 (PGC14) gamma heavy chain variable region nucleotide sequence:

GACGGCCACCTGGTTCAGTCTGGGGTTGAGGTGAAGAAGACTGGGGCTAC
 AGTCAAAATCTCCTGCAAGGTTTCTGGATACAGCTTCATCGACTACTACCT
 TCATTGGGTGCAACGGGCCCCCTGGAAAAGGCCTTGAGTGGGTGGGACTTA
 TTGATCCTGAAAATGGTGAGGCTCGATATGCAGAGAAGTTCCAGGGCAGA
 GTCACCATAATCGCGGACACGTCTATAGATACAGGCTACATGGAAATGAG
 GAGCCTGAAATCTGAGGACACGGCCGTGTATTTCTGTGCAGCAGGTGCCG
 TGGGGGCTGATTCCGGGAGCTGGTTCGACCCCTGGGGCCAGGGAACTCTG
 GTCACCGTCTCGAGC (SEQ ID NO: 115)

[0242] 1495_C14 (PGC14) gamma heavy chain amino acid sequence: expressed protein with
 variable region in bold.

DGHLVQSGVEVKKTGATVKISCKVSGYSFIDYYLHWVQRAPGKGLEWV
GLIDPENGEARYAEKFQGRVTIIADTSIDTGYMEMRSLKSEDTAVYFCAA
GAVGADSGSWFDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC
 LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQT
 YICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT
 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
 VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFF
 LYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
 24)

[0243] 1495_C14 (PGC14) gamma heavy chain variable region amino acid sequence: (Kabat
 CDRs underlined, Chothia CDRs in bold italics)

DGHLVQSGVEVKKTGATVKISCKVSGYSFIDYYLHWVQRAPGKGLEWVGLI
DPENGEARYAEKFQGRVTIIADTSIDTGYMEMRSLKSEDTAVYFCAA**GAVGA**
DSGSWFDPWGQGTLVTVSS (SEQ ID NO: 37)

[0244] 1495_C14 gamma heavy chain Kabat CDRs:

CDR 1: DYYLH (SEQ ID NO: 116)

CDR 2: LIDPENGEARYAEKFQG (SEQ ID NO: 117)

CDR 3: GAVGADSGSWFDP (SEQ ID NO: 10)

[0245] 1495_C14 gamma heavy chain Chothia CDRs:

CDR 1: GYSFID (SEQ ID NO: 102)

CDR 2: LIDPENGAR (SEQ ID NO: 103)

CDR 3: GAVGADSGSWFDP (SEQ ID NO: 10)

[0246] 1495_C14 (PGC14) lambda light chain nucleotide sequence: 1495_C14 3 coding sequence (variable region in bold)

ATGGCCTGGATCCCTCTCTTCCTCGGCGTCCTTGCTTACTGCACAGATTCC
GTAGTCTCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCA
GGACAGACAGCCAGCATCACCTGTTCTGGATCTAAATTGGGGGATAA
ATATGTTTCCTGGTATCAACTGAGGCCAGGCCAGTCCCCATACTGG
TCATGTATGAAAATGACAGGCGGCCCTCCGGGATCCCTGAGCGATT
TCCGGTTCCAATTCTGGCGACACTGCCACTCTGACCATCAGCGGGAC
CCAGGCTTTGGATGAGGCTGACTTCTACTGTCAGGCGTGGGAGACCA
CCACCACCCTTTTGTTCCTTCGGCGGAGGGAGCCAGCTGACCGTT
CTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCT
GAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTT
CTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTC
AAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAGCAACAACAAGT
ACGCGGCCAGCAGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCAC
AAAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGA
CAGTGGCCCCCTACAGAATGTTCATAG (SEQ ID NO: 25)

[0247] 1495_C14 (PGC14) lambda light chain variable region nucleotide sequence:

TCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCAAGGACAGAC
AGCCAGCATCACCTGTTCTGGATCTAAATTGGGGGATAAATATGTTTCCTG
GTATCAACTGAGGCCAGGCCAGTCCCCATACTGGTCATGTATGAAAATG
ACAGGCGGCCCTCCGGGATCCCTGAGCGATTCTCCGGTTCCAATTCTGGC
GACACTGCCACTCTGACCATCAGCGGGAGCCAGGCTTTGGATGAGGCTGA
CTTCTACTGTCAGGCGTGGGAGACCACCACCACCCTTTTGTTCCTTCGG
CGGAGGGAGCCAGCTGACCGTTCTA (SEQ ID NO: 119)

[0248] 1495_C14 (PGC14) lambda light chain amino acid sequence: expressed protein with variable region in bold.

SYELTQPPSVSVSPGQTASITCSGSKLGDKYVSWYQLRPGQSPILVMYEN
DRRPSGIPERFSGSNSGDTATLTISGTQALDEADFYCQAWETTTTTTFVFFG
GGTQLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKA
DSSPVKAGVETTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTV
EKTVAPECS (SEQ ID NO: 26)

[0249] 1495_C14 (PGC14) lambda light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

SYELTQPPSVSVSPGQTASITC**SGSKLGDKYVS**SWYQLRPGQSPILVMY**ENDRR**
PSGIPERFSGSNSGDTATLTISGTQALDEADFYC**QAWETTTTTFVF**FGGGTQL
 TVL (SEQ ID NO: 38)

[0250] 1495_C14 (PGC14) lambda light chain Kabat CDRs:

CDR 1: SGSKLGDKYVS (SEQ ID NO: 120)

CDR 2: ENDRRPS (SEQ ID NO: 121)

CDR 3: QAWETTTTTFVF (SEQ ID NO: 44)

[0251] 1495_C14 (PGC14) lambda light chain Chothia CDRs:

CDR 1: SGSKLGDKYVS (SEQ ID NO: 120)

CDR 2: ENDRRPS (SEQ ID NO: 121)

CDR 3: QAWETTTTTFVF (SEQ ID NO: 44)

[0252] 1496_C09 (PG9) (TCN-109) gamma heavy chain nucleotide sequence: 1496_C09 γ 3
 coding sequence (variable region in bold)

ATGGAGTTTGGGCTGAGCTGGGTTTTCCTCGTTGCTTTCTTAAGAGGTGTC
 CAGTGT**CAGCGATTAGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGG**
GTCGTCCTGAGACTCTCCTGTGCAGCGTCCGGATTCTGACTTCAGTA
GACAAGGCATGCACTGGGTCCGCCAGGCTCCAGGCCAGGGGCTGGA
GTGGGTGGCATTATTAATAATATGATGGAAGTGAGAAATATCATGCTG
ACTCCGTATGGGGCCGACTCAGCATCTCCAGAGACAATCCAAGGAT
ACGCTTTATCTCCAAATGAATAGCCTGAGAGTCGAGGACACGGCTAC
ATATTTTGTGTGAGAGAGGCTGGTGGGCCCCGACTACCGTAATGGGT
ACAACTATTACGATTTCTATGATGGTTATTATA**ACTACCACTATATGG**
ACGTCTGGGGCAAAGGGACCACGGT**CA**CCGTCTCGAGCGCCTCCACC
 AAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGG
 GGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGG
 TGACGGTGTCTGGA**ACTCAGGCGCCCTGACCAGCGGCGTGACACCTTC**
CCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAC
CGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATC
ACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTG
TGACAAAACTCACACATGCCACCGTGCCAGCACCTGA**ACTCCTGGGGG**
GACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCT
CCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGA
CCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG
CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGT
CAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACA
AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATC
TCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCC
CATCCCGGGAGGAGATGACCAAGAACCAGGTACGCCTGACCTGCCTGGTC
AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGC
AGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGG
CTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGC

AGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 27)

[0253] 1496_C09 (PG9) (TCN-109) gamma heavy chain variable region nucleotide sequence:

CAGCGATTAGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGTCGTCCCT
GAGACTCTCCTGTGCAGCGTCCGGATTGACTTCAGTAGACAAGGCATGC
ACTGGGTCCGCCAGGCTCCAGGCCAGGGGCTGGAGTGGGTGGCATTATT
AAATATGATGGAAGTGAGAAATATCATGCTGACTCCGTATGGGGCCGACT
CAGCATCTCCAGAGACAATTCCAAGGATACGCTTTATCTCCAAATGAATA
GCCTGAGAGTCGAGGACACGGCTACATATTTTGTGTGAGAGAGGCTGGT
GGGCCCCGACTACCGTAATGGGTACAATTACGATTTCTATGATGGTTAT
TATAACTACCACTATATGGACGTCTGGGGCAAAGGGACCACGGTCACCGT
CTCGAGC (SEQ ID NO: 122)

[0254] 1496_C09 (PG9) (TCN-109) gamma heavy chain amino acid sequence: expressed protein with variable region in bold.

QRLVESGGGVVQPGSSRLSCLAASGFDFSRQGMHWVRQAPQGGLWVAFIK
YDGSEKYHADSVWGRLSISRDN SKDTLYLQMNSLRVEDTATYFCVREAGGP
DYRNGYNYDFYDGYNYHYMDVWGKGTTVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV
VTPVSSSLGTQTYICNVNHKPSNTKVKDKRVEPKSCDKTHTCPPCPAPELLGPP
SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
TPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSP
GK (SEQ ID NO: 28)

[0255] 1496_C09 (PG9) (TCN-109) gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

QRLVESGGGVVQPGSSRLSCLAAS***GFDFSRQGMH***WVRQAPQGGLWVAFI
KYDGSEKYHADSVWGRLSISRDNSKDTLYLQMNSLRVEDTATYFCV***REAGG***
PDYRNGYNYDFYDGYNYHYMDVWGKGTTVTVSS (SEQ ID NO: 39)

[0256] 1496_C09 (PG9) (TCN-109) gamma heavy chain Kabat CDRs:

CDR 1: RQGMH (SEQ ID NO: 123)

CDR 2: FIKYDGSEKYHADSVWG (SEQ ID NO: 124)

CDR 3: EAGGPDYRNGYNYDFYDGYNYHYMDV (SEQ ID NO: 7)

[0257] 1496_C09 (PG9) (TCN-109) gamma heavy chain Chothia CDRs:

CDR 1: GFDFSR (SEQ ID NO: 118)

CDR 2: FIKYDGSEKY (SEQ ID NO: 272)

CDR 3: EAGGPDYRNGYNYDFYDGYNYHYMDV (SEQ ID NO: 7)

[0258] 1496_C09 (PG9) (TCN-109) lambda light chain nucleotide sequence: 1496_C09 λ 2 coding sequence (variable region in bold)

ATGGCCTGGGCTCTGCTTTTCCTCACCCCTCCTCACTCAGGGCACAGGGTCC
TGGGCCCAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCT
GGACAGTCGATCACCATCTCCTGCAATGGAACCAGCAATGATGTTGG
TGGCTATGAATCTGTCTCCTGGTACCAACAACATCCCGGCAAAGCCC
CCAAAGTCGTGATTTATGATGTCAGTAAACGGCCCTCAGGGGTTTCT
AATCGCTTCTCTGGCTCCAAGTCCGGCAACACGGCCTCCCTGACCAT
CTCTGGGCTCCAGGCTGAGGACGAGGGTGACTATTACTGCAAGTCTC
TGACAAGCACGAGACGTCCGGTTTTTCGGCACTGGGACCAAGCTGACC
GTTCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTC
CTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTG
ACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCC
GTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACA
AGTACGCGGCCAGCAGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCC
CACAAAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGA
AGACAGTGGCCCCTACAGAATGTTTCATAG (SEQ ID NO: 29)

[0259] 1496_C09 (PG9) (TCN-109) lambda light chain variable region nucleotide sequence:

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCG
ATCACCATCTCCTGCAATGGAACCAGCAATGATGTTGGTGGCTATGAATC
TGTCTCCTGGTACCAACAACATCCCGGCAAAGCCCCCAAAGTCGTGATTT
ATGATGTCAGTAAACGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTCCA
AGTCCGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGAC
GAGGGTGACTATTACTGCAAGTCTCTGACAAGCACGAGACGTCCGGGTTTT
CGGCACTGGGACCAAGCTGACCGTTCTA (SEQ ID NO: 125)

[0260] 1496_C09 (PG9) (TCN-109) lambda light chain amino acid sequence: expressed protein with variable region in bold.

QSALTQPASVSGSPGQSITISCNGTSNDVGGYESVSWYQQHPGKAPKVVI
YDVSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEGDYYCKSLTSTRRRV
FGTGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAW
KADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGS
TVEKTVAPTECS (SEQ ID NO: 30)

[0261] 1496_C09 (PG9) (TCN-109) lambda light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

QSALTQPASVSGSPGQSITISC**NGTSNDVGGYESVSWYQQHPGKAPKVVI****YDV**
SKRPSGVSNRFSGSKSGNTASLTISGLQAEDEGDYYC**KSLTSTRRRV**FGTGTK
LTVL (SEQ ID NO: 40)

[0262] 1496_C09 (PG9) (TCN-109) lambda light chain Kabat CDRs:

CDR 1: NGTSNDVGGYESVS (SEQ ID NO: 126)

CDR 2: DVSKRPS (SEQ ID NO: 127)

CDR 3: KSLTSTRRRV (SEQ ID NO: 45)

[0263] 1496_C09 (PG9) (TCN-109) lambda light chain Chothia CDRs:

CDR 1: NGTSNDVGGYESVS (SEQ ID NO: 126)

CDR 2: DVSKRPS (SEQ ID NO: 127)

CDR 3: KSLTSTRRRV (SEQ ID NO: 45)

[0264] The 1443_C16 (PG16) antibody includes a heavy chain variable region (SEQ ID NO: 31), encoded by the nucleic acid sequence shown in SEQ ID NO: 99, and a light chain variable region (SEQ ID NO: 32) encoded by the nucleic acid sequence shown in SEQ ID NO: 100.

[0265] The heavy chain CDRs of the 1443_C16 (PG16) antibody have the following sequences per Kabat definition: KYGMH (SEQ ID NO: 88), LISDDGMRKYHSDSMWG (SEQ ID NO: 89), and EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6). The light chain CDRs of the 1443_C16 (PG16) antibody have the following sequences per Kabat definition: NGTSSDVGGFDSVS (SEQ ID NO: 97), DVSHRPS (SEQ ID NO: 95), and SSLTDRSHRI (SEQ ID NO: 41).

[0266] The heavy chain CDRs of the 1443_C16 (PG16) antibody have the following sequences per Chothia definition: GFTFHK (SEQ ID NO: 266), LISDDGMRKY (SEQ ID NO: 267), and EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6). The light chain CDRs of the 1443_C16 (PG16) antibody have the following sequences per Chothia definition: NGTSSDVGGFDSVS (SEQ ID NO: 97), DVSHRPS (SEQ ID NO: 95), and SSLTDRSHRI (SEQ ID NO: 41).

[0267] The 1456_P20 (PG20) antibody includes a heavy chain variable region (SEQ ID NO: 33), encoded by the nucleic acid sequence shown in SEQ ID NO: 101, and a light chain variable region (SEQ ID NO: 34) encoded by the nucleic acid sequence shown in SEQ ID NO: 106.

[0268] The heavy chain CDRs of the 1456_P20 (PG20) antibody have the following sequences per Kabat definition: SYAFT (SEQ ID NO: 104), MVTPIFGAEAKYSQRFEG (SEQ ID NO: 105), and DRRAPVIATDNWLDP (SEQ ID NO: 9). The light chain CDRs of the 1456_P20 (PG20) antibody have the following sequences per Kabat definition: RASQTINNYLN (SEQ ID NO: 107), GASNLQN (SEQ ID NO: 108), and QQSFSPTPT (SEQ ID NO: 42).

[0269] The heavy chain CDRs of the 1456_ P20 (PG20) antibody have the following sequences per Chothia definition: GGTFSS (SEQ ID NO: 268), MVTPIFGGEAK (SEQ ID NO: 269), and DRRVPIATDNWLDP (SEQ ID NO: 9). The light chain CDRs of the 1456_ P20 (PG20) antibody have the following sequences per Chothia definition: RASQTINNYLN (SEQ ID NO: 107), GASNLQN (SEQ ID NO: 108), and QQSFSPTPT (SEQ ID NO: 42).

[0270] The 1460_G14 (PGG14) antibody includes a heavy chain variable region (SEQ ID NO: 35), encoded by the nucleic acid sequence shown in SEQ ID NO: 109, and a light chain variable region (SEQ ID NO: 36) encoded by the nucleic acid sequence shown in SEQ ID NO: 112.

[0271] The heavy chain CDRs of the 1460_G14 (PGG14) antibody have the following sequences per Kabat definition: SYAFS (SEQ ID NO: 110), MITPVFGETKYAPRFQG (SEQ ID NO: 111), and DRRVVPMTDNWLDP (SEQ ID NO: 8). The light chain CDRs of the 1460_G14 (PGG14) antibody have the following sequences per Kabat definition: RASQTIHTYLN (SEQ ID NO: 113), GASTLQS (SEQ ID NO: 114), QQSYSTPT (SEQ ID NO: 43).

[0272] The heavy chain CDRs of the 1460_G14 (PGG14) antibody have the following sequences per Chothia definition: GGAFSS (SEQ ID NO: 270), MITPVFGETK (SEQ ID NO: 271), DRRVVPMTDNWLDP (SEQ ID NO: 8). The light chain CDRs of the 1460_G14 (PGG14) antibody have the following sequences per Chothia definition: RASQTIHTYLN (SEQ ID NO: 113), GASTLQS (SEQ ID NO: 114), QQSYSTPT (SEQ ID NO: 43).

[0273] The 1495_C14 (PGC14) antibody includes a heavy chain variable region (SEQ ID NO: 37), encoded by the nucleic acid sequence shown in SEQ ID NO: 115, and a light chain variable region (SEQ ID NO: 38) encoded by the nucleic acid sequence shown in SEQ ID NO: 119.

[0274] The heavy chain CDRs of the 1495_C14 (PGC14) antibody have the following sequences per Kabat definition: DYYLH (SEQ ID NO: 116), LIDPENGGEARYAEKFQG (SEQ ID NO: 117), GAVGADSGSWFDP (SEQ ID NO: 10). The light chain CDRs of the 1495_C14 (PGC14) antibody have the following sequences per Kabat definition: SGSKLGDKYVS (SEQ ID NO: 120), ENDRRPS (SEQ ID NO: 121), and QAWETTTTTFVF (SEQ ID NO: 44).

[0275] The heavy chain CDRs of the 1495_C14 (PGC14) antibody have the following sequences per Chothia definition: GYSFID (SEQ ID NO: 102), LIDPENGGEAR (SEQ ID NO:

[0278] The heavy chain CDRs of the 1496_C09 (PG9) antibody have the following sequences per Chothia definition: GFD~~F~~SR (SEQ ID NO: 118), FIKYD~~G~~SEKY (SEQ ID NO: 272), and EAGGPDYRNGYNYDFYDGYNYHYMDV (SEQ ID NO: 7). The light chain CDRs of the 1496_C09 (PG9) antibody have the following sequences per Chothia definition: NGTSNDVGGYESVS (SEQ ID NO: 126), DVSKRPS (SEQ ID NO: 127), and KSLTSTRRRV (SEQ ID NO: 45).

[illegible]

	7C	29	S9	49	59	89																																																															
A49_C14_L3.ref	S	Y	E	L	T	G	-	F	P	S	V	S	V	S	P	G	Q	T	A	I	T	C	S	G	S	K	-	-	L	G	D	K	V	S	W	M	V	Q	L	R	F	G	Q	S	P	I	L	M	V	N	O	R	F	S	G	I	P	E	R	F	S	G	S	N					
A49_C14_K1.ref	D	I	O	L	T	G	-	G	G	-	G	A	G	V	G	O	D	R	V	T	T	G	R	A	S	Q	T	-	-	I	I	I	T	L	N	W	Q	T	-	F	G	K	A	P	K	L	L	I	Y	C	A	S	T	L	G	S	V	V	S	R	F	G	C	G	O				
A49_P20_K1.ref	D	I	O	L	T	G	-	G	G	-	G	A	G	V	G	O	D	R	V	T	T	G	R	A	S	Q	T	-	-	I	N	N	L	N	W	Q	T	-	F	G	K	A	P	K	L	L	I	Y	C	A	S	N	L	Q	N	V	S	R	F	S	G	S	G						
A43_C16_L2.ref	G	A	L	T	G	-	F	A	D	V	S	V	S	G	S	P	G	Q	S	I	T	T	C	G	N	G	T	S	D	V	G	G	T	D	V	G	G	-	G	A	G	V	G	O	D	R	V	T	T	G	R	A	S	Q	T	-	-	G	C	K	G	K							
A49_C09_L2.ref	G	A	L	T	G	-	F	A	D	V	S	V	S	G	S	P	G	Q	S	I	T	T	C	G	N	G	T	S	D	V	G	G	T	D	V	G	G	-	E	S	V	W	V	Q	H	F	G	K	A	P	K	V	I	D	V	S	K	R	P	S	G	V	N	R	F	S	G	S	K

	7G	89	99	15K	17B																																							
A49_C14_L3.ref	B	G	D	T	A	T	L	T	I	S	G	L	T	Q	A	L	D	E	A	D	F	Y	C	Q	A	W	E	T	T	-	T	F	V	F	G	G	O	G	T	L	T	V	L	G
A49_C14_K1.ref	B	G	D	T	L	T	I	N	S	L	Q	P	E	D	F	A	T	Y	C	Q	Q	-	-	S	V	S	-	P	R	T	F	G	G	O	T	R	L	D	I	K	-			
A49_P20_K1.ref	B	G	D	T	L	T	I	S	L	Q	P	E	D	F	A	T	Y	C	Q	Q	-	-	S	V	S	-	F	S	F	-	P	R	T	F	G	G	O	T	R	L	D	I	K	-
A43_C16_L2.ref	B	G	N	T	A	S	L	T	I	S	G	L	I	E	D	E	G	O	Y	F	C	S	-	-	L	T	D	R	S	H	R	I	F	G	G	T	K	V	T	V	L	G		
A49_C09_L2.ref	S	G	N	T	A	S	L	T	I	S	G	L	Q	A	E	D	E	G	O	Y	F	C	S	-	-	L	T	S	T	R	R	R	V	F	G	T	G	T	K	L	T	V	L	G

[0279] The sequences of sister clones to human monoclonal antibody 1443_C16 (PG16) were determined, including the sequences of the variable regions of the Gamma heavy and Kappa or Lambda light chains. In addition, the sequence of each of the polynucleotides encoding the antibody sequences was determined. Shown below are the polypeptide and polynucleotide sequences of the gamma heavy chains and kappa light chains, with the signal peptides at the N-terminus (or 5' end) and the constant regions at the C-terminus (or 3' end) of the variable regions, which are shown in bolded text.

[0280] 1469_M23 (PG16) (TCN-118) gamma heavy chain nucleotide sequence: 1469_M23 γ 3 coding sequence (variable region in bold)

ATGGAGTTTGGGCTGAGCTGGGTTTTCTCGCAACTCTGTAAAGAGTTGTG
AAGTGTCAAGGAAAACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCC
GGGGGGGTCCCTGAGACTCTCCTGTTTAGCGTCTGGATTACCTTTC
ACAAATATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGCCTG
GAGTGGGTGGCACTCATCTCAGATGACGGAATGAGGAAATATCATTC
AGACTCCATGTGGGGCCGAGTCACCATCTCCAGAGACAATTCCAAGA
ACACTCTATATCTGCAATTCaGCAGCCTGAAAGTCGAAGACACGGCTA
TGTTCTTCTGTGCGAGAGAGGCTGGTGGGCCAATCTGGCATGACGAC
GTCAAATATTACGATTTTAATGACGGCTACTACAACTACCACTACATG
GACGTCTGGGGCAAGGGGACCACGGTCACCGTCTCCTCAGCGTCGACC
AAGGGCCCATCGGTCTTCCCTCTGGCACCATCATCCAAGTCGACCTCTGG
GGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGG
TGACGGTGTCTGGAAGTCAAGGCGCCCTGACCAGCGGCGTGCACACCTTC
CCGGCTGTCTTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAC
CGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATC
ACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTG
TGACAAAACCTCACACATGCCCACCGTGCCACAGCACCTGAACTCCTGGGGG
GACCGTCAGTCTTCTTCCCCCAAAACCCAAGGACACCCTCATGATCT
CCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGA
CCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG
CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGT
CAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACA
AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
TCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCC
CATCCCGGGAGGAGATGACCAAGAACCAGGTACGCCTGACCTGCCTGGTC
AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGC
AGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGG
CTCCTTCTTCTCTATAGCAAGCTACCGTGGACAAGAGCAGGTGGCAGC
AGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 138)

[0281] 1469_M23 (PG16) (TCN-118) gamma heavy chain variable region nucleotide sequence:

CAGGAAAACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCGGGGGGGT
 CCCTGAGACTCTCCTGTTTAGCGTCTGGATTACCTTTCACAAATATGGCA
 TGC ACTGGGTCCGCCAGGCTCCAGGCAAGGGCCTGGAGTGGGTGGCACTC
 ATCTCAGATGACGGAATGAGGAAATATCATTCAGACTCCATGTGGGGCCG
 AGTCACCATCTCCAGAGACAATTCCAAGAACTCTATATCTGCAATTCaG
 CAGCCTGAAAGTCGAAGACACGGCTATGTTCTTCTGTGCGAGAGAGGCTG
 GTGGGCCAATCTGGCATGACGACGTCAAATATTACGATTTTAATGACGGC
 TACTACAACTACCACTACATGGACGTCTGGGGCAAGGGGACCACGGTCAC
 CGtCTCCTCA (SEQ ID NO: 128)

[0282] 1469_M23 (PG16) (TCN-118) gamma heavy chain amino acid sequence: expressed protein with variable region in bold.

QEKLVESGGGVVQPGGSLRLSCLASGFTFHKYGMHWVRQAPGKGLEW
VALISDDGMRKYHSDSMWGRVTISRDN SKNTLYLQFSSLKVEDTAMFFC
AREAGGPIWHDDVKYYDFNDGYNYHYMDVWGKGTTTVTVSSASTKGPS
 VFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP
 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
 KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY
 TQKSLSLSPGK (SEQ ID NO: 139)

[0283] 1469_M23 (PG16) (TCN-118) gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

QEKLVESGGGVVQPGGSLRLSCLAS***GFTFHKYGMHWVRQAPGKGLEW******VAL***
ISDDGMRKYHSDSMWGRVTISRDN***SKNTLYLQFSSLKVEDTAMFFCAREAG***
GPIWHDDVKYYDFNDGYNYHYMDVWGKGTTTVTVSS (SEQ ID NO: 140)

[0284] 1469_M23 (PG16) (TCN-118) gamma heavy chain Kabat CDRs:

CDR 1: KYGMH (SEQ ID NO: 88)

CDR 2: LISDDGMRKYHSDSMWG (SEQ ID NO: 89)

CDR 3: EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6)

[0285] 1469_M23 (PG16) (TCN-118) gamma heavy chain Chothia CDRs:

CDR 1: GFTFHK (SEQ ID NO: 266)

CDR 2: LISDDGMRKY (SEQ ID NO: 267)

CDR 3: EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6)

[0286] 1469_M23(PG16) (TCN-118) lambda light chain nucleotide sequence: 1469_M23
 λ2 coding sequence (variable region in bold)

ATGGCCTGGGCTCTGCTATTCTCACCCTCTTCACTCAGGGCACAGGGTCC
 TGGGGCCAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCT
 GGACAGACGATCACCATCTCCTGCAATGGAACCAGAAGTGACGTTGG
 TGGATTTGACTCTGTCTCCTGGTACCAACAATCCCCAGGGAGAGCCC
 CCAAAGTCATGGTTTTTGTATGTCAGTCATCGGCCCTCAGGTATCTCTA
 ATCGCTTCTCTGGCTCCAAGTCCGGCAACACGGCCTCCCTGACCATC
 TCTGGGCTCCACATTGAGGACGAGGGCGATTATTTCTGCTCTTCACT
 GACAGACAGAAGCCATCGCATATTTCGGCGGGCGGGACCAAGCTGACC
 GTTCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTC
 CTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTG
 ACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCC
 GTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACA
 AGTACGCGGCCAGCAGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCC
 CACAAAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGA
 AGACAGTGGCCCCCTACAGAATGTTTCATAG (SEQ ID NO: 141)

[0287] 1469_M23 (PG16) (TCN-118) lambda light chain variable region nucleotide sequence:

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGACG
 ATCACCATCTCCTGCAATGGAACCAGAAGTGACGTTGGTGGATTTGACTC
 TGTCTCCTGGTACCAACAATCCCCAGGGAGAGCCCCCAAAGTCATGGTTT
 TTGATGTCAGTCATCGGCCCTCAGGTATCTCTAATCGCTTCTCTGGCTCCA
 AGTCCGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCACATTGAGGAC
 GAGGGCGATTATTTCTGCTCTTCACTGACAGACAGAAGCCATCGCATATT
 CGGCGGCGGGACCAAGCTGACCGTTCTA (SEQ ID NO: 129)

[0288] 1469_M23 (PG16) (TCN-118) lambda light chain amino acid sequence: expressed protein with variable region in bold.

QSALTQPASVSGSPGQTITISCNGTRSDVGGFDSVSWYQQSPGRAPKVMV
FDVSHRPSGISNRFSGSKSGNTASLTISGLHIEDEGDYFCSSLTDRSHRIFG
GGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKA
 DSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTV
 EKTVAPECS (SEQ ID NO: 142)

[0289] 1469_M23 (PG16) (TCN-118) lambda light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

QSALTQPASVSGSPGQTITISC**NGTRSDVGGFDSV**SWYQQSPGRAPKVMV**FD**
VSHRPSGISNRFSGSKSGNTASLTISGLHIEDEGDYFC**SSLTDRSHRI**FGGGTKL
 TVL (SEQ ID NO: 96)

[0290] 1469_M23 (PG16) (TCN-118) lambda light chain Kabat CDRs:

CDR 1: NGTRSDVGGFDSVS (SEQ ID NO: 92)

CDR 2: DVSHRPS (SEQ ID NO: 95)

CDR 3: SSLTDRSHRI (SEQ ID NO: 41)

[0291] 1469_M23(PG16) (TCN-118) lambda light chain Chothia CDRs:

CDR 1: NGTRSDVGGFDSVS (SEQ ID NO: 92)

CDR 2: DVSHRPS (SEQ ID NO: 95)

CDR 3: SSLTDRSHRI (SEQ ID NO: 41)

[0292] 1456_A12 (PG16) (TCN-117) gamma heavy chain nucleotide sequence: 1456_A12
 γ 3 coding sequence (variable region in bold)

ATGGAGTTTGGGCTGAGCTGGGTTTTCCTCGCAACTCTGTTAAGAGTTGTG
 AAGTGTCACGAACAACCTGGTGGAGGCCGGGGGAGGCGTGGTCCAGC
CGGGGGGGTCCCTGAGACTCTCCTGTTTAGCGTCTGGATTACGTTT
CACAAATATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGCCT
GGAGTGGGTGGCACTCATCTCAGATGACGGAATGAGGAAATATCATT
CAGACTCCATGTGGGGCCGAGTCACCATCTCCAGAGACAATTCCAAG
AACACTCTTTATCTGCAATTCAGCAGCCTGAGAGTCGAAGACACGGC
TATGTTCTTCTGTGCGAGAGAGGCCGGTGGGCCAATCTGGCATGACG
ACGTCAAATATTACGATTTTAATGACGGCTACTACAACCTATCACTACA
TGGACGTCTGGGGCAAGGGGACCAAGGTCACCGTCTCCTCAGCGTCG
 ACCAAGGGCCCATCGGTCTTCCCTCTGGCACCATCATCCAAGTCGACCTCT
 GGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACC
 GGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGCACACCT
 TCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGA
 CCGTGCCCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTGAAT
 CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTT
 GTGACAAAACCTCACACATGCCCACCGTGCCCAAGCACCTGAACCTCCTGGGG
 GGACCGTCAGTCTTCCCTCTTCCCCCAAAACCCAAGGACACCCTCATGAT
 CTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAG
 ACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT
 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
 TCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
 AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT
 CTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCC
 CCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGT
 CAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG
 CAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCTGGACTCCGACG
 GCTCCTTCTTCCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA
 CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:
 46)

[0293] 1456_A12 (PG16) (TCN-117) gamma heavy chain variable region nucleotide
 sequence:

CACGAACAACCTGGTGGAGGCCGGGGGAGGCGTGGTCCAGCCGGGGGGGT
 CCCTGAGACTCTCCTGTTTAGCGTCTGGATTACGTTTCACAAATATGGCA
 TGCCTGGGTCCGCCAGGCTCCAGGCAAGGGCCTGGAGTGGGTGGCACTC
 ATCTCAGATGACGGAATGAGGAAATATCATTCAGACTCCATGTGGGGCCG
 AGTCACCATCTCCAGAGACAATTCCAAGAACACTCTTTATCTGCAATTCA
 GCAGCCTGAGAGTCGAAGACACGGCTATGTTCTTCTGTGCGAGAGAGGCC
 GGTGGGCCAATCTGGCATGACGACGTCAAATATTACGATTTAATGACGG
 CTACTACAACCTATCACTACATGGACGTCTGGGGCAAGGGGACCAAGGTCA
 CCGTCTCCTCA (SEQ ID NO: 130)

[0294] 1456_A12 (PG16) (TCN-117) gamma heavy chain amino acid sequence: expressed protein with variable region in bold.

HEQLVEAGGGVVQPGGSLRLSCLASGFTFHKYGMHWVRQAPGKGLEW
VALISDDGMRKYHSDSMWGRVTISRDN SKNTLYLQFSSLRVEDTAMFFC
AREAGGPIWHDDVKYYDFNDGYNYHYMDVWVGKGTKVTVSSASTKGPS
 VFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP
 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
 KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
 QPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY
 TQKSLSLSPGK (SEQ ID NO: 47)

[0295] 1456_A12 (PG16) (TCN-117) gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

HEQLVEAGGGVVQPGGSLRLSCLAS***GFTFHKYGMHWVRQAPGKGLEWVAL***
ISDDGMRKYHSDSMWGRVTISRDN SKNTLYLQFSSLRVEDTAMFFCAREAG
GPIWHDDVKYYDFNDGYNYHYMDVWVGKGTKVTVSS (SEQ ID NO: 48)

[0296] 1456_A12 (PG16) (TCN-117) gamma heavy chain Kabat CDRs:

CDR 1: KYGMH (SEQ ID NO: 88)

CDR 2: LISDDGMRKYHSDSMWG (SEQ ID NO: 89)

CDR 3: EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6)

[0297] 1456_A12 (PG16) (TCN-117) gamma heavy chain Chothia CDRs:

CDR 1: GFTFHK (SEQ ID NO: 266)

CDR 2: LISDDGMRKY (SEQ ID NO: 267)

CDR 3: EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6)

[0298] 1456_A12 (PG16) (TCN-117) lambda light chain nucleotide sequence: 1456_A12 λ 2 coding sequence (variable region in bold)

ATGGCCTGGGCTTGCTATTCCTCACCCCTCTTCACTCAGGGCACAGGGTCCT
 GGGGCCAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCT
 GGACAGACGATCACCATCTCCTGCAATGGAACCAGCCGTGACGTTGG
 TGGATTTGACTCTGTCTCCTGGTATCAACAATCCCCAGGGAAAGCCC
 CCAAAGTCATGGTTTTTTGATGTGATCATCGGCCCTCAGGTATGTCTA
 ATCGCTTCTCTGGCTCCAAGTCCGGCAACACGGCCTCCCTGACCATT
 TCTGGGCTCCACATTGAGGACGAGGGCGATTATTTCTGCTCTTCATT
 GACAGACAGAAGCCATCGCATATTCGGCGGGCGGGACCAAGCTGACC
 GTTCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTC
 CTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTG
 ACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCC
 GTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACA
 AGTACGCGGCCAGCAGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCC
 CACAAAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGA
 AGACAGTGGCCCCCTACAGAATGTTTCATAG (SEQ ID NO: 49)

[0299] 1456_A12 (PG16) (TCN-117) lambda light chain variable region nucleotide sequence:

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGACG
 ATCACCATCTCCTGCAATGGAACCAGCCGTGACGTTGGTGGATTTGACTCT
 GTCTCCTGGTATCAACAATCCCCAGGGAAAGCCCCCAAAGTCATGGTTTT
 TGATGTGATCATCGGCCCTCAGGTATGTCTAATCGCTTCTCTGGCTCCAA
 GTCCGGCAACACGGCCTCCCTGACCATTCTGGGCTCCACATTGAGGACG
 AGGGCGATTATTTCTGCTCTTCATTGACAGACAGAAGCCATCGCATATTCG
 CGGGCGGGACCAAGCTGACCGTTCTA (SEQ ID NO: 131)

[0300] 1456_A12 (PG16) (TCN-117) lambda light chain amino acid sequence: expressed protein with variable region in bold.

QSALTQPASVSGSPGQTITISCNGTSRDVGGFDSVSWYQQSPGKAPKVMV
FDVSHRPSGMSNRFSGSKSGNTASLTISGLHIEDEGDYFCSSLTDRSHRIF
GGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAW
 KADSSPVKAGVETTTPSKQSNKYAASSYLSLTPEQWKSHKSYSCQVTHEGS
 TVEKTVAPTECS (SEQ ID NO: 50)

[0301] 1456_A12 (PG16) (TCN-117) lambda light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

QSALTQPASVSGSPGQTITISC*NGTSRDVGGFDSV*SWYQQSPGKAPKVMV*FD*
*VSHRPS*GMSNRFSGSKSGNTASLTISGLHIEDEGDYFC*SSLTDRSHRI*FGGGTK
 LTVL (SEQ ID NO: 51)

[0302] 1456_A12 (PG16) (TCN-117) lambda light chain Kabat CDRs:

CDR 1: NGTSRDVGGFDSVS (SEQ ID NO: 93)

CDR 2: DVSHRPS (SEQ ID NO: 95)

CDR 3: SSLTDRSHRI (SEQ ID NO: 41)

[0303] 1456_A12 (PG16) (TCN-117) lambda light chain Chothia CDRs:

CDR 1: NGTSRDVGGFDSVS (SEQ ID NO: 93)

CDR 2: DVSHRPS (SEQ ID NO: 95)

CDR 3: SSLTDRSHRI (SEQ ID NO: 41)

[0304] 1503_H05 (PG16) (TCN-119) gamma heavy chain nucleotide sequence: 1503_H05
 γ 3 coding sequence (variable region in bold)

ATGGAGTTTGGCTGAGCTGGGTTTTCTCGCAACTCTGTTAAGAGTTGTGA
 AGTGT**CAGGAAAACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCG**
GGGGGGTCCCTGAGACTCTCCTGTTTAGCGTCTGGATTACCTTTCA
CAAATATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGCCTGG
AGTGGGTGGCACTCATCTCAGATGACGGAATGAGGAAATATCATTCA
GACTCCATGTGGGGCCGAGTCACCATCTCCAGAGACAATTCCAAGAA
CACTTTATATCTGCAATTCAGCAGCCTGAAAGTCGAAGACACGGCTA
TGTTCTTCTGTGCGAGAGAGGCTGGTGGGCCAATCTGGCATGACGAC
GTCAAATATTACGATTTTAATGACGGCTACTACAATTACCACTACATG
GACGTCTGGGGCAAGGGGACCATTGTACCGTCTCCTCAGCGTCGAC
CAAGGGCCCATCGGTCTTCCCTCTGGCACCATCATCCAAGTCGACCTCTG
GGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG
GTGACGGTGTCTGTGGAATCAGGCGCCCTGACCAGCGGCGTGACACCTT
CCCGGTGTCTTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGA
CCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTT
GTGACAAAACCTCACACATGCCCACCGTGCCCAAGCACCTGAACCTCTGGGG
GGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGAT
CTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAG
ACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGAGGTGCATAAT
GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
TCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT
CTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCC
CCATCCCGGGAGGAGATGACCAAGAACCAGGTACGCTGACCTGCCTGGT
CAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG
CAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCTGGACTCCGACG
GCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA
CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:
 52)

[0305] 1503_H05 (PG16) (TCN-119) gamma heavy chain variable region nucleotide
 sequence:

CAGGAAAACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCGGGGGGGT
 CCCTGAGACTCTCCTGTTTAGCGTCTGGATTACCTTTCACAAATATGGCA
 TGCCTGGGTCCGCCAGGCTCCAGGCAAGGGCCTGGAGTGGGTGGCACTC
 ATCTCAGATGACGGAATGAGGAAATATCATTCAGACTCCATGTGGGGCCG
 AGTCACCATCTCCAGAGACAATTCCAAGAACAACCTTTATATCTGCAATTCA
 GCAGCCTGAAAGTCGAAGACACGGCTATGTTCTTCTGTGCGAGAGAGGCT
 GGTGGGCCAATCTGGCATGACGACGTCAAATATTACGATTTTAATGACGG
 CTACTACAATTACCACTACATGGACGTCTGGGGCAAGGGGACCATTGTCA
 CCGTCTCCTCA (SEQ ID NO: 132)

[0306] 1503_H05 (PG16) (TCN-119) gamma heavy chain amino acid sequence: expressed protein with variable region in bold.

QEKLVESGGGVVQPGGSLRLSCLASGFTFHKYGMHWVRQAPGKGLEW
VALISDDGMRKYHSDSMWGRVTISRDN SKNTLYLQFSSLKVEDTAMFFC
AREAGGPIWHDDVKYYDFNDGYNYHYMDVWGKGTIVTVSSASTKGPS
 VFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP
 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
 KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
 QPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY
 TQKSLSLSPGK (SEQ ID NO: 53).

[0307] 1503_H05 (PG16) (TCN-119) gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

QEKLVESGGGVVQPGGSLRLSCLAS***GFTFHKYGMHWVRQAPGKGLEW******VAL***
ISDDGMRKYHSDSMWGRVTISRDN***SKNTLYLQFSSLKVEDTAMFFCAREAG***
GPIWHDDVKYYDFNDGYNYHYMDVWGKGTIVTVSS (SEQ ID NO: 54)

[0308] 1503_H05 (PG16) (TCN-119) gamma heavy chain Kabat CDRs:

CDR 1: KYGMH (SEQ ID NO: 88)

CDR 2: LISDDGMRKYHSDSMWG (SEQ ID NO: 89)

CDR 3: EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6)

[0309] 1503_H05 (PG16) (TCN-119) gamma heavy chain Chothia CDRs:

CDR 1: GFTFHK (SEQ ID NO: 266)

CDR 2: LISDDGMRKY (SEQ ID NO: 267)

CDR 3: EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6)

[0310] 1503_H05 (PG16) (TCN-119) lambda light chain nucleotide sequence: 1503_H05 λ 2 coding sequence (variable region in bold)

ATGGCCTGGGCTTGCTATTCCTCACCCCTCTTCACTCAGGGCACAGGGTCCT
 GGGGCCAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCT
 GGACAGACGATCACCATCTCCTGCAATGGAACCAGAAGTGACGTTGG
 TGGATTTGACTCTGTCTCCTGGTACCAACAATCCCCAGGGAAAGCCC
 CCAAAGTCATGGTTTTTTGATGTGTCAGTCATCGGCCCTCAGGTATCTCTA
 ATCGCTTCTCTGGCTCCAAGTCCGGCAACACGGCCTCCCTGACCATC
 TCTGGGCTCCACATTGAGGACGAGGGCGATTATTTCTGCTCTTCACT
 GACAGACAGAAGCCATCGCATATTTCGGCGGGCGGGACCAAGGTGACC
 GTTCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTC
 CTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTG
 ACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCC
 GTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACA
 AGTACGCGGCCAGCAGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCC
 CACAAAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGA
 AGACAGTGGCCCCCTACAGAATGTTTCATAG (SEQ ID NO: 55)

[0311] 1503_H05 (PG16) (TCN-119) lambda light chain variable region nucleotide sequence:

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGACG
 ATCACCATCTCCTGCAATGGAACCAGAAGTGACGTTGGTGGATTTGACTC
 TGTCTCCTGGTACCAACAATCCCCAGGGAAAGCCCCCAAAGTCATGGTTT
 TTGATGTGTCAGTCATCGGCCCTCAGGTATCTCTAATCGCTTCTCTGGCTCCA
 AGTCCGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCACATTGAGGAC
 GAGGGCGATTATTTCTGCTCTTCACTGACAGACAGAAGCCATCGCATATT
 CGGCGGCGGGACCAAGGTGACCGTTCTA (SEQ ID NO: 133)

[0312] 1503_H05 (PG16) (TCN-119) lambda light chain amino acid sequence: expressed protein with variable region in bold.

QSALTQPASVSGSPGQTITISCNGTRSDVGGFDSVSWYQQSPGKAPKVMV
FDVSHRPSGISNRFSGSKSGNTASLTISGLHIEDEGDYFCSSLTDRSHRIFG
GGTKVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWK
 ADSSPVKAGVETTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGST
 VEKTVAPTECS (SEQ ID NO: 56)

[0313] 1503_H05 (PG16) (TCN-119) lambda light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

QSALTQPASVSGSPGQTITISC*NGTRSDVGGFDSV*SWYQQSPGKAPKVMV*FD*
*VSHRPS*GISNRFSGSKSGNTASLTISGLHIEDEGDYFC*SSLTDRSHRIF*GGGGTK
 VTVL (SEQ ID NO: 57)

[0314] 1503_H05 (PG16) (TCN-119) lambda light chain Kabat CDRs:

CDR 1: NGTRSDVGGFDSVS (SEQ ID NO: 92)

CDR 2: DVSHRPS (SEQ ID NO: 95)

CDR 3: SSLTDRSHRI (SEQ ID NO: 41)

[0315] 1503_H05 (PG16) (TCN-119) lambda light chain Chothia CDRs:

CDR 1: NGTRSDVGGFDSVS (SEQ ID NO: 92)

CDR 2: DVSHRPS (SEQ ID NO: 95)

CDR 3: SSLTDRSHRI (SEQ ID NO: 41)

[0316] 1489_I13 (PG16) (TCN-120) gamma heavy chain nucleotide sequence: 1489_I13 γ 3 coding sequence (variable region in bold)

ATGGAGTTTGGGCTGAGCTGGGTTTTCCTCGCAACTCTGTTAAGAGTTGTG
AAGTGT**CAGGAACA**ACTGTTGGAGTCTGGGGGAGGCGTGGTCCAGCC
GGGGGGGTCCCTGAGACTCTCCTGTTTAGCGTCTGGATTCACGTTTC
ACAAATATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGCCTG
GAGTGGGTGGCACTCATCTCAGATGACGGAATGAGGAAATATCATTC
AAACTCCATGTGGGGCCGAGTCACCATCTCCAGAGACAATTCCAAGA
ACACTCTTTATCTGCAATTCAGCAGCCTGAAAGTCGAAGACACGGCT
ATGTTCTTCTGTGCGAGAGAGGCTGGTGGGCCAATCTGGCATGACGA
CGTCAAATATTACGATTTTAATGACGGCTACTACA**ACTACCACTACAT**
GGACGTCTGGGGCAAGGGGACCACGGTCACCGTCTCCTCAGCGTCGA
CCAAGGGCCCATCGGTCTTCCCTCTGGCACCATCATCCAAGTCGACCTCTG
GGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG
GTGACGGTGTCTGTGGA**ACTCAGGCGCCCTGACCAGCGGCGTG**CACACCTT
CCCGGTGTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGA
CCGTGCCCTCCAGCAGCTTGGG**CACCCAGACCTACATCTGCAACGTGAAT**
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTT
GTGACAAA**ACTCACACATGCCCACCGTGCCCAGCACCTGA**ACTCCTGGGG
GGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCCTCATGAT
CTCCCGGACCCCTGAGGT**CACATGCGTGGTGGTGGACGTGAGCCACGAAG**
ACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT
GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
TCAGCGTCTCACCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT
CTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCC
CCATCCCGGGAGGAGATGACCAAGAACCAGGT**CAGCCTGACCTGCCTGGT**
CAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG
CAGCCGGAGAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG
GCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA
CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:
58)

[0317] 1489_I13 (PG16) (TCN-120) gamma heavy chain variable region nucleotide sequence:

CAGGAACAACCTGTTGGAGTCTGGGGGAGGCGTGGTCCAGCCGGGGGGGT
 CCCTGAGACTCTCCTGTTTAGCGTCTGGATTACGTTTCACAAATATGGCA
 TGCCTGGGTCCGCCAGGCTCCAGGCAAGGGCCTGGAGTGGGTGGCACTC
 ATCTCAGATGACGGAATGAGGAAATATCATTCAAACTCCATGTGGGGCCG
 AGTCACCATCTCCAGAGACAATTCCAAGAACACTCTTTATCTGCAATTCA
 GCAGCCTGAAAGTCGAAGACACGGCTATGTTCTTCTGTGCGAGAGAGGCT
 GGTGGGGCCAATCTGGCATGACGACGTCAAATATTACGATTTTAATGACGG
 CTACTACAACCTACCACTACATGGACGTCTGGGGCAAGGGGACCACGGTCA
 CCGTCTCCTCA (SEQ ID NO: 134)

[0318] 1489_I13 (PG16) (TCN-120) gamma heavy chain amino acid sequence: expressed protein with variable region in bold.

QEQLLESGGGVVQPGGSLRLSCLAS**GFTFH**KYGMHWVRQAPGKGLEW
 VALISDDGMRKYHSNSMWGRVTISRDN**SKNTLYLQFSS**LKVEDTAMFFC
AREAGGPIWHDDVKYYDFNDGYNYHYMDVW**GKGTT**TVTVSSASTKGPS
 VFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP
 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGV
 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
 KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
 QPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY
 TQKSLSLSPGK (SEQ ID NO: 59)

[0319] 1489_I13 (PG16) (TCN-120) gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

QEQLLESGGGVVQPGGSLRLSCLAS***GFTFH***KYGMHWVRQAPGKGLEWVAL
ISDDGMRKYHSNSMWGRVTISRDN***SKNTLYLQFSS***LKVEDTAMFFC***EAG***
GPIWHDDVKYYDFNDGYNYHYMDVW***GKGTT***TVTVSS (SEQ ID NO: 60)

[0320] 1489_I13 (PG16) (TCN-120) gamma heavy chain Kabat CDRs:

CDR 1: KYGMH (SEQ ID NO: 88)

CDR 2: LISDDGMRKYHSNSMWG (SEQ ID NO: 98)

CDR 3: EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6)

[0321] 1489_I13 (PG16) (TCN-120) gamma heavy chain Chothia CDRs:

CDR 1: GFTFHK (SEQ ID NO: 266)

CDR 2: LISDDGMRKY (SEQ ID NO: 267)

CDR 3: EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6)

[0322] 1489_I13 (PG16) (TCN-120) lambda light chain nucleotide sequence: 1489_I13 λ 2 coding sequence (variable region in bold)

ATGGCCTGGGCTCTGCTATTCTCACCCTCTTCACTCAGGGCACAGGGTCC
 CGGGGCCAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCT
 GGACAGACGATCACCATCTCCTGCAATGGAACCAGCAGTGACGTTGG
 TGGATTTGACTCTGTCTCCTGGTATCAACAATCCCCAGGGAAAGCCC
 CCAAAGTCATGGTTTTTGTATGTCAGTCATCGGCCCTCAGGTATCTCTA
 ATCGCTTCTCTGGCTCCAAGTCCGGCAACACGGCCTCCCTGACCATC
 TCTGGGCTCCACATTGAGGACGAGGGCGATTATTTCTGCTCTTCACT
 GACAGACAGAAGCCATCGCATATTTCGGCGGGCGGGACCAAGGTGACC
 GTTCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTC
 CTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTG
 ACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCC
 GTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACA
 AGTACGCGGCCAGCAGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCC
 CACAAAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGA
 AGACAGTGGCCCCCTACAGAATGTTTCATAG (SEQ ID NO: 61)

[0323] 1489_I13 (PG16) (TCN-120) lambda light chain variable region nucleotide sequence:

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGACG
 ATCACCATCTCCTGCAATGGAACCAGCAGTGACGTTGGTGGATTTGACTC
 TGTCTCCTGGTATCAACAATCCCCAGGGAAAGCCCCCAAAGTCATGGTTT
 TTGATGTCAGTCATCGGCCCTCAGGTATCTCTAATCGCTTCTCTGGCTCCA
 AGTCCGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCACATTGAGGAC
 GAGGGCGATTATTTCTGCTCTTCACTGACAGACAGAAGCCATCGCATATT
 CGGCGGCGGGACCAAGGTGACCGTTCTA (SEQ ID NO: 135)

[0324] 1489_I13 (PG16) (TCN-120) lambda light chain amino acid sequence: expressed protein with variable region in bold.

QSALTQPASVSGSPGQTITISCNGTSSDVGGFDSVSWYQQSPGKAPKVMV
 FDVSHRPSGISNRFSGSKSGNTASLTISGLHIEDEGDYFCSSLTDRSHRIFG
 GGTKVTVLGPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWK
 ADSSPVKAGVETTPSKQSNKYAASSYLSLTPEQWKSHKSYSCQVTHEGST
 VEKTVAPTECS (SEQ ID NO: 14)

[0325] 1489_I13 (PG16) (TCN-120) lambda light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics).

QSALTQPASVSGSPGQTITISCNGTSSDVGGFDSVSWYQQSPGKAPKVMVFD
VSHRPSGISNRFSGSKSGNTASLTISGLHIEDEGDYFCSSLTDRSHRIFGGGTK
 VTVL (SEQ ID NO: 32)

[0326] 1489_I13 (PG16) (TCN-120) lambda light chain Kabat CDRs:

CDR 1: NGTSSDVGGFDSVS (SEQ ID NO: 97)

CDR 2: DVSHRPS (SEQ ID NO: 95)

CDR 3: SSLTDRSHRI (SEQ ID NO: 41)

[0327] 1489_I13 (PG16) (TCN-120) lambda light chain Chothia CDRs:

CDR 1: NGTSSDVGGFDSVS (SEQ ID NO: 97)

CDR 2: DVSHRPS (SEQ ID NO: 95)

CDR 3: SSLTDRSHRI (SEQ ID NO: 41)

[0328] 1480_I08 gamma heavy chain nucleotide sequence: 1480_I08 γ 3 coding sequence
(variable region in bold)

ATGGAGTTTGGCTGAGCTGGGTTTTCTCGCAACTCTGTTAAGAGTTGTGA
AGTGT**CAGGAACA**ACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCG
GGGGGGTCCCTGAGACTCTCCTGTTTAGCGTCTGGATTACGTTTCA
CAAATATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGCCTGG
AGTGGGTGGCACTCATCTCAGATGACGGAATGAGGAAATATCATTCA
GACTCCATGTGGGGCCGAGTCACCATCTCCAGAGACAATTCCAAGAA
CACTCTTTATCTGCAATTCAGCAGCCTGAAAGTCGAAGACACGGCTA
TGTTCTTCTGTGCGAGAGAGGCTGGTGGGCCAATCTGGCATGACGAC
GTCAAATATTACGATTTTAATGACGGCTACTACAACTACCACTACATG
GACGTCTGGGGCAAGGGGACCACGGTCACCGTCTCCTCAGCGTCGAC
CAAGGGCCCATCGGTCTTCCCTCTGGCACCATCATCCAAGTCGACCTCTG
GGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG
GTGACGGTGTCTGTGGAATCAGGCGCCCTGACCAGCGGCGTGCACACCTT
CCCGGTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGA
CCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTT
GTGACAAAACCTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGG
GGACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGAT
CTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAG
ACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT
GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
TCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
AAGTGCAAGGTCTCCAACAAGCCCTCCCAGCCCCATCGAGAAAACCAT
CTCCAAGGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCC
CCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGT
CAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG
CAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG
GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA
CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:
64)

[0329] 1480_I08 gamma heavy chain variable region nucleotide sequence:

CAGGAACA**ACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCGGGGGGGT**
CCCTGAGACTCTCCTGTTTAGCGTCTGGATTACGTTTCACAAATATGGCA
TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGCCTGGAGTGGGTGGCACTC
ATCTCAGATGACGGAATGAGGAAATATCATTCACTCCATGTGGGGCCG

AGTCACCATCTCCAGAGACAATTCCAAGAACAACACTCTTTATCTGCAATTCA
GCAGCCTGAAAGTCGAAGACACGGCTATGTTCTTCTGTGCGAGAGAGGCT
GGTGGGCCAATCTGGCATGACGACGTCAAATATTACGATTTTAATGACGG
CTACTACAACCTACCACTACATGGACGTCTGGGGCAAGGGGACCACGGTCA
CCGTCTCCTCA (SEQ ID NO: 136)

[0330] 1480_I08 gamma heavy chain amino acid sequence: expressed protein with variable region in bold.

QEQLVESGGGVVQPGGSLRLSCLASGFTFHKYGMHWVRQAPGKGLEW
VALISDDGMRKYHSDSMWGRVTISRDN SKNTLYLQFSSLKVEDTAMFFC
AREAGGPIWHDDVKYYDFNDGYNYHYMDVWGKGTTTVTVSSASTKGPS
VFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP
APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGV
EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHY
TQKSLSLSPGK (SEQ ID NO: 65)

[0331] 1480_I08 gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

QEQLVESGGGVVQPGGSLRLSCLAS***GFTFHKYGMHWVRQAPGKGLEW******VAL***
ISDDGMRKYHSDSMWGRVTISRDN SKNTLYLQFSSLKVEDTAMFFCAREAG
GPIWHDDVKYYDFNDGYNYHYMDVWGKGTTTVTVSS (SEQ ID NO: 31)

[0332] 1480_I08 gamma heavy chain Kabat CDRs:

CDR 1: KYGMH (SEQ ID NO: 88)

CDR 2: LISDDGMRKYHSDSMWG (SEQ ID NO: 89)

CDR 3: EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6)

[0333] 1480_I08 gamma heavy chain Chothia CDRs:

CDR 1: GFTFHK (SEQ ID NO: 266)

CDR 2: LISDDGMRKY (SEQ ID NO: 267)

CDR 3: EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6)

[0334] 1480_I08 lambda light chain nucleotide sequence: 1480_I08 2 coding sequence (variable region in bold)

ATGGCCTGGGCTCTGCTATTCGTCACCCTCCTCACTCAGGGCACAGGGTCC
TGGGGCCAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCT
GGACAGACGATCACCATCTCCTGCAATGGAACCAGCAGTGACGTTGG
TGGATTTGACTCTGTCTCCTGGTATCAACAATCCCCAGGGAAAGCCC
CCAAAGTCATGGTTTTTGTATGTCAGTCATCGGCCCTCAGGTATCTCTA

ATCGCTTCTCTGGCTCCAAGTCCGGCAACACGGCCTCCCTGACCATC
TCTGGGCTCCACATTGAGGACGAGGGCGATTATTTCTGCTCTTCACT
GACAGACAGAAGCCATCGCATATTCGGCGGGCGGGACCAAGGTGACC
GTTCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTC
CTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTG
ACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCC
GTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACA
AGTACGCGGCCAGCAGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCC
CACAAAAGCTACAGCTGCCAGGTACGCATGAAGGGAGCACCGTGGAGA
AGACAGTGGCCCCTACAGAATGTTCATAG (SEQ ID NO: 67)

[0335] 1480_I08 lambda light chain variable region nucleotide sequence:

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGACG
ATCACCATCTCCTGCAATGGAACCAGCAGTGACGTTGGTGGATTTGACTC
TGTCTCCTGGTATCAACAATCCCCAGGGAAAGCCCCCAAAGTCATGGTTT
TTGATGTCAGTCATCGGCCCTCAGGTATCTCTAATCGCTTCTCTGGCTCCA
AGTCCGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCACATTGAGGAC
GAGGGCGATTATTTCTGCTCTTCACTGACAGACAGAAGCCATCGCATATT
CGGCGGCGGGACCAAGGTGACCGTTCTA (SEQ ID NO: 137)

[0336] 1480_I08 lambda light chain amino acid sequence: expressed protein with variable region in bold.

QSALTQPASVSGSPGQTITISCNGTSSDVGGFDSVSWYQQSPGKAPKVMV
FDVSHRPSGISNRFSGSKSGNTASLTISGLHIEDEGDYFCSSLTDRSHRIFG
GGTKVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWK
ADSSPVKAGVETTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGST
VEKTVAPTECS (SEQ ID NO: 14)

[0337] 1480_I08 lambda light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

QSALTQPASVSGSPGQTITISCNGTSSDVGGFDSVSSWYQQSPGKAPKVMV***FD***
VSHRPSGISNRFSGSKSGNTASLTISGLHIEDEGDYFC***SSLTDRSHRI***FGGGTK
VTVL (SEQ ID NO: 32)

[0338] 1480_I08 lambda light chain Kabat CDRs:

CDR 1: NGTSSDVGGFDSVS (SEQ ID NO: 97)

CDR 2: DVSHRPS (SEQ ID NO: 95)

CDR 3: SSLTDRSHRI (SEQ ID NO: 41)

[0339] 1480_I08 lambda light chain Chothia CDRs:

CDR 1: NGTSSDVGGFDSVS (SEQ ID NO: 97)

CDR 2: DVSHRPS (SEQ ID NO: 95)

CDR 3: SSLTDRSHRI (SEQ ID NO: 41)

[0340] The 1469_M23 (PG16) antibody includes a heavy chain variable region (SEQ ID NO: 139), encoded by the nucleic acid sequence shown in SEQ ID NO: 128, and a light chain variable region (SEQ ID NO: 142) encoded by the nucleic acid sequence shown in SEQ ID NO: 129.

[0341] The heavy chain CDRs of the 1469_M23 (PG16) antibody have the following sequences per Kabat and Chothia definitions: KYGMH (SEQ ID NO: 88), LISDDGMRKYHSDSMWG (SEQ ID NO: 89), and EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6). The light chain CDRs of the 1469_M23 (PG16) antibody have the following sequences per Kabat and Chothia definitions: NGTRSDVGGFDSVS (SEQ ID NO: 92), DVSHRPS (SEQ ID NO: 95), and SSLTDRSHRI (SEQ ID NO: 41).

[0342] The 1456_A12 (PG16) antibody includes a heavy chain variable region (SEQ ID NO: 47), encoded by the nucleic acid sequence shown in SEQ ID NO: 130, and a light chain variable region (SEQ ID NO: 50) encoded by the nucleic acid sequence shown in SEQ ID NO: 131.

[0343] The heavy chain CDRs of the 1456_A12 (PG16) antibody have the following sequences per Kabat and Chothia definitions: KYGMH (SEQ ID NO: 88), LISDDGMRKYHSDSMWG (SEQ ID NO: 89), and EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6). The light chain CDRs of the 1456_A12 (PG16) antibody have the following sequences per Kabat and Chothia definitions: NGTSRDVGGFDSVS (SEQ ID NO: 93), DVSHRPS (SEQ ID NO: 95), and SSLTDRSHRI (SEQ ID NO: 41).

[0344] The 1503_H05 (PG16) antibody includes a heavy chain variable region (SEQ ID NO: 53), encoded by the nucleic acid sequence shown in SEQ ID NO: 132, and a light chain variable region (SEQ ID NO: 56) encoded by the nucleic acid sequence shown in SEQ ID NO: 133.

[0345] The heavy chain CDRs of the 1503_H05 (PG16) antibody have the following sequences per Kabat and Chothia definitions: KYGMH (SEQ ID NO: 88), LISDDGMRKYHSDSMWG (SEQ ID NO: 89), and EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6). The light chain CDRs of the 1503_H05 (PG16) antibody have the following sequences per Kabat and Chothia definitions:

NGTRSDVGGFDSVS (SEQ ID NO: 92), DVSHRPS (SEQ ID NO: 95), and SSLTDRSHRI (SEQ ID NO: 41).

[0346] The 1489_I13 (PG16) antibody includes a heavy chain variable region (SEQ ID NO: 59), encoded by the nucleic acid sequence shown in SEQ ID NO: 134, and a light chain variable region (SEQ ID NO: 14) encoded by the nucleic acid sequence shown in SEQ ID NO: 135.

[0347] The heavy chain CDRs of the 1489_I13 (PG16) antibody have the following sequences per Kabat and Chothia definitions: KYGMH (SEQ ID NO: 88), LISDDGMRKYHSNSMWG (SEQ ID NO: 98), and EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6). The light chain CDRs of the 1489_I13 (PG16) antibody have the following sequences per Kabat and Chothia definitions: NGTSSDVGGFDSVS (SEQ ID NO: 97), DVSHRPS (SEQ ID NO: 95), and SSLTDRSHRI (SEQ ID NO: 41).

[0348] The 1480_I08 (PG16) antibody includes a heavy chain variable region (SEQ ID NO: 65), encoded by the nucleic acid sequence shown in SEQ ID NO: 136, and a light chain variable region (SEQ ID NO: 14) encoded by the nucleic acid sequence shown in SEQ ID NO: 137.

[0349] The heavy chain CDRs of the 1480_I08 (PG16) antibody have the following sequences per Kabat and Chothia definitions: KYGMH (SEQ ID NO: 88), LISDDGMRKYHSDSMWG (SEQ ID NO: 89), and EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6). The light chain CDRs of the 1480_I08 (PG16) antibody have the following sequences per Kabat and Chothia definitions: NGTSSDVGGFDSVS (SEQ ID NO: 97), DVSHRPS (SEQ ID NO: 95), and SSLTDRSHRI (SEQ ID NO: 41).

[0350] The sequences of additional human monoclonal antibodies were determined, including the sequences of the variable regions of the Gamma heavy and Kappa or Lambda light chains. In addition, the sequence of each of the polynucleotides encoding the antibody sequences was determined. Shown below are the polypeptide and polynucleotide sequences of the gamma heavy chains and kappa light chains, with the signal peptides at the N-terminus (or 5' end) and the constant regions at the C-terminus (or 3' end) of the variable regions, which are shown in bolded text.

[0351] 4838_L06 (PGT-121) gamma heavy chain nucleotide sequence: coding sequence (variable region in bold)

ATGAAACACCTGTGGTTCTTCTTCTCCTGGTGGCAGCTCCCAGATGGGTC
 CTGTCACAGATGCAGTTACAGGAGTCGGGCCCCGGACTGGTGAAGCC
 TTCGGAACCCCTGTCCCTCACGTGCAGTGTGTCTGGTGCCTCCATAA
 GTGACAGTTACTGGAGCTGGATCCGGCGGTCCCCAGGGAAGGGACTT
 GAGTGGATTGGGTATGTCCACAAAAGCGGCGACACAAATTACAGCCC
 CTCCTCAAGAGTCGAGTCAACTTGTCGTTAGACACGTCCAAAAATC
 AGGTGTCCCTGAGCCTTGTGGCCGCGACCGCTGCGGACTCGGGCAA
 TATTATTGCGCGAGAACACTGCACGGGAGGAGAATTTATGGAATCGT
 TGCCTTCAATGAGTGGTTCACCTACTTCTACATGGACGTCTGGGGCA
 ATGGGACTCAGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGG
 TCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCC
 CTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTG
 GAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTAC
 AGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC
 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAA
 CACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCAC
 ACATGCCACCCGTGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTT
 CCTCTTCCCCCCTCAAGGACACCCTCATGATCTCCCGGACCCCTG
 AGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA
 GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG
 CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCTAC
 CGTCTGCAACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCT
 CCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA
 GGGCAGCCCCGAGAACACAGGTGTACACCCTGCCCCCATCCCGGGAGG
 AGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT
 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGACA
 ACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCT
 ATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTT
 CTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGA
 GCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 62)

[0352] 4838_L06 (PGT-121) gamma heavy chain variable region nucleotide sequence:

CAGATGCAGTTACAGGAGTCGGGCCCCGGACTGGTGAAGCCTTCGGAAA
 CCCTGTCCCTCACGTGCAGTGTGTCTGGTGCCTCCATAAGTGACAGTTACT
 GGAGCTGGATCCGGCGGTCCCCAGGGAAGGGACTTGAGTGGATTGGGTAT
 GTCCACAAAAGCGGCGACACAAATTACAGCCCCCTCCCTCAAGAGTCGAGT
 CAACTTGTCGTTAGACACGTCCAAAAATCAGGTGTCCCTGAGCCTTGTGG
 CCGCGACCGCTGCGGACTCGGGCAAATATTATTGCGCGAGAACACTGCAC
 GGGAGGAGAATTTATGGAATCGTTGCCTTCAATGAGTGGTTCACCTACTT
 CTACATGGACGTCTGGGGCAATGGGACTCAGGTCACCGTCTCCTCA (SEQ
 ID NO: 63)

[0353] 4838_L06 (PGT-121) gamma heavy chain amino acid sequence: expressed protein
 with variable region in bold.

QMQLQESGPGGLVKPSETLSLTCSVSGASISDSYWSWIRRS PGKGLEWIGY
 VHKS GDTNYS PSLKSRVNLSLDT SKNQVSLSLVAATAADSGKY YCAR TLH
 GRRIYGIVAFNEWFTYFYMDVWGN GTQVTVSSASTKGPSVFPLAPSSKSTS
 GGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTV
 PSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVF
 LFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
 EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP
 VLDS DGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK
 (SEQ ID NO: 66)

[0354] 4838_L06 (PGT-121) gamma heavy chain variable region amino acid sequence:
 (Kabat CDRs underlined, Chothia CDRs in bold italics)

QMQLQESGPGGLVKPSETLSLTCSVSGASISDSYWSWIRRS PGKGLEWIGY **YVHK**
SGDTNYS PSLKSRVNLSLDT SKNQVSLSLVAATAADSGKY YCAR **TLHGRR**
YIVAFNEWFTYFYMDVWGN GTQVTVSS (SEQ ID NO: 79)

[0355] 4838_L06 (PGT-121) gamma heavy chain Kabat CDRs:

CDR 1: DSYWS (SEQ ID NO: 90)

CDR 2: YVHKSGDTNYS PSLKS (SEQ ID NO: 265)

CDR 3: TLHGRRYIGIVAFNEWFTYFYMDV (SEQ ID NO: 143)

[0356] 4838_L06 (PGT-121) gamma heavy chain Chothia CDRs:

CDR 1: GASISD (SEQ ID NO: 144)

CDR 2: YVHKSGDTN (SEQ ID NO: 145)

CDR 3: TLHGRRYIGIVAFNEWFTYFYMDV (SEQ ID NO: 143)

[0357] 4838_L06 (PGT-121) lambda light chain nucleotide sequence: coding sequence
 (variable region in bold)

ATGGCCTGGACCTTTCTCCTCCTCGGCCTCCTCTCTCACTGCACAGCCTCT
 GTGACCTCCGATATATCTGTGGCCCCAGGAGAGACGGCCAGGATTTC
 CTGTGGGGAAAAGAGCCTTGGAAGTAGAGCTGTACAATGGTATCAAC
 ACAGGGCCCGCCAGGCCCCCTCTTTAATCATATATAATAATCAGGAC
 CGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCCTGACTCCCC
 TTTTGGGACCACGGCCACCCTGACCATCACCAGTGTCGAAGCCGGGG
 ATGAGGCCGACTATTACTGT CATATATGGGATAGTAGAGTTCCCACC
 AAATGGGTCTTCGGCGGAGGGACCACGCTGACCGTGTTAGGTCAGCC
 CAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCA
 AGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAG
 CCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGT
 GGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGC
 AGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAAAAGCTACA

GCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCC
TACAGAATGTTTCATAG (SEQ ID NO: 146)

[0358] 4838_L06 (PGT-121) lambda light chain variable region nucleotide sequence:

TCCGATATATCTGTGGCCCCAGGAGAGACGGCCAGGATTTCTGTGGGGA
AAAGAGCCTTGGAAGTAGAGCTGTACAATGGTATCAACACAGGGCCGGC
CAGGCCCCCTCTTTAATCATATATAATAATCAGGACCGGCCCTCAGGGAT
CCCTGAGCGATTCTCTGGCTCCCCTGACTCCCCTTTTGGGACCACGGCCAC
CCTGACCATCACCAGTGTCTGAAGCCGGGGATGAGGCCGACTATTACTGTC
ATATATGGGATAGTAGAGTTCCACCAAATGGGTCTTCGGCGGAGGGACC
ACGCTGACCGTGTTA (SEQ ID NO: 147)

[0359] 4838_L06 (PGT-121) lambda light chain amino acid sequence: expressed protein
with variable region in bold.

SDISVAPGETARISCGEKSLSRAVQWYQHRAGQAPSLIYNNQDRPSGIP
ERFSGSPDSPFGTTATLTITSVEAGDEADYYCHIWDSRVPTKWVFGGGTT
LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSP
VKAGVETTTPSKQSNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTV
APTECS (SEQ ID NO: 148)

[0360] 4838_L06 (PGT-121) lambda light chain variable region amino acid sequence:
(Kabat CDRs underlined, Chothia CDRs in bold italics)

SDISVAPGETARISCGEKSLSRAVQWYQHRAGQAPSLIYNNQDRPSGIPERF
SGSPDSPFGTTATLTITSVEAGDEADYYCHIWDSRVPTKWVFGGGTTTLVL
(SEQ ID NO: 149)

[0361] 4838_L06 (PGT-121) lambda light chain Kabat CDRs:

CDR 1: GEKSLGSRAVQ (SEQ ID NO: 150)

CDR 2: NNQDRPS (SEQ ID NO: 151)

CDR 3: HIWDSRVPTKWV (SEQ ID NO: 152)

[0362] 4838_L06 (PGT-121) lambda light chain Chothia CDRs:

CDR 1: GEKSLGSRAVQ (SEQ ID NO: 150)

CDR 2: NNQDRPS (SEQ ID NO: 151)

CDR 3: HIWDSRVPTKWV (SEQ ID NO: 152)

[0363] 4873_E03 (PGT-121) gamma heavy chain nucleotide sequence: coding sequence
(variable region in bold)

ATGAAACACCTGTGGTTCTTCCTTCTCCTGGTGGCAGCTCCCAGATGGGTC
CTGTCCAGATGCAGTTACAGGAGTCGGGCCCCGGACTGGTGAAGCCT
TCGGAAACCCTGTCCCTCACGTGCAGTGTGTCTGGTGCCTCCATAAG

TGACAGTTACTGGAGCTGGATCCGGCGGTCCCCAGGGAAGGGACTTG
 AGTGGATTGGGTATGTCCACAAAAGCGGCGACACAAATTACATCCCC
 TCCCTCAAGAGTCGAGTCAACTTGTTCGTTAGACACGTCCAAAAATCA
 GGTGTCCCTGAGCCTTGTGGCCGCGACCGCTGCGGACTCGGGCAAAT
 ATTATTGCGCGAGAACAACACTGCACGGGAGGAGAATTTATGGAATCGTT
 GCCTTCAATGAGTGGTTCACCTACTTCTACATGGACGTCTGGGGCAA
 TGGGACTCAGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTC
 TTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCT
 GGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTTCGTGGA
 ACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAG
 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAG
 CTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACA
 CCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACAC
 ATGCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCC
 TCTTCCCCCCCCAAAACCCAAGGACACCCCTCATGATCTCCCGGACCCCTGAG
 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTT
 CAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG
 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCACCCT
 CCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCC
 AACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAG
 GGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA
 GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATC
 CCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAA
 CTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTA
 TAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC
 TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAG
 CCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 62)

[0364] 4873_E03 (PGT-121) gamma heavy chain variable region nucleotide sequence:

CAGATGCAGTTACAGGAGTCGGGCCCCGGACTGGTGAAGCCTTCGGAAA
 CCCTGTCCCTCACGTGCAGTGTGTCTGGTGCCTCCATAAGTGACAGTTACT
 GGAGCTGGATCCGGCGGTCCCCAGGGAAGGGACTTGAGTGGATTGGGTAT
 GTCCACAAAAGCGGCGACACAAATTACAGCCCCCTCCCTCAAGAGTCGAGT
 CAACTTGTTCGTTAGACACGTCCAAAAATCAGGTGTCCCTGAGCCTTGTGG
 CCGCGACCGCTGCGGACTCGGGCAAATATTATTGCGCGAGAACAACACTGCAC
 GGGAGGAGAATTTATGGAATCGTTGCCTTCAATGAGTGGTTCACCTACTT
 CTACATGGACGTCTGGGGCAATGGGACTCAGGTCACCGTCTCCTCA (SEQ
 ID NO: 63)

[0365] 4873_E03 (PGT-121) gamma heavy chain amino acid sequence: expressed protein
 with variable region in bold.

MKHLWFFLLLVAAPRWVLSQMQLQESGPLVKPSETLSLTCSVSGASIS
 DSYWSWIRRS PGKGLEWIGYVHKSGDTNYIPSLKSRVNLSLDTSKNQVSL
SLVAATAADSGKYYCARTLHGRRIYGIVAFNEWFTYFYMDVWNGTQV
 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG

VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKRVEPKS
 CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
 KVSNAKALPAIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
 SDIAVEWESNGQPENNYKTTPVLDSGSFFLYSKLTVDKSRWQQGNVFCSS
 VMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 66)

[0366] 4873_E03 (PGT-121) gamma heavy chain variable region amino acid sequence:
 (Kabat CDRs underlined, Chothia CDRs in bold italics)

QMQLQESGPGLVKPSETLSLTCSVSG***ASISDSYWS***WIRRS***PGKGLEWIGYVHK***
SGDTNYSPSLKSRVNLSDT***SKNQVSLSLVAATAADSGKY***CAR***TLHGRR******Y***
GIVAFNEWFTYFYMDVWGNGTQVT***VSS*** (SEQ ID NO: 79)

[0367] 4873_E03 (PGT-121) gamma heavy chain Kabat CDRs:

CDR 1: DSYWS (SEQ ID NO: 90)

CDR 2: YVHKSGDTNYSPSLKS (SEQ ID NO: 265)

CDR 3: TLHGRRY***GIVAFNEWFTYFYMDV*** (SEQ ID NO: 143)

[0368] 4873_E03 (PGT-121) gamma heavy chain Chothia CDRs:

CDR 1: GASISD (SEQ ID NO: 144)

CDR 2: YVHKSGDTN (SEQ ID NO: 145)

CDR 3: TLHGRRY***GIVAFNEWFTYFYMDV*** (SEQ ID NO: 143)

[0369] 4873_E03 (PGT-121) lambda light chain nucleotide sequence: coding sequence
 (variable region in bold)

ATGGCCTGGACCTTTCTCCTCCTCGGCCTCCTCTCTCACTGCACAGCCTCT
 GTGACCTCCGATATATCTGTGGCCCCAGGAGAGACGGCCAGGATTTC
 CTGTGGGGAAAAGAGCCTTGGAAGTAGAGCTGTACAATGGTATCAAC
 ACAGGGCCGGCCAGGCCCCCTCTTTAATCATATATAATAATCAGGAC
 CGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCCTGACTCCCC
TTTTGGGACCACGGCCACCCTGACCATCACCAGTGTCGAAGCCGGGG
ATGAGGCCGACTATTACTGTCATATATGGGATAGTAGAGTTCCCACC
 AAATGGGTCTT**CGGCGGAGGGACCACGCTGACCGTGTTAGGTCAGCC**
 CAAGGCTGCCCCCTCGGTCACTCTGT**TCCCGCCCTCCTCTGAGGAGCTTCA**
 AGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGA**CTTCTACCCGGGAG**
 CCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGT
 GGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGC
 AGCTACCTGAGCCTGACGCTGAGCAGTGGAAGTCCCACAAAAGCTACA
 GCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCC
 TACAGAATGTT**CATAG** (SEQ ID NO: 146)

[0370] 4873_E03 (PGT-121) lambda light chain variable region nucleotide sequence:

TCCGATATATCTGTGGCCCCAGGAGAGACGGCCAGGATTTCCTGTGGGGA
 AAAGAGCCTTGGAAAGTAGAGCTGTACAATGGTATCAACACAGGGCCCGC
 CAGGCCCCCTCTTTAATCATATATAATAATCAGGACCGGCCCTCAGGGAT
 CCCTGAGCGATTCTCTGGCTCCCCTGACTCCCCTTTTGGGACCACGGCCAC
 CCTGACCATCACCAGTGTCTGAAGCCGGGGATGAGGCCGACTATTACTGTC
 ATATATGGGATAGTAGAGTTCCCACCAAATGGGTCTTCGGCGGAGGGACC
 ACGCTGACCGTGTTA (SEQ ID NO: 147)

[0371] 4873_E03 (PGT-121) lambda light chain amino acid sequence: expressed protein with variable region in bold.

MAWTFLLLGLLSHCTASVTS~~DISVAPGETARISC~~**GEKSLGSRAVQWYQH**
RAGQAPSLIIYNNQDRPSGIPERFSGSPDSPFGTTATLTITSVEAGDEADYY
CHIWD~~SRVPTKWV~~FGGGTTTLTVLGQPKAAPSVTLFPPSSEELQANKATLVC
 LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWK
 SHKSYSCQVTHEGSTVEKTVAPTECS (SEQ ID NO: 148)

[0372] 4873_E03 (PGT-121) lambda light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

SDISVAPGETARISC**GEKSLGSRAVQ**WYQHRAGQAPSLIIY**NNQDRPS**GIPERF
 SGSPDSPFGTTATLTITSVEAGDEADYY**CHIWD~~SRVPTKWV~~FGGGTTTLTVL**
 (SEQ ID NO: 149)

[0373] 4873_E03 (PGT-121) lambda light chain Kabat CDRs:

CDR 1: GEKSLGSRAVQ (SEQ ID NO: 150)

CDR 2: NNQDRPS (SEQ ID NO: 151)

CDR 3: HIWDSRVPTKWV (SEQ ID NO: 152)

[0374] 4873_E03 (PGT-121) lambda light chain Chothia CDRs:

CDR 1: GEKSLGSRAVQ (SEQ ID NO: 150)

CDR 2: NNQDRPS (SEQ ID NO: 151)

CDR 3: HIWDSRVPTKWV (SEQ ID NO: 152)

[0375] 4877_D15 (PGT-122) gamma heavy chain nucleotide sequence: coding sequence (variable region in bold)

ATGAAACACCTGTGGTTCTTCCTTCTCCTGGTGGCAGCTCCCAGATGGGTC
 CTGTCCCAGGTTTCATCTGCAGGAGTCGGGCCCCGGACTGGTGAAGCC
TTCGGAGACCCTGTCCCTCACGTGCAATGTGTCTGGGACCCTCGTGC
GTGATAACTACTGGAGCTGGATCAGACAACCCCTCGGGAAGCAACCT
GAGTGGATTGGCTATGTCCATGACAGCGGGGACACGAATTACAACCC
CTCCCTGAAGAGTCGAGTCCACTTATCGTTGGACAAGTCCAAAAACC
TGGTGTCCCTGAGGCTGACCGGCGTGACCGCCGCGGACTCGGCCATA
TATTATTGCGCGACAACAAAACACGGGAGGAGGATTTATGGCGTCGT

TGCCTTCAAAGAGTGGTTACCTATTTCTACATGGACGTCTGGGGCA
AAGGGACTTCGGTCACCGTCTCCTCAGCCTCCACCAAGGGGCCATCGG
TCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGACACAGCGGCC
CTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTG
GAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTAC
AGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC
AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAA
CACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCAC
ACATGCCCACCGTGCCCAGCACCTGAACCTCCTGGGGGGACCGTCAGTCTT
CCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTG
AGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA
GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG
CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCCTCAC
CGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCT
CCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA
GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGG
AGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACA
ACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCT
ATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTT
CTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGA
GCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 153)

[0376] 4877_D15 (PGT-122) gamma heavy chain variable region nucleotide sequence:

CAGGTTTCATCTGCAGGAGTCGGGCCCCGGACTGGTGAAGCCTTCGGAGAC
CCTGTCCCTCACGTGCAATGTGTCTGGGACCCTCGTGCGTGATACTACTG
GAGCTGGATCAGACAACCCCTCGGGAAGCAACCTGAGTGGATTGGCTATG
TCCATGACAGCGGGGACACGAATTACAACCCCTCCCTGAAGAGTCGAGTC
CACTTATCGTTGGACAAGTCCAAAAACCTGGTGTCCCTGAGGCTGACCGG
CGTGACCGCCGCGGACTCGGCCATATATTATTGCGCGACAACAAAACACG
GGAGGAGGATTTATGGCGTCGTTGCCTTCAAAGAGTGGTTCACCTATTTCT
ACATGGACGTCTGGGGCAAAGGGACTTCGGTTCACCGTCTCCTCA (SEQ ID
NO: 154)

[0377] 4877_D15 (PGT-122) gamma heavy chain amino acid sequence: expressed protein
with variable region in bold.

MKHLWFFLLLVAAPRWVLSQVHLQESGPGLVKPSETLSLTCNVSGTLVR
DNYWSWIRQLGKQPEWIGYVHDSGDTNYNPSLKS RVHLSLDKSKNLVS
LRLTGVTAAADSAIYYCATTKHGRRIYGVVAFKEWFTYFYMDVWGKGS
VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPK
SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP

SDIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 155)

[0378] 4877_D15 (PGT-122) gamma heavy chain variable region amino acid sequence:
(Kabat CDRs underlined, Chothia CDRs in bold italics)

QVHLQESGPGLVKPSETLSLTCNVSGTLVRDNYWSWIRQPLGKQPEWIGYVH
DSGDTNYPNPSLKSRVHLSLDKSKNLVSLRLTGVTAAADSAIYYCATTKHGRRRI
YGVVAFKEWFTYFYMDVWGKGTSVTVSS (SEQ ID NO: 156)

[0379] 4877_D15 (PGT-122) gamma heavy chain Kabat CDRs:

CDR 1: DNYWS (SEQ ID NO: 261)

CDR 2: YVHDSGDTNYPNPSLKS (SEQ ID NO: 157)

CDR 3: TKHGRRRIYGVVAFKEWFTYFYMDV (SEQ ID NO: 262)

[0380] 4877_D15 (PGT-122) gamma heavy chain Chothia CDRs:

CDR 1: GTLVRD (SEQ ID NO: 263)

CDR 2: YVHDSGDTN (SEQ ID NO: 264)

CDR 3: TKHGRRRIYGVVAFKEWFTYFYMDV (SEQ ID NO: 262)

[0381] 4877_D15 (PGT-122) lambda light chain nucleotide sequence: coding sequence
(variable region in bold)

ATGGCCTGGACCGTTCTCCTCCTCGGCCTCCTCTCTCACTGCACAGGCGCG
GTGTCTACCTTTGTGTCTAGTGGCCCCAGGACAGACGGCCAGGATTACT
TGTGGGGAAGAGAGCCTTGGAAGTAGATCTGTTATTTGGTATCAACA
GAGGCCAGGCCAGGCCCTTCATTAATCATCTATAATAATAATGACC
GGCCTCAGGGATTCTTGACCGATTTTCTGGGTCCCCTGGCTCCACT
TTTGGGACCACGGCCACCCTGACCATCACCAGTGTCGAAGCCGGGGA
TGAGGCCGACTATTATTGTCTATCTGGGATAGTAGACGACCAACCA
ATTGGGTCTTCGGCGAAGGGACCACACTGATCGTGTTAGGTCAGCCCA
AGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAG
CCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCC
GTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGG
AGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAG
CTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAAAAGCTACAGCT
GCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCCTAC
AGAATGTTTCATAG (SEQ ID NO: 158)

[0382] 4877_D15 (PGT-122) lambda light chain variable region nucleotide sequence:

ACCTTTGTGTCTAGTGGCCCCAGGACAGACGGCCAGGATTACTTGTGGGGA
AGAGAGCCTTGGAAGTAGATCTGTTATTTGGTATCAACAGAGGCCAGGCC
AGGCCCTTCATTAATCATCTATAATAATAATGACCGGCCCTCAGGGATTCT
CTGACCGATTTTCTGGGTCCCCTGGCTCCACTTTTGGGACCACGGCCACCC

TGACCATCACCAGTGTCTGAAGCCGGGGATGAGGCCGACTATTATTGTCAT
ATCTGGGATAGTAGACGACCAACCAATTGGGTCTTCGGCGAAGGGACCAC
ACTGATCGTGTTA (SEQ ID NO: 159)

[0383] 4877_D15 (PGT-122) lambda light chain amino acid sequence: expressed protein with variable region in bold.

MAWTVLLLGLLSHCTGAVSTFVSVAPGQTARITCGEESLGSRSVIYQQ
RPGQAPSLIIYNNNDRPSGIPDRFSGSPSTFGTTATLTITSVEAGDEADYY
CHIWDSSRRPTNWVFGEGTTLIVLGQPKAAPSVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADSSPVKAGVETTPSKQSNKYAASSYLSLTPEQWK
SHKSYSCQVTHEGSTVEKTVAPTECS (SEQ ID NO: 160)

[0384] 4877_D15 (PGT-122) lambda light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

TFVSVAPGQTARITC**GEESLGSRSVI**YQQRPGQAPSLIIY**NNDRPS**GIPDRF
SGSPGSTFGTTATLTITSVEAGDEADYY**CHIWDSSRRPTNWV**FGEGTTLIVL
(SEQ ID NO: 161)

[0385] 4877_D15 (PGT-122) lambda light chain Kabat CDRs:

CDR 1: GEESLGSRSVI (SEQ ID NO: 162)

CDR 2: NNDRPS (SEQ ID NO: 163)

CDR 3: HIWDSSRRPTNWV (SEQ ID NO: 164)

[0386] 4877_D15 (PGT-122) lambda light chain Chothia CDRs:

CDR 1: GEESLGSRSVI (SEQ ID NO: 162)

CDR 2: NNDRPS (SEQ ID NO: 163)

CDR 3: HIWDSSRRPTNWV (SEQ ID NO: 164)

[0387] 4858_P08 (PGT-123) gamma heavy chain nucleotide sequence: coding sequence (variable region in bold)

ATGAAACACCTGTGGATCTTCCTTCTCCTGGTGGCAACTCCCAGATGGGTC
GAGTCCCAGCTGCACCTGCAGGAGTCGGGCCCAGGGCTGGTGAAGCC
TCCGGAGACCCTGTCCCTCACGTGTAGTGTGTCTGGCGCCTCCATCA
ATGATGCCTATTGGAGTTGGATTCGGCAGTCCCAGGGAAGCGGCCT
GAGTGGGTTGGATATGTCCATCACAGCGGTGACACAAATTATAATCC
CTCACTCAAGAGGCGCGTCACGTTTTTCATTAGACACGGCCAAGAATG
AAGTGTCCCTGAAATTAGTAGACCTGACCGCTGCGGACTCGGCCACA
TATTTTTGTGCGCGAGCACTTCACGGGAAGAGGATTTATGGGATAGT
TGCCCTCGGAGAGTTGTTACCTACTTCTACATGGACGTCTGGGGCA
AGGGGACTGCGGTACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGG
TCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCC
CTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTG

GAAGTCAGGCGCCCTGACCAGCGGCGTGACACACCTTCCCGGCTGTCCTAC
 AGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC
 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAA
 CACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCAC
 ACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTT
 CCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTG
 AGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA
 GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG
 CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCCTCAC
 CGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCT
 CCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA
 GGGCAGCCCCGAGAACACAGGTGTACACCCTGCCCCCATCCCGGGAGG
 AGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT
 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAA
 ACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCT
 ATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTT
 CTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGA
 GCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 165)

[0388] 4858_P08 (PGT-123) gamma heavy chain variable region nucleotide sequence:

CAGCTGCACCTGCAGGAGTCGGGCCCAGGGCTGGTGAAGCCTCCGGAGA
 CCCTGTCCCTCACGTGTAGTGTGTCTGGCGCCTCCATCAATGATGCCTATT
 GGAGTTGGATTTCGGCAGTCCCCAGGGAAGCGGCCTGAGTGGGTGGATAT
 GTCCATCACAGCGGTGACACAAATTATAATCCCTCACTCAAGAGGCGCGT
 CACGTTTTATTAGACACGGCCAAGAATGAAGTGTCCCTGAAATTAGTAG
 ACCTGACCGCTGCGGACTCGGCCACATATTTTTGTGCGCGAGCACTTCAC
 GGGAAGAGGATTTATGGGATAGTTGCCCTCGGAGAGTTGTTACCTACTT
 CTACATGGACGTCTGGGGCAAGGGGACTGCGGTCACCGTCTCCTCA (SEQ
 ID NO: 166)

[0389] 4858_P08 (PGT-123) gamma heavy chain amino acid sequence: expressed protein
 with variable region in bold.

MKHLWIFLLLVATPRWVESQLHLQESGPGLVKPPETLSLTCSVSGASIND
AYWSWIRQSPGKRPEWVG YVHSGDTNYPNPSLKRRVTFSLDTAKNEVS
LKLVDLTAADSATYFCARALHGKRIYGI VALGELFTYFYMDVWGKGTA
VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPK
SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS
VMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 167)

[0390] 4858_P08 (PGT-123) gamma heavy chain variable region amino acid sequence:
 (Kabat CDRs underlined, Chothia CDRs in bold italics)

QLHLQESGPGLVKPPETLSLTCSVSGASINDAYWSWIRQSPGKRPEWVG**YVH**
HSGDTNYNPSLKRRVTFSLDTAKNEVSLKLVDLTAADSATYFCAR**ALHGKRI**
YGIVALGELFTYFYMDVWGKGTAVTVSS (SEQ ID NO: 168)

[0391] 4858_P08 (PGT-123) gamma heavy chain Kabat CDRs:

CDR 1: DAYWS (SEQ ID NO: 169)

CDR 2: YVHHS GDTN YNPSLKR (SEQ ID NO: 170)

CDR 3: ALHGKRI YGIVALGELFTYFYMDV (SEQ ID NO: 171)

[0392] 4858_P08 (PGT-123) gamma heavy chain Chothia CDRs:

CDR 1: GASIND (SEQ ID NO: 172)

CDR 2: YVHHS GDTN (SEQ ID NO: 173)

CDR 3: ALHGKRI YGIVALGELFTYFYMDV (SEQ ID NO: 171)

[0393] 4858_P08 (PGT-123) lambda light chain nucleotide sequence: coding sequence
(variable region in bold)

ATGGCCTGGACCGTTCTCCTCCTCGGCCTCCTCTCTCACTGCACAGGCTCT
CTGGCCTCCTCTATGTCCGTGTCCCCGGGGGAGACGGCCAAGATCTC
CTGTGGAAAAGAGAGCATTGGTAGCAGAGCTGTGCAATGGTATCAGC
AGAAGCCAGGCCAGCCCCCTCATTGATTATCTATAATAATCAGGAC
CGCCCCGCAGGGGTCCCTGAGCGATTCTCTGCCTCCCCTGACTTCCG
TCCTGGGACCACGGCCACCCTGACCATCACCAATGTCGACGCCGAGG
ATGAGGCCGACTATTACTGTCATATATATGATGCTAGAGGTGGCACC
AATTGGGTCTTCGACAGAGGGACCACACTGACCGTCTTAGGTCAGCCC
AAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAA
GCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGC
CGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTG
GAGACCACCACACCCTCCAAACAAGCAACAACAAGTACGCGGCCAGCA
GCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCACAAAAGCTACAGC
TGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCCTA
CAGAATGTTCATAG (SEQ ID NO: 174)

[0394] 4858_P08 (PGT-123) lambda light chain variable region nucleotide sequence:

TCCTCTATGTCCGTGTCCCCGGGGGAGACGGCCAAGATCTCCTGTGGAAA
AGAGAGCATTGGTAGCAGAGCTGTGCAATGGTATCAGCAGAAGCCAGGC
CAGCCCCCTCATTGATTATCTATAATAATCAGGACCGCCCCGCAGGGGT
CCCTGAGCGATTCTCTGCCTCCCCTGACTTCCGTCCTGGGACCACGGCCAC
CCTGACCATCACCAATGTCGACGCCGAGGATGAGGCCGACTATTACTGTC
ATATATATGATGCTAGAGGTGGCACCAATTGGGTCTTCGACAGAGGGACC
ACACTGACCGTCTTA (SEQ ID NO: 175)

[0395] 4858_P08 (PGT-123) lambda light chain amino acid sequence: expressed protein
with variable region in bold.

MAWTVLLLGLLSHCTGSLASSMSVSPGETAKISCGKESIGSRAVQWYQQ
 KPGQPPSLIYNNQDRPAGVPERFSASPDFRPGTTATLTITNVDAEDEADY
 YCHYDARGGTNWVFDRTTLTVLGQPKAAPSVTLFPPSSEELQANKATLV
 CLISDFYPGAVTVAWKADSSPVKAGVETTTSPKQSNNKYAASSYLSLTPEQW
 KSHKSYSCQVTHEGSTVEKTVAPTECS (SEQ ID NO: 176)

[0396] 4858_P08 (PGT-123) lambda light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

SSMSVSPGETAKISCG***KESIGSRAVQ***WYQQKPGQPPSLIY***NNQDRPA***GVPER
 FSASPDFRPGTTATLTITNVDAEDEADY***YCHYDARGGTNWV***FDRTTLTVL
 (SEQ ID NO: 177)

[0397] 4858_P08 (PGT-123) lambda light chain Kabat CDRs:

CDR 1: GKESIGSRAVQ (SEQ ID NO: 178)

CDR 2: NNQDRPA (SEQ ID NO: 179)

CDR 3: HIYDARGGTNWV (SEQ ID NO: 180)

[0398] 4858_P08 (PGT-123) lambda light chain Chothia CDRs:

CDR 1: GKESIGSRAVQ (SEQ ID NO: 178)

CDR 2: NNQDRPA (SEQ ID NO: 179)

CDR 3: HIYDARGGTNWV (SEQ ID NO: 180)

[0399] 5123_A06 (PGT-125) gamma heavy chain nucleotide sequence: coding sequence
 (variable region in bold)

ATGAAACACCTGTGGTTCTTCTTCCTGCTGGTGGCGGCTCCCAGATGCGTC
 CTGTCCCAGTCGCAGCTGCAGGAGTCGGGCCCACGACTGGTGGAGGC
 CTCGGAGACCCTGTCACTCACGTGCAATGTGTCCGGCGAGTCCACTG
 GTGCCTGTACTTATTTCTGGGGCTGGGTCCGGCAGGCCCCAGGGAAG
 GGGCTGGAGTGGATCGGGAGTTTGTCCCATTTGTCAGAGTTTCTGGGG
 TTCCGGTTGGACCTTCCACAACCCGTCTCTCAAGAGTCGACTCACGA
 TTTCACCTCGACACGCCCAAGAATCAGGTCTTCCTCAAGCTCACTTCTC
 TGACTGCCGCGGACACGGCCACTTACTACTGTGCGCGATTTCGACGGC
 GAAGTCTTGGTCTATAATCATTGGCCAAAGCCGGCCTGGGTGGACCT
 CTGGGGCCGCGGAATACCGGTCAACGTCTCCTCAGCCTCCACCAAGGG
 CCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCA
 CAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACG
 GTGTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGC
 TGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC
 CTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC
 CCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAA
 AACTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGGACCGT
 CAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA
 CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAG

GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGAC
 AAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
 CTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA
 GGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
 CCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
 GAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCT
 TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA
 GAACAACCTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCT
 TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA
 CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC
 AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 181)

[0400] 5123_A06 (PGT-125) gamma heavy chain variable region nucleotide sequence:

CAGTCGCAGCTGCAGGAGTCGGGCCCACGACTGGTGGAGGCCTCGGAGA
 CCCTGTCACTCACGTGCAATGTGTCCGGCGAGTCCACTGGTGCCTGTACTT
 ATTTCTGGGGCTGGGTCCGGCAGGCCCCAGGGAAGGGGCTGGAGTGGATC
 GGGAGTTTGTCCATTGTGTCAGAGTTTCTGGGGTTCCGGTTGGACCTTCCAC
 AACCCGTCTCTCAAGAGTCGACTCACGATTTCACTCGACACGCCCAAGAA
 TCAGGTCTTCTCAAGCTCACTTCTGACTGCCGCGGACACGGCCACTTA
 CTA CTGTGCGCGATTGACGGCGAAGTCTTGGTCTATAATCATTGGCCAA
 AGCCGGCCTGGGTGGACCTCTGGGGCCGCGGAATACCGGTCACCGTCTCC
 TCA (SEQ ID NO: 182)

[0401] 5123_A06 (PGT-125) gamma heavy chain amino acid sequence: expressed protein with variable region in bold.

MKHLWFFFLVAAPRCVLSQSQLQESGPRLVEASETSLSLTCNVSGESTG
ACTYFWGWVRQAPGKGLEWIGSLSHCQSFWGSWTFHNPSLKSRLTIS
L DTPKNQVFLKLTS**LAADTATYYCARFDGEVLVYNHWP****KPAWVDLW**
GRGIPVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS
 GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK
 RVEPKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVS
 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
 EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
 GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNV
 FSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 183)

[0402] 5123_A06 (PGT-125) gamma heavy chain variable region amino acid sequence:
 (Kabat CDRs underlined, Chothia CDRs in bold italics)

QSQLQESGPRLVEASETSLSLTCNVSGESTG***ACTYFWGWVRQAPGKGLEWIGS***
L***SHCQSFWGSWTFHNPSLKSRLTIS******L******DTPKNQVFLKLTS******LAADTATYYCA***
R***FDGEVLVYNHWP******KPAWVDLW***GRGIPVTVSS (SEQ ID NO: 184)

[0403] 5123_A06 (PGT-125) gamma heavy chain Kabat CDRs:

CDR 1: ACTYFWG (SEQ ID NO: 185)

CDR 2: SLSHCQSFWGSWTFHNP SLKS (SEQ ID NO: 186)

CDR 3: FDGEVLVYNHWP KPAWVDL (SEQ ID NO: 187)

[0404] 5123_A06 (PGT-125) gamma heavy chain Chothia CDRs:

CDR 1: GESTGACT (SEQ ID NO: 188)

CDR 2: SLSHCQSFWGSWTF (SEQ ID NO: 189)

CDR 3: FDGEVLVYNHWP KPAWVDL (SEQ ID NO: 187)

[0405] 5123_A06 (PGT-125) lambda light chain nucleotide sequence: coding sequence
(variable region in bold)

ATGGCCTGGGCTCTGCTCCTCCTCACCCTCCTCACTCAGGGCACAGGGGC
CTGGGCCCAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCC
TGGACAGTCAATCACCATCTCCTGCAATGGAACCGCCACTAACTTTGT
CTCCTGGTACCAACAATTCCCAGACAAGGCCCCCAAATCATCATTTT
TGGGGTTCGATAAGCGCCCCCCCCGGTGTCCCCGATCGTTTCTCTGGCT
CCCGGTCTGGCACGACGGCCTCCCTTACCGTCTCCCGACTCCAGACT
GACGATGAGGCTGTCTATTATTGCGGTTCACTTGTCGGCAACTGGGA
TGTGATTTTCGGCGGAGGGACCACCTTGACCGTCCTAGGTCAGCCCCA
GGCTGCCCCCTCGGTCACTCTGTTCCCCGCCCTCCTCTGAGGAGCTTCAAGC
CAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCG
TGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGA
GACCACCACACCTCCAAACAAGCAACAACAAGTACGCGGCCAGCAGC
TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAAAAGCTACAGCTG
CCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCCTACA
GAATGTTTCATAG (SEQ ID NO: 190)

[0406] 5123_A06 (PGT-125) lambda light chain variable region nucleotide sequence:

CAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCCTGGACAGTCA
ATCACCATCTCCTGCAATGGAACCGCCACTAACTTTGTCTCCTGGTACCAA
CAATTCCCAGACAAGGCCCCCAAATCATCATTTTGGGGTTCGATAAGCG
CCCCCCCCGGTGTCCCCGATCGTTTCTCTGGCTCCCGGTCTGGCACGACGGC
CTCCCTTACCGTCTCCCGACTCCAGACTGACGATGAGGCTGTCTATTATTG
CGGTTCACTTGTCGGCAACTGGGATGTGATTTTCGGCGGAGGGACCACCT
TGACCGTCCTA (SEQ ID NO: 191)

[0407] 5123_A06 (PGT-125) lambda light chain amino acid sequence: expressed protein
with variable region in bold.

MAWALLLLTLLTQGTGAWAQSALTQPPSASGSPGQSITISCNGTATNFVS
WYQQFPDKAPKLIIFGVDKRPPGVDPDRFSGSRSGTTASLTVSRLQTDDEA
VYYCGSLVGNWDVIFGGGTTTLTVLGQPKAAPSVTLFPPSSEELQANKATLV
CLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQW
KSHKSYSCQVTHEGSTVEKTVAPTECS (SEQ ID NO: 192)

[0408] 5123_A06 (PGT-125) lambda light chain variable region amino acid sequence:
(Kabat CDRs underlined, Chothia CDRs in bold italics)

QSALTQPPSASGSPGQSITISC**NGTATNFV**SWYQQFPDKAPKLII**FGVDKRPP**G
VPDRFSGSRSGTTASLTVSRLQTDDEAVYYC**GSLVGNWDVI**FGGGTTLTVL
(SEQ ID NO: 193)

[0409] 5123_A06 (PGT-125) lambda light chain Kabat CDRs:

CDR 1: NGTATNFVS (SEQ ID NO: 194)

CDR 2: GVDKRPP (SEQ ID NO: 195)

CDR 3: GSLVGNWDVI (SEQ ID NO: 196)

[0410] 5123_A06 (PGT-125) lambda light chain Chothia CDRs:

CDR 1: NGTATNFVS (SEQ ID NO: 194)

CDR 2: GVDKRPP (SEQ ID NO: 195)

CDR 3: GSLVGNWDVI (SEQ ID NO: 196)

[0411] 5141_B17 (PGT-126) gamma heavy chain nucleotide sequence: coding sequence
(variable region in bold)

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCGGCTCCCAGATGGGTC
CTGTCCCAGCCGCAGCTGCAGGAGTCGGGGCCAGGACTGGTGGAGGC
TTCGGAGACCCTGTCCCTCACCTGCACTGTGTCCGGCGACTCCACTG
CTGCTTGTGACTATTTCTGGGGCTGGGTCCGGCAGCCCCCAGGGAAG
GGCCTGGAGTGGATTGGGGGTTTGTACATTGTGCAGGTTACTACAA
TACTGGCTGGACCTACCACAACCCGTCTCTCAAGAGTCGGCTCACGA
TTTCACTCGACACCCCCAAGAATCAGGTCTTCCTGAAGTTAAATTCTG
TGACCGCCGCGGACACGGCCATTTACTACTGTGCGCGATTTCGACGGC
GAAGTTTTGGTGTACCACGATTGGCCAAAGCCGGCCTGGGTTCGACCT
CTGGGGCCGGGGAACTTTGGTCAACCGTCTCCTCAGCCTCCACCAAGGG
CCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCA
CAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACG
GTGTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGC
TGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC
CTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC
CCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAA
AACTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGGACCGT
CAGTCTTCCTCTTCCCCCAAACCCAAAGGACACCCTCATGATCTCCCGGA
CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAG
GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGAC
AAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
CTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA
GGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
CCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
GAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCT

TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA
GAACAAC TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCT
TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA
CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC
AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 197)

[0412] 5141_B17 (PGT-126) gamma heavy chain variable region nucleotide sequence:

CAGCCGCAGCTGCAGGAGTCGGGGCCAGGACTGGTGGAGGCTTCGGAGA
CCCTGTCCCTCACCTGCACTGTGTCCGGCGACTCCACTGCTGCTTGTGACT
ATTTCTGGGGCTGGGTCCGGCAGCCCCCAGGGAAGGGCCTGGAGTGGATT
GGGGGTTTGTACATTGTGCAGGTTACTACAATACTGGCTGGACCTACCA
CAACCCGTCTCTCAAGAGTCGGCTCACGATTTCACTCGACACCCCAAGA
ATCAGGTCTTCCTGAAGTTAAATTCTGTGACCGCCGCGGACACGGCCATTT
ACTACTGTGCGCGATTTCGACGGCGAAGTTTTTGGTGTACCACGATTGGCCA
AAGCCGGCCTGGGTTCGACCTCTGGGGCCGGGGAAC TTTGGTCACCGTCTC
CTCA (SEQ ID NO: 198)

[0413] 5141_B17 (PGT-126) gamma heavy chain amino acid sequence: expressed protein with variable region in bold.

MKHLWFFLLLVAAPRWVLSQPQLQESGPGLVEASETLSLTCTVSGDSTA
ACDYFWGWVRQPPGKGLEWIGGLSHCAGYYNTGWTYHNPSLKSRLTIS
LDTPKNQVFLKLNSVTAADTAIYYCARFDGEVLVYHDWPKPAWVDLWG
RGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNS
GALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK
RVEPKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPDSIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNV
FSCSV MHEALHNHYTQKSLSLSPGK (SEQ ID NO: 199)

[0414] 5141_B17 (PGT-126) gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

QPQLQESGPGLVEASETLSLTCTVSGDSTA***ACDYFWGWVRQPPGKGLEWIG***
LSHCAGYYNTGWTYHNPSLKSRLTISLDTPKNQVFLKLNSVTAADTAIYYCAR
FDGEVLVYHDWPKPAWVDLWGRGTLVTVSS (SEQ ID NO: 200)

[0415] 5141_B17 (PGT-126) gamma heavy chain Kabat CDRs:

CDR 1: ACDYFWG (SEQ ID NO: 201)

CDR 2: GLSHCAGYYNTGWTYHNPSLKS (SEQ ID NO: 202)

CDR 3: FDGEVLVYHDWPKPAWVDL (SEQ ID NO: 203)

[0416] 5141_B17 (PGT-126) gamma heavy chain Chothia CDRs:

CDR 1: GDSTAACD (SEQ ID NO: 204)

CDR 2: GLSHCAGYYNTGWTY (SEQ ID NO: 205)

CDR 3: FDGEVLVYHDWPKPAWVDL (SEQ ID NO: 203)

[0417] 5141_B17 (PGT-126) lambda light chain nucleotide sequence: coding sequence
(variable region in bold)

ATGGCCTGGGCTCTGCTCCTCCTCACCCCTCCTCACTCAGGGCACAGGGGC
CTGGGCCCAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCC
TGGACAGTCAATCTCCATCTCCTGCACTGGAACCAGCAATAGGTTTG
TCTCCTGGTACCAGCAACACCCAGGCAAGGCCCCCAAACTCGTCATT
TATGGGGTCAATAAGCGCCCCCTCAGGTGTCCCTGATCGTTTTTCTGG
CTCCAAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGGCTCCAGA
CTGACGATGAGGCTGTCTATTACTGCAGCTCACTTGTAGGCAACTGG
GATGTGATTTTCGGCGGAGGGACCAAGTTGACCGTCCTGGGTCAGCC
CAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCA
AGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAG
CCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGT
GGAGACCACACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGC
AGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAAAAGCTACA
GCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCC
TACAGAATGTTTCATAG (SEQ ID NO: 206)

[0418] 5141_B17 (PGT-126) lambda light chain variable region nucleotide sequence:

CAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCCTGGACAGTCA
ATCTCCATCTCCTGCACTGGAACCAGCAATAGGTTTGTCTCCTGGTACCAG
CAACACCCAGGCAAGGCCCCCAAACTCGTCATTTATGGGGTCAATAAGCG
CCCCCTCAGGTGTCCCTGATCGTTTTTCTGGCTCCAAGTCTGGCAACACGGC
CTCCCTGACCGTCTCTGGGCTCCAGACTGACGATGAGGCTGTCTATTACTG
CAGCTCACTTGTTAGGCAACTGGGATGTGATTTTCGGCGGAGGGACCAAGT
TGACCGTCCTG (SEQ ID NO: 207)

[0419] 5141_B17 (PGT-126) lambda light chain amino acid sequence: expressed protein
with variable region in bold.

MAWALLLLTLLTQGTGAWAQSAQTQPPSASGSPGQSSISISCTGTSNRFVS
WYQQHPGKAPKLVIYGVNKRPSGVPDRFSGSKSGNTASLTVSGLQTDDE
AVYYCSSLVGNWDVIFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATL
VCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNKYYAASSYLSLTPEQ
WKSHKSYSCQVTHEGSTVEKTVAPTECS (SEQ ID NO: 208)

[0420] 5141_B17 (PGT-126) lambda light chain variable region amino acid sequence:
(Kabat CDRs underlined, Chothia CDRs in bold italics)

QSALTQPPSASGSPGQSSISISCTGTGTSNRFVSWYQQHPGKAPKLVIYGVNKRPS
GVPDRFSGSKSGNTASLTVSGLQTDDEAVYYCSSLVGNWDVIFGGGTKLTVL
(SEQ ID NO: 209)

[0421] 5141_B17 (PGT-126) lambda light chain Kabat CDRs:

CDR 1: TGTSNRFVS (SEQ ID NO: 210)

CDR 2: GVNKRPS (SEQ ID NO: 211)

CDR 3: SSLVGNWDVI (SEQ ID NO: 212)

[0422] 5141_B17 (PGT-126) lambda light chain Chothia CDRs:

CDR 1: TGTSNRFVS (SEQ ID NO: 210)

CDR 2: GVNKRPS (SEQ ID NO: 211)

CDR 3: SSLVGNWDVI (SEQ ID NO: 212)

[0423] 5147_N06 (PGT-130) gamma heavy chain nucleotide sequence: coding sequence
(variable region in bold)

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCGGCTCCCAGATGGGTC
CTGTCCCAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCC
TGCGGAGACCCTGTCCCTCACCTGCAGTGTCTCTGGAGAATCTATCA
ATACTGGTCATTACTACTGGGGCTGGGTCCGTCAGGTCCCAGGGAAG
GGACTTGAGTGGATAGGTCATATCCATTATACGACGGCTGTCCTGCA
CAACCCGTCCCTCAAGAGTCGACTCACCATCAAAATTTACACGTTGA
GAAACCAGATTACCCTGAGGCTCAGTAATGTGACGGCCGCGGACACG
GCCGTCTATCACTGCGTACGATCCGGCGGCGACATCTTATATTATTAT
GAGTGGCAAAAGCCGCACTGGTTCTCTCCCTGGGGCCCCGGGAATCCA
CGTCACCGTCTCGAGCGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG
GCACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT
GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACCTCAGGCG
CCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGA
CTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC
CCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG
GACAAGAGAGTTGAGCCCAAATCTTGAGACAAACTCACACATGCCCACC
GTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCC
AAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCG
TGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC
AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG
GA CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC
TCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCG
AGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG
AACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACAT
CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACA ACTACAAGACC
ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTC
ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGT
GATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGT
CTCCGGGTAAATGA (SEQ ID NO: 213)

[0424] 5147_N06 (PGT-130) gamma heavy chain variable region nucleotide sequence:

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTGCGGAGA
 CCCTGTCCCTCACCTGCAGTGTCTCTGGAGAATCTATCAATACTGGTCATT
 ACTACTGGGGCTGGGTCCGTCAGGTCCCAGGGAAGGGACTTGAGTGGATA
 GGTCAATATCCATTATACGACGGCTGTCTGCACAACCCGTCCTCAAGAG
 TCGACTCACCATCAAAATTTACACGTTGAGAAACCAGATTACCCTGAGGC
 TCAGTAATGTGACGGCCGCGGACACGGCCGTCTATCACTGCGTACGATCC
 GCGGCGGACATCTTATATTATTATGAGTGGCAAAAGCCGCACTGGTTCTC
 TCCCTGGGGCCCCGGGAATCCACGTCACCGTCTCGAGC (SEQ ID NO:214)

[0425] 5147_N06 (PGT-130) gamma heavy chain amino acid sequence: expressed protein with variable region in bold.

MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPAETLSLTCSVSGESIN
TGHYYWGWVRQVPGKGLEWIGHIHYTTAVLHNPSLKSRLTIKIYTLRN
QITLRLSNVTAADTAVYHCVRSGGDILYYYEWQKPHWFSPWGPPIHVTV
SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCD
KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS
NKALPAIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI
AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVM
HEALHNHYTQKSLSLSPGK (SEQ ID NO: 215)

[0426] 5147_N06 (PGT-130) gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

QVQLQESGPGLVKPAETLSLTCSVSGESIN***TGHYYWGWVRQVPGKGLEWIG***
HHIHYTTAVLHNPSLKSRLTIKIYTLRNQITLRLSNVTAADTAVYHCVR***SGGDIL***
YYYEWQKPHWFSPWGPPIHVTVSS (SEQ ID NO: 216)

[0427] 5147_N06 (PGT-130) gamma heavy chain Kabat CDRs:

CDR 1: TGHYYWG (SEQ ID NO: 217)

CDR 2: HHHYTTAVLHNPSLKS (SEQ ID NO: 218)

CDR 3: SGGDILYYYEWQKPHWFSP (SEQ ID NO: 219)

[0428] 5147_N06 (PGT-130) gamma heavy chain Chothia CDRs:

CDR 1: GESINTGH (SEQ ID NO: 220)

CDR 2: HHHYTTAVL (SEQ ID NO: 221)

CDR 3: SGGDILYYYEWQKPHWFSP (SEQ ID NO: 219)

[0429] 5147_N06 (PGT-130) lambda light chain nucleotide sequence: coding sequence (variable region in bold)

ATGGCCTGGGCTCTGCTCCTCCTCACCCCTCCTCACTCAGGGCACAGGGTCC
 TGGGCCAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCTT

GGACAGTCAGTCACCATCTCCTGCAATGGAACCAGCAGTGACATTGG
 CGGTTGGAATTTTGTCTCCTGGTATCAACAGTTCCCGGGCAGAGCCC
 CCAGACTCATTATTTTGTAGAGTCAATAAGCGGCCCTCAGGGGTCCCT
 GGTGCTTCTCTGGCTCCAAGTCGGGCAATTCGGCCTCCCTGACCGT
 CTCTGGGCTCCAGTCTGACGATGAGGGTCAATATTTCTGCAGTTCAC
 TTTTCGGCAGGTGGGATGTTGTTTTTGGCGGGGGGACCAAGCTGACC
 GTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTC
 CTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTG
 ACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCC
 GTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACA
 AGTACGCGGCCAGCAGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCC
 CACAAAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGA
 AGACAGTGGCCCCTACAGAATGTTTCATAG (SEQ ID NO: 222)

[0430] 5147_N06 (PGT-130) lambda light chain variable region nucleotide sequence:

CAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCTTGGACAGTCA
 GTCACCATCTCCTGCAATGGAACCAGCAGTGACATTGGCGGTTGGAATTT
 TGTCTCCTGGTATCAACAGTTCCCGGGCAGAGCCCCCAGACTCATTATTTT
 TGAGGTCAATAAGCGGCCCTCAGGGGTCCCTGGTCGCTTCTCTGGCTCCA
 AGTCGGGCAATTCGGCCTCCCTGACCGTCTCTGGGCTCCAGTCTGACGAT
 GAGGGTCAATATTTCTGCAGTTCACTTTTTCGGCAGGTGGGATGTTGTTTT
 GCGGGGGGACCAAGCTGACCGTCCTA (SEQ ID NO: 223)

[0431] 5147_N06 (PGT-130) lambda light chain amino acid sequence: expressed protein with variable region in bold.

MAWALLLLTLLTQGTGSWAQSALTQPPSASGSLGQSVTISCNGTSSDIGG
 WNFVSWYQQFPGRAPRLIIFEVNKRPSGVPGRFSGSKSGNSASLTVSGLQ
SDDEGQYFCSSLFGRWDVVFGGG**TKLTV**LGQPKAAPSVTLFPPSSEELQAN
 KATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNKYAASSYLSL
 TPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS (SEQ ID NO: 224)

[0432] 5147_N06 (PGT-130) lambda light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

QSALTQPPSASGSLGQSVTISC**NGTSSDIGGWNFV**SWYQQFPGRAPRLIIFE**VN**
KRPSGVPGRFSGSKSGNSASLTVSGLQSDDEGQYFC**SSLFGRWDVV**FGGGTK
 LTVL (SEQ ID NO: 225)

[0433] 5147_N06 (PGT-130) lambda light chain Kabat CDRs:

CDR 1: NGTSSDIGGWNFVS (SEQ ID NO: 226)

CDR 2: EVNKRPS (SEQ ID NO: 227)

CDR 3: SSLFGRWDVV (SEQ ID NO: 228)

[0434] 5147_N06 (PGT-130) lambda light chain Chothia CDRs:

CDR 1: NGTSSDIGGWNFVS (SEQ ID NO: 226)

CDR 2: EVNKRPS (SEQ ID NO: 227)

CDR 3: SSLFGRWDVV (SEQ ID NO: 228)

[0435] 5343_B08 (PGT-135) gamma heavy chain nucleotide sequence: coding sequence
(variable region in bold)

ATGAAACACCTGTGGTTCTTCCTCTTGCTGGTGGCGGCTCCCAGATGGGTC
CTGTCCCAGTTGCAGATGCAGGAGTCGGGCCCAGGACTGGTGAAGCC
TTCGGAGACCCTGTCTCTGAGTTGCACTGTCTCTGGTGACTCCATAA
GGGGTGGCGAGTGGGGCGATAAAGATTATCATTGGGGCTGGGTCCG
CCACTCAGCAGGAAAGGGCCTGGAGTGGATTGGGAGTATCCATTGGA
GGGGGACCACCCACTACAAAGAGTCCCTCAGGAGAAGAGTGAGTATG
TCGATCGACACGTCCAGGAATTGGTTCTCCCTGAGGCTGGCCTCTGT
GACCGCCGCGGACACGGCCGTCTACTTTTGTGCGAGACACCGACATC
ATGATGTTTTTCATGTTGGTCCCTATTGCGGGCTGGTTCGACGTCTGG
GGCCCGGGAGTCCAGGTCACCGTCTCGAGCGCCTCCACCAAGGGCCCA
TCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGC
GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGT
CGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCGGCTGTC
CTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC
AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAG
CAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAAC
CACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGT
CTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCC
TGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCA
AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAA
GCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC
ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGG
TCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCC
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG
AGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTC
TATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGA
ACAACCTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTC
CTCTATAGCAAGCTACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACG
TCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
AAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 229)

[0436] 5343_B08 (PGT-135) gamma heavy chain variable region nucleotide sequence:

CAGTTGCAGATGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGA
CCCTGTCTCTGAGTTGCACTGTCTCTGGTGACTCCATAAGGGGTGGCGAGT
GGGGCGATAAAGATTATCATTGGGGCTGGGTCCGCCACTCAGCAGGAAA
GGGCCTGGAGTGGATTGGGAGTATCCATTGGAGGGGGACCACCCACTACA
AAGAGTCCCTCAGGAGAAGAGTGAGTATGTGATCGACACGTCCAGGAA
TTGGTTCTCCCTGAGGCTGGCCTCTGTGACCGCCGCGGACACGGCCGTCT
ACTTTTGTGCGAGACACCGACATCATGATGTTTTTCATGTTGGTCCCTATTG

CGGGCTGGTTCGACGTCTGGGGCCCCGGGAGTCCAGGTCACCGTCTCGAGC
(SEQ ID NO: 230)

[0437] 5343_B08 (PGT-135) gamma heavy chain amino acid sequence: expressed protein with variable region in bold.

**MKHLWFFLLLVAAPRWVLSQLQMQUESGPGLVKPSSETLSLSCTVSGDSIR
GGEWGDKDYHWGWVRHSAGKGLEWIGSIHWRGTTHYKESLRRRVSM
SIDTSRNWFSRLASVTAADTAVYFCARHRHHDVFMLVPIAGWFDVWGP
GVQVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG
ALTSKVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKR
VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV
FSCSVMHEALHNHYTQKSLSLSPGK** (SEQ ID NO: 231)

[0438] 5343_B08 (PGT-135) gamma heavy chain variable region amino acid sequence:
(Kabat CDRs underlined, Chothia CDRs in bold italics)

QLQMQUESGPGLVKPSSETLSLSCTVSGDSIR**GGEWGDKDYHWGWVRHSAGK
GLEWIGSIHWRGTTHYKESLRRRVSM****SIDTSRNWFSRLASVTAADTAVYFC
AR****HRHHDVFMLVPIAGWFDV****WGPVQVTVSS** (SEQ ID NO: 232)

[0439] 5343_B08 (PGT-135) gamma heavy chain Kabat CDRs:

CDR 1: GGEWGDKDYHWG (SEQ ID NO: 233)

CDR 2: SIHWRGTTHYKESLRR (SEQ ID NO: 234)

CDR 3: HRHHDVFMLVPIAGWFDV (SEQ ID NO: 235)

[0440] 5343_B08 (PGT-135) gamma heavy chain Chothia CDRs:

CDR 1: GDSIRGGEWGDKD (SEQ ID NO: 236)

CDR 2: SIHWRGTTH (SEQ ID NO: 237)

CDR 3: HRHHDVFMLVPIAGWFDV (SEQ ID NO: 235)

[0441] 5343_B08 (PGT-135) kappa light chain nucleotide sequence: coding sequence
(variable region in bold)

ATGGAAACCCAGCTCAGCTTCTCTCCTCCTGCTACTCTGGCTCCCAGAT
ACCACTGGAGAAATTGTGATGACGCAGTCTCCCGACACCTGTCTGTC
TCTCCAGGGGAGACAGTCACACTCTCCTGCAGGGCCAGTCAGAATAT
TAACAAGAATTTAGCCTGGTACCAATACAAACCTGGCCAGTCTCCCA
GGCTCGTAATTTTGAACATATAGCAAGATCGCTGCTTTCCCTGCCA
GGTTCGTTGCCAGTGGTTCTGGGACAGAGTTCACCTCTCACCATCAAC
AACATGCAGTCTGAAGATGTTGCAGTTTATTACTGTCAACAATATGAA
GAGTGGCCTCGGACGTTCTGGGCAAGGGACCAAGGTGGATATCAAACG

TACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT
GAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAG
AGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAAC
TCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCC
TCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGT
CTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGA
GCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO: 238)

[0442] 5343_B08 (PGT-135) kappa light chain variable region nucleotide sequence:

GAAATTGTGATGACGCAGTCTCCCGACACCCTGTCTGTCTCTCCAGGGGA
GACAGTCACACTCTCCTGCAGGGCCAGTCAGAATATTAACAAGAATTTAG
CCTGGTACCAATACAAACCTGGCCAGTCTCCCAGGCTCGTAATTTTTGAA
ACATATAGCAAGATCGCTGCTTTCCCTGCCAGGTTTCGTTGCCAGTGGTTCT
GGGACAGAGTTCACTCTCACCATCAACAACATGCAGTCTGAAGATGTTGC
AGTTTATTACTGTCAACAATATGAAGAGTGGCCTCGGACGTTCTGGGCAAG
GGACCAAGGTGGATATCAAA (SEQ ID NO: 239)

[0443] 5343_B08 (PGT-135) kappa light chain amino acid sequence: expressed protein with variable region in bold.

METPAQLLFLLLLWLPDTTGEIVMTQSPDTLSVSPGETVTLSCRASQNIN
KNLAWYQYKPGQSPRLVIFETYSKIAAFPARFVASGSGTEFTLTINNMQS
EDVAVYYCQYEEWPRTFGQG**TKVDIKRTVAAPSVFIFPPSDEQLKSGTAS**
VVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSK
ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 240)

[0444] 5343_B08 (PGT-135) kappa light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

EIVMTQSPDTLSVSPGETVTLS***CRASONINKNLA***WYQYKPGQSPRLVIF***ETYS***
KIAAFPARFVASGSGTEFTLTINNMQSE***DAVYYCQYEEWPRT***FGQG***TKVD***
IK (SEQ ID NO: 242)

[0445] 5343_B08 (PGT-135) kappa light chain Kabat CDRs:

CDR 1: RASQNINKNLA (SEQ ID NO: 243)

CDR 2: ETYSKIA (SEQ ID NO: 244)

CDR 3: QYEEWPRT (SEQ ID NO: 245)

[0446] 5343_B08 (PGT-135) kappa light chain Chothia CDRs:

CDR 1: RASQNINKNLA (SEQ ID NO: 243)

CDR 2: ETYSKIA (SEQ ID NO: 244)

CDR 3: QYEEWPRT (SEQ ID NO: 245)

[0447] 5344_E16 (PGT-135) gamma heavy chain nucleotide sequence: coding sequence
(variable region in bold)

ATGAAACACCTGTGGTTCTTCCTCTTGCTGGTGGCGGCTCCCAGATGGGTC
CTGTCCCAGTTGCAGATGCAGGAGTCGGGCCCAGGACTGGTGAAGCC
TTCGGAGACCCTGTCTCTGAGTTGCACTGTCTCTGGTGACTCCATAA
GGGGTGGCGAGTGGGGCGATAAAGATTATCATTGGGGCTGGGTCCG
CCACTCAGCAGGAAAGGGCCTGGAGTGGATTGGGAGTATCCATTGGA
GGGGGACCACCCACTACAAAGAGTCCCTCAGGAGAAGAGTGAGTATG
TCGATCGACACGTCCAGGAATTGGTTCTCCCTGAGGCTGGCCTCTGT
GACCGCCGCGGACACGGCCGTCTACTTTTGTGCGAGACACCGACATC
ATGATGTTTTTCATGTTGGTCCCTATTGCGGGCTGGTTCGACGTCTGG
GGCCCGGGAGTCCAGGTCACCGTCTCGAGCGCCTCCACCAAGGGCCCA
TCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGACAGC
GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGT
CGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTC
CTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC
AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAG
CAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGAGACAAAAT
CACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGT
CTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCC
TGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCA
AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAA
GCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC
ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGG
TCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAGCC
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG
AGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTC
TATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGA
ACAACCTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTC
CTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACG
TCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
AAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 229)

[0448] 5344_E16 (PGT-135) gamma heavy chain variable region nucleotide sequence:

CAGTTGCAGATGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGA
CCCTGTCTCTGAGTTGCACTGTCTCTGGTGACTCCATAAGGGGTGGCGAGT
GGGGCGATAAAGATTATCATTGGGGCTGGGTCCGCCACTCAGCAGGAAA
GGGCCTGGAGTGGATTGGGAGTATCCATTGGAGGGGGACCACCCACTACA
AAGAGTCCCTCAGGAGAAGAGTGAGTATGTGATCGACACGTCCAGGAA
TTGGTTCTCCCTGAGGCTGGCCTCTGTGACCGCCGCGGACACGGCCGTCT
ACTTTTGTGCGAGACACCGACATCATGATGTTTTTCATGTTGGTCCCTATTG
CGGGCTGGTTCGACGTCTGGGGCCCCGGGAGTCCAGGTCACCGTCTCGAGC
(SEQ ID NO: 230)

[0449] 5344_E16 (PGT-135) gamma heavy chain amino acid sequence: expressed protein with variable region in bold.

MKHLWFFLLLVAAPRWVLSQLQMQUESGPGLVKPSETLSLSCTVSGDSIR
GGEWGDKDYHWGWVRHSAGKGLEWIGSIHWRGTTHYKESLRRRVSM
SIDTSRNWFSRLASVTAADTAVYFCARHRHHDVFMLVPIAGWFDVWGP
GVQVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG
ALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKR
VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV
FSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 231)

[0450] 5344_E16 (PGT-135) gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

QLQMQUESGPGLVKPSETLSLSCTVSGDSIR***GGEWGDKDYHWGW***VRHSAGK
GLEWIG***SIHWRGTTHYKESLRRRVSM***SIDTSRNWFSRLASVTAADTAVYFC
AR***HRHHDVFMLVPIAGWFDV***WGPVQVTVSS (SEQ ID NO: 232)

[0451] 5344_E16 (PGT-135) gamma heavy chain Kabat CDRs:

CDR 1: GGEWGDKDYHWG (SEQ ID NO: 233)

CDR 2: SIHWRGTTHYKESLRR (SEQ ID NO: 234)

CDR 3: HRHHDVFMLVPIAGWFDV (SEQ ID NO: 235)

[0452] 5344_E16 (PGT-135) gamma heavy chain Chothia CDRs:

CDR 1: GDSIRGGEWGDKD (SEQ ID NO: 236)

CDR 2: SIHWRGTTH (SEQ ID NO: 237)

CDR 3: HRHHDVFMLVPIAGWFDV (SEQ ID NO: 235)

[0453] 5344_E16 (PGT-135) kappa light chain nucleotide sequence: coding sequence (variable region in bold)

ATGGAAACCCAGCTCAGCTTCTCTCCTCCTGCTACTCTGGCTCCCAGAT
ACCACTGGAGAAATTGTGATGACGCAGTCTCCCGACACCCTGTCTGTC
TCTCCAGGGGAGACAGTCACACTCTCCTGCAGGGCCAGTCAGAATAT
TAACAAGAATTTAGCCTGGTACCAATACAAACCTGGCCAGTCTCCCA
GGCTCGTAATTTTGAACATATAGCAAGATCGCTGCTTTCCCTGCCA
GGTTCGTTGCCAGTGGTTCTGGGACAGAGTTCACCTCTCACCATCAAC
AACATGCAGTCTGAAGATGTTGCAGTTTATTACTGTCAACAATATGAA
GAGTGGCCTCGGACGTTCCGGCAAGGGACCAAGGTGGATATCAAACG
TACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT
GAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAG
AGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAAC

TCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCC
TCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGT
CTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGA
GCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO: 238)

[0454] 5344_E16 (PGT-135) kappa light chain variable region nucleotide sequence:

GAAATTGTGATGACGCAGTCTCCCGACACCCTGTCTGTCTCTCCAGGGGA
GACAGTCACACTCTCCTGCAGGGCCAGTCAGAATATTAACAAGAATTTAG
CCTGGTACCAATACAAACCTGGCCAGTCTCCCAGGCTCGTAATTTTTGAA
ACATATAGCAAGATCGCTGCTTTCCCTGCCAGGTTTCGTTGCCAGTGGTTCT
GGGACAGAGTTCACTCTCACCATCAACAACATGCAGTCTGAAGATGTTGC
AGTTTATTACTGTCAACAATATGAAGAGTGGCCTCGGACGTTCTGGGCAAG
GGACCAAGGTGGATATCAAA (SEQ ID NO: 239)

[0455] 5344_E16 (PGT-135) kappa light chain amino acid sequence: expressed protein with variable region in bold.

METPAQLLFLLLLWLPDTTGEIVMTQSPDTLSVSPGETVTLS**CRASQNIN**
KNLAWYQYKPGQSPRLVIFETYSKIAAFPARFVASGSGTEFTLTINNMQS
EDVAVYYCQQYEEWPRTFGQGTKVDIKRTVAAPSVFIFPPSDEQLKSGTAS
VVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTLSSTLTLSK
ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 240)

[0456] 5344_E16 (PGT-135) kappa light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

EIVMTQSPDTLSVSPGETVTLS***CRASONINKNLA***WYQYKPGQSPRLVIF***ETYS***
KIAAFPARFVASGSGTEFTLTINNMQSE***EDVAVYYCQQYEEWPRT***FGQGTKVD
IK (SEQ ID NO: 242)

[0457] 5344_E16 (PGT-135) kappa light chain Kabat CDRs:

CDR 1: RASQNINKNLA (SEQ ID NO: 243)

CDR 2: ETYSKIA (SEQ ID NO: 244)

CDR 3: QQYEEWPRT (SEQ ID NO: 245)

[0458] 5344_E16 (PGT-135) kappa light chain Chothia CDRs:

CDR 1: RASQNINKNLA (SEQ ID NO: 243)

CDR 2: ETYSKIA (SEQ ID NO: 244)

CDR 3: QQYEEWPRT (SEQ ID NO: 245)

[0459] 5329_C19 (PGT-136) gamma heavy chain nucleotide sequence: coding sequence (variable region in bold)

ATGAAACACCTGTGGTTCTTCCTCCTGCTAGTGGCGGCTCCCAGATGGGTC
 CTGTCGCAGCTGCAGTTGCAGGAATCGGGCCCAGGACTGGTGAAGCC
 TTCGGAGACCCTGTCCCTGACTTGCACAGTTTCTGGTGGCTCCATGA
 GGGGCACCGACTGGGGCGAGAATGACTTCCACTACGGCTGGATCCG
 CCAGTCCTCCGCAAAGGGGCTGGAGTGGATTGGGAGCATCCATTGGA
 GGGGGAGGACCACCCACTACAAGACGTCCTTCAGGAGTCGGGGCCAC
 CTTGTGCGATAGACACGTCCAATAATCGCTTCTCCCTGACGTTTAGTTT
 TGTGACCGCCGCGGACACGGCCGTCTACTATTGTGCGAGACATAAAT
 ATCATGATATTTTCAGGGTGGTCCCTGTTGCGGGCTGGTTCGACCCC
 TGGGGCCAGGGATTACTGGTCACCGTCTCGAGCGCCTCCACCAAGGGC
 CCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCAC
 AGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG
 TGTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCT
 GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC
 CTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC
 CCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAA
 AACTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGT
 CAGTCTTCTCTTCCCCC AAAACCCAAGGACACCTCATGATCTCCCGGA
 CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAG
 GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGAC
 AAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
 CTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA
 GGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAG
 CCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
 GAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCT
 TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA
 GAACAACCTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCT
 TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA
 CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC
 AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 246)

[0460] 5329_C19 (PGT-136) gamma heavy chain variable region nucleotide sequence:

CAGCTGCAGTTGCAGGAATCGGGCCCAGGACTGGTGAAGCCTTCGGAGA
 CCCTGTCCCTGACTTGCACAGTTTCTGGTGGCTCCATGAGGGGACCGACT
 GGGGCGAGAATGACTTCCACTACGGCTGGATCCGCCAGTCCTCCGCAAAG
 GGGCTGGAGTGGATTGGGAGCATCCATTGGAGGGGGAGGACCACCCACT
 ACAAGACGTCCTTCAGGAGTCGGGCCACCTTGTGCGATAGACACGTCCAAT
 AATCGCTTCTCCCTGACGTTTAGTTTTGTGACCGCCGCGGACACGGCCGTC
 TACTATTGTGCGAGACATAAATATCATGATATTTTCAGGGTGGTCCCTGTT
 GCGGGCTGGTTCGACCCCTGGGGCCAGGGATTACTGGTCACCGTCTCGAG
 C (SEQ ID NO: 247)

[0461] 5329_C19 (PGT-136) gamma heavy chain amino acid sequence: expressed protein with variable region in bold.

**MKHLWFFLLLVAAPRWVLSQLQLQESGPGLVKPSETLSLTCTVSGGSM
RGTDWGENDFHYGWIRQSSAKGLEWIGSIHWRGRTHYKTSFRSRATLS
IDTSNNRFSLTFSFVTAADTAVYYCARHKYHDIRVVPVAGWFDPWGQG
LLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL
TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVE
PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
CSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 248)**

[0462] 5329_C19 (PGT-136) gamma heavy chain variable region amino acid sequence:
(Kabat CDRs underlined, Chothia CDRs in bold italics)

**QLQLQESGPGLVKPSETLSLTCTVSGGSMRGTDWGENDFHYGWIRQSSAKG
LEWIGSIHWRGRTHYKTSFRSRATLSIDTSNNRFSLTFSFVTAADTAVYYCA
RHKYHDIRVVPVAGWFDPWGQG**LLVTVSS (SEQ ID NO: 249)

[0463] 5329_C19 (PGT-136) gamma heavy chain Kabat CDRs:

CDR 1: GTDWGENDFHYG (SEQ ID NO: 250)

CDR 2: SIHWRGRTHYKTSFRS (SEQ ID NO: 251)

CDR 3: HKYHDIRVVPVAGWFDP (SEQ ID NO: 252)

[0464] 5329_C19 (PGT-136) gamma heavy chain Chothia CDRs:

CDR 1: GGSMRGTDWGEND (SEQ ID NO: 253)

CDR 2: SIHWRGRTH (SEQ ID NO: 254)

CDR 3: HKYHDIRVVPVAGWFDP (SEQ ID NO: 252)

[0465] 5329_C19 (PGT-136) kappa light chain nucleotide sequence: coding sequence
(variable region in bold)

ATGGAAACCCAGCTCAGCTTCTCTTCCTCCTGCTACTCTGGCTCCCAGAT
AGCACTGGAGAAATAGTGATGACGCAGTCTCCACCCACCCTGTCTGTG
**TCTCCAGGGGAAACAGCCACACTCTCCTGTAGGGCCAGTCAGAATGT
TAAGAATAATTTAGCCTGGTACCAGCTGAAACCTGGCCAGGCTCCCA
GGCTCCTCATCTTTGATGCGTCCAGCAGGGCCGGTGGTATTCCTGAC
AGGTTCAGTGGCAGCGGTATGGGACAGACTTCACTCTCACCGTCAA
CAGTGTGCAGTCCGAAGATTTTGGAGATTATTTTGTGTCAGCAATATGA
AGAGTGGCCTCGGACGTTTCGGCCAAGGGACCAAGGTGGATATCAAAC
GTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGT
TGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCA
GAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAA
CTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGC
CTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAG**

TCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAG
AGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO: 255)

[0466] 5329_C19 (PGT-136) kappa light chain variable region nucleotide sequence:

GAAATAGTGATGACGCAGTCTCCACCCACCCTGTCTGTGTCTCCAGGGGA
AACAGCCACACTCTCCTGTAGGGCCAGTCAGAATGTTAAGAATAATTTAG
CCTGGTACCAGCTGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTTTGAT
GCGTCCAGCAGGGCCGGTGGTATTCCTGACAGGTTTCAGTGGCAGCGGTTA
TGGGACAGACTTCACTCTCACCGTCAACAGTGTGCAGTCCGAAGATTTTG
GAGATTATTTTGTGTCAGCAATATGAAGAGTGGCCTCGGACGTTCCGCCAA
GGGACCAAGGTGGATATCAAA (SEQ ID NO: 256)

[0467] 5329_C19 (PGT-136) kappa light chain amino acid sequence: expressed protein with
variable region in bold.

METPAQLLFLLLLWLPDSTGEIVMTQSPPTLSVSPGETATLSCRASQNVK
NNLAWYQLKPGQAPRLLIFDASSRAGGIPDRFSGSGYGTDFTLTVNSVQS
EDFGDYFCQQYEEWPRTFGQGTKVDIKRTVAAPSVFIFPPSDEQLKSGTAS
VVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSK
ADYEKHKVYACEVTHQGLSPVTKSFNRGEC (SEQ ID NO: 257)

[0468] 5329_C19 (PGT-136) kappa light chain variable region amino acid sequence: (Kabat
CDRs underlined, Chothia CDRs in bold italics)

EIVMTQSPPTLSVSPGETATLSC***RASQNVKNNLA***WYQLKPGQAPRLLIF***DASS***
RAGGIPDRFSGSGYGTDFTLTVNSVQSEDFGDYFC***QQYEEWPRT***FGQGTKVD
IK (SEQ ID NO: 258)

[0469] 5329_C19 (PGT-136) kappa light chain Kabat CDRs:

CDR 1: RASQNVKNNLA (SEQ ID NO: 259)

CDR 2: DASSRAG (SEQ ID NO: 260)

CDR 3: QQYEEWPRT (SEQ ID NO: 245)

[0470] 5329_C19 (PGT-136) kappa light chain Chothia CDRs:

CDR 1: RASQNVKNNLA (SEQ ID NO: 259)

CDR 2: DASSRAG (SEQ ID NO: 260)

CDR 3: QQYEEWPRT (SEQ ID NO: 245)

[0471] 5366_P21 (PGT-136) gamma heavy chain nucleotide sequence: coding sequence
(variable region in bold)

ATGAAACACCTGTGGTTCTTCCTCCTGCTAGTGGCGGCTCCCAGATGGGTC
CTGTCGCAGCTGCAGTTGCAGGAATCGGGCCCAGGACTGGTGAAGCC
TTCGGAGACCCTGTCCCTGACTTGCACAGTTTCTGGTGGCTCCATGA

GGGGCACC GACTGGGGCGAGAATGACTTCCACTACGGCTGGATCCG
 CCAGTCCTCCGCAAAGGGGCTGGAGTGGATTGGGAGCATCCATTGGA
 GGGGGAGGACCACCCACTACAAGACGTCCTTCAGGAGTCGGGGCCAC
 CTTGTGCGATAGACACGTCCAATAATCGCTTCTCCCTGACGTTTAGTTT
 TGTGACCGCCGCGGACACGGCCGTCTACTATTGTGCGAGACATAAAT
 ATCATGATATTTTCAGGGTGGTCCCTGTTGCGGGCTGGTTCGACCCC
 TGGGGCCAGGGATTACTGGTCACCGTCTCGAGCGCCTCCACCAAGGGC
 CCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCAC
 AGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG
 TGTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCGGCT
 GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC
 CTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC
 CCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAA
 AACTCACACATGCCCACCGTGCCAGCACCTGAACCTCCTGGGGGGACCGT
 CAGTCTTCCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA
 CCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAG
 GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGAC
 AAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
 CTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA
 GGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
 CCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
 GAGGAGATGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGCT
 TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA
 GAACAACATAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCT
 TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA
 CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC
 AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 246)

[0472] 5366_P21 (PGT-136) gamma heavy chain variable region nucleotide sequence:

CAGCTGCAGTTGCAGGAATCGGGCCCAGGACTGGTGAAGCCTTCGGAGA
 CCCTGTCCCTGACTTGCACAGTTTCTGGTGGCTCCATGAGGGGGCACC GACT
 GGGGCGAGAATGACTTCCACTACGGCTGGATCCGCCAGTCCTCCGCAAAG
 GGGCTGGAGTGGATTGGGAGCATCCATTGGAGGGGGAGGACCACCCACT
 ACAAGACGTCCTTCAGGAGTCGGGCCACCTTGTCGATAGACACGTCCAAT
 AATCGCTTCTCCCTGACGTTTAGTTTTGTGACCGCCGCGGACACGGCCGTC
 TACTATTGTGCGAGACATAAATATCATGATATTTTCAGGGTGGTCCCTGTT
 GCGGGCTGGTTCGACCCCTGGGGCCAGGGATTACTGGTCACCGTCTCGAG
 C (SEQ ID NO: 247)

[0473] 5366_P21 (PGT-136) gamma heavy chain amino acid sequence: expressed protein
 with variable region in bold.

MKHLWFFLLLVAAPRWVLSQLQLQESGPGLVKPSETLSLTCTVSGGSM
RGTDWGENDFHYGWIRQSSAKGLEWIGSIHWRGRTHYKTSFRSRATLS
IDTSNNRFSLTFSFVTAADTAVYYCARHKYHDI**FRVVPVAGWFD****PWGQG**
LLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL

TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVE
PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTTPVLDSGSSFLYSLKLTVDKSRWQQGNVFS
CSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 248)

[0474] 5366_P21 (PGT-136) gamma heavy chain variable region amino acid sequence:
(Kabat CDRs underlined, Chothia CDRs in bold italics)

QLQLQESGPGLVKPSETLSLTCTVSGGSMRGTDWGENDFHYGWIRQSSAKG
LEWIG***SIHWRGRTHYKTSFRS***RATLSIDTSNNRFSLTFSFVTAADTAVYYCA
R***HKYHDIFRVVPVAGWFDP***WGQGLLVTVSS (SEQ ID NO: 249)

[0475] 5366_P21 (PGT-136) gamma heavy chain Kabat CDRs:

CDR 1: GTDWGENDFHYG (SEQ ID NO: 250)

CDR 2: SIHWRGRTHYKTSFRS (SEQ ID NO: 251)

CDR 3: HKYHDIFRVVPVAGWFDP (SEQ ID NO: 252)

[0476] 5366_P21 (PGT-136) gamma heavy chain Chothia CDRs:

CDR 1: GGSMRGTDWGEND (SEQ ID NO: 253)

CDR 2: SIHWRGRTH (SEQ ID NO: 254)

CDR 3: HKYHDIFRVVPVAGWFDP (SEQ ID NO: 252)

[0477] 5366_P21 (PGT-136) kappa light chain nucleotide sequence: coding sequence
(variable region in bold)

ATGGAAACCCAGCTCAGCTTCTCTTCCTCCTGCTACTCTGGCTCCCAGAT
AGCACTGGAGAAATAGTGATGACGCAGTCTCCACCCACCTGTCTGTG
TCTCCAGGGGAAACAGCCACACTCTCCTGTAGGGCCAGTCAGAATGT
TAAGAATAATTTAGCCTGGTACCAGCTGAAACCTGGCCAGGCTCCCA
GGCTCCTCATCTTTGATGCGTCCAGCAGGGCCGGTGGTATTCCTGAC
AGGTTCAGTGGCAGCGGTTATGGGACAGACTTCACTCTCACCGTCAA
CAGTGTGCAGTCCGAAGATTTTGGAGATTATTTTGTGTCAGCAATATGA
AGAGTGGCCTCGGACGTTCCGGCCAAGGGACCAAGGTGGATATCAAAC
GTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGT
TGAAATCTGGAAGTGCCTCTGTTGTGTGCTGCTGAATAACTTCTATCCCA
GAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAA
CTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGC
CTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAG
TCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAG
AGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO: 255)

[0478] 5366_P21 (PGT-136) kappa light chain variable region nucleotide sequence:

GAAATAGTGATGACGCAGTCTCCACCCACCCTGTCTGTGTCTCCAGGGGA
 AACAGCCACACTCTCCTGTAGGGCCAGTCAGAATGTTAAGAATAATTTAG
 CCTGGTACCAGCTGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTTTGAT
 GCGTCCAGCAGGGCCGGTGGTATTCCTGACAGGTTCACTGGCAGCGGTTA
 TGGGACAGACTTCACTCTCACCGTCAACAGTGTGCAGTCCGAAGATTTTG
 GAGATTATTTTGTGAGCAATATGAAGAGTGGCCTCGGACGTTCGGCCAA
 GGGACCAAGGTGGATATCAAA (SEQ ID NO: 256)

[0479] 5366_P21 (PGT-136) kappa light chain amino acid sequence: expressed protein with variable region in bold.

METPAQLLFLLLWLPDSTGEIVMTQSPPTLSVSPGETATLSCRASQNVK
NNLAWYQLKPGQAPRLLIFDASSRAGGIPDRFSGSGYGTDFTLTVNSVQS
EDFGDYFCQQYEEWPRTFGQGTKVDIKRTVAAPSVFIFPPSDEQLKSGTAS
VVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSLTLSK
ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 257)

[0480] 5366_P21 (PGT-136) kappa light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

EIVMTQSPPTLSVSPGETATLSC**RASONVKNNLA**WYQLKPGQAPRLLIF**DASS**
RAGGIPDRFSGSGYGTDFTLTVNSVQSEDFGDYFC**QQYEEWPRT**FGQGTKVD
 IK (SEQ ID NO: 258)

[0481] 5366_P21 (PGT-136) kappa light chain Kabat CDRs:

CDR 1: RASQNVKNNLA (SEQ ID NO: 259)

CDR 2: DASSRAG (SEQ ID NO: 260)

CDR 3: QQYEEWPRT (SEQ ID NO: 245)

[0482] 5366_P21 (PGT-136) kappa light chain Chothia CDRs:

CDR 1: RASQNVKNNLA (SEQ ID NO: 259)

CDR 2: DASSRAG (SEQ ID NO: 260)

CDR 3: QQYEEWPRT (SEQ ID NO: 245)

[0483] 4964_G22 (PGT-141) gamma heavy chain nucleotide sequence: coding sequence (variable region in bold)

ATGGACTGGATTTGGAGGATCCTCTTCTTGGTGGCAGCAGTTGCAAGTGC
 CCACTCGCAGGTGCAGCTGGTGCAGTCTGGGCCGGAGGTGAAGAAGC
 CTGGGTCTCAGTGAAGGTCTCCTGCAAGGCCTCTGGAAACACCTTC
 AGTAAATATGATGTCCACTGGGTACGACAGGCCACTGGACAGGGGCT
 TGAATGGGTGGGATGGATGAGTCATGAGGGTGATAAGACAGAATCTG
 CACAGAGATTTAAGGGCCGAGTCACCTTCACGAGGGACACTTCCGCA
 AGCACAGCCTACATGGAAGTGCAGCGGCCTGACATCTGACGACACGGC
 CATCTATTATTGTACGAGAGGCTCAAAACATCGTTTGCGAGACTACGT

TCTCTACGATGACTACGGCTTAATTAATTATCAAGAGTGGAATGACTA
 CCTTGAATTTTGGACGTCTGGGGCCATGGAACCGCGGTACCGTCT
 CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCC
 AAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACT
 ACTTCCCCGAACCGGTGACGGTGTCGTGGAACCTCAGGCGCCCTGACCAGC
 GGC GTGCACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTC
 AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
 CTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTT
 GAGCCCAAATCTTGTGACAAACTCACACATGCCACCGTGCCAGCACC
 TGA ACTCCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCCAAGG
 ACACCCCTCATGATCTCCCGGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT
 GTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT
 GGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
 ACGTACCGTGTGGTCAGCGTCCTACCGTCTGCACCAGGACTGGCTGAA
 TGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCA
 TCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
 GTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGC
 CTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTG
 GGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTG
 CTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTACCGTGGACAA
 GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGG
 CTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
 TGA (SEQ ID NO: 273)

[0484] 4964_G22 (PGT-141) gamma heavy chain variable region nucleotide sequence:

CAGGTGCAGCTGGTGCAGTCTGGGCCGGAGGTGAAGAAGCCTGGGT
 CCTCAGTGAAGGTCTCCTGCAAGGCCTCTGGAAACACCTTCAGTAAA
 TATGATGTCCACTGGGTACGACAGGCCACTGGACAGGGGCTTGAATG
 GGTGGGATGGATGAGTCATGAGGGTGATAAGACAGAATCTGCACAGA
 GATTTAAGGGCCGAGTCACCTTCACGAGGGACACTTCCGCAAGCACA
 GCCTACATGGAAGTGC GCGGCCTGACATCTGACGACACGGCCATCTA
 TTATTGTACGAGAGGCTCAAAACATCGTTTGCGAGACTACGTTCTCTA
 CGATGACTACGGCTTAATTAATTATCAAGAGTGGAATGACTACCTTGA
 ATTTTGGACGTCTGGGGCCATGGAACCGCGGTACCGTCTCCTCA
 (SEQ ID NO: 274)

[0485] 4964_G22 (PGT-141) gamma heavy chain amino acid sequence: expressed protein
 with leader sequence in italics and variable region in bold.

*MDWIWRILFLVA AVASAH***SQVQLVQSGPEVKKPGSSVKV***SCKASGNTFSKY*
DVHWVRQATGQGLEWVGWMSHEGDKTESAQR*FKGRVTFTRDTSASTA*
Y*MELRGLTSDDTAIYYCTR***GS***KHRLRDYVLYDDYGLINYQEWNDYLEFL*
DVWGHGTA*VT***VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT**
SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
KVDKR*VEPK***SCDK***TH***TCPP***CPAPELLG***GPSVFLFPPKPKDTLMISRTPEV**
TCV*VVDVSHEDPEVKFNWYVDGVEVHNA***TKPREEQYNSTYRVVSVLTVLHQD**

WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS
 LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
 WQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 275)

[0486] 4964_G22 (PGT-141) gamma heavy chain variable region amino acid sequence:
 (Kabat CDRs underlined, Chothia CDRs in bold italics)

QVQLVQSGPEVKKPGSSVKVSCKAS***GNTFSKYDVH***WVRQATGQGLEWVG
WMSHEGDKTESAQRFKGRVTFTTRDTSASTAYMELRGLTSDDTAIYYCTRG***S***
KHRLRDYVLYDDYGLINYQEWNDYLEFLDVWGHGTAFTVSS (SEQ ID NO:
 276)

[0487] 4964_G22 (PGT-141) gamma heavy chain Kabat CDRs:

CDR 1: KYDVH (SEQ ID NO: 277)

CDR 2: WMSHEGDKTESAQRFKG (SEQ ID NO: 278)

CDR 3: GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (SEQ ID NO: 279)

[0488] 4964_G22 (PGT-141) gamma heavy chain Chothia CDRs:

CDR 1: GNTFSK (SEQ ID NO: 280)

CDR 2: WMSHEGDKTE (SEQ ID NO: 281)

CDR 3: GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (SEQ ID NO: 279)

[0489] 4964_G22 (PGT-141) kappa light chain nucleotide sequence: coding sequence
 (variable region in bold)

ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGGTCTCTGGA
 TCCAGTGC GGATACTGTCGTGACTCAGTCTCCACTCTCCCTGCCCCGTC
 ACCCCTGGAGAGGCGGCCTCCATGTCCTGTTTCGTCTGACTCAGAGCCT
 CCGGCATAGTAATGGAGCCAACTATTTGGCTTGGTATCAGCACAAAC
 CGGGGCAGTCTCCACGACTCCTAATCCGTTTAGGTTCTCAACGGGCC
 TCCGGGGTCCCTGACAGATTCAGTGGCAGTGGATCAGGCACTCATT
TACACTGAAAATCAGTAGAGTGGAGGCTGAAGATGCTGCAATTTATT
ATTGCATGCAAGGTCTGAACCGTCCCTGGACGTTTCGGCAAGGGGACC
AAGTTGGAAATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCC
 GCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCT
 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAAC
 GCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCA
 AGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGA
 CTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGA
 GCTCGCCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG(SEQ ID NO:
 282)

[0490] 4964_G22 (PGT-141) kappa light chain variable region nucleotide sequence:

GATACTGTCGTGACTCAGTCTCCACTCTCCCTGCCCCGTCACCCCTGG
 AGAGGCGGCCTCCATGTCCTGTTCTGTCGACTCAGAGCCTCCGGCATA
 GTAATGGAGCCAACTATTTGGCTTGGTATCAGCACAAACCGGGGCAG
 TCTCCACGACTCCTAATCCGTTTAGGTTCTCAACGGGCCTCCGGGGT
 CCCTGACAGATTGAGTGGCAGTGGATCAGGCACTCATTTTACACTGA
 AAATCAGTAGAGTGGAGGCTGAAGATGCTGCAATTTATTATTGCATG
 CAAGGTCTGAACCGTCCCTGGACGTTCTGGCAAGGGGACCAAGTTGGA
 AATCAAA (SEQ ID NO: 283)

[0491] 4964_G22 (PGT-141) kappa light chain amino acid sequence: expressed protein with leader sequence in *italics* and variable region in **bold**.

*MRI PAQLI GLIMLWVSGSSADTVVTQSPLSLPVT*PGEAASMSCSSTQSLRHS
 NGANYLAWYQHKGQSPRLIRLGSQRASGVDPDRFSGSGSGTHFTLKISR
 VEAEDAIIYYCMQGLNRPWTFGKGTKLEIKRTVAAPSVFIFPPSDEQLKSG
 TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLT
 LSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC (SEQ ID NO: 284)

[0492] 4964_G22 (PGT-141) kappa light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in **bold italics**)

DTVVTQSPLSLPVTPGEAASMSC***SSTQSLRHS***NGANYLAWYQHKGQSPRLI
RLGSORASGVDPDRFSGSGSGTHFTLKISRVEAEDAIIYYC***MQGLNRPWT***FGK
 GTKLEIK (SEQ ID NO: 285)

[0493] 4964_G22 (PGT-141) kappa light chain Kabat CDRs:

CDR 1: SSTQSLRHSNGANYLA (SEQ ID NO: 286)

CDR 2: LGSQRAS (SEQ ID NO: 287)

CDR 3: MQGLNRPWT (SEQ ID NO: 288)

[0494] 4964_G22 (PGT-141) kappa light chain Chothia CDRs:

CDR 1: SSTQSLRHSNGANYLA (SEQ ID NO: 286)

CDR 2: LGSQRAS (SEQ ID NO: 287)

CDR 3: MQGLNRPWT (SEQ ID NO: 288)

[0495] 4993_K13 (PGT-141) gamma heavy chain nucleotide sequence: coding sequence (variable region in **bold**)

ATGGACTGGATTTGGAGGATCCTCTTCTTGGTGGCAGCAGTTGCAAGTGC
 CCACTCGCAGGTGCAGCTGGTGCAGTCTGGGCCTGAGGTGAAGAAGC
 CTGGGTCTCAGTGAAGGTCTCCTGCAAGGCCTCTGGAAACACCTTC
 AGTAAATATGATGTCCACTGGGTACGGCAGGCCACTGGACAGGGGCT
 TGAATGGGTGGGATGGATGAGTCATGAGGGTGATAAGACAGAATCTG
 CACAGAGATTTAAGGGCCGAGTCACCTTCACGAGGGGACACTTCCGCA
 AGCACAGCCTACATGGAAGTGCAGCGGCCTGACATCTGACGACACGGC

CATTTATTATTGTACGAGAGGCTCAAAACATCGCTTGCGAGACTATGT
TCTCTACGATGACTACGGCTTAATTAATTATCAAGAGTGGAATGACTA
CCTTGAATTTTTGGACGTCTGGGGCCATGGAACCGCGGTACACCGTCT
CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCC
AAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACT
ACTTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCCTGACCAGC
GGCGTGACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTC
AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
CTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAGAGTT
GAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACC
TGAACCTCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGG
ACACCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGAC
GTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT
GGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAA
TGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCA
TCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
GTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGC
CTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTG
GGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTG
CTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAA
GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGG
CTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
TGA (SEQ ID NO: 289)

[0496] 4993_K13 (PGT-141) gamma heavy chain variable region nucleotide sequence:

CAGGTGCAGCTGGTGCAGTCTGGGCCTGAGGTGAAGAAGCCTGGGT
CCTCAGTGAAGGTCTCCTGCAAGGCCTCTGGAAACACCTTCAGTAAA
TATGATGTCCACTGGGTACGGCAGGCCACTGGACAGGGGCTTGAATG
GGTGGGATGGATGAGTCATGAGGGTGATAAGACAGAATCTGCACAGA
GATTTAAGGGCCGAGTCACCTTCACGAGGGACACTTCCGCAAGCACA
GCCTACATGGAACCTGCGCGGCCTGACATCTGACGACACGGCCATTTA
TTATTGTACGAGAGGCTCAAAACATCGCTTGCGAGACTATGTTCTCTA
CGATGACTACGGCTTAATTAATTATCAAGAGTGGAATGACTACCTTGA
ATTTTTGGACGTCTGGGGCCATGGAACCGCGGTACACCGTCTCCTCA(S
EQ ID NO: 290)

[0497] 4993_K13 (PGT-141) gamma heavy chain amino acid sequence: expressed protein
with leader sequence in italics and variable region in bold.

*MDWIWRILFLVA AVASAH***SQVQLVQSGPEVKKPGSSVKV***SCKASGNTFSKY*
DVHWVRQATGQGLEWV*GWMSHEGDKTESAQR***FKGRVTFTRDTSASTA**
YMELRGLTSDDTAIYYCT*RGSKHRLRDYVLYDDYGLIN***YQEWNDYLEFL**
DVWGHGTA*VTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT*
SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
KVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV

VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
 WLNQKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS
 LTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR
 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 275)

[0498] 4993_K13 (PGT-141) gamma heavy chain variable region amino acid sequence:
 (Kabat CDRs underlined, Chothia CDRs in bold italics)

QVQLVQSGPEVKKPGSSVKVSCKAS***GNTFSKYDV***HWVRQATGQGLEWVG
WMSHEGDKTESAQRFKGRVTFTRDTSASTAYMELRGLTSDDTAIYYCTRG***S***
KHRLRDYVLYDDYGLINYQEWNDYLEFLDVWGHGTA VTVSS (SEQ ID NO:
 276)

[0499] 4993_K13 (PGT-141) gamma heavy chain Kabat CDRs:

CDR 1: KYDVH (SEQ ID NO: 277)

CDR 2: WMSHEGDKTESAQRFKG (SEQ ID NO: 278)

CDR 3: GSKHRLRDYVLYDDYGLINYQE WNDYLEFLDV (SEQ ID NO: 279)

[0500] 4993_K13 (PGT-141) gamma heavy chain Chothia CDRs:

CDR 1: GNTFSK (SEQ ID NO: 280)

CDR 2: WMSHEGDKTE (SEQ ID NO: 281)

CDR 3: GSKHRLRDYVLYDDYGLINYQE WNDYLEFLDV (SEQ ID NO: 279)

[0501] 4993_K13 (PGT-141) kappa light chain nucleotide sequence: coding sequence
 (variable region in bold)

ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGGTCTCTGGA
 TCCAGTGC GGATACTGTCTGCTGACTCAGTCTCCACTCTCCCTGCCCCGTC
 ACCCCTGGAGAGGCGGCCTCCATGTCCTGTTTCGTCGACTCAGAGCCT
 CCGGCATAGTAATGGAGCCAACTATTTGGCTTGGTATCAGCACAAAC
 CGGGGCAGTCTCCACGACTCCTAATCCGTTTAGGTTCTCAACGGGCC
 TCCGGGGTCCCTGACAGATTCAAGTGGCAGTGGATCAGGCACTCATT
 TACACTGAAAATCAGTAGAGTGGAGGCTGAAGATGCTGCAATTTATT
 ATTGCATGCAAGGTCTGAACCGTCCCTGGACGTTTCGGCAAGGGGACC
 AAGTTGGAAATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCC
 GCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCT
 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAAC
 GCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCA
 AGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGA
 CTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGA
 GCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:
 282)

[0502] 4993_K13 (PGT-141) kappa light chain variable region nucleotide sequence:

GATACTGTCGTGACTCAGTCTCCACTCTCCCTGCCCCGTCACCCCTGG
 AGAGGCGGCCTCCATGTCCTGTTCTGTCGACTCAGAGCCTCCGGCATA
 GTAATGGAGCCAACTATTTGGCTTGGTATCAGCACAAACCGGGGCAG
 TCTCCACGACTCCTAATCCGTTTAGGTTCTCAACGGGCCTCCGGGGT
 CCCTGACAGATTTCAGTGGCAGTGGATCAGGCACTCATTTTACACTGA
 AAATCAGTAGAGTGGAGGCTGAAGATGCTGCAATTTATTATTGCATG
 CAAGGTCTGAACCGTCCCTGGACGTTCTGGCAAGGGGACCAAGTTGGA
 AATCAAA (SEQ ID NO: 283)

[0503] 4993_K13 (PGT-141) kappa light chain amino acid sequence: expressed protein with leader sequence in italics and variable region in bold.

*MRI PAQLI GLI MI WVS GSSADTVVTQSPLSLPVT*PGEAASMSCSSTQSLRHS
 NGANYLAWYQHKGQSPRLLIRLGSQRASGVDPDRFSGSGSGTHFTLKISR
 VEAEDAAIYYCMQGLNRPWTFGKGTKLEIKRTVAAPSVFIFPPSDEQLKSG
 TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLT
 LSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC (SEQ ID NO: 284)

[0504] 4993_K13 (PGT-141) kappa light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

DTVVTQSPLSLPVT*PGEAASMSC**SSTQSLRHS*NGANYLAWYQHKGQSPRLLI
RLGSORASGVDPDRFSGSGSGTHFTLKISRVEAEDAAIYYCMQGLNRPWTFGK
 GTKLEIK (SEQ ID NO: 285)

[0505] 4993_K13 (PGT-141) kappa light chain Kabat CDRs:

CDR 1: SSTQSLRHSNGANYLA (SEQ ID NO: 286)

CDR 2: LGSQRAS (SEQ ID NO: 287)

CDR 3: MQGLNRPWT (SEQ ID NO: 288)

[0506] 4993_K13 (PGT-141) kappa light chain Chothia CDRs:

CDR 1: SSTQSLRHSNGANYLA (SEQ ID NO: 286)

CDR 2: LGSQRAS (SEQ ID NO: 287)

CDR 3: MQGLNRPWT (SEQ ID NO: 288)

[0507] 4995_E20 (PGT-142) gamma heavy chain nucleotide sequence: coding sequence (variable region in bold)

ATGGACTGGATTTGGAGGATCCTCTTCTTGGTGGCAGCAGTTGCAAGTGC
 CCACTCGCAGGTGCAGCTGGTGCAGTCTGGGCCTGAGGTGAAGAAGC
 CTGGGTCTCAGTGAAGGTCTCCTGCAAGGCCTCTGGAAACACCTTC
 AGTAAATATGATGTCCACTGGGTACGACAGGCCACTGGACAGGGGCT
 TGAATGGGTGGGATGGATTAGTCATGAGCGTGATAAGACAGAATCTG
 CACAGAGATTTAAGGGCCGAGTCACCTTCACGAGGGGACACTTCCGCA
 ACCACAGCCTACATGGAAGTGC GCGGCCTGACATCTGACGACACGGC

CATTTATTATTGTACGAGAGGCTCAAAACATCGCTTGCGAGACTACGT
TCTCTACGATGACTACGGCTTAATTAATTATCAAGAGTGGAATGACTA
CCTTGAATTTTTGGACGTCTGGGGCCATGGAACCGCGGTACACGTCT
CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCC
AAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACT
ACTTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCCTGACCAGC
GGCGTGACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTC
AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
CTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAGAGTT
GAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACC
TGAACCTCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGG
ACACCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGAC
GTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT
GGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAA
TGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCA
TCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
GTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGC
CTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTG
GGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTG
CTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAA
GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGG
CTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
TGA (SEQ ID NO: 314)

[0508] 4995_E20 (PGT-142) gamma heavy chain variable region nucleotide sequence:

CAGGTGCAGCTGGTGCAGTCTGGGCCTGAGGTGAAGAAGCCTGGGT
CCTCAGTGAAGGTCTCCTGCAAGGCCTCTGGAAACACCTTCAGTAAA
TATGATGTCCACTGGGTACGACAGGCCACTGGACAGGGGCTTGAATG
GGTGGGATGGATTAGTCATGAGCGTGATAAGACAGAACTCTGCACAGA
GATTTAAGGGCCGAGTCACCTTCACGAGGGACACTTCCGCAACCACA
GCCTACATGGAACCTGCGCGGCCTGACATCTGACGACACGGCCATTTA
TTATTGTACGAGAGGCTCAAAACATCGCTTGCGAGACTACGTTCTCTA
CGATGACTACGGCTTAATTAATTATCAAGAGTGGAATGACTACCTTGA
ATTTTTGGACGTCTGGGGCCATGGAACCGCGGTACACGTCTCCTCA
(SEQ ID NO: 315)

[0509] 4995_E20 (PGT-142) gamma heavy chain amino acid sequence: expressed protein
with leader sequence in italics and variable region in bold.

*MDWIWRILFLVA*AVASAH**SQVQLVQSGPEVKKPGSSVKV**SCKASGNTFSKY
DVHWVRQATGQGLEWVGWISHERDKTESAQR**FKGRVTFTRDTS**ATTAY
MELRGLTSDDTAIYYCTRGSKHRLRDYVLYDDYGLINYQEWN**DYLEFLD**
VWGHGTA**VT**VSSASTKGPSVFPLAPSSKSTSGGTAA**LGCLVKDYFPEP**VTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSV**VT**VPSSSLGTQTYICNVNHKPSNTK
VDKRVEPKSCDKTHTCP**PC**PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV

VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQ
QGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 291)

[0510] 4995_E20 (PGT-142) gamma heavy chain variable region amino acid sequence:
(Kabat CDRs underlined, Chothia CDRs in bold italics)

QVQLVQSGPEVKKPGSSVKVSCKAS***GNTFSKYDV***HWVRQATGQGLEWVG
WISHERDKTESAQRFKGRVTFTRDTSATTAYMELRGLTSDDTAIYYCT***RGSK***
HRLRDYVLYDDYGLINYQEWNDYLEFLDVWGHGTA VTVSS (SEQ ID NO:
292)

[0511] 4995_E20 (PGT-142) gamma heavy chain Kabat CDRs:

CDR 1: KYDVH (SEQ ID NO: 277)

CDR 2: WISHERDKTESAQRFKG (SEQ ID NO: 293)

CDR 3: GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (SEQ ID NO: 279)

[0512] 4995_E20 (PGT-142) gamma heavy chain Chothia CDRs:

CDR 1: GNTFSK (SEQ ID NO: 280)

CDR 2: WISHERDKTE (SEQ ID NO: 294)

CDR 3: GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (SEQ ID NO: 279)

[0513] 4995_E20 (PGT-142) kappa light chain nucleotide sequence: coding sequence
(variable region in bold)

ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGGTCTCTGGA
TCCAGTGC GGATACTGTCGTGACTCAGTCTCCACTCTCCCTGCCCCGTC
ACCCCTGGAGAGGCGGCCTCCATGTCCTGTTTCGTGCTGACTCAGAGCCT
CCGGCATAGTAATGGAGCCAACTATTTGGCTTGGTATCAGCACAAAC
CGGGGCAGTCTCCACGACTCCTAATCCGTTTAGGTTCTCAACGGGCC
TCCGGGGTCCCTGACAGATTCAAGTGGCAGTGGATCAGGCACTCATT
TACACTGAAAATCAGTAGAGTGGAGGCTGAAGATGCTGCAATTTATT
ATTGCATGCAAGGTCTGAACCGTCCCTGGACGTTTCGGCAAGGGGACC
AAGTTGGAAATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCC
GCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCT
GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAAC
GCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCA
AGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGA
CTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGA
GCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:
282)

[0514] 4995_E20 (PGT-142) kappa light chain variable region nucleotide sequence:

GATACTGTCGTGACTCAGTCTCCACTCTCCCTGCCCCGTCACCCCTGG
 AGAGGCGGCCTCCATGTCCTGTTCTGTCGACTCAGAGCCTCCGGCATA
 GTAATGGAGCCAACTATTTGGCTTGGTATCAGCACAAACCGGGGCAG
 TCTCCACGACTCCTAATCCGTTTAGGTTCTCAACGGGCCTCCGGGGT
 CCCTGACAGATTTCAGTGGCAGTGGATCAGGCACTCATTTTACACTGA
 AAATCAGTAGAGTGGAGGCTGAAGATGCTGCAATTTATTATTGCATG
 CAAGGTCTGAACCGTCCCTGGACGTTCTGGCAAGGGGACCAAGTTGGA
 AATCAAA (SEQ ID NO: 283)

[0515] 4995_E20 (PGT-142) kappa light chain amino acid sequence: expressed protein with leader sequence in *italics* and variable region in **bold**.

*MRI PAQLI GLI MI WVS GSSADTVVTQSPLSLPVT*PGEAASMSCSSTQSLRHS
 NGANYLA**WYQH**KGQSPRLI**RLGSQRAS**GV**PDR**FSGSGSG**THFT**LKISR
 VEAEDAAIYYCMQGLNRPWTF**GKGT**KL**EIK**RTVAAPSVFIFPPSDEQLKSG
 TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLT
 LSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC (SEQ ID NO: 284)

[0516] 4995_E20 (PGT-142) kappa light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in **bold italics**)

DTVVTQSPLSLPVT**PGEAASMSC****SSTQSLRHS**NGANYLA**WYQH**KGQSPRLI
RLGSORASGV**PDR**FSGSGSG**THFT**LKISRVEAEDAAIYYC**MQGLNRPWT**FGK
 GTKLEIK (SEQ ID NO: 285)

[0517] 4995_E20 (PGT-142) kappa light chain Kabat CDRs:

CDR 1: SSTQSLRHSNGANYLA (SEQ ID NO: 286)

CDR 2: LGSQRAS (SEQ ID NO: 287)

CDR 3: MQGLNRPWT (SEQ ID NO: 288)

[0518] 4995_E20 (PGT-142) kappa light chain Chothia CDRs:

CDR 1: SSTQSLRHSNGANYLA (SEQ ID NO: 286)

CDR 2: LGSQRAS (SEQ ID NO: 287)

CDR 3: MQGLNRPWT (SEQ ID NO: 288)

[0519] 4980_N08 (PGT-143) gamma heavy chain nucleotide sequence: coding sequence (variable region in **bold**)

ATGGACTGGATTTGGAGGATCCTCTTCTTGGTGGCAGCAGTTGCAAGTGC
 CCACGCGCAGGTGCAGCTGGAGCAGTCTGGGGCTGAGGTGAAGAAGC
 CTGGGTCTCAGTGAAGGTCTCCTGCAAGGCCTCTGGAAACACCTTC
 AGTAAATATGATGTCCACTGGGTACGACAGGCCACTGGACAGGGGCT
 TGAATGGGTGGGATGGATGAGTCATGAGGGTGATAAGACAGAATCTG
 CACAGAGATTTAAGGGGCGAGTCACCTTCACGAGGGGACACTTCCGCA
 AGCACAGCCTACATGGAAGTGCAGCGGCCTGACATCTGACGACACGGC

CATTTATTATTGTACGAGAGGTTCAAAACATCGCTTGCGAGACTACGT
TCTCTACGATGACTACGGCTTAATTAATTATCAAGAGTGGAATGACTA
CCTTGAATTTTTGGACGTCTGGGGCCATGGAACCGCGGTACACCGTCT
CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCC
AAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACT
ACTTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCCTGACCAGC
GGCGTGACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTC
AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
CTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAGAGTT
GAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACC
TGAACCTCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGG
ACACCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGAC
GTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT
GGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAA
TGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCA
TCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
GTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGC
CTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTG
GGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTG
CTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAA
GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGG
CTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
TGA (SEQ ID NO: 295)

[0520] 4980_N08 (PGT-143) gamma heavy chain variable region nucleotide sequence:

CAGGTGCAGCTGGAGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGT
CCTCAGTGAAGGTCTCCTGCAAGGCCTCTGGAAACACCTTCAGTAAA
TATGATGTCCACTGGGTACGACAGGCCACTGGACAGGGGCTTGAATG
GGTGGGATGGATGAGTCATGAGGGTGATAAGACAGAATCTGCACAGA
GATTTAAGGGGCGAGTCACCTTACGAGGGACACTTCCGCAAGCACA
GCCTACATGGAACCTGCGCGGCCTGACATCTGACGACACGGCCATTTA
TTATTGTACGAGAGGTTCAAAACATCGCTTGCGAGACTACGTTCTCTA
CGATGACTACGGCTTAATTAATTATCAAGAGTGGAATGACTACCTTGA
ATTTTTGGACGTCTGGGGCCATGGAACCGCGGTACACGTCTCCTCA
(SEQ ID NO: 296)

[0521] 4980_N08 (PGT-143) gamma heavy chain amino acid sequence: expressed protein
with leader sequence in italics and variable region in bold.

*MDWIWRILFLVA*AVASAH**AQVQLEQSGAEVKKPGSSVKV**SCKASGNTFSKY
DVHWVRQATGQGLEWVGWMSHEGDKTESAQRFKGRVTFTRDTSASTA
YMELRGLTSDDTAIYYCTRGSKHRLRDYVLYDDYGLINYQEWNDYLEFL
DVWGHGTAIVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV
SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
KVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV

VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
 WLNQKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS
 LTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR
 WQQGNVVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 297)

[0522] 4980_N08 (PGT-143) gamma heavy chain variable region amino acid sequence:
 (Kabat CDRs underlined, Chothia CDRs in bold italics)

QVQLEQSGAEVKKPGSSVKVSCKAS***GNTFSKYDVH***WVRQATGQGLEWVG
WMSHEGDKTESAQRFKGRVTFTRDTSASTAYMELRGLTSDDTAIYYCTRG***S***
KHRLRDYVLYDDYGLINYQEWNDYLEFLDVWGHGTA VTVSS (SEQ ID NO:
 298)

[0523] 4980_N08 (PGT-143) gamma heavy chain Kabat CDRs:

CDR 1: KYDVH (SEQ ID NO: 277)

CDR 2: WMSHEGDKTESAQRFKG (SEQ ID NO: 278)

CDR 3: GSKHRLRDYVLYDDYGLINYQE WNDYLEFLDV (SEQ ID NO: 279)

[0524] 4980_N08 (PGT-143) gamma heavy chain Chothia CDRs:

CDR 1: GNTFSK (SEQ ID NO: 280)

CDR 2: WMSHEGDKTE (SEQ ID NO: 281)

CDR 3: GSKHRLRDYVLYDDYGLINYQE WNDYLEFLDV (SEQ ID NO: 279)

[0525] 4980_N08 (PGT-143) kappa light chain nucleotide sequence: coding sequence
 (variable region in bold)

ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGGTCTCTGGA
 TCCAGTGC GGATACTGTCGTGACTCAGTCTCCACTCTCCCTGCCCCGTC
 ACCCCTGGAGAGGCGGCCTCCATGTCCTGTACGTCGACTCAGAGCCT
 CCGTCATAGTAATGGAGCCAACTATTTGGCTTGGTACCAGCACAAAC
 CAGGGCAGTCTCCACGACTCCTAATCCGTTTAGGTTCTCAACGGGCC
 TCCGGGGTCCCTGACAGATTCAAGTGGCAGTGGATCAGGCACTCATT
 TACACTGAAAATCAGTCGAGTGGAGCCTGAAGATGCTGCAATTTATT
 ATTGCATGCAAGGTCTGAACCGTCCCTGGACGTTTCGGCAAGGGGACC
 AAGTTGGAAATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCC
 GCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCT
 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAAC
 GCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCA
 AGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGA
 CTACGAGAAACACAAAGTCTACGCCTGCGAAGTACCCATCAGGGCCTGA
 GCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:
 299)

[0526] 4980_N08 (PGT-143) kappa light chain variable region nucleotide sequence:

GATACTGTCGTGACTCAGTCTCCACTCTCCCTGCCCCGTCACCCCTGG
 AGAGGCGGCCTCCATGTCCTGTACGTCGACTCAGAGCCTCCGTCATA
 GTAATGGAGCCAACTATTTGGCTTGGTACCAGCACAAACCAGGGCAG
 TCTCCACGACTCCTAATCCGTTTAGGTTCTCAACGGGCCTCCGGGGT
 CCCTGACAGATTTCAGTGGCAGTGGATCAGGCACTCATTTTACACTGA
 AAATCAGTCGAGTGGAGCCTGAAGATGCTGCAATTTATTATTGCATG
 CAAGGTCTGAACCGTCCCTGGACGTTCTGGCAAGGGGACCAAGTTGGA
 AATCAAA (SEQ ID NO: 300)

[0527] 4980_N08 (PGT-143) kappa light chain amino acid sequence: expressed protein with leader sequence in *italics* and variable region in **bold**.

*MRI PAQLI GLIMLWVSGSSADTVVTQSPLSLPVT*PGEAASMSCTSTQSLRHS
 NGANYLAWYQHKPGQSPRLIRLGSQRASGVDPDRFSGSGSGTHFTLKISR
 VEPEDAIIYYCMQGLNRPWTFGKGTKLEIKRTVAAPSVFIFPPSDEQLKSG
 TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLT
 LSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC (SEQ ID NO: 301)

[0528] 4980_N08 (PGT-143) kappa light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in **bold italics**)

DTVVTQSPLSLPVTPGEAASMSCT***TSTQSLRHS***NGANYLAWYQHKPGQSPRLI
RLGSORASGVDPDRFSGSGSGTHFTLKISRV***EPEDAIIYYCMOGLNRPWT***FGK
 GTKLEIK (SEQ ID NO: 302)

[0529] 4980_N08 (PGT-143) kappa light chain Kabat CDRs:

CDR 1: TSTQSLRHSNGANYLA (SEQ ID NO: 303)

CDR 2: LGSQRAS (SEQ ID NO: 287)

CDR 3: MQGLNRPWT (SEQ ID NO: 288)

[0530] 4980_N08 (PGT-143) kappa light chain Chothia CDRs:

CDR 1: TSTQSLRHSNGANYLA (SEQ ID NO: 303)

CDR 2: LGSQRAS (SEQ ID NO: 287)

CDR 3: MQGLNRPWT (SEQ ID NO: 288)

[0531] 4970_K22 (PGT-144) gamma heavy chain nucleotide sequence: coding sequence (variable region in **bold**)

ATGGACTGGATTTGGAGGATCCTCTTCTTGGTGGCAGCAGTTGCAAGTGC
 CCACTCGCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGC
 CTGGGTCTCAGTGAAGGTCTCCTGCAAGGCCTCTGGAAACACCTTC
 AGGAAATATGATGTCCACTGGGTACGACAGGCCACTGGACAGGGGCT
 TGAATGGGTGGGATGGATGAGTCATGAGGGTGATAAGACAGAATCTG
 CACAGAGATTTAAGGGCCGAGTCTCTTTCACGAGGGGACAATCCGCA
 AGCACAGCCTACATTGAACTGCGCGGCCTGACATCTGACGACACGGC

CATTTATTATTGTACCGGAGGCTCAAAACATCGCTTGCGAGACTACGT
TCTCTACGATGATTACGGCCTAATAAATCAGCAAGAGTGGAAATGACT
ACCTTGAATTTTGGACGTCTGGGGCCATGGAACCGCGGTACCCGTC
TCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTC
CAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACT
ACTTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCCTGACCAGC
GGCGTGACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTC
AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
CTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTT
GAGCCCAAATCTTGTGACAAAACCTCACACATGCCCACCGTGCCCAGCACC
TGAACCTCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGG
ACACCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGAC
GTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT
GGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAA
TGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCA
TCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
GTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGC
CTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTG
GGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTG
CTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAA
GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGG
CTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
TGA (SEQ ID NO: 304)

[0532] 4970_K22 (PGT-144) gamma heavy chain variable region nucleotide sequence:

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGT
CCTCAGTGAAGGTCTCCTGCAAGGCCTCTGGAAACACCTTCAGGAAA
TATGATGTCCACTGGGTACGACAGGCCACTGGACAGGGGCTTGAATG
GGTGGGATGGATGAGTCATGAGGGTGATAAGACAGAATCTGCACAGA
GATTTAAGGGCCGAGTCTCTTTCACGAGGGACAATTCGCAAGCACA
GCCTACATTGAACTGCGCGGCCTGACATCTGACGACACGGCCATTTA
TTATTGTACCGGAGGCTCAAAACATCGCTTGCGAGACTACGTTCTCTA
CGATGATTACGGCCTAATAAATCAGCAAGAGTGGAAATGACTACCTTG
AATTTTGGACGTCTGGGGCCATGGAACCGCGGTACCCGTCTCCTCA
(SEQ ID NO: 305)

[0533] 4970_K22 (PGT-144) gamma heavy chain amino acid sequence: expressed protein
with leader sequence in italics and variable region in bold.

*MDWIWRILFLVA*AVASAH**SQVQLVQSGAEVKKPGSSVKV**SCKASGNTFRKY
DVHWVRQATGQGLEWVGWMSHEGDKTESAQRFKGRVSFTRDNSASTA
YIELRGLTSDDTAIYYCTGGSKHRLRDYVLYDDYGLINQQEWNDYLEFL
DVWGHGTAIVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV
SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
KVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV

VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
 WLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS
 LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
 WQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 306)

[0534] 4970_K22 (PGT-144) gamma heavy chain variable region amino acid sequence:
 (Kabat CDRs underlined, Chothia CDRs in bold italics)

QVQLVQSGAEVKKPGSSVKVSCKAS***GNTFRKYDVH***WVRQATGQGLEWVG
WMSHEGDKTESAQRFKGRVSFTRDNSASTAYIELRGLTSDDTAIYYCTG***GSK***
HRLRDYVLYDDYGLINQOEWNDYLEFLDVWGHGTAVTVSS (SEQ ID NO:
 307)

[0535] 4970_K22 (PGT-144) gamma heavy chain Kabat CDRs:

CDR 1: KYDVH (SEQ ID NO: 277)

CDR 2: WMSHEGDKTESAQRFKG (SEQ ID NO: 278)

CDR 3: GSKHRLRDYVLYDDYGLINQOEWNDYLEFLDV (SEQ ID NO: 308)

[0536] 4970_K22 (PGT-144) gamma heavy chain Chothia CDRs:

CDR 1: GNTFRK (SEQ ID NO: 309)

CDR 2: WMSHEGDKTE (SEQ ID NO: 281)

CDR 3: GSKHRLRDYVLYDDYGLINQOEWNDYLEFLDV (SEQ ID NO: 308)

[0537] 4970_K22 (PGT-144) kappa light chain nucleotide sequence: coding sequence
 (variable region in bold)

ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGGTCTCTGGA
 TCCAGTGC GGATACTGTCTGCTGACTCAGTCTCCACTCTCCCTGTCCGTC
 ACCCCTGGAGAGGCGGCCTCCATGTCTGTACGTCGACTCAGAGCCT
 CCGGCATAGTAATGGAGCCAACTATTTGGCTTGGTACCAGCACAAAC
 CAGGGCAGTCTCCACGACTCCTAATCCGTTTAGGTTCTCAACGGGCC
 TCCGGGGTCCCTGACAGATTCAAGTGGCAGTGGATCAGGCACTCATT
 TACACTGAAAATCAGTAGAGTGGAGGCTGACGATGCTGCAATTTATT
 ATTGCATGCAAGGTCTGAACCGTCCCTGGACGTTTCGGCAAGGGGACC
 AAGTTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCC
 GCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCT
 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAAC
 GCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCA
 AGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGA
 CTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGA
 GCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:
 310)

[0538] 4970_K22 (PGT-144) kappa light chain variable region nucleotide sequence:

GATACTGTCGTGACTCAGTCTCCACTCTCCCTGTCCGTCACCCCTGGA
 GAGGCGGCCTCCATGTCCTGTACGTGCGACTCAGAGCCTCCGGCATAG
 TAATGGAGCCAACTATTTGGCTTGGTACCAGCACAAACCAGGGCAGT
 CTCCACGACTCCTAATCCGTTTAGGTTCTCAACGGGCCTCCGGGGTC
 CCTGACAGATTCAGTGGCAGTGGATCAGGCACTCATTTTACACTGAA
 AATCAGTAGAGTGGAGGCTGACGATGCTGCAATTTATTATTGCATGC
 AAGGTCTGAACCGTCCCTGGACGTTTCGGCAAGGGGACCAAGTTGGAG
 ATCAAA (SEQ ID NO: 311)

[0539] 4970_K22 (PGT-144) kappa light chain amino acid sequence: expressed protein with leader sequence in *italics* and variable region in **bold**.

MRI PAQLI GLIML WVSGSSADTVVTQSPLSLSVTPGEAASMSCTSTQSLRHS
NGANYLAWYQHKGQSPRLI**RLGSQRAS**GV**PDRFSGSGSGTHFTLKISR**
VEADDAIYYCMQGLNRPWTFGKGTKLEIKRTVAAPSVFIFPPSDEQLKSG
 TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLT
 LSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC (SEQ ID NO: 312)

[0540] 4970_K22 (PGT-144) kappa light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in **bold italics**)

DTVVTQSPLSLSVTPGEAASMSCT***TSTQSLRHSNGANYLA***WYQHKGQSPRLI
RLGSORASGV***PDRFSGSGSGTHFTLKISR***VEADDAIYYC***MOGLNRPWT***FGK
 GTKLEIK (SEQ ID NO: 313)

[0541] 4970_K22 (PGT-144) kappa light chain Kabat CDRs:

CDR 1: TSTQSLRHSNGANYLA (SEQ ID NO: 303)

CDR 2: LGSQRAS (SEQ ID NO: 287)

CDR 3: MQGLNRPWT (SEQ ID NO: 288)

[0542] 4970_K22 (PGT-144) kappa light chain Chothia CDRs:

CDR 1: TSTQSLRHSNGANYLA (SEQ ID NO: 303)

CDR 2: LGSQRAS (SEQ ID NO: 287)

CDR 3: MQGLNRPWT (SEQ ID NO: 288)

[0543] The 4838_L06 (PGT-121) antibody includes a heavy chain variable region (SEQ ID NO: 79), encoded by the nucleic acid sequence shown in SEQ ID NO: 63, and a light chain variable region (SEQ ID NO: 149) encoded by the nucleic acid sequence shown in SEQ ID NO: 147.

[0544] The heavy chain CDRs of the 4838_L06 (PGT-121) antibody have the following sequences per Kabat definition: DSYWS (SEQ ID NO: 90), YVHKSGDTNYSPLKS (SEQ ID NO: 265), and TLHGRRYIGIVAFNEWFTYFYMDV (SEQ ID NO: 143). The light chain CDRs

of the 4838_L06 (PGT-121) antibody have the following sequences per Kabat definition: GEKSLGSRAVQ (SEQ ID NO: 150), NNQDRPS (SEQ ID NO: 151), and HIWDSRVPTKWV (SEQ ID NO: 152).

[0545] The heavy chain CDRs of the 4838_L06 (PGT-121) antibody have the following sequences per Chothia definition: GASISD (SEQ ID NO: 144), YVHKSGDTN (SEQ ID NO: 145), and TLHGRRIGIVAFNEWFTYFYMDV (SEQ ID NO: 143). The light chain CDRs of the 4838_L06 (PGT-121) antibody have the following sequences per Chothia definition: GEKSLGSRAVQ (SEQ ID NO: 150), NNQDRPS (SEQ ID NO: 151), and HIWDSRVPTKWV (SEQ ID NO: 152).

[0546] The 4873_E03 (PGT-121) antibody includes a heavy chain variable region (SEQ ID NO: 79), encoded by the nucleic acid sequence shown in SEQ ID NO: 63, and a light chain variable region (SEQ ID NO: 149) encoded by the nucleic acid sequence shown in SEQ ID NO: 147.

[0547] The heavy chain CDRs of the 4873_E03 (PGT-121) antibody have the following sequences per Kabat definition: DSYWS (SEQ ID NO: 90), YVHKSGDTNYSPLKS (SEQ ID NO: 265), and TLHGRRIGIVAFNEWFTYFYMDV (SEQ ID NO: 143). The light chain CDRs of the 4873_E03 (PGT-121) antibody have the following sequences per Kabat definition: GEKSLGSRAVQ (SEQ ID NO: 150), NNQDRPS (SEQ ID NO: 151), and HIWDSRVPTKWV (SEQ ID NO: 152).

[0548] The heavy chain CDRs of the 4873_E03 (PGT-121) antibody have the following sequences per Chothia definition: GASISD (SEQ ID NO: 144), YVHKSGDTN (SEQ ID NO: 145), and TLHGRRIGIVAFNEWFTYFYMDV (SEQ ID NO: 143). The light chain CDRs of the 4873_E03 (PGT-121) antibody have the following sequences per Chothia definition: GEKSLGSRAVQ (SEQ ID NO: 150), NNQDRPS (SEQ ID NO: 151), and HIWDSRVPTKWV (SEQ ID NO: 152).

[0549] The 4877_D15 (PGT-122) antibody includes a heavy chain variable region (SEQ ID NO: 156), encoded by the nucleic acid sequence shown in SEQ ID NO: 154, and a light chain variable region (SEQ ID NO: 161) encoded by the nucleic acid sequence shown in SEQ ID NO: 159.

[0550] The heavy chain CDRs of the 4877_D15 (PGT-122) antibody have the following sequences per Kabat definition: DNYWS (SEQ ID NO: 261), YVHDSGDTNYPNPSLKS (SEQ

ID NO: 157), and TKHGRRYGVVAFKEWFTYFYMDV (SEQ ID NO: 262). The light chain CDRs of the 4877_D15 (PGT-122) antibody have the following sequences per Kabat definition: GEESLGSRSVI (SEQ ID NO: 162), NNNDRPS (SEQ ID NO: 163), and HIWDSRRPTNWV (SEQ ID NO: 164).

[0551] The heavy chain CDRs of the 4877_D15 (PGT-122) antibody have the following sequences per Chothia definition: GTLVRD (SEQ ID NO: 263), YVHDSGDTN (SEQ ID NO: 264), and TKHGRRYGVVAFKEWFTYFYMDV (SEQ ID NO: 262). The light chain CDRs of the 4877_D15 (PGT-122) antibody have the following sequences per Chothia definition: GEESLGSRSVI (SEQ ID NO: 162), NNNDRPS (SEQ ID NO: 163), and HIWDSRRPTNWV (SEQ ID NO: 164).

[0552] The 4858_P08 (PGT-123) antibody includes a heavy chain variable region (SEQ ID NO: 168), encoded by the nucleic acid sequence shown in SEQ ID NO: 166, and a light chain variable region (SEQ ID NO: 177) encoded by the nucleic acid sequence shown in SEQ ID NO: 175.

[0553] The heavy chain CDRs of the 4858_P08 (PGT-123) antibody have the following sequences per Kabat definition: DAYWS (SEQ ID NO: 169), YVHHSGDTNYPNPSLKR (SEQ ID NO: 170), ALHGKRIYGI VALGELFTYFYMDV (SEQ ID NO: 171). The light chain CDRs of the 4858_P08 (PGT-123) antibody have the following sequences per Kabat definition: GKESIGSRAVQ (SEQ ID NO: 178), NNQDRPA (SEQ ID NO: 179), and HIYDARGGTNWV (SEQ ID NO: 180).

[0554] The heavy chain CDRs of the 4858_P08 (PGT-123) antibody have the following sequences per Chothia definition: GASIND (SEQ ID NO: 172), YVHHSGDTN (SEQ ID NO: 173), ALHGKRIYGI VALGELFTYFYMDV (SEQ ID NO: 171). The light chain CDRs of the 4858_P08 (PGT-123) antibody have the following sequences per Chothia definition: GKESIGSRAVQ (SEQ ID NO: 178), NNQDRPA (SEQ ID NO: 179), HIYDARGGTNWV (SEQ ID NO: 180).

[0555] The 5123_A06 (PGT-125) antibody includes a heavy chain variable region (SEQ ID NO: 164), encoded by the nucleic acid sequence shown in SEQ ID NO: 182, and a light chain variable region (SEQ ID NO: 193) encoded by the nucleic acid sequence shown in SEQ ID NO: 191.

[0556] The heavy chain CDRs of the 5123_A06 (PGT-125) antibody have the following sequences per Kabat definition: ACTYFWG (SEQ ID NO: 185), SLSHCQSFWSGSGWTFHNPSLKS (SEQ ID NO: 186), and FDGEVLVYNHWPKPAWVDL (SEQ ID NO: 187). The light chain CDRs of the 5123_A06 (PGT-125) antibody have the following sequences per Kabat definition: NGTATNFVS (SEQ ID NO: 194), GVDKRPP (SEQ ID NO: 195), and GSLVGNWDVI (SEQ ID NO: 196).

[0557] The heavy chain CDRs of the 5123_A06 (PGT-125) antibody have the following sequences per Chothia definition: GESTGACT (SEQ ID NO: 188), SLSHCQSFWSGSGWTF (SEQ ID NO: 189), and FDGEVLVYNHWPKPAWVDL (SEQ ID NO: 187). The light chain CDRs of the 5123_A06 (PGT-125) antibody have the following sequences per Chothia definition: NGTATNFVS (SEQ ID NO: 194), GVDKRPP (SEQ ID NO: 195), and GSLVGNWDVI (SEQ ID NO: 196).

[0558] The 5141_B17 (PGT-126) antibody includes a heavy chain variable region (SEQ ID NO: 200), encoded by the nucleic acid sequence shown in SEQ ID NO: 198, and a light chain variable region (SEQ ID NO: 209) encoded by the nucleic acid sequence shown in SEQ ID NO: 207.

[0559] The heavy chain CDRs of the 5141_B17 (PGT-126) antibody have the following sequences per Kabat definition: ACDYFWG (SEQ ID NO: 201), GLSHCAGYYNTGWTYHNPSLKS (SEQ ID NO: 202), and FDGEVLVYHDWPKPAWVDL (SEQ ID NO: 203). The light chain CDRs of the 5141_B17 (PGT-126) antibody have the following sequences per Kabat definition: TGTSNRFVS (SEQ ID NO: 210), GVNKRPS (SEQ ID NO: 211), and SSLVGNWDVI (SEQ ID NO: 212).

[0560] The heavy chain CDRs of the 5141_B17 (PGT-126) antibody have the following sequences per Chothia definition: GDSTAACD (SEQ ID NO: 204), GLSHCAGYYNTGWTY (SEQ ID NO: 205), and FDGEVLVYHDWPKPAWVDL (SEQ ID NO: 203). The light chain CDRs of the 5141_B17 (PGT-126) antibody have the following sequences per Chothia definition: TGTSNRFVS (SEQ ID NO: 210), GVNKRPS (SEQ ID NO: 211), and SSLVGNWDVI (SEQ ID NO: 212).

[0561] The 5147_N06 (PGT-130) antibody includes a heavy chain variable region (SEQ ID NO: 216), encoded by the nucleic acid sequence shown in SEQ ID NO: 214, and a light chain

variable region (SEQ ID NO: 225) encoded by the nucleic acid sequence shown in SEQ ID NO: 223.

[0562] The heavy chain CDRs of the 5147_N06 (PGT-130) antibody have the following sequences per Kabat definition: TGHYYWG (SEQ ID NO: 217), HIIHYTTAVLHNPSLKS (SEQ ID NO: 218), and SGGDILYYEWWQKPHWFSP (SEQ ID NO: 219). The light chain CDRs of the 5147_N06 (PGT-130) antibody have the following sequences per Kabat definition: NGTSSDIGGWNFVS (SEQ ID NO: 226), EVNKRPS (SEQ ID NO: 227), and SSLFGRWDVV (SEQ ID NO: 228).

[0563] The heavy chain CDRs of the 5147_N06 (PGT-130) antibody have the following sequences per Chothia definition: GESINTGH (SEQ ID NO: 220), HIIHYTTAVL (SEQ ID NO: 221), and SGGDILYYEWWQKPHWFSP (SEQ ID NO: 219). The light chain CDRs of the 5147_N06 (PGT-130) antibody have the following sequences per Chothia definition: NGTSSDIGGWNFVS (SEQ ID NO: 226), EVNKRPS (SEQ ID NO: 227), and SSLFGRWDVV (SEQ ID NO: 228).

[0564] The 5343_B08 (PGT-135) antibody includes a heavy chain variable region (SEQ ID NO: 232), encoded by the nucleic acid sequence shown in SEQ ID NO: 230, and a light chain variable region (SEQ ID NO: 242) encoded by the nucleic acid sequence shown in SEQ ID NO: 239.

[0565] The heavy chain CDRs of the 5343_B08 (PGT-135) antibody have the following sequences per Kabat definition: GGEWGDKDYHWG (SEQ ID NO: 233), SIHWRGTTHYKESLRR (SEQ ID NO: 234), and HRHHDVFMLVPIAGWFDV (SEQ ID NO: 235). The light chain CDRs of the 5343_B08 (PGT-135) antibody have the following sequences per Kabat definition: RASQNINKNLA (SEQ ID NO: 243), ETYSKIA (SEQ ID NO: 244), and QQYEEWPRT (SEQ ID NO: 245).

[0566] The heavy chain CDRs of the 5343_B08 (PGT-135) antibody have the following sequences per Chothia definition: GDSIRGGEWGDKD (SEQ ID NO: 236), SIHWRGTTH (SEQ ID NO: 237), and HRHHDVFMLVPIAGWFDV (SEQ ID NO: 235). The light chain CDRs of the 5343_B08 (PGT-135) antibody have the following sequences per Chothia definition: RASQNINKNLA (SEQ ID NO: 243), ETYSKIA (SEQ ID NO: 244), and QQYEEWPRT (SEQ ID NO: 245).

[0567] The 5344_E16 (PGT-135) antibody includes a heavy chain variable region (SEQ ID NO: 232), encoded by the nucleic acid sequence shown in SEQ ID NO: 230, and a light chain variable region (SEQ ID NO: 242) encoded by the nucleic acid sequence shown in SEQ ID NO: 239.

[0568] The heavy chain CDRs of the 5344_E16 (PGT-135) antibody have the following sequences per Kabat definition: GGEWGDKDYHWG (SEQ ID NO: 233), SIHWRGTTTHYKESLRR (SEQ ID NO: 234), and HRHHDVFMLVPIAGWFDV (SEQ ID NO: 235). The light chain CDRs of the 5344_E16 (PGT-135) antibody have the following sequences per Kabat definition: RASQNINKNLA (SEQ ID NO: 243), ETYSKIA (SEQ ID NO: 244), and QQYEEWPRT (SEQ ID NO: 245).

[0569] The heavy chain CDRs of the 5344_E16 (PGT-135) antibody have the following sequences per Chothia definition: GDSIRGGEWGDKD (SEQ ID NO: 236), SIHWRGTTTH (SEQ ID NO: 237), and HRHHDVFMLVPIAGWFDV (SEQ ID NO: 235). The light chain CDRs of the 5344_E16 (PGT-135) antibody have the following sequences per Chothia definition: RASQNINKNLA (SEQ ID NO: 243), ETYSKIA (SEQ ID NO: 244), and QQYEEWPRT (SEQ ID NO: 245).

[0570] The 5329_C19 (PGT-136) antibody includes a heavy chain variable region (SEQ ID NO: 249), encoded by the nucleic acid sequence shown in SEQ ID NO: 247, and a light chain variable region (SEQ ID NO: 258) encoded by the nucleic acid sequence shown in SEQ ID NO: 256.

[0571] The heavy chain CDRs of the 5329_C19 (PGT-136) antibody have the following sequences per Kabat definition: GTDWGENDFHYG (SEQ ID NO: 250), SIHWRGRTTHYKTSFRS (SEQ ID NO: 251), and HKYHDIFRVVPVAGWFDP (SEQ ID NO: 252). The light chain CDRs of the 5329_C19 (PGT-136) antibody have the following sequences per Kabat definition: RASQNVKNNLA (SEQ ID NO: 259), DASSRAG (SEQ ID NO: 260), and QQYEEWPRT (SEQ ID NO: 245).

[0572] The heavy chain CDRs of the 5329_C19 (PGT-136) antibody have the following sequences per Chothia definition: GGSMRGTDWGEND (SEQ ID NO: 253), SIHWRGRTTH (SEQ ID NO: 254), and HKYHDIFRVVPVAGWFDP (SEQ ID NO: 252). The light chain CDRs of the 5329_C19 (PGT-136) antibody have the following sequences per Chothia definition:

RASQNVKNNLA (SEQ ID NO: 259), DASSRAG (SEQ ID NO: 260), and QQYEEWPRT (SEQ ID NO: 245).

[0573] The 5366_P21 (PGT-136) antibody includes a heavy chain variable region (SEQ ID NO: 249), encoded by the nucleic acid sequence shown in SEQ ID NO: 247, and a light chain variable region (SEQ ID NO: 258) encoded by the nucleic acid sequence shown in SEQ ID NO: 256.

[0574] The heavy chain CDRs of the 5366_P21 (PGT-136) antibody have the following sequences per Kabat definition: GTDWGENDFHYG (SEQ ID NO: 250), SIHWRGRTTHYKTSFRS (SEQ ID NO: 251), and HKYHDIFRVVPVAGWFDP (SEQ ID NO: 252). The light chain CDRs of the 5366_P21 (PGT-136) antibody have the following sequences per Kabat definition: RASQNVKNNLA (SEQ ID NO: 259), DASSRAG (SEQ ID NO: 260), and QQYEEWPRT (SEQ ID NO: 245).

[0575] The heavy chain CDRs of the 5366_P21 (PGT-136) antibody have the following sequences per Chothia definition: GGSMRGTDWGEND (SEQ ID NO: 253), SIHWRGRTTH (SEQ ID NO: 254), and HKYHDIFRVVPVAGWFDP (SEQ ID NO: 252). The light chain CDRs of the 5366_P21 (PGT-136) antibody have the following sequences per Chothia definition: RASQNVKNNLA (SEQ ID NO: 259), DASSRAG (SEQ ID NO: 260), and QQYEEWPRT (SEQ ID NO: 245).

[0576] The 5964_G22 (PGT-141) antibody includes a heavy chain variable region (SEQ ID NO: 276), encoded by the nucleic acid sequence shown in SEQ ID NO: 274, and a light chain variable region (SEQ ID NO: 285) encoded by the nucleic acid sequence shown in SEQ ID NO: 283.

[0577] The heavy chain CDRs of the 5964_G22 (PGT-141) antibody have the following sequences per Kabat definition: KYDVH (SEQ ID NO: 277), WMSHEGDKTESAQRFGK (SEQ ID NO: 278), and GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (SEQ ID NO: 279). The light chain CDRs of the 5964_G22 (PGT-141) antibody have the following sequences per Kabat definition: SSTQSLRHSNGANYLA (SEQ ID NO: 286), LGSQRAS (SEQ ID NO: 287), and MQGLNRPWT (SEQ ID NO: 288).

[0578] The heavy chain CDRs of the 5964_G22 (PGT-141) antibody have the following sequences per Chothia definition: GNTFSK (SEQ ID NO: 280), WMSHEGDKTE (SEQ ID NO: 281), and GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (SEQ ID NO: 279). The light

chain CDRs of the 5964_G22 (PGT-141) antibody have the following sequences per Chothia definition: SSTQSLRHSNGANYLA (SEQ ID NO: 286), LGSQRAS (SEQ ID NO: 287), and MQGLNRPWT (SEQ ID NO: 288).

[0579] The 4993_K13 (PGT-141) antibody includes a heavy chain variable region (SEQ ID NO: 276), encoded by the nucleic acid sequence shown in SEQ ID NO: 290, and a light chain variable region (SEQ ID NO: 285) encoded by the nucleic acid sequence shown in SEQ ID NO: 283.

[0580] The heavy chain CDRs of the 4993_K13 (PGT-141) antibody have the following sequences per Kabat definition: KYDVH (SEQ ID NO: 277), WMSHEGDKTESAQRFKG (SEQ ID NO: 278), and GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (SEQ ID NO: 279). The light chain CDRs of the 4993_K13 (PGT-141) antibody have the following sequences per Kabat definition: SSTQSLRHSNGANYLA (SEQ ID NO: 286), LGSQRAS (SEQ ID NO: 287), and MQGLNRPWT (SEQ ID NO: 288).

[0581] The heavy chain CDRs of the 4993_K13 (PGT-141) antibody have the following sequences per Chothia definition: GNTFSK (SEQ ID NO: 280), WMSHEGDKTE (SEQ ID NO: 281), and GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (SEQ ID NO: 279). The light chain CDRs of the 4993_K13 (PGT-141) antibody have the following sequences per Chothia definition: SSTQSLRHSNGANYLA (SEQ ID NO: 286), LGSQRAS (SEQ ID NO: 287), and MQGLNRPWT (SEQ ID NO: 288).

[0582] The 4995_E20 (PGT-142) antibody includes a heavy chain variable region (SEQ ID NO: 292), encoded by the nucleic acid sequence shown in SEQ ID NO: 315, and a light chain variable region (SEQ ID NO: 285) encoded by the nucleic acid sequence shown in SEQ ID NO: 283.

[0583] The heavy chain CDRs of the 4995_E20 (PGT-142) antibody have the following sequences per Kabat definition: KYDVH (SEQ ID NO: 277), WISHERDKTESAQRFKG (SEQ ID NO: 293), and GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (SEQ ID NO: 279). The light chain CDRs of the 4995_E20 (PGT-142) antibody have the following sequences per Kabat definition: SSTQSLRHSNGANYLA (SEQ ID NO: 286), LGSQRAS (SEQ ID NO: 287), and MQGLNRPWT (SEQ ID NO: 288).

[0584] The heavy chain CDRs of the 4995_E20 (PGT-142) antibody have the following sequences per Chothia definition: GNTFSK (SEQ ID NO: 280), WISHERDKTE (SEQ ID NO:

294), and GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (SEQ ID NO: 279). The light chain CDRs of the 4995_E20 (PGT-142) antibody have the following sequences per Chothia definition: SSTQSLRHSNGANYLA (SEQ ID NO: 286), LGSQRAS (SEQ ID NO: 287), and MQGLNRPWT (SEQ ID NO: 288).

[0585] The 4980_N08 (PGT-143) antibody includes a heavy chain variable region (SEQ ID NO: 298), encoded by the nucleic acid sequence shown in SEQ ID NO: 296, and a light chain variable region (SEQ ID NO: 302) encoded by the nucleic acid sequence shown in SEQ ID NO: 300.

[0586] The heavy chain CDRs of the 4980_N08 (PGT-143) antibody have the following sequences per Kabat definition: KYDVH (SEQ ID NO: 277), WMSHEGDKTESAQRFGK (SEQ ID NO: 278), and GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (SEQ ID NO: 279). The light chain CDRs of the 4980_N08 (PGT-143) antibody have the following sequences per Kabat definition: TSTQSLRHSNGANYLA (SEQ ID NO: 303), LGSQRAS (SEQ ID NO: 287), and MQGLNRPWT (SEQ ID NO: 288).

[0587] The heavy chain CDRs of the 4980_N08 (PGT-143) antibody have the following sequences per Chothia definition: GNTFSK (SEQ ID NO: 280), WMSHEGDKTE (SEQ ID NO: 281), and GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (SEQ ID NO: 279). The light chain CDRs of the 4980_N08 (PGT-143) antibody have the following sequences per Chothia definition: TSTQSLRHSNGANYLA (SEQ ID NO: 303), LGSQRAS (SEQ ID NO: 287), and MQGLNRPWT (SEQ ID NO: 288).

[0588] The 4970_K22 (PGT-144) antibody includes a heavy chain variable region (SEQ ID NO: 307), encoded by the nucleic acid sequence shown in SEQ ID NO: 305, and a light chain variable region (SEQ ID NO: 313) encoded by the nucleic acid sequence shown in SEQ ID NO: 311.

[0589] The heavy chain CDRs of the 4970_K22 (PGT-144) antibody have the following sequences per Kabat definition: KYDVH (SEQ ID NO: 277), WMSHEGDKTESAQRFGK (SEQ ID NO: 278), and GSKHRLRDYVLYDDYGLINQQEWNDYLEFLDV (SEQ ID NO: 308). The light chain CDRs of the 4970_K22 (PGT-144) antibody have the following sequences per Kabat definition: TSTQSLRHSNGANYLA (SEQ ID NO: 303), LGSQRAS (SEQ ID NO: 287), and MQGLNRPWT (SEQ ID NO: 288).

[0590] The heavy chain CDRs of the 4970_K22 (PGT-144) antibody have the following sequences per Chothia definition: GNTFRK (SEQ ID NO: 309), WMSHEGDKTE (SEQ ID NO: 281), and GSKHRLRDYVLYDDYGLINQQEWNDYLEFLDV (SEQ ID NO: 308). The light chain CDRs of the 4970_K22 (PGT-144) antibody have the following sequences per Chothia definition: TSTQSLRHSNGANYLA (SEQ ID NO: 303), LGSQRAS (SEQ ID NO: 287), and MQGLNRPWT (SEQ ID NO: 288).

[0591] The sequences of additional human monoclonal antibodies were determined, including the sequences of the variable regions of the Gamma heavy and Kappa or Lambda light chains. In addition, the sequence of each of the polynucleotides encoding the antibody sequences was determined. Shown below are the polypeptide and polynucleotide sequences of the gamma heavy chains and kappa light chains, with the signal peptides at the N-terminus (or 5' end) and the constant regions at the C-terminus (or 3' end) of the variable regions, which are shown in bolded text.

[0592] 5145_B14 (PGT-127) gamma heavy chain nucleotide sequence: coding sequence (variable region in bold)

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCGGCTCCCAGATGGGTC
 CTGTCCCAGCCGCAGCTGCAGGAGTCGGGCCAGGACTGGTGGAGGC
TTCGGAGACCCTGTCCCTCACGTGCACTGTGTCCGGCGACTCCACTG
GTCGTTGTAATTATTTCTGGGGCTGGGTCCGGCAGCCCCAGGGAAG
GGGCTGGAGTGGATTGGGAGTTTGTCCCACTGTAGAAGTTACTACAA
TACTGACTGGACCTACCACAACCCGTCTCTCAAGAGTCGACTCACTAT
TTCCTCGACACGCCCAAGAATCAGGTCTTCCTGAGATTGACCTCTGT
GACCGCCGCGGACACGGCCACTTATTACTGTGCGCGATTCCGGCGGCG
AAGTTCTAGTGTAACAGAGATTGGCCAAAGCCGGCCTGGGTCCGACCTC
TGGGGCCGGGGAACGCTGGTTCGTCACCGTCTCGAGCGCCTCCACCAA
 GGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGG
 GCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTG
 ACGGTGTCGTGGAATCAGGCGCCCTGACCAGCGCGTGCACACCTTCCC
 GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG
 TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCAC
 AAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTG TG
 ACAAACACTCACACATGCCCACCGTGCCAGCACCTGAACTCCTGGGGGGA
 CCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCC
 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACC
 CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCC
 AAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCA
 GCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG
 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTC
 CAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA

TCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCA
 AAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCA
 GCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCT
 CCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
 GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTA
 CACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 316)

[0593] 5145_B14 (PGT-127) gamma heavy chain variable region nucleotide sequence:

CAGCCGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGGAGGCTTCGGAGA
 CCCTGTCCCTCACGTGCACTGTGTCCGGCGACTCCACTGGTCGTTGTAATT
 ATTTCTGGGGCTGGGTCCGGCAGCCCCCAGGGAAGGGGCTGGAGTGGATT
 GGGAGTTTGTCCCACTGTAGAAGTTACTACAATACTGACTGGACCTACCA
 CAACCCGTCTCTCAAGAGTCGACTCACTATTTCACTCGACACGCCCAAGA
 ATCAGGTCTTCTGAGATTGACCTCTGTGACCGCCGCGGACACGGCCACT
 TATTACTGTGCGCGATTCCGGCGGCGAAGTTCTAGTGTACAGAGATTGGCC
 AAAGCCGGCCTGGGTCGACCTCTGGGGCCGGGGAACGCTGGTCGTCACCG
 TCTCGAGC (SEQ ID NO: 317)

[0594] 5145_B14 (PGT-127) gamma heavy chain amino acid sequence: expressed protein with leader sequence in *italics* and variable region in **bold**.

MKHLWFFLLVAAPRWVLSQPQLQESGPGLVEASETLSLTCTVSGDSTGRC
NYFWGWVRQPPGKGLEWIGSLSHCRSYNTDWTYHNPSLKSRLTISLDT
PKNQVFLRLTSVTAADTATYYCARFGGEVLVYRDWPKPAWVDLWGRG
TLVVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG
 ALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKR
 VEPKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVS
 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
 EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
 GFYPSTDAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV
 FSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 318)

[0595] 5145_B14 (PGT-127) gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in **bold italics**)

QPQLQESGPGLVEASETLSLTCTVSGDSTGRC***NYFWGWVRQPPGKGLEWIGS***
LSHCRSYNTDWTYHNPSLKSRLTISLDT***PKNQVFLRLTSVTAADTATYYCAR***
FGGEVLVYRDWPKPAWVDLWGRGTLVVTVSS (SEQ ID NO: 319)

[0596] 5145_B14 (PGT-127) gamma heavy chain Kabat CDRs:

CDR 1: RCNYFWG (SEQ ID NO: 320)

CDR 2: SLSHCRSYNTDWTYHNPSLKS (SEQ ID NO: 321)

CDR 3: FGGEVLVYRDWPKPAWVDL (SEQ ID NO: 322)

[0597] 5145_B14 (PGT-127) gamma heavy chain Chothia CDRs:

CDR 1: GDSTGRCN (SEQ ID NO: 323)

CDR 2: SLSHCRSYNTDWTY (SEQ ID NO: 324)

CDR 3: FGGEVLVYRDWPKPAWVDL (SEQ ID NO: 322)

[0598] 5145_B14 (PGT-127) lambda light chain nucleotide sequence: coding sequence
(variable region in bold)

ATGGCCTGGGCTCTGCTCCTCCTCACCCTCCTCACTCAGGGCACAGGGGC
CTGGGCCCAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCC
TGGACAGTCAATCACCATCTCCTGCACTGGAACCAGCAATAACTTTGT
CTCCTGGTACCAACAATAACCCAGGCAAGGCCCCCAAAC**TCGTCATTT**
ATGAGGTCAATAAGCGCCCCTCAGGTGTCCCTGATCGTTTCTCTGGC
TCCAAGTCTGGCAGCACGGCCTCCCTGACCGTCTCTGGACTCCAGGC
TGACGATGAGGGTGTCTATTATTGTAGTTCACTTGTAGGCAACTGGG
ATGTGATTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGTCAGCCCA
AGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAG
CCAACAAGGCCCACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCC
GTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGG
AGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAG
CTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCT
GCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCCTAC
AGAATGTTTCATAG (SEQ ID NO:327)

[0599] 5145_B14 (PGT-127) lambda light chain variable region nucleotide sequence:

CAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCCTGGACAGTCA
ATCACCATCTCCTGCACTGGAACCAGCAATAACTTTGTCTCCTGGTACCAA
CAATACCCAGGCAAGGCCCCCAAAC**TCGTCATTTATGAGGTCAATAAGCG**
CCCCTCAGGTGTCCCTGATCGTTTCTCTGGCTCCAAGTCTGGCAGCACGGC
CTCCCTGACCGTCTCTGGACTCCAGGCTGACGATGAGGGTGTCTATTATTG
TAGTTCACTTGTAGGCAACTGGGATGTGATTTTCGGCGGAGGGACCAAGT
TGACCGTCCTA (SEQ ID NO: 328)

[0600] 5145_B14 (PGT-127) lambda light chain amino acid sequence: expressed protein
with leader sequence in italics and variable region in bold.

MAWALLLTLLTQGTGAWAQSALTQPPSASGSPGQSITISCTGTSNNFVSWY
QQYPGKAPKLVIYEVNKRPSGVPDRFSGSKSGSTASLTVSGLQADDEGVY
YCSSLVGNWDVIFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKS
HRSYSCQVTHEGSTVEKTVAPTECS (SEQ ID NO: 329)

[0601] 5145_B14 (PGT-127) lambda light chain variable region amino acid sequence:
(Kabat CDRs underlined, Chothia CDRs in bold italics)

QSALTQPPSASGSPGQSITISC**TGTSNNFVS**WYQQYPGKAPKLVIY**EVNKRPS**
 GVPDRFSGSKSGSTASLTVSGLQADDEGVYYC**SSLVGNWDVI**FGGGTKLTVL
 (SEQ ID NO: 330)

[0602] 5145_B14 (PGT-127) lambda light chain Kabat CDRs:

CDR 1: TGTSNNFVS (SEQ ID NO: 325)

CDR 2: EVNKRPS (SEQ ID NO: 227)

CDR 3: SSLVGNWDVI (SEQ ID NO: 212)

[0603] 5145_B14 (PGT-127) lambda light chain Chothia CDRs:

CDR 1: TGTSNNFVS (SEQ ID NO: 325)

CDR 2: EVNKRPS (SEQ ID NO: 227)

CDR 3: SSLVGNWDVI (SEQ ID NO: 212)

[0604] 5114_A19 (PGT-128) gamma heavy chain nucleotide sequence: coding sequence
 (variable region in bold)

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCGGCTCCCAGATGGGTC
 CTGTCCCAGCCGCAGCTGCAGGAGTCGGGCCCAACACTGGTGGAGGC
TTCGGAGACTCTGTCCCTCACCTGCGCTGTGTCCGGCGACTCCACTG
CTGCATGTAATTCTTTCTGGGGCTGGGTCCGGCAGCCCCAGGGAAG
GGGCTGGAGTGGGTTGGGAGTTTGTCCCATTTGTGCAAGCTATTGGAA
TCGTGGGTGGACCTACCACAACCCGTCTCTCAAGAGTCGGCTCACGC
TTGCTCTCGACACACCCAAGAATCTGGTCTTCCTCAAATTAAATTCTG
TGACTGCCGCGGACACGGCCACTTACTACTGTGCGCGATTCCGGCGGC
GAAGTTTTACGCTACACGGATTGGCCAAAGCCGGCCTGGGTTCGACCT
CTGGGGCCCGGGGAACGCTGGTCACCGTCTCGAGCGCCTCCACCAAGG
 GCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGC
 ACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGAC
 GGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCGG
 CTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGC
 CCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAG
 CCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACA
 AAATCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCG
 TCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG
 ACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
 GGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA
 CAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGT
 CCTACCGTCTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCA
 AGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAA
 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCC
 GGAGGAGATGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGC
 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG
 AGAACAACACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC
 TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGA

ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACG
CAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA(SEQ ID NO: 331)

[0605] 5114_A19 (PGT-128) gamma heavy chain variable region nucleotide sequence:

CAGCCGCAGCTGCAGGAGTCGGGCCCCAACACTGGTGGAGGCTTCGGAGA
CTCTGTCCCTCACCTGCGCTGTGTCCGGCGACTCCACTGCTGCATGTAATT
CTTTCTGGGGCTGGGTCCGGCAGCCCCCAGGGAAGGGGCTGGAGTGGGTT
GGGAGTTTGTCCCATTTGTGCAAGCTATTGGAATCGTGGGTGGACCTACCA
CAACCCGTCTCTCAAGAGTCGGCTCACGCTTGCTCTCGACACACCCAAGA
ATCTGGTCTTCTCAAATTAATTCTGTGACTGCCGCGGACACGGCCACTT
ACTACTGTGCGCGATTTCGGCGGCGAAGTTTTACGCTACACGGATTGGCCA
AAGCCGGCCTGGGTTCGACCTCTGGGGCCGGGGAACGCTGGTCACCGTCTC
GAGC (SEQ ID NO:332)

[0606] 5114_A19 (PGT-128) gamma heavy chain amino acid sequence: expressed protein
with leader sequence in *italics* and variable region in **bold**.

*MKHLWFFLLVAAPRWVLSQPQLQESGPTLVEASET***LSLTC***AVSGDSTAAC*
NSFWGWVRQPPGKGLEWVGSLSHCASYWNRGW*TYHNPSLKSRLTLAL*
DTPKNLVFLKLNSVTAADTATYYCARFGGEVLRYTDWPKPAWVDLWG
RGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNS
GALTS*GVHTFPAVLQSSGLYSLSSV***TV***PSSSLGTQTYICNVNHKPSNTK***V***DK*
*RVEPKSCDKHTHTCP***PC***PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVS*
*HEDPEVKFNWYVDGVEVHNA***TK***PREEQYNSTYRVVSVLTVLHQDWLNGK*
EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
*GFYP***SDIAVEWESNGQPENNYK***TT***PVLDSDGSFFLYSKLTV***DKSRWQQGNV*
*FSCSV***MHEALHNHYTQKSLSLSPGK** (SEQ ID NO: 333)

[0607] 5114_A19 (PGT-128) gamma heavy chain variable region amino acid sequence:
(Kabat CDRs underlined, Chothia CDRs in **bold italics**)

*QPQLQESGPTLVEASET***LSLTC***AVSGDSTAAC****NSFWGWVRQPPGKGLEWVG***
SLSHCASYWNRGW***TYHNPSLKSRLTLALDTPKNLVFLKLNSVTAADTATYYC***
ARFGGEVLRYTDWPKPAWVDL*WG***RGTLVTVSS** (SEQ ID NO: 334)

[0608] 5114_A19 (PGT-128) gamma heavy chain Kabat CDRs:

CDR 1: ACNSFWG (SEQ ID NO: 326)

CDR 2: SLSHCASYWNRGWTYHNPSLKS (SEQ ID NO: 335)

CDR 3: FGGEVLRYTDWPKPAWVDL (SEQ ID NO: 336)

[0609] 5114_A19 (PGT-128) gamma heavy chain Chothia CDRs:

CDR 1: GDSTAACN (SEQ ID NO: 337)

CDR 2: SLSHCASYWNRGWTY (SEQ ID NO: 338)

CDR 3: FGGEVLRYTDWPKPAWVDL (SEQ ID NO: 336)

[0610] 5114_A19 (PGT-128) lambda light chain nucleotide sequence: coding sequence
(variable region in bold)

ATGGCCTGGGCTCTGCTCCTCCTCACCCTCCTCACTCAGGGCACAGGGGC
CTGGGCCCAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCC
TGGACAGTCAATCACCATCTCCTGCACTGGAACCAGCAATAACTTTGT
CTCCTGGTACCAGCAACACGCAGGCAAGGCCCCCAAGCTCGTCATTT
ATGACGTCAATAAGCGCCCCTCAGGTGTCCCTGATCGTTTCTCTGGC
TCCAAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGACTCCAGAC
TGACGATGAGGCTGTCTATTACTGCGGCTCACTTGTAGGCAACTGGG
ATGTGATTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGTCAGCCCA
AGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAG
CCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCC
GTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGG
AGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAG
CTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCT
GCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTAC
AGAATGTTCATAG(SEQ ID NO: 390)

[0611] 5114_A19 (PGT-128) lambda light chain variable region nucleotide sequence:

CAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCCTGGACAGTCA
ATCACCATCTCCTGCACTGGAACCAGCAATAACTTTGTCTCCTGGTACCAG
CAACACGCAGGCAAGGCCCCCAAGCTCGTCATTTATGACGTCAATAAGCG
CCCCCTCAGGTGTCCCTGATCGTTTCTCTGGCTCCAAGTCTGGCAACACGGC
CTCCCTGACCGTCTCTGGACTCCAGACTGACGATGAGGCTGTCTATTACTG
CGGCTCACTTGTAGGCAACTGGGATGTGATTTTCGGCGGAGGGACCAAGT
TGACCGTCCTA(SEQ ID NO: 391)

[0612] 5114_A19 (PGT-128) lambda light chain amino acid sequence: expressed protein
with leader sequence in italics and variable region in bold.

MAWALLLLTLLTQGTGAWAQSALTQPPSASGSPGQSITISCTGTSNNFVSWY
QQHAGKAPKLVIYDVNKRPSGVPDRFSGSKSGNTASLTVSGLQTDDEAV
YYCGSLVGNWDVIFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADSSPVKAGVETTPSKQSNNKYAASSYLSLTPEQWK
SHRSYSCQVTHEGSTVEKTVAPTECS (SEQ ID NO: 392)

[0613] 5114_A19 (PGT-128) lambda light chain variable region amino acid sequence:
(Kabat CDRs underlined, Chothia CDRs in bold italics)

QSALTQPPSASGSPGQSITISCT***TGTSNNFV***SWYQQHAGKAPKLVIY***DVNKRPS***
GVPDRFSGSKSGNTASLTVSGLQTDDEAVYYC***CGSLVGNWDVIF***GGGTKLTVL
(SEQ ID NO: 393)

[0614] 5114_A19 (PGT-128) lambda light chain Kabat CDRs:

CDR 1: TGTSNNFVS (SEQ ID NO: 325)

CDR 2: DVNKRPS (SEQ ID NO: 343)

CDR 3: GSLVGNWDVI (SEQ ID NO: 196)

[0615] 5114_A19 (PGT-128) lambda light chain Chothia CDRs:

CDR 1: TGTSNNFVS (SEQ ID NO: 325)

CDR 2: DVNKRPS (SEQ ID NO: 343)

CDR 3: GSLVGNWDVI (SEQ ID NO: 196)

[0616] 5136_H01 (PGT-131) gamma heavy chain nucleotide sequence: coding sequence
(variable region in bold)

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCGGCTCCCAGATGGGTC
CTTCCCAGGTGCAACTACAGGAGTCGGGCCCAGGACTGGTGAAGCC
TTCGGAGACCCTTTCCTCACCTGCACTGTCTCTGGTGAATCCATCAA
CACTGGTCATCACTACTGGGGCTGGGTCCGTCAGGTCCCAGGGAAGG
GACCGGAATGGATTGCTCACATCCACTATAATACGGCTGTCTTACAC
AATCCGGCCCTCAAGAGTCGAGTCACCATTTCGATTTTCACCCTGAA
GAATCTGATTACCCTGAGCCTCAGTAATGTGACCGCCGCGGACACGG
CCGTCTATTTCTGCGTTCGATCCGGCGGCGACATTTTATACTATATTG
AGTGGCAAAAACCCCACTGGTTCTATCCCTGGGGCCCCGGGAATTTTG
GTCACCGTCTCGAGCGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGG
CACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTG
GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCGC
CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTTACAGTCCTCAGGAC
TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGG
ACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCG
TGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCTTCCCCCA
AAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGT
GGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACG
TGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCA
GTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGG
ACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCT
CCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA
GAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGA
ACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATC
GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCA
CGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCA
CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG
ATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTC
TCCGGGTAAATGA(SEQ ID NO: 344)

[0617] 5136_H01 (PGT-131) gamma heavy chain variable region nucleotide sequence:

CAGGTGCAACTACAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGA
CCCTTTCCTCACCTGCACTGTCTCTGGTGAATCCATCAACACTGGTCATC

ACTACTGGGGCTGGGTCCGTCAGGTCCCAGGGAAGGGACCGGAATGGATT
 GCTCACATCCACTATAATACGGCTGTCTTACACAATCCGGCCCTCAAGAG
 TCGAGTCACCATTTTCGATTTTCACCCTGAAGAATCTGATTACCCTGAGCCT
 CAGTAATGTGACCGCCGCGGACACGGCCGTCTATTTCTGCGTTCGATCCG
 GCGGCGACATTTTATACTATATTGAGTGGCAAAAACCCCACTGGTTCTATC
 CCTGGGGCCCCGGAATTTTGGTCACCGTCTCGAGC(SEQ ID NO: 345)

[0618] 5136_H01 (PGT-131) gamma heavy chain amino acid sequence: expressed protein with leader sequence in *italics* and variable region in **bold**.

*MKHLWFFLLVAAPRWVLSQVQLQESG***PGLVKPSETLSLTCTVSGDSINTGH**
HYWGWVRQVPGKGPEWIAHIHYNTAVLHNPALKSRVTISIFTLKNLITLS
LSNVTAA*DTAVYFCVRS***GGDILYYIEWQKPHW***FYPWGP***GILTVSSASTK**
 GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
 QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCP
 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
 PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES
 NGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHN
 HYTQKSLSLSPGK (SEQ ID NO: 346)

[0619] 5136_H01 (PGT-131) gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in **bold italics**)

*QVQLQESG***PGLVKPSETLSLTCTVSGDSINTGH***HYWGWVRQVPGKGPEWIA*
HIHYNTAVLHNPALKSRVTISIFTLKNLITLS*LSNVTAA****DTAVYFCVRS******GGDIL***
YYIEWOKPHW*FYPWGP***GILTVSS** (SEQ ID NO: 347)

[0620] 5136_H01 (PGT-131) gamma heavy chain Kabat CDRs:

CDR 1: TGHHYWG (SEQ ID NO: 348)

CDR 2: HIHYNTAVLHNPALKS (SEQ ID NO: 349)

CDR 3: SGGDILYYIEWQKPHWFYP (SEQ ID NO: 350)

[0621] 5136_H01 (PGT-131) gamma heavy chain Chothia CDRs:

CDR 1: GDSINTGH (SEQ ID NO: 351)

CDR 2: HIHYNTAVL (SEQ ID NO: 352)

CDR 3: SGGDILYYIEWQKPHWFYP (SEQ ID NO: 350)

[0622] 5136_H01 (PGT-131) lambda light chain nucleotide sequence: coding sequence (variable region in **bold**)

ATGGCCTGGGCTCTGCTCCTCCTCACCCTCCTCACTCAGGGCACAGGGTCC
 TGGGCCCAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCTT
GGACAGTCACTCACCATCTCCTGCAGTGGAACCGGCAGTGACATTGG
CAGTTGGAATTTTGTCTCCTGGTATCAACAATTCCCAGGCAGAGCCC

CCAACCTCATTATTTTTGAGGTCAATAGGCGGCGATCAGGGGTCCCT
 GATCGCTTCTCTGGTTCCAAGTCGGGCAATACGGCCTCCCTGACCGT
 CTCTGGGCTCCGGTCTGAGGATGAGGCTGAATATTTTTGACAGTTCCC
 TTTCAGGCAGGTGGGACATTGTTTTTTGGCGGAGGGACCAAGGTGACC
 GTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTC
 CTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTG
 ACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCC
 GTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAGCAACAACA
 AGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCC
 CACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGA
 AGACAGTGGCCCCTACAGAATGTTTCATAG (SEQ ID NO:353)

[0623] 5136_H01 (PGT-131) lambda light chain variable region nucleotide sequence:

CAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCTTGGACAGTCA
 CTCACCATCTCCTGCAGTGGAACCGGCAGTGACATTGGCAGTTGGAATTT
 TGTCTCCTGGTATCAACAATTCCCAGGCAGAGCCCCCAACCTCATTATTTT
 TGAGGTCAATAGGCGGCGATCAGGGGTCCCTGATCGCTTCTCTGGTTCCA
 AGTCGGGCAATACGGCCTCCCTGACCGTCTCTGGGCTCCGGTCTGAGGAT
 GAGGCTGAATATTTTTGCAGTTCCCTTTCAGGCAGGTGGGACATTGTTTTT
 GGCGGAGGGACCAAGGTGACCGTCCTA (SEQ ID NO:354)

[0624] 5136_H01 (PGT-131) lambda light chain amino acid sequence: expressed protein with leader sequence in italics and variable region in bold.

*MAWALLLLTLLTQGTGSWA***QSALTQPPSASGSLGQSLTISC***SGTGSDIGSWNF*
VSWYQQFPGRAPNLIIFEVNR*RRSGVPDRFSGSKSGNTASLTVSGLRSEDE*
AEYFCSSLSGRWDIVFGGGTKVTVLGQPKAAPS*VTLP***PPSSEELQANKATL**
*VCLISDFYPGAVTVAWKADSSPVKAGVETTT***PSKQSNKYAASSYLSLTPEQ**
WKSHRSYSCQVTHEGSTVEKTVAPTECS (SEQ ID NO: 355)

[0625] 5136_H01 (PGT-131) lambda light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

*QSALTQPPSASGSLGQSLTISC***SGTGSDIGSWNFV***SWYQQFPGRAPNLIIFEV*
RRR*SGVPDRFSGSKSGNTASLTVSGLRSEDEAEYFC***SSLSGRWDIV***FGGGTKV*
TVL (SEQ ID NO: 356)

[0626] 5136_H01 (PGT-131) lambda light chain Kabat CDRs:

CDR 1: SGTGSDIGSWNFVS (SEQ ID NO: 357)

CDR 2: EVNRRRS (SEQ ID NO: 358)

CDR 3: SSLSGRWDIV (SEQ ID NO: 359)

[0627] 5136_H01 (PGT-131) lambda light chain Chothia CDRs:

CDR 1: SGTGSDIGSWNFVS (SEQ ID NO: 357)

CDR 2: EVNRRRS (SEQ ID NO: 358)

CDR 3: SSLSGRWDIV (SEQ ID NO: 359)

[0628] 5345_I01 (PGT-137) gamma heavy chain nucleotide sequence: coding sequence
(variable region in bold)

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTTGCGGCTCCCAGATGTGTC
CTGTCT**GAGGTGCATCTGGAGGAGTCGGGCCCAGGACTGGTGAGGCC**
CTCGGAGACCTTGTCCCTGACTTGACGGCCTCTGGTGGCTCCATAA
GGGGGGGCGAGTGGGGCGATAGTGACTACCACTGGGGCTGGGTCCG
CCACTCTCCCGAAAAGGGACTGGAATGGATTGGAAGTATTCATTGGC
GGGGGACCACCCACTACAACGCGCCCTTCCGGGGGCGAGGCAGATT
GTCGATAGACCTCTCCCGGAATCAATTCTCCCTGCGCCTGACGTCTG
TGACCGCCGAAGACACTGCCGTCTATTATTGTGTGAAGCACAAATAT
CATGACATTGTCATGGTGGTCCCCATTGCGGGCTGGTTCGACCCCTG
GGGCCAGGGACTCCAGGTCACCGTCTCGAGCGCCTCCACCAAGGGCCC
ATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAG
CGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTG
TCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCGGCTGT
CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTC
CAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCA
GCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAAC
TCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTCAG
TCTTCCTCTTCCCCCAAAACCCAAGGACACCTCATGATCTCCCGGACCC
CTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTG
AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAA
AGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCT
CACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAG
GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGC
CAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
GAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCT
TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA
GAACAACCTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCT
TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA
CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC
AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:360)

[0629] 5345_I01 (PGT-137) gamma heavy chain variable region nucleotide sequence:

GAGGTGCATCTGGAGGAGTCGGGCCCAGGACTGGTGAGGCCCTCGGAGA
CCTTGTCCCTGACTTGACGGCCTCTGGTGGCTCCATAAGGGGGGGCGAG
TGGGGCGATAGTGACTACCACTGGGGCTGGGTCCGCCACTCTCCCGAAAA
GGGACTGGAATGGATTGGAAGTATTCATTGGCGGGGGACCACCCACTACA
ACGCGCCCTTCCGGGGGCGAGGCAGATTGTCGATAGACCTCTCCCGGAAT
CAATTCTCCCTGCGCCTGACGTCTGTGACCGCCGAAGACACTGCCGTCTAT
TATTGTGTGAAGCACAAATATCATGACATTGTCATGGTGGTCCCCATTGCG

GGCTGGTTCGACCCCTGGGGCCAGGGACTCCAGGTCACCGTCTCGAGC(SEQ ID NO:361)

[0630] 5345_I01 (PGT-137) gamma heavy chain amino acid sequence: expressed protein with leader sequence in italics and variable region in bold.

*MKHLWFFLLVAA***PRCVLSEVHLEESGPGLVRPSETLSLTCTASGG****SIRGGE**
WGDS**SDYHWGWVRHSPEKGLEWIGSIHWRGTTHYNAPFRGRGRLSIDLS**
RNQFSLRLTSVTAEDTAVYYCVKHKYH**DIVMVVPIAGWFDPWGQGLQV**
TVSS**ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG**
VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS
CDKTH**TCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE**
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPVLDS**DGSFFLYSKLTVDKSRWQQGNV****FSCS**
VMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 362)

[0631] 5345_I01 (PGT-137) gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

EVHLEESGPGLVRPSETLSLTCTASGG**SIRGGE****WGDS****SDYHWGWVRHSPEKGL**
EWIG**SIHWRGTTHYNAPFRGRGRLSIDLSRNQFSLRLTSVTAEDTAVYYCVK**
HKYHDIVMVVPIAGWFDPWGQGLQVTVSS (SEQ ID NO: 363)

[0632] 5345_I01 (PGT-137) gamma heavy chain Kabat CDRs:

CDR 1: GGEWGDSYHWG (SEQ ID NO: 364)

CDR 2: SIHWRGTTHYNAPFRG (SEQ ID NO: 365)

CDR 3: HKYHDIVMVVPIAGWFDP (SEQ ID NO: 366)

[0633] 5345_I01 (PGT-137) gamma heavy chain Chothia CDRs:

CDR 1: GGSIRGGEWGDS (SEQ ID NO: 367)

CDR 2: SIHWRGTTH (SEQ ID NO: 237)

CDR 3: HKYHDIVMVVPIAGWFDP (SEQ ID NO: 366)

[0634] 5345_I01 (PGT-137) kappa light chain nucleotide sequence: coding sequence (variable region in bold)

ATGGAACCCCCAGCTCAGCTTCTCTCCTCCTGCTACTCTGGCTCCCAGAT
 ACTACTGGAGAAATAATGATGACGCAGTCTCCAGCCATCCTGTCTGTG
TCTCCAGGAGACAGAGCCACACTCTCCTGCAGGGCCAGTCAGAGTGT
GAAGAATAATTTAGCCTGGTACCAGAAGAGACCTGGCCAGGCTCCCA
GACTCCTCATCTTTGATACATCCAGCAGGGCCTCTGGTATCCCTGCCA
GGTTCAGTGGCGGTGGTTCTGGGACAGAGTTC**ACTCTC****ACCGTCAAC**
AGCATGCAGTCTGAAGACTTTGCGACTTATTACTGTCAGCAATATGAA
GAGTGGCCTCGGACGTT**CGGCCAGGGGACCAAGGTGGAAATCAAAC**

GTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGT
 TGAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCA
 GAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAA
 CTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGC
 CTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAG
 TCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAG
 AGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO: 394)

[0635] 5345_I01 (PGT-137) kappa light chain variable region nucleotide sequence:

GAAATAATGATGACGCAGTCTCCAGCCATCCTGTCTGTGTCTCCAGGAGA
 CAGAGCCACACTCTCCTGCAGGGCCAGTCAGAGTGTGAAGAATAATTTAG
 CCTGGTACCAGAAGAGACCTGGCCAGGCTCCAGACTCCTCATCTTTGAT
 ACATCCAGCAGGGCCTCTGGTATCCCTGCCAGGTTTCAGTGGCGGTGGTTC
 TGGGACAGAGTTCACTCTCACCGTCAACAGCATGCAGTCTGAAGACTTTG
 CGACTTATTACTGTCAGCAATATGAAGAGTGGCCTCGGACGTTTCGGCCAG
 GGGACCAAGGTGGAAATCAAA (SEQ ID NO: 395)

[0636] 5345_I01 (PGT-137) kappa light chain amino acid sequence: expressed protein with leader sequence in *italics* and variable region in **bold**.

*METPAQLLFLLLLWLPDITGEIMMTQSPAILS***SVSPGDRATLSCRASQSVKNN**
LAWYQKRPGQAPRLLIFDTSSRASGIPARFSGGGSGTEFTLTVNSMQSED
FATYYCQQYEEWPRTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVV
CLLNNFYYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKAD
YEKHKVYACEVTHQGLSPVTKSFNRGEC (SEQ ID NO: 396)

[0637] 5345_I01 (PGT-137) kappa light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in **bold italics**)

EIMMTQSPAILSVPDRATLSCR**RASQSVKNNLA**WYQKRPGQAPRLLIF**DTSS**
RASGIPARFSGGGSGTEFTLTVNSMQSEDFATYYC**QQYEEWPRT**FGQGTKVEI
 K (SEQ ID NO: 397)

[0638] 5345_I01 (PGT-137) kappa light chain Kabat CDRs:

CDR 1: RASQSVKNNLA (SEQ ID NO: 372)

CDR 2: DTSSRAS (SEQ ID NO: 373)

CDR 3: QQYEEWPRT (SEQ ID NO: 245)

[0639] 5345_I01 (PGT-137) kappa light chain Chothia CDRs:

CDR 1: RASQSVKNNLA (SEQ ID NO: 372)

CDR 2: DTSSRAS (SEQ ID NO: 373)

CDR 3: QQYEEWPRT (SEQ ID NO: 245)

[0640] 4995_P16 (PGT-145) gamma heavy chain nucleotide sequence: coding sequence
(variable region in bold)

ATGGACTGGATTTGGAGGATCCTCTTCTTGGTGGCAGCAGCTACAAGTGC
CCACTCCCAGGTGCAGTTGGTGCAGTCTGGGGCTGAAGTGAAGAAGC
CTGGGTCTCAGTGAAGGTCTCCTGCAAGGCCTCTGGAAACAGTTTC
AGTAATCATGATGTCCACTGGGTACGACAGGCCACTGGACAGGGGCT
TGAATGGATGGGATGGATGAGTCATGAGGGTGATAAGACAGGCTTGG
CACAAAAGTTTCAGGGCAGAGTCACCATCACGAGGGGACAGTGGCGCA
AGTACAGTCTACATGGAGTTGCGCGGCCTGACAGCTGACGACACGGC
CATTTATTATTGTTTGACCGGCTCAAAACATCGCCTGCGAGATTATTT
TCTGTACAATGAATATGGCCCCAATTATGAAGAGTGGGGTGACTACC
TTGCGACTTTGGACGTCTGGGGCCATGGGACCGCGGTACCGTCTCG
AGCGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAA
GAGCACCTCTGGGGGCACAGCGGCCCTGGGGCTGCCTGGTCAAGGACTACT
TCCCCGAACCGGTGACGGTGTCGTGGAACCTCAGGCGCCCTGACCAGCGGC
GTGCACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG
CAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAG
CCCAAATCTTGTGACAAACTCACACATGCCACCGTGCCAGCACCTGA
ACTCCTGGGGGGACCGTCAGTCTTCTTCTTCCCCCAAAACCCAAGGACA
CCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTG
AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
AGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAC
GTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG
GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATC
GAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
ACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTACGCCT
GACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
AGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCT
GGACTCCGACGGCTCCTTCTTCTTCTATAGCAAGCTCACCGTGGACAAGA
GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT
CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATG
A (SEQ ID NO: 398)

[0641] 4995_P16 (PGT-145) gamma heavy chain variable region nucleotide sequence:

CAGGTGCAGTTGGTGCAGTCTGGGGCTGAAGTGAAGAAGCCTGGGTCTC
AGTGAAGGTCTCCTGCAAGGCCTCTGGAAACAGTTTCAGTAATCATGATG
TCCACTGGGTACGACAGGCCACTGGACAGGGGCTTGAATGGATGGGATG
GATGAGTCATGAGGGTGATAAGACAGGCTTGGCACAAAAGTTTCAGGGC
AGAGTCACCATCACGAGGGACAGTGGCGCAAGTACAGTCTACATGGAGTT
GCGCGGCCTGACAGCTGACGACACGGCCATTTATTATTGTTTGACCGGCT
CAAAACATCGCCTGCGAGATTATTTCTGTACAATGAATATGGCCCCAATT
ATGAAGAGTGGGGTGACTACCTTGGGACTTTGGACGTCTGGGGCCATGGG
ACCGCGGTACCGTCTCGAGC (SEQ ID NO:399)

[0642] 4995_P16 (PGT-145) gamma heavy chain amino acid sequence: expressed protein with leader sequence in italics and variable region in bold.

*MDWIWRILFLVAAATSAHSQVQLVQSGAEVKKPGSSVKVSC*KASGNSFSNH
DVHWVRQATGQGLEWMGWMSHEGDKTGLAQKFQGRVTITRDSGAST
VYME LRGLTADDTAIYYCLTGSKHRLRDYFLYNEYGPNYEEWGDYLAT
LDVWGHGTA VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN
TKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC
VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQV
SLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR
WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 400)

[0643] 4995_P16 (PGT-145) gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

QVQLVQSGAEVKKPGSSVKVSCKASGNSFSNHDVHWVRQATGQGLEWMG
WMSHEGDKTGLAQKFQGRVTITRDSGASTVYME LRGLTADDTAIYYCLTG
SKHRLRDYFLYNEYGPNYEEWGDYLATLDVWGHGTA VTVSS (SEQ ID NO: 401)

[0644] 4995_P16 (PGT-145) gamma heavy chain Kabat CDRs:

CDR 1: NHDVH (SEQ ID NO: 378)

CDR 2: WMSHEGDKTGLAQKFQG (SEQ ID NO: 379)

CDR 3: GSKHRLRDYFLYNEYGPNYEEWGDYLATLDV (SEQ ID NO: 380)

[0645] 4995_P16 (PGT-145) gamma heavy chain Chothia CDRs:

CDR 1: GNSFSN (SEQ ID NO: 381)

CDR 2: WMSHEGDKTG (SEQ ID NO: 382)

CDR 3: GSKHRLRDYFLYNEYGPNYEEWGDYLATLDV (SEQ ID NO: 380)

[0646] 4995_P16 (PGT-145) kappa light chain nucleotide sequence: coding sequence (variable region in bold)

ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGGTCTCTGGA
TCCGGTGCGGAGGTTGTCATAACTCAGTCTCCACTCTTCCTGCCCGTC
ACCCCTGGAGAGGCGGCCTCCTTGCTTGCAAGTGCAGCCACAGCCT
CCAACATTCAACTGGAGCCAACTATTTGGCTTGGTACCTGCAGAGAC
CAGGGCAAACCTCCACGCCTGTTGATCCATTTGGCCACTCATCGGGCC
TCCGGGGTCCCTGACAGATTCAGTGGCAGTGGATCAGGCACAGATTT
TACACTTAAAATCAGTCGAGTGGAGTCTGACGATGTTGGAACCTTATTA
TTGCATGCAGGGTCTGCACAGTCCCTGGACGTTCCGGCCAAGGGACCA
AGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCG
CCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTG

AATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACG
 CCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAA
 GGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGAC
 TACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGA
 GCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID
 NO:383)

[0647] 4995_P16 (PGT-145) kappa light chain variable region nucleotide sequence:

GAGGTTGTCATAACTCAGTCTCCACTCTTCCTGCCCGTCACCCCTGGAGAG
 GCGGCCTCCTTGTCTTGCAAGTGCAGCCACAGCCTCCAACATTCAACTGG
 AGCCAACTATTTGGCTTGGTACCTGCAGAGACCAGGGCAAACCTCCACGCC
 TGTGATCCATTTGGCCACTCATCGGGCCTCCGGGGTCCCTGACAGATTCA
 GTGGCAGTGGATCAGGCACAGATTTTACACTTAAAATCAGTCGAGTGGAG
 TCTGACGATGTTGGAACCTTATTATTGCATGCAGGGTCTGCACAGTCCCTGG
 ACGTTCGGCCAAGGGACCAAGGTGGAGATCAAA (SEQ ID NO:384)

[0648] 4995_P16 (PGT-145) kappa light chain amino acid sequence: expressed protein with
 leader sequence in italics and variable region in bold.

*MRLPAQLLGLLMLWVSGSGAEVVITQSPLFLPVT***PGEAASLSCKCSHSLQHS**
TGANYLAWYLQRPQT**PRLLIHLATHRASGV****PDRFSGSGSGTDFTLKISR**
VESDDVGTY**YCMQGLHSPWTF****GQGTKVEIKRTVAAPSVFIFPPSDEQLKS**
 GTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLST
 LTLSKADYEEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 385)

[0649] 4995_P16 (PGT-145) kappa light chain variable region amino acid sequence: (Kabat
 CDRs underlined, Chothia CDRs in bold italics)

EVVITQSPLFLPVT**PGEAASLSCK*****KCSHSLQHST******TGANYLAWYLQRPQT*****PRLLI**
HLATHRASGV**PDRFSGSGSGTDFTLKISR****VESDDVGTY****YCMQGLHSPWTF****GQ**
 GTKVEIK (SEQ ID NO: 386)

[0650] 4995_P16 (PGT-145) kappa lambda light chain Kabat CDRs:

CDR 1: KCSHSLQHSTGANYLA (SEQ ID NO: 387)

CDR 2: LATHRAS (SEQ ID NO: 388)

CDR 3: MQGLHSPWT (SEQ ID NO: 389)

[0651] 4995_P16 (PGT-145) kappa light chain Chothia CDRs:

CDR 1: KCSHSLQHSTGANYLA (SEQ ID NO: 387)

CDR 2: LATHRAS (SEQ ID NO: 388)

CDR 3: MQGLHSPWT (SEQ ID NO: 389)

[0652] The 5145_B14 (PGT-127) antibody includes a heavy chain variable region (SEQ ID
 NO: 319), encoded by the nucleic acid sequence shown in SEQ ID NO: 317, and a light chain

variable region (SEQ ID NO: 330) encoded by the nucleic acid sequence shown in SEQ ID NO: 328.

[0653] The heavy chain CDRs of the 5145_B14 (PGT-127) antibody have the following sequences per Kabat definition: RCNYFWG (SEQ ID NO: 320), SLSHCRSYYNTDWTYHNPSLKS (SEQ ID NO: 321), and FGGEVLVYRDWPKPAWVDL (SEQ ID NO: 322). The light chain CDRs of the 5145_B14 (PGT-127) antibody have the following sequences per Kabat definition: TGTSNNFVS (SEQ ID NO: 325), EVNKRPS (SEQ ID NO: 227), and SSLVGNWDVI (SEQ ID NO: 212).

[0654] The heavy chain CDRs of the 5145_B14 (PGT-127) antibody have the following sequences per Chothia definition: GDSTGRCN (SEQ ID NO: 323), SLSHCRSYYNTDWTY (SEQ ID NO: 324), and FGGEVLVYRDWPKPAWVDL (SEQ ID NO: 322). The light chain CDRs of the 5145_B14 (PGT-127) antibody have the following sequences per Chothia definition: TGTSNNFVS (SEQ ID NO: 325), EVNKRPS (SEQ ID NO: 227), and SSLVGNWDVI (SEQ ID NO: 212).

[0655] The 5114_A19 (PGT-128) antibody includes a heavy chain variable region (SEQ ID NO: 334), encoded by the nucleic acid sequence shown in SEQ ID NO: 332, and a light chain variable region (SEQ ID NO: 393) encoded by the nucleic acid sequence shown in SEQ ID NO: 391.

[0656] The heavy chain CDRs of the 5114_A19 (PGT-128) antibody have the following sequences per Kabat definition: ACNSFWG (SEQ ID NO: 326), SLSHCASYWNRGWTYHNPSLKS (SEQ ID NO: 335), and FGGEVLRYTDWPKPAWVDL (SEQ ID NO: 336). The light chain CDRs of the 5114_A19 (PGT-128) antibody have the following sequences per Kabat definition: TGTSNNFVS (SEQ ID NO: 325), DVNKRPS (SEQ ID NO: 343), GSLVGNWDVI (SEQ ID NO: 196).

[0657] The heavy chain CDRs of the 5114_A19 (PGT-128) antibody have the following sequences per Chothia definition: GDSTAACN (SEQ ID NO: 337), SLSHCASYWNRGWTY (SEQ ID NO: 338), FGGEVLRYTDWPKPAWVDL (SEQ ID NO: 336)

[0658] . The light chain CDRs of the 5114_A19 (PGT-128) antibody have the following sequences per Chothia definition: TGTSNNFVS (SEQ ID NO: 325), DVNKRPS (SEQ ID NO: 343), GSLVGNWDVI (SEQ ID NO: 196).

[0659] The 5136_H01 (PGT-131) antibody includes a heavy chain variable region (SEQ ID NO: 347), encoded by the nucleic acid sequence shown in SEQ ID NO: 345, and a light chain variable region (SEQ ID NO: 356) encoded by the nucleic acid sequence shown in SEQ ID NO: 354.

[0660] The heavy chain CDRs of the 5136_H01 (PGT-131) antibody have the following sequences per Kabat definition: TGHHYWG (SEQ ID NO: 348), HIHYNTAVLHNPALKS (SEQ ID NO: 349), and SGGDILYYIEWQKPHWFYP (SEQ ID NO: 350). The light chain CDRs of the 5136_H01 (PGT-131) antibody have the following sequences per Kabat definition: SGTGSDIGSWNFVS (SEQ ID NO: 357), EVNRRRS (SEQ ID NO: 358), and SSLSGRWDIV (SEQ ID NO: 359).

[0661] The heavy chain CDRs of the 5136_H01 (PGT-131) antibody have the following sequences per Chothia definition: GDSINTGH (SEQ ID NO: 351), HIHYNTAVL (SEQ ID NO: 352), and SGGDILYYIEWQKPHWFYP (SEQ ID NO: 350). The light chain CDRs of the 5136_H01 (PGT-131) antibody have the following sequences per Chothia definition: SGTGSDIGSWNFVS (SEQ ID NO: 357), EVNRRRS (SEQ ID NO: 358), and SSLSGRWDIV (SEQ ID NO: 359).

[0662] The 5345_I01 (PGT-137) antibody includes a heavy chain variable region (SEQ ID NO: 363), encoded by the nucleic acid sequence shown in SEQ ID NO: 361, and a light chain variable region (SEQ ID NO: 397) encoded by the nucleic acid sequence shown in SEQ ID NO: 395.

[0663] The heavy chain CDRs of the 5345_I01 (PGT-137) antibody have the following sequences per Kabat definition: GGEWGDSYHWG (SEQ ID NO: 364), SIHWRGTTTHYNAPFRG (SEQ ID NO: 365), and HKYHDIVMVPPIAGWFDP (SEQ ID NO: 366). The light chain CDRs of the 5345_I01 (PGT-137) antibody have the following sequences per Kabat definition: RASQSVKNNLA (SEQ ID NO: 372), DTSSRAS (SEQ ID NO: 373), and QQYEEWPRT (SEQ ID NO: 245).

[0664] The heavy chain CDRs of the 5345_I01 (PGT-137) antibody have the following sequences per Chothia definition: GGSIRGGEWGDS (SEQ ID NO: 367), SIHWRGTTTH (SEQ ID NO: 237), and HKYHDIVMVPPIAGWFDP (SEQ ID NO: 366). The light chain CDRs of the 5345_I01 (PGT-137) antibody have the following sequences per Chothia definition:

RASQSVKNNLA (SEQ ID NO: 372), DTSSRAS (SEQ ID NO: 373), and QQYEEWPRT (SEQ ID NO: 245).

[0665] The 4995_P16 (PGT-145) antibody includes a heavy chain variable region (SEQ ID NO: 401), encoded by the nucleic acid sequence shown in SEQ ID NO: 399, and a light chain variable region (SEQ ID NO: 386) encoded by the nucleic acid sequence shown in SEQ ID NO: 384.

[0666] The heavy chain CDRs of the 4995_P16 (PGT-145) antibody have the following sequences per Kabat definition: NHDVH (SEQ ID NO: 378), WMSHEGDKTG LAQKFQG (SEQ ID NO: 379), and GSKHRLRDYFLYNEYGP NYEEWGDY LATLDV (SEQ ID NO: 380). The light chain CDRs of the 4995_P16 (PGT-145) antibody have the following sequences per Kabat definition: KCSHSLQHSTGANYLA (SEQ ID NO: 387), LATHRAS (SEQ ID NO: 388), and MQGLHSPWT (SEQ ID NO: 389).

[0667] The heavy chain CDRs of the 4995_P16 (PGT-145) antibody have the following sequences per Chothia definition: GNSFSN (SEQ ID NO: 381), WMSHEGDKTG (SEQ ID NO: 382), and GSKHRLRDYFLYNEYGP NYEEWGDY LATLDV (SEQ ID NO: 380). The light chain CDRs of the 4995_P16 (PGT-145) antibody have the following sequences per Chothia definition: KCSHSLQHSTGANYLA (SEQ ID NO: 387), LATHRAS (SEQ ID NO: 388), and MQGLHSPWT (SEQ ID NO: 389).

[0668] The sequences of additional human monoclonal antibodies were determined, including the sequences of the variable regions of the Gamma heavy and Kappa or Lambda light chains. In addition, the sequence of each of the polynucleotides encoding the antibody sequences was determined. Shown below are the polypeptide and polynucleotide sequences of the gamma heavy chains and kappa light chains, with the signal peptides at the N-terminus (or 5' end) and the constant regions at the C-terminus (or 3' end) of the variable regions, which are shown in bolded text.

[0669] 4835_F12 (PGT-124) gamma heavy chain nucleotide sequence: coding sequence (leader sequence in italics, variable region in bold)

ATGAAACACCTGTGGTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTCCT
ATCCCAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAGACCTT
CGGAGACCCTGTCCGTCACCTGCATCGTCTCTGGGGGCTCCATCAGC
AATTACTACTGGACTTGGATCCGACAGTCCCCAGGAAAGGGACTGGA
GTGGATAGGCTATATTTCTGACAGAGAAACAACGACTTACAATCCCT
CCCTCAACAGTCGAGCCGTCATATCACGAGACACGTCGAAAAACCAA

TTGTCCCTACAATTACGTTCCGTCACCACTGCGGACACGGCCATCTAT
 TTCTGTGCGACAGCGCGCCGAGGACAGAGGATTTATGGAGTGGTTTC
 ATTTGGAGAGTTCTTCTACTACTACTACATGGACGTCTGGGGCAAAG
 GGA CTGCGGTACCGTCTCCTCAGCGTCGACCAAGGGCCCATCGGTCTT
 CCCTCTGGCACCATCATCCAAGTCGACCTCTGGGGGCACAGCGGCCCTGG
 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGAAC
 TCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTC
 CTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCT
 TGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
 AAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACAT
 GCCCACCCTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTC
 TTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGT
 CACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA
 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCG
 GGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCC
 TGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAA
 CAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGG
 CAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGAT
 GACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA
 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAATA
 CAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAG
 CAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA
 TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCT
 CTCCTGTCTCCGGGTAAATGA (SEQ ID NO: 402)

[0670] 4835_F12 (PGT-124) gamma heavy chain variable region nucleotide sequence:

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAGACCTTCGG
 AGACCCTGTCCGTCACCTGCATCGTCTCTGGGGGCTCCATCAGCAAT
 TACTACTGGACTTGGATCCGACAGTCCCCAGGAAAGGGACTGGAGTG
 GATAGGCTATATTTCTGACAGAGAAACAACGACTTACAATCCCTCCCT
 CAACAGTCGAGCCGTCATATCACGAGACACGTCGAAAAACCAATTGT
 CCCTACAATTACGTTCCGTCACCACTGCGGACACGGCCATCTATTTCT
 GTGCGACAGCGCGCCGAGGACAGAGGATTTATGGAGTGGTTTTCATTT
 GGAGAGTTCTTCTACTACTACTACATGGACGTCTGGGGCAAAGGGAC
 TGCGGTACCGTCTCCTCA (SEQ ID NO: 403)

[0671] 4835_F12 (PGT-124) gamma heavy chain amino acid sequence: expressed protein
 with leader sequence in italics and variable region in bold.

*MKHLWFFLLLVAA*PRWVLSQVQLQESGPGLVRPSETLSVTCIVSGGSISNYY
WTWIRQSPGKGLEWIGYISDRETTTYNPSLNSRAVISRDTSKNQLSLQLR
SVTTADTAIYFCATARRGQRIYGVVSFGEFFYYYYMDVWGKGTAVTVSS
 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
 PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKT
 HTPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
 WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN

KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVH
EALHNHYTQKSLSLSPGK (SEQ ID NO: 404)

[0672] 4835_F12 (PGT-124) gamma heavy chain variable region amino acid sequence:
(Kabat CDRs underlined, Chothia CDRs in bold italics)

QVQLQESGPGLVRPSETLSVTCIVS***GG***SIS***NYYWT***WIRQSPGKGLEWIG***YISD***
RETTTYNPSLNSRAVISRDTSKNQSLQLRSVTTADTAIFYCAT***ARRG***QRIY***G***
VVSFGEFFYYYYMDVWGKGTA VTVSS (SEQ ID NO: 405)

[0673] 4835_F12 (PGT-124) gamma heavy chain Kabat CDRs:

CDR 1: NYYWT (SEQ ID NO: 406)

CDR 2: YISDRETTTYNPSLNS (SEQ ID NO: 407)

CDR 3: ARRQRIYGVVSFGEFFYYYYMDV (SEQ ID NO: 408)

[0674] 4835_F12 (PGT-124) gamma heavy chain Chothia CDRs:

CDR 1: GGSISN (SEQ ID NO: 409)

CDR 2: YISDRETTT (SEQ ID NO: 410)

CDR 3: ARRQRIYGVVSFGEFFYYYYMDV (SEQ ID NO: 408)

[0675] 4835_F12 (PGT-124) light chain nucleotide sequence: coding sequence (variable
region in bold)

ATGGCCTGGATCCCTCTCCTCCTCGGCCTCCTCTCTCACTGCACAGGGTCTGT
GACGTCCCTATGTGAGCCCACTGTCAGTGGCCCTGGGGGAGACGGCCA
GGATTTCTGTGGACGACAGGCCCTTGGAAGTAGAGCTGTGCAGTGG
TATCAACATAAGCCAGGCCAGGCCCTATTTTGCTCATCTATAATAAT
CAAGACCGGCCCTCAGGGATCCCTGAGCGGTCTCTGGCACCCCTGA
TATTAATTTTGGGACCACGGCCACCCTGACTATCAGCGGGGTCTGAAG
TCGGGGATGAAGCCGACTATTACTGTACATGTGGGACTCTAGAAGT
GGTTTCAGTTGGTCTTTTCGGCGGGGCGACCAGGCTGACCGTCCTAGG
TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCTCGCCCTCCTCTGAGGA
GCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACC
CGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGC
GGGAGTGGAGACCACCACACCTCCAAACAAGCAACAACAAGTACGCG
GCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAAGTCCCACAAA
GCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGT
GCCCTTACAGAATGTTTCATAG (SEQ ID NO: 411)

[0676] 4835_F12 (PGT-124) light chain variable region nucleotide sequence:

TCCTATGTGAGCCCACTGTCAGTGGCCCTGGGGGAGACGGCCAGGAT
TTCCTGTGGACGACAGGCCCTTGGAAGTAGAGCTGTGCAGTGGTATC
AACATAAGCCAGGCCAGGCCCTATTTTGCTCATCTATAATAATCAAG

ACCGGCCCTCAGGGATCCCTGAGCGGTTCTCTGGCACCCCTGATATT
 AATTTTGGGACCACGGCCACCCTGACTATCAGCGGGGTGGAAGTCGG
 GGATGAAGCCGACTATTACTGTACATGTGGGACTCTAGAAGTGGTT
 TCAGTTGGTCTTTCGGCGGGGCGACCAGGCTGACCGTCCTA (SEQ ID
 NO: 412)

[0677] 4835_F12 (PGT-124) light chain amino acid sequence: expressed protein with leader
 sequence in italics and variable region in bold.

MAWIPLLLGLLSHCTGSVTSYVSPLSVALGETARISCGRQALGSRAVQWYQ
HKPGQAPILLIYNNQDRPSGIPERFSGTPDINFGTTATLTISGVEVGDEAD
YYCHMWDSRSGFSWSFGGATRLTVLGQPKAAPSVTLFPPSSEELQANKAT
LVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNKYAASSYLSLTPE
QWKSHKSYSCQVTHEGSTVEKTVAPTECS (SEQ ID NO: 413)

[0678] 4835_F12 (PGT-124) light chain variable region amino acid sequence: (Kabat CDRs
 underlined, Chothia CDRs in bold italics)

SYVSPLSVALGETARISC**GRQALGSRAVQ**WYQHKGPGAPILLIY**NNQDRPSGI**
 PERFSGTPDINFGTTATLTISGVEVGDEADYYC**HMWDSRSGFSWSF**GGATRL
 TVL (SEQ ID NO: 414)

[0679] 4835_F12 (PGT-124) light chain Kabat CDRs:

CDR 1: GRQALGSRAVQ (SEQ ID NO: 415)

CDR 2: NNQDRPS (SEQ ID NO: 151)

CDR 3: HMWDSRSGFSWS (SEQ ID NO: 416)

[0680] 4835_F12 (PGT-124) light chain Chothia CDRs:

CDR 1: GRQALGSRAVQ (SEQ ID NO: 415)

CDR 2: NNQDRPS (SEQ ID NO: 151)

CDR 3: HMWDSRSGFSWS (SEQ ID NO: 416)

[0681] 4869_K15 (PGT-133) gamma heavy chain nucleotide sequence: coding sequence
 (variable region in bold)

ATGAAACACCTGTGGTTCTTCCTTCTCCTGGTGGCAGCTCCCAGATGGGTTCGT
*GTCC*CAGGTGCATCTGCAAGAGTCGGGGCCAGGACTGGTGACGCCTT
 CGGAAACCCTGTCCCTCACTTGCACTGTGTCTGAATGGCTCCGTCAGT
 GGTCTGCTTCTGGAGCTGGATCCGGCAGTCCCCAGGGAGAGGACTGG
 AATGGATCGGTTATTTTTCTGACACTGACAGGTCTGAATATAATCCTT
 CTCTCAGGAGTCGACTCACCTTATCAGTAGATAGATCTAAGAACCAG
 TTGTCCCTGAGATTGAAGTCCGTGACCGCTGCGGATTTCGGCCACTTA
 TTACTGTGCGAGAGCACAGCAGGGGAAGAGGATCTATGGAATAGTGT
 CTTTCGGAGAGTTCTTCTATTATTATTACATGGACGCCTGGGGCAAAG
 GGACTCCGGTCACCGTCTCCTCAGCGTCGACCAAGGGCCCATCGGTCTT

CCCTCTGGCACCATCATCCAAGTCGACCTCTGGGGGCACAGCGGCCCTGG
 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAAC
 TCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTC
 CTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCT
 TGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
 AAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACAT
 GCCCACCCTGCCAGCACCTGAACTCCTGGGGGGGACCGTCAGTCTTCCTC
 TCCCCCCTAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGT
 CACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA
 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCG
 GGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCC
 TGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAA
 CAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGG
 CAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGAT
 GACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA
 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAATA
 CAAGACCACGCCTCCCGTGTCTGGACTCCGACGGCTCCTTCTTCTCTATAG
 CAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA
 TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCT
 CTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 417)

[0682] 4869_K15 (PGT-133) gamma heavy chain variable region nucleotide sequence:

CAGGTGCATCTGCAAGAGTCGGGGCCAGGACTGGTGACGCCTTCGG
 AAACCCTGTCCCTCACTTGCAGTGTGTGCAATGGCTCCGTCACTGGT
 CGCTTCTGGAGCTGGATCCGGCAGTCCCCAGGGAGAGGACTGGAAT
 GGATCGGTTATTTTTCTGACACTGACAGGTCTGAATATAATCCTTCTC
 TCAGGAGTCGACTCACCTTATCAGTAGATAGATCTAAGAACCAGTTG
 TCCCTGAGATTGAAGTCCGTGACCGCTGCGGATTGCGCCACTTATTA
 CTGTGCGAGAGCACAGCAGGGGAAGAGGATCTATGGAATAGTGTCTT
 TCGGAGAGTTCTTCTATTATTATTACATGGACGCCTGGGGCAAAGGG
 ACTCCGGTCACCGTCTCCTCA (SEQ ID NO: 418)

[0683] 4869_K15 (PGT-133) gamma heavy chain amino acid sequence: expressed protein with leader sequence in italics and variable region in bold.

*MKHLWFFLLVAA*PRWVVS**QVHLQESG**PGLVTPSETLSLTCTVSNGSVSGRF
 WSWIRQSPGRGLEWIGYFSDTDRSEYNPSLRSRLT**LSVDRSKNQLSLRLK**
 SVTAADSATYYC**ARAQQGKRIY**GIVSFGEFFYYYMDAWGKGTPVTVSS
 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSQVHTF
 PAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCKT
 HTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
 WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN
 KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
 VEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFPSCSVMH
 EALHNHYTQKSLSLSPGK (SEQ ID NO: 419)

[0684] 4869_K15 (PGT-133) gamma heavy chain variable region amino acid sequence:
(Kabat CDRs underlined, Chothia CDRs in bold italics)

QVHLQESGPGLVTPSETLSLTCTVS***NGSVSGR******FW******SWIR******QSPGR******GLEWIG******YFSD***
TDRSEYNPSLRSRLT***LSVDRSKNQLSLRLKSV******TAADSATYYCAR******AOOGKRIY***
GIVSFGEFFYYYYMDAWGKGTPVTVSS (SEQ ID NO: 420)

[0685] 4869_K15 (PGT-133) gamma heavy chain Kabat CDRs:

CDR 1: GRFWS (SEQ ID NO: 421)

CDR 2: YFSDTDRSEYNPSLRS (SEQ ID NO: 422)

CDR 3: AQQ GKRIY GIVSFGEFFYYYYMDA (SEQ ID NO: 423)

[0686] 4869_K15 (PGT-133) gamma heavy chain Chothia CDRs:

CDR 1: NGSVSG (SEQ ID NO: 424)

CDR 2: YFSDTDRSE (SEQ ID NO: 425)

CDR 3: AQQ GKRIY GIVSFGEFFYYYYMDA (SEQ ID NO: 423)

[0687] 4869_K15 (PGT-133) light chain nucleotide sequence: coding sequence (variable region in bold)

ATGGCCTGGATCCCTCTCCTCCTCGGCCTCCTCTCTCACTGCACAGGTTCTGA
CACTTCGTTAAACCCACTGTCTGCTGGCCCCAGGAGCGACGGCCAAAA
TTCCCTGCGGAGAAAGGAGCCGTGGAAGTAGGGCTGTCCAGTGGTAT
CAGCAGAAGCCAGGCCAGGCCCCACATTGATCATTATAATAATCA
AGACCGGCCCGCAGGGGTCTCTGAACGATTTTCTGGCAATCCTGACG
TCGCTATTGGGGTGACGGCCACCCTGACCATCAGTCGGGTCTGAAGTC
GGGGATGAGGCCGACTATTATTGTCACTATTGGGACAGTAGAAGTCC
CATCAGCTGGATTTTTCGGCGGAGGGACCCAGCTGACCGTCTCTGGGTCT
AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGC
TTCAAGCCAACAAGGCCCACTGGTGTGTCTCATAAGTGACTTCTACCCG
GGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGG
GAGTGGAGACCACCAACCCCTCCAAACAAGCAACAACAAGTACGCGGC
CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAAAAGCT
ACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGC
CCCTACAGAATGTTTCATAG(SEQ ID NO: 426)

[0688] 4869_K15 (PGT-133) light chain variable region nucleotide sequence:

TCGTTAAACCCACTGTCTGCTGGCCCCAGGAGCGACGGCCAAAATTCC
CTGCGGAGAAAGGAGCCGTGGAAGTAGGGCTGTCCAGTGGTATCAG
CAGAAGCCAGGCCAGGCCCCACATTGATCATTATAATAATCAAGA
CCGGCCCCGAGGGGTCTCTGAACGATTTTCTGGCAATCCTGACGTCTG
CTATTGGGGTGACGGCCACCCTGACCATCAGTCGGGTCTGAAGTCTGGG
GATGAGGCCGACTATTATTGTCACTATTGGGACAGTAGAAGTCCCAT

CAGCTGGATTTTCGGCGGAGGGACCCAGCTGACCGTCCTG(SEQ ID NO: 427)

[0689] 4869_K15 (PGT-133) light chain amino acid sequence: expressed protein with leader sequence in italics and variable region in bold.

*MAWIPLLGLLSHCTGSDTSLNPLSLAPGATAKIPCGERSRGSRAVQWYQQ
KPGQAPTLIIYNNQDRPAGVSEFSGNPDVAIGVTATLTISRVEVGDEADY
YCHYWDSRSPISWIFGGGTQLTVLGQPKAAPSVTLFPPSSEELQANKATLV
CLISDFYPGAVTVAWKADSSPVKAGVETTPSKQSNNKYAASSYLSLTPEQW
KSHKSYSCQVTHEGSTVEKTVAPTECS* (SEQ ID NO: 428)

[0690] 4869_K15 (PGT-133) light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

*SLNPLSLAPGATAKIPCGERSRGSRAVQWYQQKPGQAPTLIIYNNQDRPAGVS
ERFSGNPDVAIGVTATLTISRVEVGDEADYYCHYWDSRSPISWIFGGGTQLTV
L* (SEQ ID NO: 429)

[0691] 4869_K15 (PGT-133) light chain Kabat CDRs:

CDR 1: GERSRGSRAVQ (SEQ ID NO: 430)

CDR 2: NNQDRPA (SEQ ID NO: 179)

CDR 3: HYWDSRSPISWI (SEQ ID NO: 431)

[0692] 4869_K15 (PGT-133) light chain Chothia CDRs:

CDR 1: GERSRGSRAVQ (SEQ ID NO: 430)

CDR 2: NNQDRPA (SEQ ID NO: 179)

CDR 3: HYWDSRSPISWI (SEQ ID NO: 431)

[0693] 4876_M06 (PGT-134) gamma heavy chain nucleotide sequence: coding sequence (variable region in bold)

*ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTCGT
GTCCCAGGTGCATCTGCAAGAGTCGGGGCCAGGACTGGTGACGCCTT
CGGAAACCCTGTCCCTCACTTGCACTGTGTCGAATGGCTCCGTCAGT
GGTCGCTTCTGGAGCTGGATCCGGCAGTCCCCAGGGAGAGGACTGG
AATGGATCGGTTATTTTTCTGACACTGACAGGTCTGAATATAATCCTT
CTCTCAGGAGTCGACTCACCTTATCAGTCGATAGATCCAAGAACCAG
TTGTCCCTAAAATTGAAGTCCGTGACCGCTGCGGATTTCGGCCACTTA
TACTGTGCGAGAGCACAAACAGGGGAAGAGGATCTATGGAATAGTGT
CTTTCGGAGAGTTGTTCTATTATTACATGGACGCCTGGGGCAA
GGGACTCCGGTCACCGTCTCCTCAGCGTCGACCAAGGGCCCATCGGTC
TTCCCTCTGGCACCATCATCCAAGTCGACCTCTGGGGGCACAGCGGCCCT
GGGCTGCCTGGTCAAGGACTACTCCCCGAACCGGTGACGGTGTCGTGGA
ACTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCGGCTGTCTACAG*

TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAG
 CTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACA
 CCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAACTCACAC
 ATGCCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCC
 TCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTT
 CAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG
 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGT
 CCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCC
 AACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAG
 GGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA
 GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATC
 CCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAA
 CTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTA
 TAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC
 TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAG
 CCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 432)

[0694] 4876_M06 (PGT-134) gamma heavy chain variable region nucleotide sequence:

CAGGTGCATCTGCAAGAGTCGGGGCCAGGACTGGTGACGCCTTCGG
AAACCCTGTCCCTCACTTGCACGTGTGTGCAATGGCTCCGTCAAGTGGT
CGTTCTTGAGCTGGATCCGGCAGTCCCCAGGGAGAGGACTGGAAT
GGATCGGTTATTTTTCTGACACTGACAGGTCTGAATATAATCCTTCTC
TCAGGAGTCGACTCACCTTATCAGTCGATAGATCCAAGAACCAGTTG
TCCCTAAATTGAAGTCCGTGACCGCTGCGGATTCCGGCCACTTATTA
CTGTGCGAGAGCACAAACAGGGGAAGAGGATCTATGGAATAGTGTCTT
TCGGAGAGTTGTTCTATTATTATTACATGGACGCCTGGGGCAAAGGG
ACTCCGGTCACCGTCTCCTCA (SEQ ID NO: 433)

[0695] 4876_M06 (PGT-134) gamma heavy chain amino acid sequence: expressed protein with leader sequence in italics and variable region in bold.

*MKHLWFFLLVAA***PRWVVSQVHLQESGPGLVTPSETLSLTCTVSNGSVSGRF**
WSWIRQSPGRGLEWIGYFSDTDRSEYNPSLRSRLT**SVDRSKNQLSLKLK**
SVTAADSATYYCARAQQKRIYGIVSFGELFY**YYMDAWGKGTPVTVSS**
*ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT***SVNSGALTSGVHTF**
*PAVLQSSGLYSLSSV***TVPS****SLGTQTYICNVNHKPSNTKVDKRVEPKSCDKT**
HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN
KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
*VEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNV***FSCSVMH**
EALHNHYTQKSLSLSPGK (SEQ ID NO: 434)

[0696] 4876_M06 (PGT-134) gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

QVHLQESGPGLVTPSETLSLTCTVSNGSVSGRFWSWIRQSPGRGLEWIGYFSD
TDRSEYNPSLRSRLTSLVDRSKNQLSLKLKSVTAADSATYYCARAQOGKRIY
GIVSFGELFYYYMDAWGKGTPVTVSS (SEQ ID NO: 435)

[0697] 4876_M06 (PGT-134) gamma heavy chain Kabat CDRs:

CDR 1: GRFWS (SEQ ID NO: 421)

CDR 2: YFSDTDRSEYNPSLRS (SEQ ID NO: 422)

CDR 3: AQQ GKRIYGIVSFGELFYYYMDA (SEQ ID NO: 436)

[0698] 4876_M06 (PGT-134) gamma heavy chain Chothia CDRs:

CDR 1: NGSVSG (SEQ ID NO: 424)

CDR 2: YFSDTDRSE (SEQ ID NO: 425)

CDR 3: AQQ GKRIYGIVSFGELFYYYMDA (SEQ ID NO: 436)

[0699] 4876_M06 (PGT-134) light chain nucleotide sequence: coding sequence (variable region in bold)

ATGGCCTGGATCCCTCTCCTCCTCGGCCTCCTCTCTCACTGCACAGGTTCTGA
CAC7TCGTAAACCCACTGTCTGCTGGCCCCGGGAGCGACGGCCAAAA
TTCCTGCGGAGAAAGGAGCCGTGGAAGTAGGGCTGTCCAGTGGTAT
CAGCAGAAGCCAGGCCAGGCCCCACATTGATCATTATAATAATCA
AGACCGGCCCGCAGGGGTCTCTGAACGATTTTCTGGCAATCCTGACG
TCGCTATTGGGGTGACGGCCACCCTGACCATCAGTCGGGTCGAAGTC
GGGGATGAGGGCGACTATTATTGTCACTATTGGGACAGTAGAAGTCC
CATCAGCTGGATTTTCGCCGGAGGGACCCAGTTGACCGTCCTGGGTC
AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGC
TTCAAGCCAACAAGGCCCACTGGTGTGTCTCATAAGTGACTTCTACCCG
GGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGG
GAGTGGAGACCACACACCCTCCAAACAAAGCAACAACAAGTACGCGGC
CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCACAAAAGCT
ACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGC
CCCTACAGAATGTTCATAG (SEQ ID NO: 437)

[0700] 4876_M06 (PGT-134) light chain variable region nucleotide sequence:

TCGTAAACCCACTGTCTGCTGGCCCCGGGAGCGACGGCCAAAATTCC
CTGCGGAGAAAGGAGCCGTGGAAGTAGGGCTGTCCAGTGGTATCAG
CAGAAGCCAGGCCAGGCCCCACATTGATCATTATAATAATCAAGA
CCGGCCCCGAGGGGTCTCTGAACGATTTTCTGGCAATCCTGACGTCG
CTATTGGGGTGACGGCCACCCTGACCATCAGTCGGGTCGAAGTCCCAT
GATGAGGGCGACTATTATTGTCACTATTGGGACAGTAGAAGTCCCAT
CAGCTGGATTTTCGCCGGAGGGACCCAGTTGACCGTCCTG (SEQ ID
NO: 438)

[0701] 4876_M06 (PGT-134) light chain amino acid sequence: expressed protein with leader sequence in *italics* and variable region in **bold**.

*MAWIPLLLGLLSHCTGSDTSLNPLSLAPGATAKIPCGERSRGSRAVQWYQQ
KPGQAPTLIIYNNQDRPAGVSERFSGNPDVAIGVTATLTISRVEVGDEGDY
YCHYWDSRSPISWIFAGGTQLTVLGQPKAAPSVTLFPPSSEELQANKATLV
CLISDFYPGAVTVAWKADSSPVKAGVETTPSKQSNNKYAASSYLSLTPEQW
KSHKSYSCQVTHEGSTVEKTVAPTECS* (SEQ ID NO: 439)

[0702] 4876_M06 (PGT-134) light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in **bold italics**)

SLNPLSLAPGATAKIPCG**ERSRGSRAVQ**WYQQKPGQAPTLIIY**NNQDRPAGVS**
ERFSGNPDVAIGVTATLTISRVEVGDEGDY**YCHYWDSRSPISWIFAGGTQLTV**
L (SEQ ID NO: 440)

[0703] 4876_M06 (PGT-134) light chain Kabat CDRs:

CDR 1: GERSRGSRAVQ (SEQ ID NO: 430)

CDR 2: NNQDRPA (SEQ ID NO: 179)

CDR 3: HYWDSRSPISWI (SEQ ID NO: 431)

[0704] 4876_M06 (PGT-134) light chain Chothia CDRs:

CDR 1: GERSRGSRAVQ (SEQ ID NO: 430)

CDR 2: NNQDRPA (SEQ ID NO: 179)

CDR 3: HYWDSRSPISWI (SEQ ID NO: 431)

[0705] 5131_A17 (PGT-132) gamma heavy chain nucleotide sequence: coding sequence (variable region in **bold**)

*ATGAAACACCTGTGGTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTCCT
TTCCCAGGTGCAACTACAGGAGTCGGGCCCAGGACTGGTGAAGCCTT
CGGAGACCCTTTCCCTCACCTGCACTGTCTCTGGTGACTCCATCAACA
CTGGTCATCACTACTGGGGCTGGGTCCGTCAGGTCCCAGGGAAGGGA
CCGGAATGGATTGCTCACATCCACTATAATACGGCTGTCTTGACAAAT
CCGGCCCTCAAGAGTCGAGTCACCATTTCGATTTTCACCCTGAAGAA
TCTGATTACCCTGAGGCTCAGTAATATGACCGCCGCGGACACGGCCG
TCTATTTCTGCGTTCGATCCGGCGGCGACATTTTATACTATAATGAGT
GGCAAAAACCCCACTGGTTCTATCCCTGGGGCCCGGGAATTTGGTC
ACCGTCTCGAGCGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACC
CTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCA
AGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAAGTCAAGGCGCCCTG
ACCAGCGGCGTGACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTA
CTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGA
CCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAA
GAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCC*

CAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCAAAA
 CCAAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGT
 GGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGG
 ACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTA
 CAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACT
 GGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCC
 AGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAA
 CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACC
 AGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC
 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCG
 TGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATG
 CATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCC
 GGGTAAATGA (SEQ ID NO: 441)

[0706] 5131_A17 (PGT-132) gamma heavy chain variable region nucleotide sequence:

CAGGTGCAACTACAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGG
 AGACCCTTCCCTCACCTGCACTGTCTCTGGTGACTCCATCAACTG
 GTCATCACTACTGGGGCTGGGTCCGTCAGGTCCCAGGGAAGGGACC
 GGAATGGATTGCTCACATCCACTATAATACGGCTGTCTTGACAATCC
 GGCCCTCAAGAGTCGAGTCACCATTTTCGATTTTCACCCTGAAGAATCT
 GATTACCCTGAGGCTCAGTAATATGACCGCCGCGGACACGGCCGTCT
 ATTTCTGCGTTCGATCCGGCGGCGACATTTTATACTATAATGAGTGGC
 AAAAACCCCACTGGTTCTATCCCTGGGGCCCAGGAATTTTGGTCACC
 GTCTCGAGC (SEQ ID NO: 442)

[0707] 5131_A17 (PGT-132) gamma heavy chain amino acid sequence: expressed protein with leader sequence in *italics* and variable region in **bold**.

*MKHLWFFLLVAAPRWVLSQVQLQESG***PGLVKPSETLSLTCTVSGDSINTGH**
HYWGWVRQVPGKGPEWIA*HIHYNTAVLHNPALKSRVTISIFTLKNLITL*
*RLSNMTAADTAVYFCVRS***GGDILYYNEWQKPHWFYPWGP***GILVTVSSAS*
TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHT
CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL
PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEAL
HNHYTQKSLSLSPGK (SEQ ID NO: 443)

[0708] 5131_A17 (PGT-132) gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in **bold italics**)

*QVQLQESG***PGLVKPSETLSLTCTVSGDS*****INTGHHYWGWVRQVPGKGPEWIA***
HIHYNTAVLHNPALKSRVTISIFTLKNLITLRLSNMTAADTAVYFCVRS***GGDIL***
YYNEWQKPHWFYPWGP*GILVTVSS* (SEQ ID NO: 444)

[0709] 5131_A17 (PGT-132) gamma heavy chain Kabat CDRs:

CDR 1: TGHYWG (SEQ ID NO: 348)

CDR 2: HIHYNTAVLHNPALKS (SEQ ID NO: 349)

CDR 3: SGGDILYYNEWQKPHWFYP (SEQ ID NO: 445)

[0710] 5131_A17 (PGT-132) gamma heavy chain Chothia CDRs:

CDR 1: GDSINTGH (SEQ ID NO: 351)

CDR 2: HIHYNTAVL (SEQ ID NO: 352)

CDR 3: SGGDILYYNEWQKPHWFYP (SEQ ID NO: 445)

[0711] 5131_A17 (PGT-132) light chain nucleotide sequence: coding sequence (variable region in bold)

*ATGGCCTGGGCTCTGCTCCTCCTCACCCTCCTCACTCAGGGCACAGGGTCCTG
GGCCAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCTTG
GACAGTCACTCACCATCTCCTGCAGTGGAACCGCCAGTGACATTGGC
AGTTGGAATTTTGTCTCCTGGTATCAACAATTCCCAGGCAGAGCCCC
CAACCTCATTATTTTGTAGGTCAATAGGCGGCGATCAGGGGTCCCTG
ATCGCTTCTCTGGTTCCAAGTCGGGCAATACGGCCTCCCTGACCGTC
TCTGGGCTCCGGTCTGAGGATGAGGCTGAATATTTTGCAGTTCCCT
TTCAGGCAGGTGGGACATTGTTTTTGGCGGAGGGACCAAGGTGACCG
TCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCT
CTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGAC
TTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGT
CAAGGCGGGAGTGGAGACCACACACCTCCAAACAAAGCAACAACAAG
TACGCGGCCAGCAGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCA
CAAAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAG
ACAGTGGCCCCTACAGAATGTTTCATAG(SEQ ID NO: 446)*

[0712] 5131_A17 (PGT-132) light chain variable region nucleotide sequence:

*CAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCTTGGACA
GTCACTCACCATCTCCTGCAGTGGAACCGCCAGTGACATTGGCAGTT
GGAATTTTGTCTCCTGGTATCAACAATTCCCAGGCAGAGCCCCCAAC
CTCATTATTTTGTAGGTCAATAGGCGGCGATCAGGGGTCCCTGATCG
CTTCTCTGGTTCCAAGTCGGGCAATACGGCCTCCCTGACCGTCTCTG
GGCTCCGGTCTGAGGATGAGGCTGAATATTTTGCAGTTCCCTTTCA
GGCAGGTGGGACATTGTTTTTGGCGGAGGGACCAAGGTGACCGTCCT
A(SEQ ID NO: 447)*

[0713] 5131_A17 (PGT-132) light chain amino acid sequence: expressed protein with leader sequence in italics and variable region in bold.

*MAWALLLLTLLTQGTGSWAQSALTQPPSASGSLGQSLTISCSGTASDIGSWNF
VSWYQQFPGRAPNLIIFEVNRRRSGVPDRFSGSKSGNTASLTVSGLRSEDE*

AEYFCSSLSGRWDIVFGGGTKVTVLGQPKAAPSVTLFPPSSEELQANKATL
VCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQ
WKSHKSYSCQVTHEGSTVEKTVAPTECS (SEQ ID NO: 448)

[0714] 5131_A17 (PGT-132) light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

QSALTQPPSASGSLGQSLTISC***SGTASDIGSWNFVSWYQQFPGRAPNLIIF******EVN***
RRRSGVPDRFSGSKSGNTASLTVSGLRSEDEAEYFC***SSLSGRWDIV***FGGGTKV
TVL (SEQ ID NO: 449)

[0715] 5131_A17 (PGT-132) light chain Kabat CDRs:

CDR 1: SGTASDIGSWNFVS (SEQ ID NO: 450)

CDR 2: EVNRRRS (SEQ ID NO: 358)

CDR 3: SLSGRWDIV (SEQ ID NO: 359)

[0716] 5131_A17 (PGT-132) light chain Chothia CDRs:

CDR 1: SGTASDIGSWNFVS (SEQ ID NO: 450)

CDR 2: EVNRRRS (SEQ ID NO: 358)

CDR 3: SLSGRWDIV (SEQ ID NO: 359)

[0717] 5138_G07 (PGT-138) gamma heavy chain nucleotide sequence: coding sequence (variable region in bold)

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTCCT
GTCCCAGCCGCGAGCTGCAGGAGTCGGGGCCAGGACTGGTGGAGGCTT
CGGAGACCCTGTCCCTCACCTGCACTGTGTCCGGCGACTCCACTGCT
GCTTGTGACTATTTCTGGGGCTGGGTCCGGCAGCCCCCAGGGAAGGG
GCTGGAGTGGATTGGAAGTTTGTACATTGTGCAGGTTACTACAATA
GTGGCTGGACCTACCACAACCCGTCTCTCAAGAGTCGACTCACGATT
TCACTCGACACGCCCAAGAATCAGGTCTTCCTGAAGTTAAATTCTGTG
ACCGCCGCGGACACGGCCATTTACTACTGTGCGCGATTTCGGTGGCGA
CGTTTTGGTGTACCACGATTGGCCAAAGCCGGCCTGGGTCGACCTCT
GGGGCCGGGGAGTTTTGGTCACCGTCTCGAGCGCCTCCACCAAGGGC
CCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCAC
AGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG
TGTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCT
GTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC
CTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC
CCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAA
AACTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGT
CAGTCTTCCTCTTCCCCCAAACCCAAAGGACACCCTCATGATCTCCCGGA
CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAG
GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGAC
AAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC

CTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA
GGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
CCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
GAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCT
TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA
GAACAATAACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCT
TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA
CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC
AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 451)

[0718] 5138_G07 (PGT-138) gamma heavy chain variable region nucleotide sequence:

CAGCCGCAGCTGCAGGAGTCGGGGCCAGGACTGGTGGAGGCTTCGG
AGACCCTGTCCCTCACCTGCACTGTGTCCGGCGACTCCACTGCTGCT
TGTGACTATTTCTGGGGCTGGGTCCGGCAGCCCCCAGGGAAGGGGCT
GGAGTGGATTGGAAGTTTGTACATTGTGCAGGTTACTACAATAGTG
GCTGGACCTACCACAACCCGTCTCTCAAGAGTCGACTCACGATTTC
CTCGACACGCCCAAGAATCAGGTCTTCCTGAAGTTAAATTCTGTGAC
CGCCGCGGACACGGCCATTTACTACTGTGCGCGATTCCGTGGCGACG
TTTGGTGTACCACGATTGGCCAAAGCCGGCCTGGGTGCACCTCTGG
GGCCGGGGAGTTTGGTCAACCGTCTCGAGC (SEQ ID NO: 452)

[0719] 5138_G07 (PGT-138) gamma heavy chain amino acid sequence: expressed protein with leader sequence in italics and variable region in bold.

MKHLWFFLLVAAPRWVLSQPQLQESGPGGLVEASETLSLTCTVSGDSTAAC
DYFWGWVRQPPGKGLEWIGSLSHCAGYYNSGWTYHNPSLKSRLTISLD
TPKNQVFLKLNSVTAADTAIYYCARFGGDVLVYHDWPKPAWVDLWGR
GVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG
ALTSQVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKR
VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNV
FSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 453)

[0720] 5138_G07 (PGT-138) gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

QPQLQESGPGGLVEASETLSLTCTVSGDSTAAC***CDYFWGWVRQPPGKGLEWIGS***
LSHCAGYYNSGWTYHNPSLKSRLTISLDTPKNQVFLKLNSVTAADTAIYYCAR
FGGDVLVYHDWPKPAWVDLWGRGVLVTVSS (SEQ ID NO: 454)

[0721] 5138_G07 (PGT-138) gamma heavy chain Kabat CDRs:

CDR 1: ACDYFWG (SEQ ID NO: 201)

CDR 2: SLSHCAGYYNSGWTYHNPSLKS (SEQ ID NO: 455)

CDR 3: FGGDVLVYHDWPKPAWVDL (SEQ ID NO: 456)

[0722] 5138_G07 (PGT-138) gamma heavy chain Chothia CDRs:

CDR 1: GDSTAACD (SEQ ID NO: 204)

CDR 2: SLSHCAGYYNSGWTY (SEQ ID NO: 457)

CDR 3: FGGDVLVYHDWPKPAWVDL (SEQ ID NO: 456)

[0723] 5138_G07 (PGT-138) light chain nucleotide sequence: coding sequence (variable region in bold)

*ATGGCCTGGGCTCTGCTCCTCCTCACCCTCCTCACTCAGGGCACAGGGGCCT
GGGCCCAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCCT
GGACAGTCAATCACCATCTCCTGCACTGGAAATATCAATAACTTTGTCT
TCCTGGTACCAACAACACCCTGGCAAGGCCCCCAAACCTCGTCATTTA
TGGGGTCAATAAGCGCCCCTCAGGTGTCCCTGATCGTTTTTCTGGCT
CCAAGTCTGGCAACGCGGCCTCCCTGACCGTCTCTGGACTCCAGACT
GACGATGAGGCTGTCTATTACTGCGGCTCACTTGCAGGCAACTGGGA
TGTGGTTTTTCGGCGGAGGGACCAAGTTGACTGTCCTGGGTCAGCCCAT
GGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGC
CAACAAGGCCACACTGGTGTGTCTCATAAGTGAAGTCTTACCCGGGAGCCG
TGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGA
GACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGC
TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAAAAGCTACAGCTG
CCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCCTACA
GAATGTTCATAG*(SEQ ID NO: 581)

[0724] 5138_G07 (PGT-138) light chain variable region nucleotide sequence:

*CAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCCTGGACA
GTCAATCACCATCTCCTGCACTGGAAATATCAATAACTTTGTCTCCTG
GTACCAACAACACCCTGGCAAGGCCCCCAAACCTCGTCATTTATGGGG
TCAATAAGCGCCCCTCAGGTGTCCCTGATCGTTTTTCTGGCTCCAAGT
CTGGCAACGCGGCCTCCCTGACCGTCTCTGGACTCCAGACTGACGAT
GAGGCTGTCTATTACTGCGGCTCACTTGCAGGCAACTGGGATGTGGT
TTTCGGCGGAGGGACCAAGTTGACTGTCCTG*(SEQ ID NO: 582)

[0725] 5138_G07 (PGT-138) light chain amino acid sequence: expressed protein with leader sequence in italics and variable region in bold.

*MAWALLLLTLLTQGTGAWAQSALTQPPSASGSPGQSITISCTGNINNFVSWY
QQHPGKAPKLVIYGVNKRPSGVPRFSGSKSGNAASLTVSGLQTDDEAV
YYCGSLAGNWDVVFGGGTKLTVLGQPMAPSVTLPSPSSEELQANKATLV
CLISDFYPGAVTVAWKADSSPVKAGVETTPSKQSNNKYAASSYLSLTPEQW
KSHKSYSCQVTHEGSTVEKTVAPTECS* (SEQ ID NO: 583)

[0726] 5138_G07 (PGT-138) light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

QSALTQPPSASGSPGQSITISCT**TGNINNFV**SWYQQHPGKAPKLVIY**GVNKRPS**
GVPDRFSGSKSGNAASLTVSGLQTDDEAVYYC**GSLAGNWDVV**FGGGTKLTV
L (SEQ ID NO: 584)

[0727] 5138_G07 (PGT-138) light chain Kabat CDRs:

CDR 1: TGNINNFVS (SEQ ID NO: 458)

CDR 2: GVNKRPS (SEQ ID NO: 211)

CDR 3: GSLAGNWDVV (SEQ ID NO: 459)

[0728] 5138_G07 (PGT-138) light chain Chothia CDRs:

CDR 1: TGNINNFVS (SEQ ID NO: 458)

CDR 2: GVNKRPS (SEQ ID NO: 211)

CDR 3: GSLAGNWDVV (SEQ ID NO: 459)

[0729] 5120_N10 (PGT-139) gamma heavy chain nucleotide sequence: coding sequence (variable region in bold)

ATGAAACACCTGTGGTTCTTCCTGCTGGTGGCAGCTCCAGATGGGTCCT
GTCCCAGCCGCAGCTGCAGGAGTCGGGGCCAGGACTGGTGGAGGCTT
CGGAGACCCTGTCCCTCACCTGCACTGTGTCCGGCGACTCCACTGCT
GGTTGTGACTATTTCTGGGGCTGGGTCCGGCAGCCCCCAGGGAAGG
GGCTGGAGTGGATTGGGGGTTTGTACATTGTGCAGGTTACTACAAT
ACTGGCTGGACCTACCACAACCCGTCTCTCAAGAGTCGACTCACGAT
TTCCTCGACACGCCCAAGAATCAGGTCTTCCTGAAGTTAAATTCTGT
GACCGCCGCGGACACGGCCATTTACTACTGTGCGCGATTTCGACGGCG
AAGTTTTGGTGTACAACGATTGGCCAAAGCCGGCCTGGGTTCGACCTC
TGGGGCCGGGGAACTTTGGTCAACCGTCTCGAGCGCCTCCACCAAGGG
CCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCA
CAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACG
GTGTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGC
TGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC
CTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC
CCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAA
AACTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGGACCGT
CAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA
CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAG
GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGAC
AAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
CTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA
GGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
CCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
GAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCT

TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA
 GAACAACATAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCT
 TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA
 CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC
 AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 460)

[0730] 5120_N10 (PGT-139) gamma heavy chain variable region nucleotide sequence:

CAGCCGCAGCTGCAGGAGTCGGGGCCAGGACTGGTGGAGGCTTCGG
AGACCCTGTCCCTCACCTGCACTGTGTCCGGCGACTCCACTGCTGGT
TGTGACTATTTCTGGGGCTGGGTCCGGCAGCCCCCAGGGAAGGGGCT
GGAGTGGATTGGGGGTTTGTACATTGTGCAGGTACTACAATACTG
GCTGGACCTACCACAACCCGTCTCTCAAGAGTCGACTCACGATTTC
CTCGACACGCCCAAGAATCAGGTCTTCCTGAAGTTAAATTCTGTGAC
CGCCGCGGACACGGCCATTTACTACTGTGCGCGATTTCGACGGCGAAG
TTTTGGTGTACAACGATTGGCCAAAGCCGGCCTGGGTTCGACCTCTGG
GGCCGGGGAACTTTGGTCACCGTCTCGAGC (SEQ ID NO: 461)

[0731] 5120_N10 (PGT-139) gamma heavy chain amino acid sequence: expressed protein with leader sequence in italics and variable region in bold.

MKHLWFFLLVAAPRWVLSQPQLQESGPGLVEASETSLTCTVSGDSTAGC
DYFWGWVRQPPGKGLEWIGLSHCAGYYNTGWTYHNPSLKSRLTISLD
TPKNQVFLKLNSVTAADTAIYYCARFDGEVLVYNDWPKPAWVDLWGRG
TLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL
TSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVKRVE
PKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
CSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 462)

[0732] 5120_N10 (PGT-139) gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

QPQLQESGPGLVEASETSLTCTVSGDSTAGCDYFWGWVRQPPGKGLEWIG
GLSHCAGYYNTGWTYHNPSLKSRLTISLDTPKNQVFLKLNSVTAADTAIYYC
ARFDGEVLVYNDWPKPAWVDLWGRGTLVTVSS (SEQ ID NO: 463)

[0733] 5120_N10 (PGT-139) gamma heavy chain Kabat CDRs:

CDR 1: GCDYFWG (SEQ ID NO: 464)

CDR 2: GLSHCAGYYNTGWTYHNPSLKS (SEQ ID NO: 202)

CDR 3: FDGEVLVYNDWPKPAWVDL (SEQ ID NO: 465)

[0734] 5120_N10 (PGT-139) gamma heavy chain Chothia CDRs:

CDR 1: GDSTAGCD (SEQ ID NO: 466)

CDR 2: GLSHCAGYYNTGWTY (SEQ ID NO: 205)

CDR 3: FDGEVLVYNDWPKPAWVDL (SEQ ID NO: 465)

[0735] 5120_N10 (PGT-139) light chain nucleotide sequence: coding sequence (variable region in bold)

*ATGGCCTGGGCTCTGCTCCTCCTCACCTCCTCACTCAGGGCACAGGGGCCT
GGGCCCAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCCT
GGACAGTCAATCACCATCTCCTGCACTGGAACCAGCAATAACTTTGT
CTCCTGGTACCAGCAACACCCAGCCAAGGCCCCCAAACCTCGTCATTT
ATGGGGTCAATAAGCGCCCCTCAGGTGTCCCTGATCGTTTTTCTGGC
TCCAAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGACTCCAGAC
TGACGATGAGGCTGTCTATTACTGCGGCTCACTTGTAAGGCAACTGGG
ATGTGATTTTCGGCGGAGGGACCAAGTTGACCGTCCTGGGTCAGCCC
ATGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAA
GCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGC
CGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTG
GAGACCACACACCTCCAAACAAGCAACAACAAGTACGCGGCCAGCA
GCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCAAAAAGCTACAGC
TGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCCTA
CAGAATGTTTCATAG*(SEQ ID NO: 467)

[0736] 5120_N10 (PGT-139) light chain variable region nucleotide sequence:

*CAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCCTGGACA
GTCAATCACCATCTCCTGCACTGGAACCAGCAATAACTTTGTCTCCTG
GTACCAGCAACACCCAGCCAAGGCCCCCAAACCTCGTCATTTATGGGG
TCAATAAGCGCCCCTCAGGTGTCCCTGATCGTTTTTCTGGCTCCAAGT
CTGGCAACACGGCCTCCCTGACCGTCTCTGGACTCCAGACTGACGAT
GAGGCTGTCTATTACTGCGGCTCACTTGTAAGGCAACTGGGATGTGAT
TTTCGGCGGAGGGACCAAGTTGACCGTCCTG*(SEQ ID NO: 468)

[0737] 5120_N10 (PGT-139) light chain amino acid sequence: expressed protein with leader sequence in italics and variable region in bold.

*MAWALLLLTLLTQGTGAWAQSAITQPPSASGSPGQSITISCTGTSNNFVSWY
QQHPAKAPKLVIYGVNKRPSGVPDRFSGSKSGNTASLTVSGLQTDDEAV
YYCGSLVGNWDVIFGGGTKLTVLGQPMAPSVTLFPPSSEELQANKATLV
CLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQW
KSHKSYSCQVTHEGSTVEKTVAPTECS* (SEQ ID NO: 469)

[0738] 5120_N10 (PGT-139) light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

*QSALTQPPSASGSPGQSITISCT****GTTSNNFVSWY****QQHPAKAPKLVIY****GVNKRPS***
*GVPDRFSGSKSGNTASLTVSGLQTDDEAVYYC****GSLVGNWDVI****IFGGGTKLTVL*
(SEQ ID NO: 470)

[0739] 5120_N10 (PGT-139) light chain Kabat CDRs:

CDR 1: TGTSNNFVS (SEQ ID NO: 325)

CDR 2: GVNKRPS (SEQ ID NO: 211)

CDR 3: GSLVGNWDVI (SEQ ID NO: 196)

[0740] 5120_N10 (PGT-139) light chain Chothia CDRs:

CDR 1: TGTSNNFVS (SEQ ID NO: 325)

CDR 2: GVNKRPS (SEQ ID NO: 211)

CDR 3: GSLVGNWDVI (SEQ ID NO: 196)

[0741] The 4835_F12 (PGT-124) antibody includes a heavy chain variable region (SEQ ID NO: 405), encoded by the nucleic acid sequence shown in SEQ ID NO: 403, and a light chain variable region (SEQ ID NO: 414) encoded by the nucleic acid sequence shown in SEQ ID NO: 412.

[0742] The heavy chain CDRs of the 4835_F12 (PGT-124) antibody have the following sequences per Kabat definition: NYYWT (SEQ ID NO: 406), YISDRETTTYNPSLNS (SEQ ID NO: 407), and ARRQGRIYGVVSFGGEFFYYYYMDV (SEQ ID NO: 408). The light chain CDRs of the 4835_F12 (PGT-124) antibody have the following sequences per Kabat definition: GRQALGSRAVQ (SEQ ID NO: 415), NNQDRPS (SEQ ID NO: 151), and HMWDSRSGFSWS (SEQ ID NO: 416).

[0743] The heavy chain CDRs of the 4835_F12 (PGT-124) antibody have the following sequences per Chothia definition: GGSISN (SEQ ID NO: 409), YISDRETTT (SEQ ID NO: 410), and ARRQGRIYGVVSFGGEFFYYYYMDV (SEQ ID NO: 408). The light chain CDRs of the 4835_F12 (PGT-124) antibody have the following sequences per Chothia definition: GRQALGSRAVQ (SEQ ID NO: 415), NNQDRPS (SEQ ID NO: 151), and HMWDSRSGFSWS (SEQ ID NO: 416).

[0744] The 4869_K15 (PGT-133) antibody includes a heavy chain variable region (SEQ ID NO: 420), encoded by the nucleic acid sequence shown in SEQ ID NO: 418, and a light chain variable region (SEQ ID NO: 429) encoded by the nucleic acid sequence shown in SEQ ID NO: 427.

[0745] The heavy chain CDRs of the 4869_K15 (PGT-133) antibody have the following sequences per Kabat definition: GRFWS (SEQ ID NO: 421), YFSDTDRSEYNPSLRS (SEQ ID NO: 422), and AQQGKRIYGIVSFGEFFYYYYMDA (SEQ ID NO: 423). The light chain CDRs

of the 4869_K15 (PGT-133) antibody have the following sequences per Kabat definition: GERSRGSRAVQ (SEQ ID NO: 430), NNQDRPA (SEQ ID NO: 179), and HYWDSRSPISWI (SEQ ID NO: 431).

[0746] The heavy chain CDRs of the 4869_K15 (PGT-133) antibody have the following sequences per Chothia definition: NGSVSG (SEQ ID NO: 424), YFSDTDRSE (SEQ ID NO: 425), and AQQGKRIYGIVSFGGEFFYYYYYMDA (SEQ ID NO: 423). The light chain CDRs of the 4869_K15 (PGT-133) antibody have the following sequences per Chothia definition: GERSRGSRAVQ (SEQ ID NO: 430), NNQDRPA (SEQ ID NO: 179), and HYWDSRSPISWI (SEQ ID NO: 431).

[0747] The 4876_M06 (PGT-134) antibody includes a heavy chain variable region (SEQ ID NO: 435), encoded by the nucleic acid sequence shown in SEQ ID NO: 433, and a light chain variable region (SEQ ID NO: 440) encoded by the nucleic acid sequence shown in SEQ ID NO: 438.

[0748] The heavy chain CDRs of the 4876_M06 (PGT-134) antibody have the following sequences per Kabat definition: GRFWS (SEQ ID NO: 421), YFSDTDRSEYNPSLRS (SEQ ID NO: 422), and AQQGKRIYGIVSFGELFYYYYYYMDA (SEQ ID NO: 436). The light chain CDRs of the 4876_M06 (PGT-134) antibody have the following sequences per Kabat definition: GERSRGSRAVQ (SEQ ID NO: 430), NNQDRPA (SEQ ID NO: 179), and HYWDSRSPISWI (SEQ ID NO: 431).

[0749] The heavy chain CDRs of the 4876_M06 (PGT-134) antibody have the following sequences per Chothia definition: NGSVSG (SEQ ID NO: 424), YFSDTDRSE (SEQ ID NO: 425), and AQQGKRIYGIVSFGELFYYYYYYMDA (SEQ ID NO: 436). The light chain CDRs of the 4876_M06 (PGT-134) antibody have the following sequences per Chothia definition: GERSRGSRAVQ (SEQ ID NO: 430), NNQDRPA (SEQ ID NO: 179), and HYWDSRSPISWI (SEQ ID NO: 431).

[0750] The 5131_A17 (PGT-132) antibody includes a heavy chain variable region (SEQ ID NO: 444), encoded by the nucleic acid sequence shown in SEQ ID NO: 442, and a light chain variable region (SEQ ID NO: 449) encoded by the nucleic acid sequence shown in SEQ ID NO: 447.

[0751] The heavy chain CDRs of the 5131_A17 (PGT-132) antibody have the following sequences per Kabat definition: TGHHYWG (SEQ ID NO: 348), HIIHYNTAVLHNPALKS

(SEQ ID NO: 349), and SGGDILYYNEWQKPHWFYP (SEQ ID NO: 445). The light chain CDRs of the 5131_A17 (PGT-132) antibody have the following sequences per Kabat definition: SGTASDIGSWNFVS (SEQ ID NO: 450), EVNRRRS (SEQ ID NO: 358), and SSLSGRWDIV (SEQ ID NO: 359).

[0752] The heavy chain CDRs of the 5131_A17 (PGT-132) antibody have the following sequences per Chothia definition: GDSINTGH (SEQ ID NO: 351), HIHYNTAVL (SEQ ID NO: 352), and SGGDILYYNEWQKPHWFYP (SEQ ID NO: 445). The light chain CDRs of the 5131_A17 (PGT-132) antibody have the following sequences per Chothia definition: SGTASDIGSWNFVS (SEQ ID NO: 450), EVNRRRS (SEQ ID NO: 358), and SSLSGRWDIV (SEQ ID NO: 359).

[0753] The 5138_G07 (PGT-138) antibody includes a heavy chain variable region (SEQ ID NO: 454), encoded by the nucleic acid sequence shown in SEQ ID NO: 452, and a light chain variable region (SEQ ID NO: 461) encoded by the nucleic acid sequence shown in SEQ ID NO: 459.

[0754] The heavy chain CDRs of the 5138_G07 (PGT-138) antibody have the following sequences per Kabat definition: ACDYFWG (SEQ ID NO: 201), SLSHCAGYYNSGWTYHNPSLKS (SEQ ID NO: 455), and FGGDVLVYHDWPKPAWVDL (SEQ ID NO: 456). The light chain CDRs of the 5138_G07 (PGT-138) antibody have the following sequences per Kabat definition: TGNINNFVS (SEQ ID NO: 458), GVNKRPS (SEQ ID NO: 211), and GSLAGNWDVV (SEQ ID NO: 459).

[0755] The heavy chain CDRs of the 5138_G07 (PGT-138) antibody have the following sequences per Chothia definition: GDSTAACD (SEQ ID NO: 204), SLSHCAGYYNSGWTY (SEQ ID NO: 457), and FGGDVLVYHDWPKPAWVDL (SEQ ID NO: 456). The light chain CDRs of the 5138_G07 (PGT-138) antibody have the following sequences per Chothia definition: TGNINNFVS (SEQ ID NO: 458), GVNKRPS (SEQ ID NO: 211), and GSLAGNWDVV (SEQ ID NO: 459).

[0756] The 5120_N10 (PGT-139) antibody includes a heavy chain variable region (SEQ ID NO: 463), encoded by the nucleic acid sequence shown in SEQ ID NO: 461, and a light chain variable region (SEQ ID NO: 470) encoded by the nucleic acid sequence shown in SEQ ID NO: 468.

[0757] The heavy chain CDRs of the 5120_N10 (PGT-139) antibody have the following sequences per Kabat definition: GCDYFWG (SEQ ID NO: 464), GLSHCAGYYNTGWTYHNPSLKS (SEQ ID NO: 202), and FDGEVLVYNDWPKPAWVDL (SEQ ID NO: 465). The light chain CDRs of the 5120_N10 (PGT-139) antibody have the following sequences per Kabat definition: TGTSNNFVS (SEQ ID NO: 325), GVNKRPS (SEQ ID NO: 211), and GSLVGNWDVI (SEQ ID NO: 196).

[0758] The heavy chain CDRs of the 5120_N10 (PGT-139) antibody have the following sequences per Chothia definition: GDSTAGCD (SEQ ID NO: 466), GLSHCAGYYNTGWTY (SEQ ID NO: 205), and FDGEVLVYNDWPKPAWVDL (SEQ ID NO: 465). The light chain CDRs of the 5120_N10 (PGT-139) antibody have the following sequences per Chothia definition: TGTSNNFVS (SEQ ID NO: 325), GVNKRPS (SEQ ID NO: 211), and GSLVGNWDVI (SEQ ID NO: 196).

[0759] The sequences of additional human monoclonal antibodies were determined, including the sequences of the variable regions of the Gamma heavy and Kappa or Lambda light chains. In addition, the sequence of each of the polynucleotides encoding the antibody sequences was determined. Shown below are the polypeptide and polynucleotide sequences of the gamma heavy chains and kappa light chains, with the signal peptides at the N-terminus (or 5' end) and the constant regions at the C-terminus (or 3' end) of the variable regions, which are shown in bolded text.

[0760] 6831_A21 (PGT-151) gamma heavy chain nucleotide sequence: coding sequence (leader sequence in italics, variable region in bold)

ATGGAATTGGGGCTGAGCTGGGTTTTCTCGTTGGTCTCTTAAGAGGTGTCCA
GTGTCGGGTGCAGTTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTG
GGAAGTCCGTGAGACTTTCCTGTGTAGTCTCCGATTTCCCCTTCAGCA
AGTATCCTATGTATTGGGTTTCGCCAGGCTCCAGGCAAGGGGCTGGAG
TGGGTGGCAGCCATCTCCGGTGATGCCTGGCATGTGGTCTACTCAA
TTCCGTGCAGGGCCGATTTCTCGTCTCCAGGGACAATGTCAAGAACA
CTCTATATTTAGAAATGAACAGCCTGAAAATTGAGGATACGGCCGTA
TATCGCTGCGCGAGAATGTTCCAGGAGTCTGGTCCACCACGTTTGGA
TCGTTGGAGCGGTGCAAATTATTACTATTATTCTGGTATGGACGTCTG
GGGCCAAGGGACCACGGTCACCGTCTCGAGCGCCTCCACCAAGGGCC
CATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGT
GTCGTGGAAC TCAGGCGCCCTGACCAGCGCGTGACACCTTCCCCGGCTG
TCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCT
CCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCC

AGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAA
 CTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCA
 GTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACC
 CCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
 CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA
 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC
 TCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA
 GGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
 CCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
 GAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCT
 TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA
 GAACAATAACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCT
 TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA
 CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC
 AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:471)

[0761] 6831_A21 (PGT-151) gamma heavy chain variable region nucleotide sequence:

CGGGTGCAGTTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGA
 AGTCCGTGAGACTTTCCTGTGTAGTCTCCGATTTCCTTCAGCAAGT
 ATCCTATGTATTGGGTTTCGCCAGGCTCCAGGCAAGGGGCTGGAGTGG
 GTGGCAGCCATCTCCGGTGATGCCTGGCATGTGGTCTACTCAAATTC
 CGTGCAGGGCCGATTTCTCGTCTCCAGGGACAATGTCAAGAACTC
 TATATTTAGAAATGAACAGCCTGAAAATTGAGGATACGGCCGTATAT
 CGCTGCGCGAGAATGTTCCAGGAGTCTGGTCCACCACGTTTGGATCG
 TTGGAGCGGTCGAAATTATTACTATTATTCTGGTATGGACGTCTGGG
 GCCAAGGGACCACGGTCACCGTCTCGAGC (SEQ ID NO:472)

[0762] 6831_A21 (PGT-151) gamma heavy chain amino acid sequence: expressed protein with leader sequence in *italics* and variable region in **bold**.

MELGLSWVFLVGLLRGVQCRVQLVESGGGVVQPGKSVRLSCVVSDFPFSKY
PMYWVRQAPGKGLEWVAAISGDAWHVVYSNSVQGRFLVSRDNVKNL
YLEMNSLKIEDTAVYRCARMFQESGPPRLDRWSGRNYYYYSMDVWG
QGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS
GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK
RVEPKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV
FSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 473)

[0763] 6831_A21 (PGT-151) gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in **bold italics**)

RVQLVESGGGVVQPGKSVRLSCVVSD**DFPFS**KYPMYWVRQAPGKGLEWVAA
ISGDAWHVVYSNSVQGRFLVSRDNVKNTLYLEMNSLKIEDTAVYRCAR**MFQ**
ESGPPRLDRWSGRNYYYYSGMDVWGQGTTVTVSS (SEQ ID NO: 474)

[0764] 6831_A21 (PGT-151) gamma heavy chain Kabat CDRs:

CDR 1: KYPMY (SEQ ID NO: 475)

CDR 2: AISGDAWHVVYSNSVQG (SEQ ID NO: 476)

CDR 3: MFQESGPPRLDRWSGRNYYYYSGMDV (SEQ ID NO: 477)

[0765] 6831_A21 (PGT-151) gamma heavy chain Chothia CDRs:

CDR 1: DFPFSK (SEQ ID NO: 478)

CDR 2: AISGDAWHVV (SEQ ID NO: 479)

CDR 3: MFQESGPPRLDRWSGRNYYYYSGMDV (SEQ ID NO: 477)

[0766] 6831_A21 (PGT-151) light chain nucleotide sequence: coding sequence (variable region in bold)

*ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGATACCTGAATT
 CACTGCAGACATTGTGATGACCCAGACTCCTCTCTCTTTGTCCGTCAC
 CCCTGGACAGCCGGCCTCCATCTCCTGCAAGTCCAGTGAGAGCCTCC
 GACAAAGTAATGGAAAGACCTCTTTGTATTGGTATCGGCAGAAGCCA
 GGCCAGTCTCCACAACCTCCTAGTGTTTGAAGTTTCTAATCGATTCTCT
 GGCGTGTCGGATAGGTTTGTGGCAGCGGGTCAGGGACAGACTTCAC
 ACTGAGAATCAGCCGGGTAGAGGCTGAGGATGTTGGATTTTATTACT
 GCATGCAAAGTAAAGACTTCCCACTTACATTTGGCGGGCGGGACCAAG
 GTGGATCTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCC
 ATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAA
 TAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCC
 TCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGA
 CAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTAC
 GAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTC
 GCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG* (SEQ ID NO:480)

[0767] 6831_A21 (PGT-151) light chain variable region nucleotide sequence:

*GACATTGTGATGACCCAGACTCCTCTCTCTTTGTCCGTCACCCCTGGA
 CAGCCGGCCTCCATCTCCTGCAAGTCCAGTGAGAGCCTCCGACAAAG
 TAATGGAAAGACCTCTTTGTATTGGTATCGGCAGAAGCCAGGCCAGT
 CTCCACAACCTCCTAGTGTTTGAAGTTTCTAATCGATTCTCTGGCGTGT
 CGGATAGGTTTGTGGCAGCGGGTCAGGGACAGACTTCACACTGAGA
 ATCAGCCGGGTAGAGGCTGAGGATGTTGGATTTTATTACTGCATGCA
 AAGTAAAGACTTCCCACTTACATTTGGCGGGCGGGACCAAGGTGGATC
 TCAAA* (SEQ ID NO:481)

[0768] 6831_A21 (PGT-151) light chain amino acid sequence: expressed protein with leader sequence in *italics* and variable region in **bold**.

MRI.PAQII.GLI.MI.WIPEFTADIVMTQTPLSLSVTPGQPASISCKSSESRLQSN
GKTS*LYWYRQKPGQSPQLLVFEVSNRFSGVSDRFVGS***SGSGTDFTLRISRV**
EAEDVGFYYCMQSKDFPLTFGGG**TKVDL***KRTVAAPSVFIFPPSDEQLKSGT*
*ASVVCLLN**NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT*
LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 482)

[0769] 6831_A21 (PGT-151) light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in **bold italics**)

*DIVMTQTPLSLSVTPGQPASISCK****KSSESRLQSNGKTS****LYWYRQKPGQSPQLLVF*
EVS***NRFS****GVSDRFVGS****SGSGTDFTLRISRV******EAEDVGFYYCMQSKDFPLT****FGGG*
*TKVDL**K* (SEQ ID NO: 483)

[0770] 6831_A21 (PGT-151) light chain Kabat CDRs:

CDR 1: KSSESRLQSNGKTSLY (SEQ ID NO: 484)

CDR 2: EVSNRFS (SEQ ID NO: 485)

CDR 3: MQSKDFPLT (SEQ ID NO: 486)

[0771] 6831_A21 (PGT-151) light chain Chothia CDRs:

CDR 1: KSSESRLQSNGKTSLY (SEQ ID NO: 484)

CDR 2: EVSNRFS (SEQ ID NO: 485)

CDR 3: MQSKDFPLT (SEQ ID NO: 486)

[0772] 6889_I17 (PGT-152) gamma heavy chain nucleotide sequence: coding sequence (variable region in **bold**)

ATGGAATTGGGGCTGAGCTGGGTTTTCTCGTTGGTCTCTTAAGAGGTGTCCA
CTGTCGGGTGCAGTTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTG
GGAAGTCCGTGAGACTTTCCTGTGTAGTCTCTGATTTCCCCTTCAGCA
AGTATCCTATGTATTGGGTTCGCCAGGCTCCAGGCAAGGGGCTGGAG
TGGGTGGCAGCCATCTCCGCTGATGCCTGGCATGTGGTCTACTCAGG
CTCCGTGCAGGGCCGATTTCTCGTCTCCAGGGACA**ACTCCAAGAACA**
TTCTGTATTTGGAAATGAACACCCTGAAAATTGAGGACACGGCCGTA
TATCGCTGCGCGAGAATGTTCCAGGAGTCTGGTCCACCACGTTTCGA
TTCTTGGAGCGGTCGAAATTACTACTATTACTCTGGTATGGACGTCTG
GGGCCAAGGGACCACGGTCACCGTCTCGAGCGCCTCCACCAAGGGCC
CATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGT
GTCGTGGA**ACTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCGGCTG**
TCCTACAGTCCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCT
CCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCC
AGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAA

CTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCA
 GTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACC
 CCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
 CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA
 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC
 TCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA
 GGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
 CCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
 GAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCT
 TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA
 GAACAACATAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCT
 TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA
 CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC
 AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:487)

[0773] 6889_I17 (PGT-152) gamma heavy chain variable region nucleotide sequence:

CGGGTGCAGTTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGA
 AGTCCGTGAGACTTTCCTGTGTAGTCTCTGATTTCCTTCAGCAAGT
 ATCCTATGTATTGGGTTTCGCCAGGCTCCAGGCAAGGGGCTGGAGTGG
 GTGGCAGCCATCTCCGCTGATGCCTGGCATGTGGTCTACTCAGGCTC
 CGTGCAGGGCCGATTTCTCGTCTCCAGGGACAACCTCCAAGAACATTC
 TGTATTTGGAAATGAACACCCTGAAAATTGAGGACACGGCCGTATAT
 CGCTGCGCGAGAATGTTCCAGGAGTCTGGTCCACCACGTTTCGATTC
 TTGGAGCGGTCGAAATTACTACTATTACTCTGGTATGGACGTCTGGG
 GCCAAGGGACCACGGTCACCGTCTCGAGC (SEQ ID NO:488)

[0774] 6889_I17 (PGT-152) gamma heavy chain amino acid sequence: expressed protein with leader sequence in *italics* and variable region in **bold**.

MELGLSWVFLVGLLRGVHCRVQLVESGGGVVQPGKSVRLSCVVSDFPFSKY
PMYWVRQAPGKGLEWVAAISADAWHVYSGSVQGRFLVSRDNSKNILY
LEMNTLKIEDTAVYRCARMFQESGPPRFDSWSGRNYYYYSGMDVWGQ
GTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG
ALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKR
VEPKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV
FSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 489)

[0775] 6889_I17 (PGT-152) gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in **bold italics**)

*RVQLVESGGGVVQPGKSVRLSCVVSD****FPFSKY****PMYWVRQAPGKGLEWVAA*
ISADAWHVYSGSVQGRFLVSRDNSKNILYLEMNTLKIEDTAVYRCAR***MFQ***
ESGPPRFDSWSGRNYYYYSGMDV*WGQGT**TVTVSS* (SEQ ID NO: 490)

[0776] 6889_I17 (PGT-152) gamma heavy chain Kabat CDRs:

CDR 1: KYPMY (SEQ ID NO: 475)

CDR 2: AISADAWHVYSGSVQG (SEQ ID NO: 491)

CDR 3: MFQESGPPRFDSWSGRNYYYYSGMDV (SEQ ID NO: 492)

[0777] 6889_I17 (PGT-152) gamma heavy chain Chothia CDRs:

CDR 1: DFPFSK (SEQ ID NO: 478)

CDR 2: AISADAWHV (SEQ ID NO: 493)

CDR 3: MFQESGPPRFDSWSGRNYYYYSGMDV (SEQ ID NO: 492)

[0778] 6889_I17 (PGT-152) light chain nucleotide sequence: coding sequence (variable region in bold)

*ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGATACCTGAATT
TATTGCCGACATTGTGATGACCCAGACTCCTCTCTCTTTGTCCGTCGAC
CCTGGACAGCCGGCCTCCATCTCCTGCAAGTCCAGTCAGAGCCTCCG
ACAAAGTAATGGAAAGACCTCTTTGTATTGGTATCAGCAGAAGCCAG
GCCAGTCTCCACAACCTCCTAATATTTGAAGTTTCTAATCGATTCTCTG
GCGTGTTCGGATAGGTTTGTGTTGGCAGCGGGTCAGGGACAGACTTCACA
CTGAGAATCAGCCGGGTAGAGGCTGAGGATGTTGGATTTTATTACTG
CATGCAAAGTAAAGACTTCCCACCTCACCTTTGGCGGCGGGACCAAGG
TGGATCTCAACCGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCA
TCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAAT
AACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCT
CCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGAC
AGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACG
AGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG
CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:494)*

[0779] 6889_I17 (PGT-152) light chain variable region nucleotide sequence:

**GACATTGTGATGACCCAGACTCCTCTCTCTTTGTCCGTCGACCCTGGA
CAGCCGGCCTCCATCTCCTGCAAGTCCAGTCAGAGCCTCCGACAAAG
TAATGGAAAGACCTCTTTGTATTGGTATCAGCAGAAGCCAGGCCAGT
CTCCACAACCTCCTAATATTTGAAGTTTCTAATCGATTCTCTGGCGTGT
CGGATAGGTTTGTGTTGGCAGCGGGTCAGGGACAGACTTCACACTGAGA
ATCAGCCGGGTAGAGGCTGAGGATGTTGGATTTTATTACTGCATGCA
AAGTAAAGACTTCCCACCTCACCTTTGGCGGCGGGACCAAGGTGGATC
TCAAC (SEQ ID NO:495)**

[0780] 6889_I17 (PGT-152) light chain amino acid sequence: expressed protein with leader sequence in italics and variable region in bold.

*MRLPAQLLGLLMLWIPEFIADIVMTQTPLSLVDPGQPASISCKSSQSLRQSN
GKTSLYWYQQKPGQSPQLLIFEVSNRFGVSDRFVGSVSGTDFTLRISRV*

EAEDVGFYYCMQSKDFPLTFGGGTKVDLNRTVAAPSVFIFPPSDEQLKSGT
ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT
LTKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 496)

[0781] 6889_I17 (PGT-152) light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

DIVMTQTPLSLSVDPGQPASISC***KSSQSLROSNGKTS***LYWYQQKPGQSPQLLIF
EVSNRFSGVSDRFVGS^{SG}SGTDFTLRISRVEAEDVGFYYC***MQSKDFPLT***FGGG
TKVDLN (SEQ ID NO: 497)

[0782] 6889_I17 (PGT-152) light chain Kabat CDRs:

CDR 1: KSSQSLRQSNGKTSLY (SEQ ID NO: 498)

CDR 2: EVSNRFS (SEQ ID NO: 485)

CDR 3: MQSKDFPLT (SEQ ID NO: 486)

[0783] 6889_I17 (PGT-152) light chain Chothia CDRs:

CDR 1: KSSQSLRQSNGKTSLY (SEQ ID NO: 498)

CDR 2: EVSNRFS (SEQ ID NO: 485)

CDR 3: MQSKDFPLT (SEQ ID NO: 486)

[0784] 6891_F06 (PGT-153) gamma heavy chain nucleotide sequence: coding sequence
(leader sequence in italics, variable region in bold)

ATGGAATTGGGGCTGAGCTGGGTTTTCTCGTTGCTCTCTTAAGAGGTGTCCA
GTGTCAGGTGCAGTTGGTGGAGTCGGGCGGAGGCGTGGTCCAGCCTG
GGAAGTCCCTGAGACTCTCCTGTGTAGTCTCTAATTTCTCTTCAATA
AACGTCACATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGACTAGAG
TGGATAGCAGTCATTTCTCTGATGCCATTACGCTAGACTACGCAAGT
TCCGTGCGGGGCCGATCCCTCATCTCCAGAGACAATTCCAAAAATAG
TTTATATCTAGACATGAATAACCTGAAAATTGAGGACACGGCCACATA
TTATTGTGCAAGAGATAGAGACGGATATGGTCCACCACAGATCCAGA
CTTGGAGCGGTGATACCTCCACCTTTATTCTGGAATAGACGCCTGG
GGCCTAGGGACCACGGTCACCGTCTCGAGCGCCTCCACCAAGGGCCCA
TCCGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGT
CGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCGGCTGTC
CTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC
AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAG
CAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAAT
CACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCACT
CTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCC
TGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCA
AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAA
GCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC

ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGG
TCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAGCC
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG
AGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTC
TATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGA
ACA ACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTC
CTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACG
TCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
AAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 499)

[0785] 6891_F06 (PGT-153) gamma heavy chain variable region nucleotide sequence:

CAGGTGCAGTTGGTGGAGTCGGGCGGAGGCGTGGTCCAGCCTGGGA
AGTCCCTGAGACTCTCCTGTGTAGTCTCTAATTTTCTCTTCAATAAAC
GTCACATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGACTAGAGTG
GATAGCAGTCATTTCTCTGATGCCATTCACGTAGACTACGCAAGTTC
CGTGCGGGGGCCGATCCCTCATCTCCAGAGACAATTCCAAAAATAGTT
TATATCTAGACATGAATAACCTGAAAATTGAGGACACGGCCACATATT
ATTGTGCAAGAGATAGAGACGGATATGGTCCACCACAGATCCAGACT
TGGAGCGGTCGATACCTCCACCTTTATTCTGGAATAGACGCCTGGGG
CCTAGGGACCACGGTCACCGTCTCGAGC (SEQ ID NO:500)

[0786] 6891_F06 (PGT-153) gamma heavy chain amino acid sequence: expressed protein with leader sequence in italics and variable region in bold.

MELGLSWVFLVALLRGVQCQVQLVESGGGVVQPGKSLRLSCVVSNFLFNKR
HMHWVRQAPGKGLEWIAVISSDAIHVDYASSVRGRSLISRDNSKNSLYLD
MNNLKIEDTATYYCARDRDGYGPPQIQTWSGRYLHLYSGIDAWGLGTT
VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPK
SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 501)

[0787] 6891_F06 (PGT-153) gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

*QVQLVESGGGVVQPGKSLRLSCVVS****NFLFNKR******HRMH******WVRQAPGKGLEWIA******V***
ISSDAIHVDYASSVRGRSLISRDNSKNSLYLDMNNLKIEDTATYYCARD***DRDGY***
GPPQIQTWSGRYLHLYSGIDAWGLGTTVT***VSS*** (SEQ ID NO: 502)

[0788] 6891_F06 (PGT-153) gamma heavy chain Kabat CDRs:

CDR 1: KRMH (SEQ ID NO: 503)

CDR 2: VISSDAIHVDYASSVRG (SEQ ID NO: 504)

CDR 3: DRDGYGPPQIQTWSGRYLHLYSGIDA (SEQ ID NO: 505)

[0789] 6891_F06 (PGT-153) gamma heavy chain Chothia CDRs:

CDR 1: NFLFNK (SEQ ID NO: 506)

CDR 2: VISSDAIHVD (SEQ ID NO: 507)

CDR 3: DRDGYGPPQIQTWSGRYLHLYSGIDA (SEQ ID NO: 505)

[0790] 6891_F06 (PGT-153) light chain nucleotide sequence: coding sequence (variable region in bold)

*ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGATACCTGAATT
CACTGCGGACATTGTGCTGACCCAGAGCCCCCTCTTTCTGTCCGTCAG
TCCTGGACAGCCGGCCTCCATCTCCTGTAAGTCTAGTCAGAGCCTCC
GACAAAGTAATGGAAAGACATATTTGTATTGGTACGTACAAAAGTCC
GGCCAGTCTCCACAACCCCTGATCCAGGAAGTTTCCATTCGCTTCTCT
GGAGTGCCAGGTAGATTCGCTGGCAGCGGATCAGGGACAGACTTCAC
ACTGAAAATCAGCCGGGTGGAGGCTGAAGATGTTGGAGTTTATTTCT
GCATGCAAAGTAAAGACTTTCCACTCACTTTTGGCGGAGGGACCAAG
GTGGACCTCAATCGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCC
ATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAA
TAACTTCTATCCCAGAGAGGGCCAAAGTACAGTGGAAGGTGGATAACGCCC
TCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGA
CAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTAC
GAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTC
GCCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:508)*

[0791] 6891_F06 (PGT-153) light chain variable region nucleotide sequence:

*GACATTGTGCTGACCCAGAGCCCCCTCTTTCTGTCCGTCAGTCCTGG
ACAGCCGGCCTCCATCTCCTGTAAGTCTAGTCAGAGCCTCCGACAAA
GTAATGGAAAGACATATTTGTATTGGTACGTACAAAAGTCCGGCCAG
TCTCCACAACCCCTGATCCAGGAAGTTTCCATTCGCTTCTCTGGAGTG
CCAGGTAGATTCGCTGGCAGCGGATCAGGGACAGACTTCACACTGAA
AATCAGCCGGGTGGAGGCTGAAGATGTTGGAGTTTATTTCTGCATGC
AAAGTAAAGACTTTCCACTCACTTTTGGCGGAGGGACCAAGGTGGAC
CTCAAT (SEQ ID NO:509)*

[0792] 6891_F06 (PGT-153) light chain amino acid sequence: expressed protein with leader sequence in italics and variable region in bold.

*MRLPAQLLGLLMLWIPEFTADIVLTQSPLFLSVSPGQPASISCKSSQSLRQSN
GKTYLYWYVQKSGQSPQPLIQEV SIRFSGVPGRFAGSGSGTDFTLKISRV
EAEDVG VYFCMQSKDFPLTFGGG TKVDLNRVAAPS VFIFPPSDEQLKSGT
ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTL
SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 510)*

[0793] 6891_F06 (PGT-153) light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

DIVLTQSPLFLSVSPGQPASISC**KSSQSLRQSNGKTYLY**WYVQKSGQSPQPLIQ
EVSIRFSGVPGRFAGSGSGTDFTLKISRVEAEDVG VYFC**MOSKDFPLT**FGGGT
 KVDLN (SEQ ID NO: 511)

[0794] 6891_F06 (PGT-153) light chain Kabat CDRs:

CDR 1: KSSQSLRQSNGKTYLY (SEQ ID NO: 512)

CDR 2: EVSIRFS (SEQ ID NO: 513)

CDR 3: MOSKDFPLT (SEQ ID NO: 486)

[0795] 6891_F06 (PGT-153) light chain Chothia CDRs:

CDR 1: KSSQSLRQSNGKTYLY (SEQ ID NO: 512)

CDR 2: EVSIRFS (SEQ ID NO: 513)

CDR 3: MOSKDFPLT (SEQ ID NO: 486)

[0796] 6843_G20 (PGT-154) gamma heavy chain nucleotide sequence: coding sequence (variable region in bold)

ATGGAATTGGGGCTGAGCTGGGTTTTCTCGTTGCTCTCTTAAGAGGTGTCCA
 GTGTCAGGTGCAGCTGGTGGAAATCGGGAGGAGGCGTGGTCCAGCCTG
 GAAAGTCCCTCAGACTCTCATGTGTCGTCTCTAATTTTCATCTTTAATA
 AATATCCTATGTATTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAG
 TGGGTGGCAGCCATCTCCGCTGATGCCTGGCATGTAGACTACGCAGC
 CTCCTGAAGGACCGATTTCTCATCTCCAGAGACAATTCCAAGAATG
 CTCTATATTTGGAAATGAACACCCTGAGAGTTGAAGACACGGGTATC
 TACTACTGTGCGAGAAATATAGAGGAGTTTAGTGTTCCACAGTTCGA
 TTCTTGGAGCGGTCGAAGCTACTACCACTATTTTGGGATGGACGTCT
 GGGGCCAAGGGACCACGGTCACCGTCTCGAGCGCCTCCACCAAGGGC
 CCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCAC
 AGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG
 TGTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCT
 GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC
 CTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC
 CCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAA
 AACTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGT
 CAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA
 CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAG
 GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGAC
 AAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
 CTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA
 GGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
 CCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
 GAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCT

TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA
GAACAAC TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCT
TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA
CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC
AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 514)

[0797] 6843_G20 (PGT-154) gamma heavy chain variable region nucleotide sequence:

CAGGTGCAGCTGGTGGAAATCGGGAGGAGGCGTGGTCCAGCCTGGAA
AGTCCCTCAGACTCTCATGTGTCGTCTCTAATTTTCATCTTTAATAAAT
ATCCTATGTATTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGG
GTGGCAGCCATCTCCGCTGATGCCTGGCATGTAGACTACGCAGCCTC
CGTGAAGGACCGATTTCTCATCTCCAGAGACAATTCCAAGAATGCTC
TATATTTGGAATGAACACCCTGAGAGTTGAAGACACGGGTATCTAC
TACTGTGCGAGAAATATAGAGGAGTTTAGTGTTCCACAGTTCGATTCT
TGGAGCGGTCGAAGCTACTACCACTATTTTGGGATGGACGTCTGGGG
CCAAGGGACCACGGTCACCGTCTCGAGC (SEQ ID NO: 515)

[0798] 6843_G20 (PGT-154) gamma heavy chain amino acid sequence: expressed protein with leader sequence in italics and variable region in bold.

*MELGLSWVFLVALLRGVQCQVQLVESGGGVVQPGKSLRLSCVVS***NFIFNKY**
PMYWVRQAPGKGLEWVAAISADAWHVDYAASVKDRFLISRDNSKNALY
LEMNTLRVEDTGIYYCARNIEEFSVPQFDSWSGRSYYHYFGMDVWGQG
TTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL
TSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVKDRVE
PKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
CSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 516)

[0799] 6843_G20 (PGT-154) gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

QVQLVESGGGVVQPGKSLRLSCVVS***NFIFNKY******PMYWVRQAPGKGLEWVAA***
ISADAWHVDYAASVKDRFLISRDNSKNALYLEMNTLRVEDTGIYYCARNIEE
FSVPQFDSWSGRSYYHYFGMDV***WGQGT******TVT******VSS*** (SEQ ID NO: 517)

[0800] 6843_G20 (PGT-154) gamma heavy chain Kabat CDRs:

CDR 1: KYPMY (SEQ ID NO: 475)

CDR 2: AISADAWHVDYAASVKD (SEQ ID NO: 518)

CDR 3: NIEEFSVPQFDSWSGRSYYHYFGMDV (SEQ ID NO: 519)

[0801] 6843_G20 (PGT-154) gamma heavy chain Chothia CDRs:

CDR 1: NFIFNK (SEQ ID NO: 520)

CDR 2: AISADAWHVD (SEQ ID NO: 521)

CDR 3: NIEEFSVPQFDSWSGRSYYHYFGMDV (SEQ ID NO: 519)

[0802] 6843_G20 (PGT-154) light chain nucleotide sequence: coding sequence (variable region in bold)

*ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGATACCTGAGTT
CGCTGCAGACATTGTGATGACTCAGACTCCTGTCTCTCTGTCCGTCAG
TCTTGGACAGGCGGCCTCCATCTCCTGCAGCTCCAGTGAGAGTCTCG
GACGTGGTGATGGAAGGACCTATTTGCATTGGTACCGACAGAAGCCA
GGCCAGACTCCACAATTACTCATGTATGAAGTTTCTACTCGATTCTCT
GGAGTGTCCGACAGGTTTCGCTGGCAGCGGGTCACGTACACAATTAC
ATTGAAAATTAGTCGGGTGGAGGCTGAAGATGTTGGCGTTTATTACT
GCATGCAAAGTAGAGACTTCCCAATCACTTTTGGCGGAGGGACCAGG
GTGGATCTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCC
ATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAA
TAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCC
TCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGA
CAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTAC
GAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTC
GCCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:522)*

[0803] 6843_G20 (PGT-154) light chain variable region nucleotide sequence:

*GACATTGTGATGACTCAGACTCCTGTCTCTCTGTCCGTCAGTCTTGG
CAGGCGGCCTCCATCTCCTGCAGCTCCAGTGAGAGTCTCGGACGTGG
TGATGGAAGGACCTATTTGCATTGGTACCGACAGAAGCCAGGCCAGA
CTCCACAATTACTCATGTATGAAGTTTCTACTCGATTCTCTGGAGTGT
CCGACAGGTTTCGCTGGCAGCGGGTCACGTACACAATTCACATTGAAA
ATTAGTCGGGTGGAGGCTGAAGATGTTGGCGTTTATTACTGCATGCA
AAGTAGAGACTTCCCAATCACTTTTGGCGGAGGGACCAGGGTGGATC
TCAAA (SEQ ID NO:523)*

[0804] 6843_G20 (PGT-154) light chain amino acid sequence: expressed protein with leader sequence in italics and variable region in bold.

*MRLPAQLLGLLMLWIPEFAADIVMTQTPVSLSVSLGQAASISCSSES LGRGD
GRTYLHWYRQKPGQTPQLLMYEVSTRFSGVSDRFAGSGSRTQFTLKISR
VEAEDVGVIYCMQSRDFPITFGGGTRVDLKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLT
LSKADYEEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 524)*

[0805] 6843_G20 (PGT-154) light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

DIVMTQTPVSLSVSLGQAASISC**SSSESLGRGDGRTYLH**WYRQKPGQTPQLL
 MY**EVSTRFS**GVSDRFAGSGSRTQFTLKISRVEADVGVYYC**MQSRDFPIT**FG
 GGTRVDLK (SEQ ID NO: 525)

[0806] 6843_G20 (PGT-154) light chain Kabat CDRs:

CDR 1: SSSESLGRGDGRTYLH (SEQ ID NO: 526)

CDR 2: EVSTRFS (SEQ ID NO: 527)

CDR 3: MQSRDFPIT (SEQ ID NO: 528)

[0807] 6843_G20 (PGT-154) light chain Chothia CDRs:

CDR 1: SSSESLGRGDGRTYLH (SEQ ID NO: 526)

CDR 2: EVSTRFS (SEQ ID NO: 527)

CDR 3: MQSRDFPIT (SEQ ID NO: 528)

[0808] 6892_D19 (PGT-155) gamma heavy chain nucleotide sequence: coding sequence
 (leader sequence in italics, variable region in bold)

ATGGAATTGGGGCTGAGCTGGGTTTTCTCGTCTCCTAAGAGGTGTCCA
CTGTCAGGTGCATCTGGTGGAGTCGGGGGGAGGCGTGGTCCAACCTG
GGAAGTCCCTAAGACTCTCCTGTGAAACCTCTGGCTTCATCTTCAACG
AATATCCCATGTATTGGATCCGCCAGGCTCCAGGCAAGGGACCGGAG
TGGGTGGCCGCCATCTCCGCTGACGCCTGGCATGTGGACTACGCAGG
CTCCGTGCGGGGCCGATTTACCGTCTCCAGAGACAATTCTAAGAATT
CTCTATATTTAGACATGAAGAGTCTGAAAGTTGAAGACACGGCTATAT
ATTTCTGTGCGAAAGATGGGGAGGAACACAAGGTACCACAATTGCAT
TCCTGGAGCGGACGAACTTATATCACTACACTGGTTTTGACGTCTG
GGGCCCAGGGACCACGGTCACCGTCTCGAGCGCCTCCACCAAGGGCC
CATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGT
GTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCGGCTG
TCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCT
CCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCC
AGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAA
CTCACACATGCCCACCGTGCCCAGCACCTGAACCTCTGGGGGGACCGTCA
GTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACC
CCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA
AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC
TCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA
GGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
CCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
GAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCT
TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA
GAACAACCTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCT
TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA

CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC
AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:529)

[0809] 6892_D19 (PGT-155) gamma heavy chain variable region nucleotide sequence:

**CAGGTGCATCTGGTGGAGTCGGGGGGAGGCGTGGTCCAACCTGGGA
AGTCCCTAAGACTCTCCTGTGAAACCTCTGGCTTCATCTTCAACGAAT
ATCCCATGTATTGGATCCGCCAGGCTCCAGGCAAGGGACCGGAGTGG
GTGGCCGCCATCTCCGCTGACGCCTGGCATGTGGACTACGCAGGCTC
CGTGCGGGGGCCGATTTACCGTCTCCAGAGACAATTCTAAGAATTCTC
TATATTTAGACATGAAGAGTCTGAAAGTTGAAGACACGGCTATATATT
TCTGTGCGAAAGATGGGGAGGAACACAAGGTACCACAATTGCATTCC
TGGAGCGGACGAACTTATATCACTACACTGGTTTTGACGTCTGGGG
CCCAGGGACCACGGTCACCGTCTCGAGC (SEQ ID NO:530)**

[0810] 6892_D19 (PGT-155) gamma heavy chain amino acid sequence: expressed protein with leader sequence in *italics* and variable region in **bold**.

*MELGLSWVFLVLLRGVHCQVHLVESGGGVVQPGKSLRLSCETS***GFIFNEY**
PMYWIRQAPGKGPEWVA*ISADA***WHVDYAGSVRGRFTVSRD***NSKNSLY*
LDMKSLKVEDTAIYFCAKD*GEEHKVPQLHSWSGRNLYHYTGFDVWGP*
TTVTVSS*ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT**SVNSGAL*
*TSGVHTFPAVLQSSGLYSLSSVTVPS**SSLGTQTYICNVNHKPSNTKVDKRVE*
*PKSCDKHTHTCP**CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE*
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
CSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 531)

[0811] 6892_D19 (PGT-155) gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in **bold italics**)

*QVHLVESGGGVVQPGKSLRLSCETS***GFIFNEY***PMYWIRQAPGKGPEWVA***AI**
SA**DAWHVDYAGSVRGRFTVSRD***NSKNSLYLDMKSLKVEDTAIYFCAKD***GEE**
HKVPOLHSWSGRNLYHYTGFDV*WGP***TTVTVSS** (SEQ ID NO: 532)

[0812] 6892_D19 (PGT-155) gamma heavy chain Kabat CDRs:

CDR 1: EYPMY (SEQ ID NO: 533)

CDR 2: AISADAWHVDYAGSVRG (SEQ ID NO: 534)

CDR 3: DGEEHKVPQLHSWSGRNLYHYTGFDV (SEQ ID NO: 535)

[0813] 6892_D19 (PGT-155) gamma heavy chain Chothia CDRs:

CDR 1: GFIFNE (SEQ ID NO: 536)

CDR 2: AISADAWHVD (SEQ ID NO: 521)

CDR 3: DGEEHKVPQLHSWSGRNLYHYTGFDV (SEQ ID NO: 535)

[0814] 6892_D19 (PGT-155) light chain nucleotide sequence: coding sequence (variable region in bold)

*ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGATACCTGAACT
TGCTGCAGACATTGTGATGACCCAGTCTCCTGTCTCTCTGTCCGTCAC
CCTCGGACAGCCGGCCTCCATGTCCTGCAAGTCCAGTCAGAGTGTCC
GACAGAGTGATGGCAAGACTTTCTTATATTGGTATCGACAGAAGCCA
GGCCAGTCTCCACAACTGTTAATATATGAGGGTTCGAGTCGATTCTCT
GGAGTGTGATAGGATCTCTGGCAGCGGGTCAGGGACAGACTTCAC
ACTGAGGATCAGTCGAGTGGAGGCTGAGGATGCTGGCGTTTACTTCT
GCTTGCAAACCTAAAGACTTCCCCCTCACTTTTGGCGGAGGGACCAGG
GTGGATCTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCC
ATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGTGCCTGCTGAA
TAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCC
TCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGA
CAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTAC
GAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTC
GCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:537)*

[0815] 6892_D19 (PGT-155) light chain variable region nucleotide sequence:

**GACATTGTGATGACCCAGTCTCCTGTCTCTCTGTCCGTCACCCTCGGA
CAGCCGGCCTCCATGTCCTGCAAGTCCAGTCAGAGTGTCCGACAGAG
TGATGGCAAGACTTTCTTATATTGGTATCGACAGAAGCCAGGCCAGT
CTCCACAACTGTTAATATATGAGGGTTCGAGTCGATTCTCTGGAGTGT
CAGATAGGATCTCTGGCAGCGGGTCAGGGACAGACTTCACACTGAGG
ATCAGTCGAGTGGAGGCTGAGGATGCTGGCGTTTACTTCTGCTTGCA
AACTAAAGACTTCCCCCTCACTTTTGGCGGAGGGACCAGGGTGGATC
TCAAA (SEQ ID NO:538)**

[0816] 6892_D19 (PGT-155) light chain amino acid sequence: expressed protein with leader sequence in italics and variable region in bold.

*MRLPAQLLGLLMLWIPELAADIVMTQSPVSLSVTLGQPASMSCKSSQSVRQS
DGKTFLYWYRQKPGQSPQLLIYEGSSRFSGVSDRISGSGSGTDFTLRISRV
EAEDAGVYFCLQTKDFPLTFGGGTRVDLKRVAAPSVFIFPPSDEQLKSGT
ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSLSTLTL
SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 539)*

[0817] 6892_D19 (PGT-155) light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

*DIVMTQSPVSLSVTLGQPASMSCK****KSSQSVROS******DGKTFLYWYRQKPGQSPQLLI
Y******EGSSRFS******GVSDRISGSGSGTDFTLRISRVEAEDAGVYF******CLQTKDFPLT******FGGG
TRVDLK (SEQ ID NO: 540)***

[0818] 6892_D19 (PGT-155) light chain Kabat CDRs:

CDR 1: KSSQSVRQSDGKTFLY (SEQ ID NO: 541)

CDR 2: EGSSRFS (SEQ ID NO: 542)

CDR 3: LQTKDFPLT (SEQ ID NO: 543)

[0819] 6892_D19 (PGT-155) light chain Chothia CDRs:

CDR 1: KSSQSVRQSDGKTFLY (SEQ ID NO: 541)

CDR 2: EGSSRFS (SEQ ID NO: 542)

CDR 3: LQTKDFPLT (SEQ ID NO: 543)

[0820] 6808_B09 (PGT-156) gamma heavy chain nucleotide sequence: coding sequence
(variable region in bold)

*ATGGAATTGGGGCTGAGCTGGGTTTTCTCGTCGTTCTCCTAAGAGGTGTCCA
CTGTCAGGTGCATCTGGTGGAGTCGGGGGGAGGCGTTGTCCAACCTG
GAAAGTCCCTAAGACTCTCCTGTGAAACCTCTGGCTTCATCTTCAATC
AATATCCCATGTATTGGGTCCGCCAGGCTCCAGGCAAGGGACCGGAG
TGGGTGGCCGCCATCTCCGCTGATGCCTGGCATGTGGACTACCCAGG
CTCCGTGCGGGGCCGATTTACCGTCTCCAGAGACAATTCCAAGAGTT
CTCTATATTTAGACATGAAGAGTCTGAAAGTTGAAGACACGGCTATAT
ATTTCTGTGCGAAAGATGGGGAGGAACACAAGGTACCACAATTGCAT
TCCTGGAGCGGACGAAACTTATATCACTACACTGGTTTTGACGTCTG
GGGCCCAGGGACCACGGTCACCGTCTCGAGCGCCTCCACCAAGGGCC
CATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGT
GTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCCGGCTG
TCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCT
CCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCC
AGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAA
CTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCA
GTCTTCCTCTTCCCCCAAAAACCCAAGGACACCCTCATGATCTCCCGGACC
CCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA
AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC
TCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA
GGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
CCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
GAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCT
TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA
GAACAACCTACAAGACCACGCCTCCCGTGTGGACTCCGACGGCTCCTTCT
TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA
CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC
AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 544)*

[0821] 6808_B09 (PGT-156) gamma heavy chain variable region nucleotide sequence:

CAGGTGCATCTGGTGGAGTCGGGGGGAGGCGTTGTCCAACCTGGAA
 AGTCCCTAAGACTCTCCTGTGAAACCTCTGGCTTCATCTTCAATCAAT
 ATCCCATGTATTGGGTCCGCCAGGCTCCAGGCAAGGGACCGGAGTGG
 GTGGCCGCCATCTCCGCTGATGCCTGGCATGTGGACTACCCAGGCTC
 CGTGCGGGGCGATTACCGTCTCCAGAGACAATTCCAAGAGTTCTC
 TATATTTAGACATGAAGAGTCTGAAAGTTGAAGACACGGCTATATATT
 TCTGTGCGAAAGATGGGGAGGAACACAAGGTACCACAATTGCATTCC
 TGGAGCGGACGAAACTTATATCACTACACTGGTTTTGACGTCTGGGG
 CCCAGGGACCACGGTCACCGTCTCGAGC (SEQ ID NO:545)

[0822] 6808_B09 (PGT-156) gamma heavy chain amino acid sequence: expressed protein with leader sequence in *italics* and variable region in **bold**.

MELGLSWVFLVLLRGVHCQVHLVESGGGVVQPGKSLRLSCETSGFIFNQY
PMYWVRQAPGKGPEWVAAISADAWHVDYPGSVRGRFTVSRDNSKSSLY
LDMKSLKVEDTAIFYCAKDGEHKVPQLHSWSGRNLYHYTGFDVWGPG
TTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL
 TSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVE
 PKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHE
 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
 KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
 YPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
 CSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 546)

[0823] 6808_B09 (PGT-156) gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in **bold italics**)

QVHLVESGGGVVQPGKSLRLSCETSGFIFNQYPMYWVRQAPGKGPEWVAAI
SADAWHVDYPGSVRGRFTVSRDNSKSSLYLDMKSLKVEDTAIFYCAKDGE
*HKVPQLHSWSGRNLYHYTGFDV*WGPGTTVTVSS (SEQ ID NO: 547)

[0824] 6808_B09 (PGT-156) gamma heavy chain Kabat CDRs:

CDR 1: QYPMY (SEQ ID NO: 548)

CDR 2: AISADAWHVDYPGSVRG (SEQ ID NO: 549)

CDR 3: DGEEHKVPQLHSWSGRNLYHYTGFDV (SEQ ID NO: 535)

[0825] 6808_B09 (PGT-156) gamma heavy chain Chothia CDRs:

CDR 1: GFIFNQ (SEQ ID NO: 550)

CDR 2: AISADAWHVD (SEQ ID NO: 521)

CDR 3: DGEEHKVPQLHSWSGRNLYHYTGFDV (SEQ ID NO: 535)

[0826] 6808_B09 (PGT-156) light chain nucleotide sequence: coding sequence (variable region in **bold**)

ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAAATGCTCTGGATACCTGAACT
 TGCTGCAGACATTGTGATGACCCAGTCTCCTGTCTCTCTGTCCGTCAC
 CCTCGGACAGCCGGCCTCCATGTCCTGCAAGTCCAGTCAGACTGTCC
 GACAGAGTGATGGCAAGACTTTCTTATATTGGTATCGACAGAAGGCA
 GGCCAGTCTCCACAACTGTTAATATATGAGGGTTCGAATCGATTCTCT
 GGAGTGTGATAGGATCTCTGGCAGCGGGTCGGGGACAGATTTTAC
 ACTGAGAATCAGTCGAGTGGAGGCTGAGGATGTTGGCGTTTATTTCT
 GCCTGCAAACTAAAGACTTCCCCCTCACTTTTGGCGGAGGGACCAGG
 GTGGATATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCC
 ATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAA
 TAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCC
 TCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGA
 CAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTAC
 GAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTC
 GCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:551)

[0827] 6808_B09 (PGT-156) light chain variable region nucleotide sequence:

GACATTGTGATGACCCAGTCTCCTGTCTCTCTGTCCGTCACCCCTCGGA
 CAGCCGGCCTCCATGTCCTGCAAGTCCAGTCAGACTGTCCGACAGAG
 TGATGGCAAGACTTTCTTATATTGGTATCGACAGAAGGCAGGCCAGT
 CTCCACAACTGTTAATATATGAGGGTTCGAATCGATTCTCTGGAGTGT
 CAGATAGGATCTCTGGCAGCGGGTCGGGGACAGATTTTCACTGAGA
 ATCAGTCGAGTGGAGGCTGAGGATGTTGGCGTTTATTTCTGCCTGCA
 AACTAAAGACTTCCCCCTCACTTTTGGCGGAGGGACCAGGGTGGATA
 TCAAA (SEQ ID NO:552)

[0828] 6808_B09 (PGT-156) light chain amino acid sequence: expressed protein with leader sequence in italics and variable region in bold.

MRLPAQLLGLLMLWIPELAADIVMTQSPVLSVTLGQPASMSCKSSQTVRQS
DGKTFLYWYRQKAGQSPQLLIYEGSNRFSGVSDRISGSGSGTDFTLRISR
 VEAEDVG~~VYFC~~**LOT**KDFPLTFGGGTRVDIKRTVAAPSVFIFPPSDEQLKSG
 TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTLSSTLT
 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 553)

[0829] 6808_B09 (PGT-156) light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

DIVMTQSPVLSVTLGQPASMSCK**KSSQTVRQSDGKTFLY**WYRQKAGQSPQLL
 IY**EGSNRFS**GVSDRISGSGSGTDFTLRISRVEAEDVG~~VYFC~~**LOT**KDFPLTFGG
 GTRVDIK (SEQ ID NO: 554)

[0830] 6808_B09 (PGT-156) light chain Kabat CDRs:

CDR 1: KSSQTVRQSDGKTFLY (SEQ ID NO: 555)

CDR 2: EGSNRFS (SEQ ID NO: 556)

CDR 3: LQTKDFPLT (SEQ ID NO: 543)

[0831] 6808_B09 (PGT-156) light chain Chothia CDRs:

CDR 1: KSSQTVRQSDGKTFLY (SEQ ID NO: 555)

CDR 2: EGSNRFS (SEQ ID NO: 556)

CDR 3: LQTKDFPLT (SEQ ID NO: 543)

[0832] 6892_C23 (PGT-157) gamma heavy chain nucleotide sequence: coding sequence
(leader sequence in italics, variable region in bold)

ATGGAATTGGGGCTGAGCTGGGTTTTCTCGTCGCTCTCCTAAGAGGTGTCCA
CTGTGAAGTGCATCTGGTGGAGTCGGGGGGAGGCGTGGTCCAACCTG
GAAAGTCCCTCAGACTCTCCTGTGTAACCTTCTGGCTTCATCTTCAAAC
AATATCCTATGTATTGGATCCGCCAGGCTCCAGGCAAGGGGCTGGAG
TGGGTGGCCGCCATCTCCGCTGATGCCTGGCATGTGGACTACGCAGG
CTCCGTGCGGGGCCGATTACCGTCTCCAGAGACAACCTCCAAGAATT
CTCTATATTTAGACATGAACAGTCTGACAGTTGAAGACACGGCTATAT
ATTTCTGTGCGAAAGATGGGGAAGAACACGAAGTACCACAGTTGCAC
TCCTGGAGCGGACGAAATTTATATCACTACACTGGTGTGGACATCTG
GGGCCCAGGGACCACGGTCACCGTCTCGAGCGCCTCCACCAAGGGCC
CATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGACACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGT
GTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCGGCTG
TCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCT
CCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCC
AGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAA
CTCACACATGCCCACCGTGCCAGCACCTGAACCTCCTGGGGGGACCGTCA
GTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACC
CCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA
AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC
TCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA
GGTCTCCAACAAAGCCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAG
CCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
GAGGAGATGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGCT
TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA
GAACAACCTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCT
TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA
CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC
AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:557)

[0833] 6892_C23 (PGT-157) gamma heavy chain variable region nucleotide sequence:

GAAGTGCATCTGGTGGAGTCGGGGGGAGGCGTGGTCCAACCTGGAA
AGTCCCTCAGACTCTCCTGTGTAACCTTCTGGCTTCATCTTCAAACAAT
ATCCTATGTATTGGATCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGG
GTGGCCGCCATCTCCGCTGATGCCTGGCATGTGGACTACGCAGGCTC

CGTGCGGGGCCGATTTACCGTCTCCAGAGACAACTCCAAGAATTCTC
TATATTTAGACATGAACAGTCTGACAGTTGAAGACACGGCTATATATT
TCTGTGCGAAAGATGGGGAAGAACACGAAGTACCACAGTTGCACTCC
TGGAGCGGACGAAATTTATATCACTACACTGGTGTGGACATCTGGGG
CCCAGGGACCACGGTCACCGTCTCGAGC (SEQ ID NO:558)

[0834] 6892_C23 (PGT-157) gamma heavy chain amino acid sequence: expressed protein with leader sequence in *italics* and variable region in **bold**.

MELGLSWVFLVALLRGVHCEVHLVESGGGVVQPGKSLRLSCVTSGFIFKQY
PMYWIRQAPGKGLEWVAAISADAWHVDYAGSVRGRFTVSRDNSKNSLY
*LDMNSLTVEDTAIFYCAKDGE****EEHEVPQLHSW******SGRNLYHYTGVDIWGPG***
TTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL
TSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVKDRVE
PKSCDKHTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
CSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 559)

[0835] 6892_C23 (PGT-157) gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in **bold italics**)

*EVHLVESGGGVVQPGKSLRLSCVTSG****FIFKQY******PMYWIRQAPGKGLEWVAAI***
SADAWHVDYAGSVRGRFTVSRDNSKNSLYLDMNSLTVEDTAIFYCAKD***GEE***
HEVPOLHSWSGRNLYHYTGVDI***WGPGTTVTVSS*** (SEQ ID NO: 560)

[0836] 6892_C23 (PGT-157) gamma heavy chain Kabat CDRs:

CDR 1: QYPMY (SEQ ID NO: 548)

CDR 2: AISADAWHVDYAGSVRG (SEQ ID NO: 534)

CDR 3: DGEEHEVPQLHSWSGRNLYHYTGVDI (SEQ ID NO: 561)

[0837] 6892_C23 (PGT-157) gamma heavy chain Chothia CDRs:

CDR 1: GFIFKQ (SEQ ID NO: 562)

CDR 2: AISADAWHVD (SEQ ID NO: 521)

CDR 3: DGEEHEVPQLHSWSGRNLYHYTGVDI (SEQ ID NO: 561)

[0838] 6892_C23 (PGT-157) light chain nucleotide sequence: coding sequence (variable region in **bold**)

ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGATACCTGAACT
TACTGCAGACATTGTGATGACCCAGACTCCTGTCTCTCTGTCCGTCAC
CCTCGGACAGCCGGCCTCCATGTCCTGTAAGTCCAGTCAGAGCCTCC
GACAAAGTGATGGCAAGACTTTCTTGTATTGGTATCGACAGAAGGCA
GGCCAGTCTCCACAACTCCTAATATCTGAGGCTTCGAATCGATTCTCT

GGAGTGT CAGATAGGTTCTCTGGCAGCGGTT CAGGGACAGACTTCAC
 ACTGAAAATCAGTCGGGTGGAGGCTGAGGATGTTGGCATTATTTCT
 GCATGCAAAC TAAAGACTTCCCCCTCACTTTTGGCGGAGGGACCAAG
 GTGGATCTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCC
 ATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAA
 TAACTTCTATCCCAGAGAGGGCCAAAGTACAGTGGAAGGTGGATAACGCCC
 TCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGA
 CAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTAC
 GAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTC
 GCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:563)

[0839] 6892_C23 (PGT-157) light chain variable region nucleotide sequence:

GACATTGTGATGACCCAGACTCCTGTCTCTCTGTCCGTCACCCCTCGG
 ACAGCCGGCCTCCATGTCCTGTAAGTCCAGTCAGAGCCTCCGACAAA
 GTGATGGCAAGACTTTCTTGTATTGGTATCGACAGAAGGCAGGCCAG
 TCTCCACAAC TCTAATATCTGAGGCTTCGAATCGATTCTCTGGAGTG
 TCAGATAGGTTCTCTGGCAGCGGTT CAGGGACAGACTTCACACTGAA
 AATCAGTCGGGTGGAGGCTGAGGATGTTGGCATTATTTCTGCATGC
 AAATAAAGACTTCCCCCTCACTTTTGGCGGAGGGACCAAGGTGGAT
 CTCAAA (SEQ ID NO:564)

[0840] 6892_C23 (PGT-157) light chain amino acid sequence: expressed protein with leader sequence in *italics* and variable region in **bold**.

MRLPAQLLGLLMLWIPELTADIVMTQTPVSLSVTLGQPASMSCKSSQSLRQS
DGKTFLYWYRQKAGQSPQLLISEASNRFSGVSDRFSGSGSGTDFTLKISR
VEAEDVGIYFCMQTKDFPLTFGGGTKVDLKRTVAAPSVFIFPPSDEQLKSG
 TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLT
 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 565)

[0841] 6892_C23 (PGT-157) light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in **bold italics**)

DIVMTQTPVSLSVTLGQPASMSC**KSSOSLROS****DGKTFLY**WYRQKAGQSPQLL
 ISE**ASNRF**SGVSDRFSGSGSGTDFTLKISRVEAEDVGIYFC**MOTKDFPLT**FGG
 GTKVDLK (SEQ ID NO: 566)

[0842] 6892_C23 (PGT-157) light chain Kabat CDRs:

CDR 1: KSSQSLRQSDGKTFLY (SEQ ID NO: 567)

CDR 2: EASNRF (SEQ ID NO: 568)

CDR 3: MQTKDFPLT (SEQ ID NO: 569)

[0843] 6892_C23 (PGT-157) light chain Chothia CDRs:

CDR 1: KSSQSLRQSDGKTFLY (SEQ ID NO: 567)

CDR 2: EASNRFS (SEQ ID NO: 568)

CDR 3: MQTKDFPLT (SEQ ID NO: 569)

[0844] 6881_N05 (PGT-158) gamma heavy chain nucleotide sequence: coding sequence
(variable region in bold)

*ATGGAATTGGGGCTGAGCTGGGTTTTCTCGTCGCTCTCCTAAGAGGTGTCCA
CTGTGAGGTGCGTCTGATGGAGTCGGGGGGAGGCGTGGTCCAGCCTG
GGAAGTCCCTCAGACTCTCCTGTGTAACCTCTGGCTTCATCTTCAAAA
AATATCCTATGTAAGTGGATCCGCCAGGCTCCAGGCAAGGGGCTGGAG
TGGGTGGCCGCCATCTCCGCTGATGCCTGGCATGTGGACTACCCAGG
CTCCGTGCGGGGCCGATTTACCGTCTCAAGAGACAACTCCAAGAATT
CTCTATATTTAGACATGAATAGTCTGACAGTAGAAGACACGGCTATAT
ATTTTTGTGCGAAAGATGGGGAGGAACACGAAGTCCCACAACCTGCAC
TCCTGGAGCGGACGAAATTTATATCACTACACTGGTGTAGACGTCTG
GGGCCCAGGGACCACGGTCACCGTCTCGAGCGCCTCCACCAAGGGCC
CATCGGTCTTCCCCCTGGCACCTCTCTCCAAGAGCACCTCTGGGGGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGT
GTCGTGGAACCTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGGCTG
TCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCT
CCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCC
AGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAA
CTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCA
GTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACC
CCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA
AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC
TCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA
GGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
CCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
GAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCT
TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA
GAACAACCTACAAGACCACGCCTCCCGTGTGGACTCCGACGGCTCCTTCT
TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA
CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC
AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:570)*

[0845] 6881_N05 (PGT-158) gamma heavy chain variable region nucleotide sequence:

*GAGGTGCGTCTGATGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGA
AGTCCCTCAGACTCTCCTGTGTAACCTCTGGCTTCATCTTCAAAAAAT
ATCCTATGTAAGTGGATCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGG
GTGGCCGCCATCTCCGCTGATGCCTGGCATGTGGACTACCCAGGCTC
CGTGCGGGGCCGATTTACCGTCTCAAGAGACAACTCCAAGAATTCTC
TATATTTAGACATGAATAGTCTGACAGTAGAAGACACGGCTATATATT
TTTGTGCGAAAGATGGGGAGGAACACGAAGTCCCACAACCTGCACTCC*

**TGGAGCGGACGAAATTTATATCACTACACTGGTGTAGACGTCTGGGG
CCCAGGGACCACGGTCACCGTCTCGAGC (SEQ ID NO:571)**

[0846] 6881_N05 (PGT-158) gamma heavy chain amino acid sequence: expressed protein with leader sequence in italics and variable region in bold.

*MELGLSWVFLVALLRGVHCEVRLMESGGGVVQPGKSLRLSCVTSGFIFKKY
PMYWIRQAPGKGLEWVAAISADAWHVDYPGSVRGRFTVSRDNSKNSLY
LDMNSLTVEDTAIFYCAKDGEHEVPQLHSWSGRNLYHYTGVDVWGPG
TTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL
TSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVE
PKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTTPVLDSGFFLYSKLTVDKSRWQQGNVFS
CSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 572)*

[0847] 6881_N05 (PGT-158) gamma heavy chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

*EVRLMESGGGVVQPGKSLRLSCVTSGFIFKKYPMYWIRQAPGKGLEWVAAI
SADAWHVDYPGSVRGRFTVSRDNSKNSLYLDMNSLTVEDTAIFYCAKDGE
HEVPQLHSWSGRNLYHYTGVDVWGPGTTVTVSS (SEQ ID NO: 573)*

[0848] 6881_N05 (PGT-158) gamma heavy chain Kabat CDRs:

CDR 1: KYPMY (SEQ ID NO: 475)

CDR 2: AISADAWHVDYPGSVRG (SEQ ID NO: 549)

CDR 3: DGEHEVPQLHSWSGRNLYHYTGVDV (SEQ ID NO: 574)

[0849] 6881_N05 (PGT-158) gamma heavy chain Chothia CDRs:

CDR 1: GFIFKK (SEQ ID NO: 575)

CDR 2: AISADAWHVD (SEQ ID NO: 521)

CDR 3: DGEHEVPQLHSWSGRNLYHYTGVDV (SEQ ID NO: 574)

[0850] 6881_N05 (PGT-158) light chain nucleotide sequence: coding sequence (variable region in bold)

*ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGATACCTGAAGT
GACTGCAGACATTGTGATGACCCAGACTCCTGTCTCTGTGTCCGTCAC
CCTCGGACAGCCGGCCTCCATGTCCTGCAAGTCCAGTCAGAGCGTCC
GACAAAGTGATGGCAAGACTTTTTTATATTGGTATCGACAGAAGGCA
GGCCAGTCTCCACAACCTCTTAATATATGAGGCTTCGAAGCGATTCTCT
GGAGTGTGATAGGTTCTCTGGCAGCGGGTCAGGGACAGACTTCAC
ACTGAAAATCAGTCGGGTGGGGGCTGAGGATGTTGGCGTTTATTCT
GCATGCAAACTAAAGACTTCCCCCTTACTTTTGGCGGAGGGACCAAG*

GTGGATCTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCC
ATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAA
TAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCC
TCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGA
CAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTAC
GAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTC
GCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:576)

[0851] 6881_N05 (PGT-158) light chain variable region nucleotide sequence:

GACATTGTGATGACCCAGACTCCTGTCTCTGTGTCCGTCACCCCTCGG
ACAGCCGGCCTCCATGTCCTGCAAGTCCAGTCAGAGCGTCCGACAAA
GTGATGGCAAGACTTTTTTATATTGGTATCGACAGAAGGCAGGCCAG
TCTCCACAACCTCTTAATATATGAGGCTTCGAAGCGATTCTCTGGAGTG
TCAGATAGGTTCTCTGGCAGCGGGTCAGGGACAGACTTCACACTGAA
AATCAGTCGGGTGGGGGCTGAGGATGTTGGCGTTTATTTCTGCATGC
AACTAAAGACTTCCCCCTTACTTTTGGCGGAGGGACCAAGGTGGAT
CTCAA (SEQ ID NO:577)

[0852] 6881_N05 (PGT-158) light chain amino acid sequence: expressed protein with leader sequence in *italics* and variable region in **bold**.

MRLPAQLLGLLMLWIPEVTADIVMTQTPVSVSVTLGQPASMSCKSSQSVRQS
DGKTFLYWYRQKAGQSPQLLIYEASKRFS*GVSDRFS***SGSGTDFTLKISR**
VGAEDVG*VYFCMQTKDFPLT***FGGGTKVDL***KRTVAAPS**VFIFPPS**DEQLKS*
*GTASVVCLLNNFY**PREAKVQWKVDNALQSGNSQES**VT**EQDSKD**STYLSST*
*LTLSKADY**EKH**KVYACEVTHQGLSSPVTKS**FN**R**GEC (SEQ ID NO: 578)*

[0853] 6881_N05 (PGT-158) light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in **bold italics**)

*DIVMTQTPVSVSVTLGQPASMSCK****SSOSVROSDGKTFLY****WYRQKAGQSPQLL*
*IY****EASKRFS****GVSDRFS**SGSGTDFTLKISR**VGAEDVG**VYFC****MQTKDFPLT****FGG*
GTKVDLK (SEQ ID NO: 579)

[0854] 6881_N05 (PGT-158) light chain Kabat CDRs:

CDR 1: KSSQSVRQSDGKTFLY (SEQ ID NO: 541)

CDR 2: EASKRFS (SEQ ID NO: 580)

CDR 3: MQTKDFPLT (SEQ ID NO: 569)

[0855] 6881_N05 (PGT-158) light chain Chothia CDRs:

CDR 1: KSSQSVRQSDGKTFLY (SEQ ID NO: 541)

CDR 2: EASKRFS (SEQ ID NO: 580)

CDR 3: MQTKDFPLT (SEQ ID NO: 569)

[0856] The 6831_A21 (PGT-151) antibody includes a heavy chain variable region (SEQ ID NO: 474), encoded by the nucleic acid sequence shown in SEQ ID NO: 472, and a light chain variable region (SEQ ID NO: 483) encoded by the nucleic acid sequence shown in SEQ ID NO: 481.

[0857] The heavy chain CDRs of the 6831_A21 (PGT-151) antibody have the following sequences per Kabat definition: KYPMY (SEQ ID NO: 475), AISGDAWHVVYSNSVQG (SEQ ID NO: 476), and MFQESGPPRLDRWSGRNYYYYSGMDV (SEQ ID NO: 477). The light chain CDRs of the 6831_A21 (PGT-151) antibody have the following sequences per Kabat definition: KSSESLRQSNGKTSLY (SEQ ID NO: 484), EVSNRFS (SEQ ID NO: 485), and MQSKDFPLT (SEQ ID NO: 486).

[0858] The heavy chain CDRs of the 6831_A21 (PGT-151) antibody have the following sequences per Chothia definition: DFPFSK (SEQ ID NO: 478), AISGDAWHVV (SEQ ID NO: 479), and MFQESGPPRLDRWSGRNYYYYSGMDV (SEQ ID NO: 477). The light chain CDRs of the 6831_A21 (PGT-151) antibody have the following sequences per Chothia definition: KSSESLRQSNGKTSLY (SEQ ID NO: 484), EVSNRFS (SEQ ID NO: 485), and MQSKDFPLT (SEQ ID NO: 486).

[0859] The 6889_I17 (PGT-152) antibody includes a heavy chain variable region (SEQ ID NO: 490), encoded by the nucleic acid sequence shown in SEQ ID NO: 488, and a light chain variable region (SEQ ID NO: 497) encoded by the nucleic acid sequence shown in SEQ ID NO: 495.

[0860] The heavy chain CDRs of the 6889_I17 (PGT-152) antibody have the following sequences per Kabat definition: KYPMY (SEQ ID NO: 475), AISADAWHVVYSGSVQG (SEQ ID NO: 491), and MFQESGPPRFDSWSGRNYYYYSGMDV (SEQ ID NO: 492). The light chain CDRs of the 6889_I17 (PGT-152) antibody have the following sequences per Kabat definition: KSSQSLRQSNGKTSLY (SEQ ID NO: 498), EVSNRFS (SEQ ID NO: 485), and MQSKDFPLT (SEQ ID NO: 486).

[0861] The heavy chain CDRs of the 6889_I17 (PGT-152) antibody have the following sequences per Chothia definition: DFPFSK (SEQ ID NO: 478), AISADAWHVV (SEQ ID NO: 493), and MFQESGPPRFDSWSGRNYYYYSGMDV (SEQ ID NO: 492). The light chain CDRs of the 6889_I17 (PGT-152) antibody have the following sequences per Chothia definition:

KSSQSLRQSNKGKTSLY (SEQ ID NO: 498), EVSNRFS (SEQ ID NO: 485), and MQSKDFPLT (SEQ ID NO: 486).

[0862] The 6891_F06 (PGT-153) antibody includes a heavy chain variable region (SEQ ID NO: 502), encoded by the nucleic acid sequence shown in SEQ ID NO: 500, and a light chain variable region (SEQ ID NO: 511) encoded by the nucleic acid sequence shown in SEQ ID NO: 509.

[0863] The heavy chain CDRs of the 6891_F06 (PGT-153) antibody have the following sequences per Kabat definition: KRHHM (SEQ ID NO: 503), VISSDAIHVDYASSVRG (SEQ ID NO: 504), and DRDGYGPPQIQTWSGRYLHLYSGIDA (SEQ ID NO: 505). The light chain CDRs of the 6891_F06 (PGT-153) antibody have the following sequences per Kabat definition: KSSQSLRQSNKGKTYLY (SEQ ID NO: 512), EVSIRFS (SEQ ID NO: 513), and MQSKDFPLT (SEQ ID NO: 486).

[0864] The heavy chain CDRs of the 6891_F06 (PGT-153) antibody have the following sequences per Chothia definition: NFLFNK (SEQ ID NO: 506), VISSDAIHVD (SEQ ID NO: 507), and DRDGYGPPQIQTWSGRYLHLYSGIDA (SEQ ID NO: 505). The light chain CDRs of the 6891_F06 (PGT-153) antibody have the following sequences per Chothia definition: KSSQSLRQSNKGKTYLY (SEQ ID NO: 512), EVSIRFS (SEQ ID NO: 513), and MQSKDFPLT (SEQ ID NO: 486).

[0865] The 6843_G20 (PGT-154) antibody includes a heavy chain variable region (SEQ ID NO: 517), encoded by the nucleic acid sequence shown in SEQ ID NO: 515, and a light chain variable region (SEQ ID NO: 525) encoded by the nucleic acid sequence shown in SEQ ID NO: 523.

[0866] The heavy chain CDRs of the 6843_G20 (PGT-154) antibody have the following sequences per Kabat definition: KYPMY (SEQ ID NO: 475), AISADAWHVDYAASVKD (SEQ ID NO: 518), and NIEEFSVPQFDSWSGRSYYHYFGMDV (SEQ ID NO: 519). The light chain CDRs of the 6843_G20 (PGT-154) antibody have the following sequences per Kabat definition: SSSESLGRGDGRTYLH (SEQ ID NO: 526), EVSTRFS (SEQ ID NO: 527), and MQSRDFPIT (SEQ ID NO: 528).

[0867] The heavy chain CDRs of the 6843_G20 (PGT-154) antibody have the following sequences per Chothia definition: NFIFNK (SEQ ID NO: 520), AISADAWHVD (SEQ ID NO: 521), and NIEEFSVPQFDSWSGRSYYHYFGMDV (SEQ ID NO: 519). The light chain CDRs

of the 6843_G20 (PGT-154) antibody have the following sequences per Chothia definition: SSSESLGRGDGRITYLH (SEQ ID NO: 526), EVSTRFS (SEQ ID NO: 527), and MQSRDFPIT (SEQ ID NO: 528).

[0868] The 6892_D19 (PGT-155) antibody includes a heavy chain variable region (SEQ ID NO: 532), encoded by the nucleic acid sequence shown in SEQ ID NO: 530, and a light chain variable region (SEQ ID NO: 540) encoded by the nucleic acid sequence shown in SEQ ID NO: 538.

[0869] The heavy chain CDRs of the 6892_D19 (PGT-155) antibody have the following sequences per Kabat definition: EYPMY (SEQ ID NO: 533), AISADAWHVDYAGSVRG (SEQ ID NO: 534), and DGEEHKVPQLHSWSGRNLYHYTGFDV (SEQ ID NO: 535). The light chain CDRs of the 6892_D19 (PGT-155) antibody have the following sequences per Kabat definition: KSSQSVRQSDGKTFLY (SEQ ID NO: 541), EGSSRFS (SEQ ID NO: 542), and LQTKDFPLT (SEQ ID NO: 543).

[0870] The heavy chain CDRs of the 6892_D19 (PGT-155) antibody have the following sequences per Chothia definition: GFIFNE (SEQ ID NO: 536), AISADAWHVD (SEQ ID NO: 521), and DGEEHKVPQLHSWSGRNLYHYTGFDV (SEQ ID NO: 535). The light chain CDRs of the 6892_D19 (PGT-155) antibody have the following sequences per Chothia definition: KSSQSVRQSDGKTFLY (SEQ ID NO: 541), EGSSRFS (SEQ ID NO: 542), and LQTKDFPLT (SEQ ID NO: 543).

[0871] The 6808_B09 (PGT-156) antibody includes a heavy chain variable region (SEQ ID NO: 547), encoded by the nucleic acid sequence shown in SEQ ID NO: 545, and a light chain variable region (SEQ ID NO: 554) encoded by the nucleic acid sequence shown in SEQ ID NO: 552.

[0872] The heavy chain CDRs of the 6808_B09 (PGT-156) antibody have the following sequences per Kabat definition: QYPMY (SEQ ID NO: 548), AISADAWHVDYPGSVRG (SEQ ID NO: 549), and DGEEHKVPQLHSWSGRNLYHYTGFDV (SEQ ID NO: 535). The light chain CDRs of the 6808_B09 (PGT-156) antibody have the following sequences per Kabat definition: KSSQTVRQSDGKTFLY (SEQ ID NO: 555), EGSNRFS (SEQ ID NO: 556), and LQTKDFPLT (SEQ ID NO: 543).

[0873] The heavy chain CDRs of the 6808_B09 (PGT-156) antibody have the following sequences per Chothia definition: GFIFNQ (SEQ ID NO: 550), AISADAWHVD (SEQ ID NO:

521), and DGEEHKVPQLHSWSGRNLYHYTGFDV (SEQ ID NO: 535). The light chain CDRs of the 6808_B09 (PGT-156) antibody have the following sequences per Chothia definition: KSSQTVRQSDGKTFLY (SEQ ID NO: 555), EGSNRFS (SEQ ID NO: 556), and LQTKDFPLT (SEQ ID NO: 543).

[0874] The 6892_C23 (PGT-157) antibody includes a heavy chain variable region (SEQ ID NO: 560), encoded by the nucleic acid sequence shown in SEQ ID NO: 558, and a light chain variable region (SEQ ID NO: 566) encoded by the nucleic acid sequence shown in SEQ ID NO: 564.

[0875] The heavy chain CDRs of the 6892_C23 (PGT-157) antibody have the following sequences per Kabat definition: QYPMY (SEQ ID NO: 548), AISADAWHVDYAGSVRG (SEQ ID NO: 534), and DGEEHEVPQLHSWSGRNLYHYTGVDI (SEQ ID NO: 561). The light chain CDRs of the 6892_C23 (PGT-157) antibody have the following sequences per Kabat definition: KSSQSLRQSDGKTFLY (SEQ ID NO: 567), EASNRFS (SEQ ID NO: 568), and MQTKDFPLT (SEQ ID NO: 569).

[0876] The heavy chain CDRs of the 6892_C23 (PGT-157) antibody have the following sequences per Chothia definition: GFIFKQ (SEQ ID NO: 562), AISADAWHVD (SEQ ID NO: 521), and DGEEHEVPQLHSWSGRNLYHYTGVDI (SEQ ID NO: 561). The light chain CDRs of the 6892_C23 (PGT-157) antibody have the following sequences per Chothia definition: KSSQSLRQSDGKTFLY (SEQ ID NO: 567), EASNRFS (SEQ ID NO: 568), and MQTKDFPLT (SEQ ID NO: 569).

[0877] The 6881_N05 (PGT-158) antibody includes a heavy chain variable region (SEQ ID NO: 573), encoded by the nucleic acid sequence shown in SEQ ID NO: 571, and a light chain variable region (SEQ ID NO: 579) encoded by the nucleic acid sequence shown in SEQ ID NO: 577.

[0878] The heavy chain CDRs of the 6881_N05 (PGT-158) antibody have the following sequences per Kabat definition: KYPMY (SEQ ID NO: 475), AISADAWHVDYPGSVRG (SEQ ID NO: 549), and DGEEHEVPQLHSWSGRNLYHYTGVDV (SEQ ID NO: 574). The light chain CDRs of the 6881_N05 (PGT-158) antibody have the following sequences per Kabat definition: KSSQSVRQSDGKTFLY (SEQ ID NO: 541), EASKRFS (SEQ ID NO: 580), and MQTKDFPLT (SEQ ID NO: 569).

[0879] The heavy chain CDRs of the 6881_N05 (PGT-158) antibody have the following sequences per Chothia definition: GFIFKK (SEQ ID NO: 575), AISADAWHVD (SEQ ID NO: 521), and DGEEHEVPQLHSWSGRNLYHYTGVDV (SEQ ID NO: 574). The light chain CDRs of the 6881_N05 (PGT-158) antibody have the following sequences per Chothia definition: KSSQSVRQSDGKTFLY (SEQ ID NO: 541), EASKRFS (SEQ ID NO: 580), and MQTKDFPLT (SEQ ID NO: 569).

[0880] In one aspect, an antibody according to the invention contains a heavy chain having the amino acid sequence of SEQ ID NOs: 12, 16, 20, 24, 28, 139, 47, 53, 59, 65, 62, 153, 165, 181, 197, 213, 229, 246, 275, 291, 297, 306, 318, 333, 346, 362, 400, 404, 419, 434, 443, 453, 462, 473, 489, 501, 516, 531, 546, 559, or 572, and a light chain having the amino acid sequence of SEQ ID NOs: 14, 18, 22, 26, 30, 142, 50, 56, 148, 158, 174, 190, 206, 222, 238, 255, 284, 301, 312, 329, 392, 355, 396, 385, 413, 428, 439, 448, 583, 469, 482, 496, 510, 524, 539, 553, 565, or 578. Alternatively, an antibody according to the invention contains a heavy chain variable region having the amino acid sequence of SEQ ID NOs: 31, 33, 35, 37, 39, 140, 48, 54, 60, 79, 156, 168, 184, 200, 216, 232, 149, 276, 292, 298, 307, 319, 334, 347, 363, 401, 405, 420, 435, 444, 454, 463, 474, 490, 502, 517, 532, 547, 560, or 573, and a light chain variable region having the amino acid sequence of SEQ ID NOs: 32, 34, 36, 38, 40, 96, 51, 57, 149, 161, 177, 193, 209, 225, 242, 258, 285, 302, 313, 330, 393, 356, 397, 386, 414, 429, 440, 449, 584, 470, 483, 497, 511, 525, 540, 554, 566, or 579.

[0881] In another aspect, an antibody according to the invention contains a heavy chain having the amino acid sequence encoded by the nucleic acid sequence of SEQ ID NOs: 11, 15, 19, 23, 27, 138, 46, 52, 58, 64, 66, 166, 167, 183, 199, 215, 231, 248, 273, 289, 295, 304, 314, 316, 331, 344, 360, 398, 402, 417, 432, 441, 451, 460, 471, 487, 499, 514, 529, 544, 557, or 570, and a light chain having the amino acid sequence encoded by the nucleic acid sequence of SEQ ID NOs: 13, 17, 21, 25, 29, 141, 49, 55, 61, 67, 146, 160, 176, 192, 208, 224, 240, 257, 282, 299, 310, 327, 390, 353, 394, 383, 411, 426, 437, 446, 581, 467, 480, 494, 508, 522, 537, 551, 563, or 576. Alternatively, an antibody according to the invention contains a heavy chain variable region having the amino acid sequence encoded by the nucleic acid sequence of SEQ ID NOs: 99, 101, 109, 115, 122, 128, 130, 132, 134, 136, 63, 154, 166, 182, 198, 214, 230, 247, 274, 290, 296, 305, 315, 317, 332, 345, 361, 399, 403, 418, 433, 442, 452, 461, 472, 488, 500, 515, 530, 545, 558, or 571, and a light chain variable region having the amino acid sequence encoded by the

nucleic acid sequence of SEQ ID NOs: 100, 106, 112, 119, 125, 129, 131, 133, 135, 137, 147, 159, 175, 191, 207, 223, 239, 256, 283, 300, 311, 328, 391, 354, 395, 384, 412, 427, 438, 447, 582, 468, 481, 495, 509, 523, 538, 552, 564, or 577. Furthermore, an antibody according to the invention contains a heavy chain having the amino acid sequence encoded by a nucleic acid sequence of SEQ ID NOs: 11, 15, 19, 23, 27, 138, 46, 52, 58, 64, 66, 166, 167, 183, 199, 215, 231, 248, 273, 289, 295, 304, 314, 316, 331, 344, 360, 398, 402, 417, 432, 441, 451, 460, 471, 487, 499, 514, 529, 544, 557, or 570, which contains a silent or degenerate mutation, and a light chain having the amino acid sequence encoded by the nucleic acid sequence of SEQ ID NOs: 13, 17, 21, 25, 29, 141, 49, 55, 61, 67, 146, 160, 176, 192, 208, 224, 240, 257, 282, 299, 310, 327, 390, 353, 394, 383, 411, 426, 437, 446, 581, 467, 480, 494, 508, 522, 537, 551, 563, or 576, which contains a silent or degenerate mutation. Silent and degenerate mutations alter the nucleic acid sequence, but do not alter the resultant amino acid sequence.

[0882] Preferably the three heavy chain CDRs include an amino acid sequence of at least 90%, 92%, 95%, 97%, 98%, 99%, or more identical to the amino acid sequence of KYGMH (SEQ ID NO: 88), LISDDGMRKYHSDSMWG (SEQ ID NO: 89), EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6), SYAFT (SEQ ID NO: 104), MVTPIFGEAKYSQRFEG (SEQ ID NO: 105), DRRVPIATDNWLDP (SEQ ID NO: 9), SYAFS (SEQ ID NO: 110), MITPVFGETKYAPRFQG (SEQ ID NO: 111), DRRVPMATDNWLDP (SEQ ID NO: 8), DYVLH (SEQ ID NO: 116), LIDPENGEARYAEKFQG (SEQ ID NO: 117), GAVGADSGSWFDP (SEQ ID NO: 10), RQGMH (SEQ ID NO: 123), FIKYDGSEKYHADSVWG (SEQ ID NO: 124), EAGGPDYRNGYNYDFYDGYNYHYMDV (SEQ ID NO: 7), LISDDGMRKYHSNSMWG (SEQ ID NO: 98), DSYWS (SEQ ID NO: 90), YVHKSGDTNYSPLKS (SEQ ID NO: 265), TLHGRRIGIVAFNEWFTYFYMDV (SEQ ID NO: 143), DNYWS (SEQ ID NO: 261), YVHDSGDTNYPNPSLKS (SEQ ID NO: 157), TKHGRRIGVVAFKEWFTYFYMDV (SEQ ID NO: 262), DAYWS (SEQ ID NO: 169), YVHHSGDTNYPNPSLKR (SEQ ID NO: 170), ALHGKRIYGIVALGELFTYFYMDV (SEQ ID NO: 171), ACTYFWG (SEQ ID NO: 185), SLSHCQSFWGSWTFHNPSLKS (SEQ ID NO: 186), FDGEVLVYNHWPKEWVDL (SEQ ID NO: 187), ACDYFWG (SEQ ID NO: 201), GLSHCAGYYNTGWTYHNPSLKS (SEQ ID NO: 202), FDGEVLVYHDWPKPAWVDL (SEQ ID NO: 203), TGHYYWG (SEQ ID NO: 217), HHHYTTAVLHNPSLKS (SEQ ID NO:

218), SGGDILYYEWQKPHWFSP (SEQ ID NO: 219), GGEWGDKDYHWG (SEQ ID NO: 233), SIHWRTTTHYKESLRR (SEQ ID NO: 234), HRHHDVFMLVPIAGWFDV (SEQ ID NO: 235), GTDWGENDFHYG (SEQ ID NO: 250), SIHWRTTTHYKTSFRS (SEQ ID NO: 251), HKYHDIFRVVPVAGWFDP (SEQ ID NO: 252), KYDVH (SEQ ID NO: 277), WMSHEGDKTESAQRFKG (SEQ ID NO: 278), GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (SEQ ID NO: 279), WISHERDKTESAQRFKG (SEQ ID NO: 293), GSKHRLRDYVLYDDYGLINQQEWNDYLEFLDV (SEQ ID NO: 308), RCNYFWG (SEQ ID NO: 320), SLSHCRSYYNTDWTYHNPSLKS (SEQ ID NO: 321), FGGEVLVYRDWPKPAWVDL (SEQ ID NO: 322), ACNSFWG (SEQ ID NO: 326), SLSHCASYWNRGWTYHNPSLKS (SEQ ID NO: 335), FGGEVLRYTDWPKPAWVDL (SEQ ID NO: 336), TGHHYWG (SEQ ID NO: 348), HIHYNTAVLHNPALKS (SEQ ID NO: 349), SGGDILYYIEWQKPHWFYP (SEQ ID NO: 350), GGEWGDSDYHWG (SEQ ID NO: 364), SIHWRTTTHYNAPFRG (SEQ ID NO: 365), HKYHDIVMVVPIAGWFDP (SEQ ID NO: 366), NHDVH (SEQ ID NO: 378), WMSHEGDKTGLAQKFQG (SEQ ID NO: 379), GSKHRLRDYFLYNEYGPNYEEWGDYLATLDV (SEQ ID NO: 380), NYYWT (SEQ ID NO: 406), YISDRETTTYNPSLNS (SEQ ID NO: 407), ARRGQRIYGVVSFGEFFYYYYMDV (SEQ ID NO: 408), GRFWS (SEQ ID NO: 421), YFSDTDRSEYNPSLRS (SEQ ID NO: 422), AQQGKRIYGIVSFGEFFYYYYMDA (SEQ ID NO: 423), AQQGKRIYGIVSFGELFYYYYMDA (SEQ ID NO: 436), SGGDILYYNEWQKPHWFYP (SEQ ID NO: 445), SLSHCAGYYNSGWTYHNPSLKS (SEQ ID NO: 455), FGGDVLVYHDWPKPAWVDL (SEQ ID NO: 456), GCDYFWG (SEQ ID NO: 464), FDGEVLVYNDWPKPAWVDL (SEQ ID NO: 465), KYPMY (SEQ ID NO: 475), AISGDAWHVVYNSVQG (SEQ ID NO: 476), MFQESGPPRLDRWSGRNYYYYSGMDV (SEQ ID NO: 477), AISADAWHVYSGSVQG (SEQ ID NO: 491), MFQESGPPRFDSWSGRNYYYYSGMDV (SEQ ID NO: 492), KRHMH (SEQ ID NO: 503), VISSDAIHVDYASSVRG (SEQ ID NO: 504), DRDGYGPPQIQTWSGRYLHLYSGIDA (SEQ ID NO: 505), AISADAWHVDYAASVKD (SEQ ID NO: 518), NIEEFSVPQFDSWSGRSYYHYFGMDV (SEQ ID NO: 519), EYPMY (SEQ ID NO: 533), AISADAWHVDYAGSVRG (SEQ ID NO: 534), DGEEHKVPQLHSWSGRNLYHYTGFDV (SEQ ID NO: 535), QYPMY (SEQ ID NO: 548), AISADAWHVDYPGSVRG (SEQ ID NO:

549), DGEEHEVPQLHSWSGRNLYHYTGVDI (SEQ ID NO: 561), DGEEHEVPQLHSWSGRNLYHYTGVDV (SEQ ID NO: 574), (as determined by the Kabat method) or GFTFHK (SEQ ID NO: 266), LISDDGMRKY (SEQ ID NO: 267), EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6), GGTFSS (SEQ ID NO: 268), MVTPIFGEAK (SEQ ID NO: 269), DRRVPIATDNWLDP (SEQ ID NO: 9), GGAFSS (SEQ ID NO: 270), MITPVFGETK (SEQ ID NO: 271), DRRVVPMDTNWLDP (SEQ ID NO: 8), GYSFID (SEQ ID NO: 102), LIDPENGAR (SEQ ID NO: 103), GAVGADSGSWFDP (SEQ ID NO: 10), GFDFSR (SEQ ID NO: 118), FIKYDGSEKY (SEQ ID NO: 272), EAGGPDYRNGYNYDFYDGYNYHYMDV (SEQ ID NO: 7), GASISD (SEQ ID NO: 144), YVHKSGDTN (SEQ ID NO: 145), TLHGRRYGVAFNEWFTYFYMDV (SEQ ID NO: 143), GTLVRD (SEQ ID NO: 263), YVHDSGDTN (SEQ ID NO: 264), TKHGRRYGVVAFKEWFTYFYMDV (SEQ ID NO: 262), GASIND (SEQ ID NO: 172), YVHHSMDTN (SEQ ID NO: 173), ALHGKRIYGVAFALGELFTYFYMDV (SEQ ID NO: 171), GESTGACT (SEQ ID NO: 188), SLSHCQSFWSGSGWTF (SEQ ID NO: 189), FDGEVLVYNHWPKPAWVDL (SEQ ID NO: 187), GDSTAACD (SEQ ID NO: 204), GLSHCAGYYNTGWTY (SEQ ID NO: 205), FDGEVLVYHDWPKPAWVDL (SEQ ID NO: 203), GESINTGH (SEQ ID NO: 220), HHHYTTAVL (SEQ ID NO: 221), SGGDILYYEWQKPHWFSP (SEQ ID NO: 219), GDSIRGGEWGDKD (SEQ ID NO: 236), SIHWRGTH (SEQ ID NO: 237), HRHHDVFMVLVPIAGWFDV (SEQ ID NO: 235), GGSMRGTDWGEND (SEQ ID NO: 253), SIHWRGTH (SEQ ID NO: 254), HKYHDIFRVVPVAGWFDV (SEQ ID NO: 252), GNTFSK (SEQ ID NO: 280), WMSHEGDKTE (SEQ ID NO: 281), GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (SEQ ID NO: 279), WISHERDKTE (SEQ ID NO: 294), GSKHRLRDYVLYDDYGLINQQEWNDYLEFLDV (SEQ ID NO: 308), or GNTFRK (SEQ ID NO: 309), GDSTGRCN (SEQ ID NO: 323), SLSHCRSYNTDWTY (SEQ ID NO: 324), FGGEVLVYRDWPKPAWVDL (SEQ ID NO: 322), GDSTAACN (SEQ ID NO: 337), SLSHCASYWNRGWTY (SEQ ID NO: 338), FGGEVLRYTDWPKPAWVDL (SEQ ID NO: 336), GDSINTGH (SEQ ID NO: 351), HHHYNTAVL (SEQ ID NO: 352), SGGDILYYIEWQKPHWFYP (SEQ ID NO: 350), GGSIRGGEWGDS (SEQ ID NO: 367), SIHWRGTH (SEQ ID NO: 237), HKYHDIVMVVPIAGWFDV (SEQ ID NO: 366), GNSFSN (SEQ ID NO: 381), WMSHEGDKTG (SEQ ID NO: 382),

GSKHRLRDYFLYNEYGPNYEEWGDYLATLDV (SEQ ID NO: 380), GGSISN (SEQ ID NO: 409), YISDRETTT (SEQ ID NO: 410), ARRGQRIYGVVSFGEFFYYYYMDV (SEQ ID NO: 408), NGSVSG (SEQ ID NO: 424), YFSDTDRSE (SEQ ID NO: 425), AQQGKRIYGIVSFGEFFYYYYMDA (SEQ ID NO: 423), AQQGKRIYGIVSGELFYYYYMDA (SEQ ID NO: 436), SGGDILYYNEWQKPHWFYP (SEQ ID NO: 445), SLSHCAGYYNSGWTY (SEQ ID NO: 457), FGGDVLVYHDWPKPAWVDL (SEQ ID NO: 456), GDSTAGCD (SEQ ID NO: 466), FDGEVLVYNDWPKPAWVDL (SEQ ID NO: 465), DFPFSK (SEQ ID NO: 478), AISGDAWHVV (SEQ ID NO: 479), MFQESGPPRLDRWSGRNYYYYSGMDV (SEQ ID NO: 477), AISADAWHVV (SEQ ID NO: 493), MFQESGPPRFDSWSGRNYYYYSGMDV (SEQ ID NO: 492), NFLFNK (SEQ ID NO: 506), VISSDAIHVD (SEQ ID NO: 507), DRDGYGPPQIQTWSGRYLHLYSGIDA (SEQ ID NO: 505), NFIFNK (SEQ ID NO: 520), AISADAWHVD (SEQ ID NO: 521), NIEEFSVPQFDSWSGRSYHYHYFGMDV (SEQ ID NO: 519), GFIFNE (SEQ ID NO: 536), DGEEHKVPQLHSWSGRNLYHYTGFDV (SEQ ID NO: 535), GFIFNQ (SEQ ID NO: 550), GFIFKQ (SEQ ID NO: 562), DGEEHEVPQLHSWSGRNLYHYTGVDI (SEQ ID NO: 561), GFIFKK (SEQ ID NO: 575), DGEEHEVPQLHSWSGRNLYHYTGVDV (SEQ ID NO: 574), (as determined by the Chothia method), and a light chain with three CDRs that include an amino acid sequence of at least 90%, 92%, 95%, 97%, 98%, 99%, or more identical to the amino acid sequence of NGTSSDVGGFDSVS (SEQ ID NO: 97), DVSHRPS (SEQ ID NO: 95), SSLTDRSHRI (SEQ ID NO: 41), RASQTINNYLN (SEQ ID NO: 107), GASNLQN (SEQ ID NO: 108), QQSFSTPRT (SEQ ID NO: 42), RASQTIHTYLN (SEQ ID NO: 113), GASTLQS (SEQ ID NO: 114), QQSYSTPRT (SEQ ID NO: 43), SGSKLGDKYVS (SEQ ID NO: 120), ENDRRPS (SEQ ID NO: 121), QAWETTTTTTFVF (SEQ ID NO: 44), NGTSNDVGGYESVS (SEQ ID NO: 126), DVSKRPS (SEQ ID NO: 127), KSLTSTRRRV (SEQ ID NO: 45), NGTRSDVGGFDSVS (SEQ ID NO: 92), NGTSRDVGGFDSVS (SEQ ID NO: 93), GEKSLGSRAVQ (SEQ ID NO: 150), NNQDRPS (SEQ ID NO: 151), HIWDSRVPTKWV (SEQ ID NO: 152), GEESLGSRSVI (SEQ ID NO: 162), NNNDRPS (SEQ ID NO: 163), HIWDSRRPTNWV (SEQ ID NO: 164), GKESIGSRAVQ (SEQ ID NO: 178), NNQDRPA (SEQ ID NO: 179), HIYDARGGTNWV (SEQ ID NO: 180), NGTATNFVS (SEQ ID NO: 194), GVDKRPP (SEQ ID NO: 195), GSLVGNWDVI (SEQ ID NO: 196), TGTSNRFVS (SEQ ID NO: 210), GVNKRPS (SEQ ID

NO: 211), SSLVGNWDVI (SEQ ID NO: 212), NGTSSDIGGWNFVS (SEQ ID NO: 226), EVNKRPS (SEQ ID NO: 227), SSLFGRWDVV (SEQ ID NO: 228), RASQNINKNLA (SEQ ID NO: 243), ETYSKIA (SEQ ID NO: 244), QQYEEWPRT (SEQ ID NO: 245), RASQNVKNNLA (SEQ ID NO: 259), DASSRAG (SEQ ID NO: 260), SSTQSLRHSNGANYLA (SEQ ID NO: 286), LGSQRAS (SEQ ID NO: 287), MQGLNRPWT (SEQ ID NO: 288), or TSTQSLRHSNGANYLA (SEQ ID NO: 303), TGTSNNFVS (SEQ ID NO: 325), DVNKRPS (SEQ ID NO: 343), GSLVGNWDVI (SEQ ID NO: 196), SGTGSDIGSWNFVS (SEQ ID NO: 357), EVNRRRS (SEQ ID NO: 358), SSLSGRWDIV (SEQ ID NO: 359), RASQSVKNNLA (SEQ ID NO: 372), DTSSRAS (SEQ ID NO: 373), KCSHSLQHSTGANYLA (SEQ ID NO: 387), LATHRAS (SEQ ID NO: 388), MQGLHSPWT (SEQ ID NO: 389), GRQALGSRAVQ (SEQ ID NO: 415), HMWDSRSGFSWS (SEQ ID NO: 416), GERSRGSRAVQ (SEQ ID NO: 430), HYWDSRSPISWI (SEQ ID NO: 431), SGTASDIGSWNFVS (SEQ ID NO: 450), TGNINNFVS (SEQ ID NO: 458), GSLAGNWDVV (SEQ ID NO: 459), KSSESLRQSNGKTSLY (SEQ ID NO: 484), EVSNRFS (SEQ ID NO: 485), MQSKDFPLT (SEQ ID NO: 486), KSSQSLRQSNGKTSLY (SEQ ID NO: 498), KSSQSLRQSNGKTYLY (SEQ ID NO: 512), EVSIRFS (SEQ ID NO: 513), SSSESLGRGDGRTYLH (SEQ ID NO: 526), EVSTRFS (SEQ ID NO: 527), MQSRDFPIT (SEQ ID NO: 528), KSSQSVRQSDGKTFLY (SEQ ID NO: 541), EGSSRFS (SEQ ID NO: 542), LQTKDFPLT (SEQ ID NO: 543), KSSQTVRQSDGKTFLY (SEQ ID NO: 555), EGSNRFS (SEQ ID NO: 556), KSSQSLRQSDGKTFLY (SEQ ID NO: 567), EASNRFS (SEQ ID NO: 568), MQTKDFPLT (SEQ ID NO: 569), EASKRFS (SEQ ID NO: 580), (as determined by the Kabat method), or NGTSSDVGGFDSVS (SEQ ID NO: 97), DVSHRPS (SEQ ID NO: 95), SSLTDRSHRI (SEQ ID NO: 41), RASQTINNYLN (SEQ ID NO: 107), GASNLQN (SEQ ID NO: 108), QQSFTPRT (SEQ ID NO: 42), RASQTIHTYLN (SEQ ID NO: 113), GASTLQS (SEQ ID NO: 114), QQSYSTPRT (SEQ ID NO: 43), SGSKLGDKYVS (SEQ ID NO: 120), ENDRRPS (SEQ ID NO: 121), QAWETTTTTTFVF (SEQ ID NO: 44), NGTSNDVGGYESVS (SEQ ID NO: 126), DVSKRPS (SEQ ID NO: 127), KSLTSTRRRV (SEQ ID NO: 45), NGTRSDVGGFDSVS (SEQ ID NO: 92), NGTSRDVGGFDSVS (SEQ ID NO: 93), GEKSLGSRAVQ (SEQ ID NO: 150), NNQDRPS (SEQ ID NO: 151), HIWDSRVPTKWV (SEQ ID NO: 152), GEESLGSRSVI (SEQ ID NO: 162), NNNDRPS (SEQ ID NO: 163), HIWDSRRPTNWV (SEQ ID NO: 164), GKESIGSRAVQ (SEQ ID NO: 178), NNQDRPA

(SEQ ID NO: 179), HIYDARGGTNWV (SEQ ID NO: 180), NGTATNFVS (SEQ ID NO: 194), GVDKRPP (SEQ ID NO: 195), GSLVGNWDVI (SEQ ID NO: 196), TGTSNRFVS (SEQ ID NO: 210), GVNKRPS (SEQ ID NO: 211), SSLVGNWDVI (SEQ ID NO: 212), NGTSSDIGGWNFVS (SEQ ID NO: 226), EVNKRPS (SEQ ID NO: 227), SSLFGRWDVV (SEQ ID NO: 228), RASQNINKNLA (SEQ ID NO: 243), ETYSKIA (SEQ ID NO: 244), QQYEEWPRT (SEQ ID NO: 245), RASQNVKNNLA (SEQ ID NO: 259), DASSRAG (SEQ ID NO: 260), SSTQSLRHSNGANYLA (SEQ ID NO: 286), LGSQRAS (SEQ ID NO: 287), MQGLNRPWT (SEQ ID NO: 288), TSTQSLRHSNGANYLA (SEQ ID NO: 303), TGTSNNFVS (SEQ ID NO: 325), DVNKRPS (SEQ ID NO: 343), GSLVGNWDVI (SEQ ID NO: 196), SGTGSDIGSWNFVS (SEQ ID NO: 357), EVNRRRS (SEQ ID NO: 358), SSLSGRWDIV (SEQ ID NO: 359), RASQSVKNNLA (SEQ ID NO: 372), DTSSRAS (SEQ ID NO: 373), KCSHSLQHSTGANYLA (SEQ ID NO: 387), LATHRAS (SEQ ID NO: 388), MQGLHSPWT (SEQ ID NO: 389), GRQALGSRAVQ (SEQ ID NO: 415), HMWDSRSGFSWS (SEQ ID NO: 416), GERSRGSRAVQ (SEQ ID NO: 430), HYWDSRSPISWI (SEQ ID NO: 431), SGTASDIGSWNFVS (SEQ ID NO: 450), TGNINNFVS (SEQ ID NO: 458), GSLAGNWDVV (SEQ ID NO: 459), KSSESLRQSNGKTSLY (SEQ ID NO: 484), EVSNRFS (SEQ ID NO: 485), MQSKDFPLT (SEQ ID NO: 486), KSSQSLRQSNGKTSLY (SEQ ID NO: 498), KSSQSLRQSNGKTYLY (SEQ ID NO: 512), EVSIRFS (SEQ ID NO: 513), SSSESLGRGDGRTYLH (SEQ ID NO: 526), EVSTRFS (SEQ ID NO: 527), MQSRDFPIT (SEQ ID NO: 528), KSSQSVRQSDGKTFLY (SEQ ID NO: 541), EGSSRFS (SEQ ID NO: 542), LQTKDFPLT (SEQ ID NO: 543), KSSQTVRQSDGKTFLY (SEQ ID NO: 555), EGSNRFS (SEQ ID NO: 556), KSSQSLRQSDGKTFLY (SEQ ID NO: 567), EASNRFS (SEQ ID NO: 568), MQTKDFPLT (SEQ ID NO: 569), EASKRFS (SEQ ID NO: 580), (as determined by the Chothia method).

[0883] The heavy chain of the anti-HIV monoclonal antibody is derived from a germ line variable (V) gene such as, for example, the IGHV1, IGHV3, or IGHV4 germline gene or an allele thereof.

[0884] The anti-HIV antibodies of the invention include a variable heavy chain (V_H) region encoded by a human IGHV1, IGHV3, or IGHV4 germline gene sequence or an allele thereof. Antibodies of the invention are derived from the IGHV1-2, IGHV1-8, or IGHV1-46 genes, or an allele thereof. Exemplary alleles of the IGHV1 germline gene include, but are not limited to,

IGHV1-2*02, IGHV1-2*04, IGHV1-8*01, IGHV1-46*01, IGHV1-46*02, or IGHV1-46*03. IGHV1 germline gene sequences are shown, *e.g.*, in Accession numbers L22582, X27506, X92340, M83132, X67905, L22583, Z29978, Z14309, Z14307, Z14300, Z14296, and Z14301. IGHV3 germline gene sequences are shown, *e.g.*, in Accession numbers AB019439, M99665, M77305, M77335, and M77334. Antibodies of the invention are derived from the IGHV4-59, IGHV4-64, IGHV4-b, IGHV4-39, or IGHV4-28 genes, or an allele thereof. Exemplary alleles of the IGHV4 germline gene include, but are not limited to, IGHV4-59*01, IGHV4-59*07, IGHV4-59*02, IGHV4-59*03, IGHV4-59*04, IGHV4-61*08, IGHV4-b*02, IGHV4-b*01, IGHV4-39*07, IGHV4-39*03, IGHV4-39*06, IGHV4-39*01, IGHV4-39*02, or IGHV4-28*05. IGHV4 germline gene sequences are shown, *e.g.*, in Accession numbers AB019439, L10094, X05715, X92259, X92297, M95116, Z14236, AM940222, X54447, X56362, Z14075, Z75352, AB019438, M29812, M95114, M95117, M95118, M95119, X56360, X87091, Z75359, Z14243, L10088, U03896, X56355, X56359, X92248, X92296, Z12371, M29811, L10097, X92230, X92250, X56356, Z75347, Z75348, AB019437, M95111, X92249, X92251, Z12366, Z75346, Z75361, Z12367, X56365, and X92289. The anti-HIV antibodies of the invention include a V_H region that is encoded by a nucleic acid sequence that is at least 80% homologous to the IGHV1, IGHV3, or IGHV4 germline gene sequence or an allele thereof. Preferably, the nucleic acid sequence is at least 90%, 95%, 96%, 97% homologous to the IGHV1, IGHV3, or IGHV4 germline gene sequence, and more preferably, at least 98%, 99% homologous to the IGHV1, IGHV3, or IGHV4 germline gene sequence or an allele thereof. The V_H region of the anti-HIV antibody is at least 80% homologous to the amino acid sequence of the V_H region encoded by the IGHV1, IGHV3, or IGHV4 germline gene sequence or an allele thereof. Preferably, the amino acid sequence of V_H region of the anti-HIV antibody is at least 90%, 95%, 96%, 97% homologous to the amino acid sequence encoded by the IGHV1, IGHV3, or IGHV4 germline gene sequence or an allele thereof, and more preferably, at least 98%, 99% homologous to the sequence encoded by the IGHV1, IGHV3, or IGHV4 germline gene sequence or an allele thereof.

[0885] The light chain of the anti-HIV monoclonal antibody is derived from a germ line variable (V) gene such as, for example, the IGLV2, IGLV3, IGKV1, IGKV2, IGKV2D, or IGKV3 germline gene or an allele thereof.

[0886] The anti-HIV antibodies of the invention also include a variable light chain (V_L) region encoded by a human IGLV2, IGLV3, IGKV1, IGKV2, IGKV2D, IGKV3, or IGKV3D germline gene or an allele thereof. A human IGLV2 V_L germline gene sequence is shown, *e.g.*, Accession numbers Z73664, L27822, Y12412, and Y12413. A human IGLV3 V_L germline gene sequence is shown, *e.g.*, Accession number X57826. Antibodies of the invention are derived from the IGLV2-8 germline gene, or an allele thereof.

[0887] Exemplary alleles of the IGLV2-8 germline gene include, but are not limited to, IGLV2-8*01 and IGLV2-8*02. Antibodies of the invention are derived from the IGLV3-21 germline gene, or an allele thereof. Exemplary alleles of the IGLV3-21 germline gene include, but are not limited to, IGLV3-21*01, IGLV3-21*02, and IGLV3-21*03. Antibodies of the invention are derived from the IGKV2-28 and IGKV2D-28 germline genes, or an allele thereof. Exemplary alleles of the IGKV2-28 and IGKV2D-28 germline genes include, but are not limited to, IGKV2-28*01 and IGKV2D-28*01. Antibodies of the invention are derived from the IGKV3-15 and IGKV3D-15 germline genes, or an allele thereof. Exemplary alleles of the IGKV3-15 and IGKV3D-15 germline genes include, but are not limited to, IGKV3-15*01, IGKV3D-15*01, and IGKV3D-15*02(P).

[0888] A human IGLV2 V_L germline gene sequence is shown, *e.g.*, Accession numbers Z73657, Z73664, Z73642, X14616, X97466, Z73643, D87013, Z73641, X97462, D87021, Y12417, L27695, and Z22209. A human IGLV3 V_L germline gene sequence is shown, *e.g.*, Accession numbers X57826, X97464, Z73658, X97463, D87015, X97471, X97472, X56178, X97468, X71966, D87007, M94115, Z73666, X71968, X97474, X97467, D86994, Z73644, Z73646, X97469, Z73645, D87024, X97465, X97470, and X97473. A human IGKV1 V_L germline gene sequence is shown, *e.g.*, Accession numbers AF306358, AF490911, L12062, L12064, L12065, L12066, L12068, L12072, L12075, L12076, L12079, L12080, L12081, L12082, L12083, L12084, L12085, L12086, :12088, L12091, L12093, L12101, L12106, L12108, L12110, L12112, M95721, M95722, M95723, X73855, X73860, X98972, X98973, Z15073, Z15074, Z15075, Z15077, Z15079, Z15081. A human IGKV3 V_L germline gene sequence is shown, *e.g.*, Accession numbers X01668, M23090, X12686, X06583, X71883, X71891, X02725, L37728, L37727, L37730, L19271, L19272, X17264, X72815, X12687, X71886, X71896, X71895, X72820.

[0889] Alternatively, the anti-HIV antibodies include a V_L region that is encoded by a nucleic acid sequence that is at least 80% homologous to the IGLV2, IGLV3, IGKV1, IGKV2, IGKV2D, IGKV3, or IGKV3D germline gene or an allele thereof. Preferably, the nucleic acid sequence is at least 90%, 95%, 96%, 97% homologous to the IGLV2, IGLV3, IGKV1, IGKV2, IGKV2D, IGKV3, or IGKV3D germline gene or an allele thereof, and more preferably, at least 98%, 99% homologous to the IGLV2, IGLV3, IGKV1, IGKV2, IGKV2D, IGKV3, or IGKV3D germline gene or an allele thereof. The V_L region of the anti-HIV antibody is at least 80% homologous to the amino acid sequence of the V_L region encoded the IGLV2, IGLV3, IGKV1, IGKV2, IGKV2D, IGKV3, or IGKV3D germline gene or an allele thereof. Preferably, the amino acid sequence of V_L region of the anti-HIV antibody is at least 90%, 95%, 96%, 97% homologous to the amino acid sequence encoded by the IGLV2, IGLV3, IGKV1, IGKV2, IGKV2D, IGKV3, or IGKV3D germline gene or an allele thereof, and more preferably, at least 98%, 99% homologous to the sequence encoded by the IGLV2, IGLV3, IGKV1, IGKV2, IGKV2D, IGKV3, or IGKV3D germline gene or an allele thereof.

Kabat CDR sequences for the PG16 sister clones are highlighted in boxes.

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Table 8. Alignment of light chain coding sequences of the variable domain of 1443 C16 sister clones to 1443 C16 and 1496 C09.

Kabat CDR sequences for the PG16 sister clones are highlighted in boxes.

1496 C09 L2 refseq	10	20	30	40	50	60	70	80	90	100	110	120	130	140	150	160	170	180	190	200	210	220	230	240	250	260	270	280	290	300	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450	460	470	480	490	500	510	520	530	540	550	560	570	580	590	600	610	620	630	640	650	660	670	680	690	700	710	720	730	740	750	760	770	780	790	800	810	820	830	840	850	860	870	880	890	900	910	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430	1440	1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560	1570	1580	1590	1600	1610	1620	1630	1640	1650	1660	1670	1680	1690	1700	1710	1720	1730	1740	1750	1760	1770	1780	1790	1800	1810	1820	1830	1840	1850	1860	1870	1880	1890	1900	1910	1920	1930	1940	1950	1960	1970	1980	1990	2000	2010	2020	2030	2040	2050	2060	2070	2080	2090	2100	2110	2120	2130	2140	2150	2160	2170	2180	2190	2200	2210	2220	2230	2240	2250	2260	2270	2280	2290	2300	2310	2320	2330	2340	2350	2360	2370	2380	2390	2400	2410	2420	2430	2440	2450	2460	2470	2480	2490	2500	2510	2520	2530	2540	2550	2560	2570	2580	2590	2600	2610	2620	2630	2640	2650	2660	2670	2680	2690	2700	2710	2720	2730	2740	2750	2760	2770	2780	2790	2800	2810	2820	2830	2840	2850	2860	2870	2880	2890	2900	2910	2920	2930	2940	2950	2960	2970	2980	2990	3000	3010	3020	3030	3040	3050	3060	3070	3080	3090	3100	3110	3120	3130	3140	3150	3160	3170	3180	3190	3200	3210	3220	3230	3240	3250	3260	3270	3280	3290	3300	3310	3320	3330	3340	3350	3360	3370	3380	3390	3400	3410	3420	3430	3440	3450	3460	3470	3480	3490	3500	3510	3520	3530	3540	3550	3560	3570	3580	3590	3600	3610	3620	3630	3640	3650	3660	3670	3680	3690	3700	3710	3720	3730	3740	3750	3760	3770	3780	3790	3800	3810	3820	3830	3840	3850	3860	3870	3880	3890	3900	3910	3920	3930	3940	3950	3960	3970	3980	3990	4000	4010	4020	4030	4040	4050	4060	4070	4080	4090	4100	4110	4120	4130	4140	4150	4160	4170	4180	4190	4200	4210	4220	4230	4240	4250	4260	4270	4280	4290	4300	4310	4320	4330	4340	4350	4360	4370	4380	4390	4400	4410	4420	4430	4440	4450	4460	4470	4480	4490	4500	4510	4520	4530	4540	4550	4560	4570	4580	4590	4600	4610	4620	4630	4640	4650	4660	4670	4680	4690	4700	4710	4720	4730	4740	4750	4760	4770	4780	4790	4800	4810	4820	4830	4840	4850	4860	4870	4880	4890	4900	4910	4920	4930	4940	4950	4960	4970	4980	4990	5000	5010	5020	5030	5040	5050	5060	5070	5080	5090	5100	5110	5120	5130	5140	5150	5160	5170	5180	5190	5200	5210	5220	5230	5240	5250	5260	5270	5280	5290	5300	5310	5320	5330	5340	5350	5360	5370	5380	5390	5400	5410	5420	5430	5440	5450	5460	5470	5480	5490	5500	5510	5520	5530	5540	5550	5560	5570	5580	5590	5600	5610	5620	5630	5640	5650	5660	5670	5680	5690	5700	5710	5720	5730	5740	5750	5760	5770	5780	5790	5800	5810	5820	5830	5840	5850	5860	5870	5880	5890	5900	5910	5920	5930	5940	5950	5960	5970	5980	5990	6000	6010	6020	6030	6040	6050	6060	6070	6080	6090	6100	6110	6120	6130	6140	6150	6160	6170	6180	6190	6200	6210	6220	6230	6240	6250	6260	6270	6280	6290	6300	6310	6320	6330	6340	6350	6360	6370	6380	6390	6400	6410	6420	6430	6440	6450	6460	6470	6480	6490	6500	6510	6520	6530	6540	6550	6560	6570	6580	6590	6600	6610	6620	6630	6640	6650	6660	6670	6680	6690	6700	6710	6720	6730	6740	6750	6760	6770	6780	6790	6800	6810	6820	6830	6840	6850	6860	6870	6880	6890	6900	6910	6920	6930	6940	6950	6960	6970	6980	6990	7000	7010	7020	7030	7040	7050	7060	7070	7080	7090	7100	7110	7120	7130	7140	7150	7160	7170	7180	7190	7200	7210	7220	7230	7240	7250	7260	7270	7280	7290	7300	7310	7320	7330	7340	7350	7360	7370	7380	7390	7400	7410	7420	7430	7440	7450	7460	7470	7480	7490	7500	7510	7520	7530	7540	7550	7560	7570	7580	7590	7600	7610	7620	7630	7640	7650	7660	7670	7680	7690	7700	7710	7720	7730	7740	7750	7760	7770	7780	7790	7800	7810	7820	7830	7840	7850	7860	7870	7880	7890	7900	7910	7920	7930	7940	7950	7960	7970	7980	7990	8000	8010	8020	8030	8040	8050	8060	8070	8080	8090	8100	8110	8120	8130	8140	8150	8160	8170	8180	8190	8200	8210	8220	8230	8240	8250	8260	8270	8280	8290	8300	8310	8320	8330	8340	8350	8360	8370	8380	8390	8400	8410	8420	8430	8440	8450	8460	8470	8480	8490	8500	8510	8520	8530	8540	8550	8560	8570	8580	8590	8600	8610	8620	8630	8640	8650	8660	8670	8680	8690	8700	8710	8720	8730	8740	8750	8760	8770	8780	8790	8800	8810	8820	8830	8840	8850	8860	8870	8880	8890	8900	8910	8920	8930	8940	8950	8960	8970	8980	8990	9000	9010	9020	9030	9040	9050	9060	9070	9080	9090	9100	9110	9120	9130	9140	9150	9160	9170	9180	9190	9200	9210	9220	9230	9240	9250	9260	9270	9280	9290	9300	9310	9320	9330	9340	9350	9360	9370	9380	9390	9400	9410	9420	9430	9440	9450	9460	9470	9480	9490	9500	9510	9520	9530	9540	9550	9560	9570	9580	9590	9600	9610	9620	9630	9640	9650	9660	9670	9680	9690	9700	9710	9720	9730	9740	9750	9760	9770	9780	9790	9800	9810	9820	9830	9840	9850	9860	9870	9880	9890	9900	9910	9920	9930	9940	9950	9960	9970	9980	9990	10000	10010	10020	10030	10040	10050	10060	10070	10080	10090	10100	10110	10120	10130	10140	10150	10160	10170	10180	10190	10200	10210	10220	10230	10240	10250	10260	10270	10280	10290	10300	10310	10320	10330	10340	10350	10360	10370	10380	10390	10400	10410	10420	10430	10440	10450	10460	10470	10480	10490	10500	10510	10520	10530	10540	10550	10560	10570	10580	10590	10600	10610	10620	10630	10640	10650	10660	10670	10680	10690	10700	10710	10720	10730	10740	10750	10760	10770	10780	10790	10800	10810	10820	10830	10840	10850	10860	10870	10880	10890	10900	10910	10920	10930	10940	10950	10960	10970	10980	10990	11000	11010	11020	11030	11040	11050	11060	11070	11080	11090	11100	11110	11120	11130	11140	11150	11160	11170	11180	11190	11200	11210	11220	11230	11240	11250	11260	11270	11280	11290	11300	11310	11320	11330	11340	11350	11360	11370	11380	11390	11400	11410	11420	11430	11440	11450	11460	11470	11480	11490	11500	11510	11520	11530	11540	11550	11560	11570	11580	11590	11600	11610	11620	11630	11640	11650	11660	11670	11680	11690	11700	11710	11720	11730	11740	11750	11760	11770	11780	11790	11800	11810	11820	11830	11840	11850	11860	11870	11880	11890	11900	11910	1

Table 9. Alignment of heavy chain protein sequences of the variable domain of 1443 C16 sister clones to 1443 C16 and 1496 C09.

Kabat CDR sequences for the PG16 sister clones are highlighted in boxes.

1469_M23_G3_refseq	K																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						

Table 10. Alignment of light chain protein sequences of the variable domain of 1443 C16 sister clones to 1443 C16 and 1496 C09.

Kabat CDR sequences for the PG16 sister clones are highlighted in black boxes.

Table 11. Consensus nucleotide sequences of Kabat CDRs of heavy chains of 1443 PG16 sister clones.CDR1 (kabat):

1443 C16	AAATATGGCATGCAC (SEQ ID NO: 68)
1469 M23	AAATATGGCATGCAC (SEQ ID NO: 68)
1456 A12	AAATATGGCATGCAC (SEQ ID NO: 68)
1503 H05	AAATATGGCATGCAC (SEQ ID NO: 68)
1489 I13	AAATATGGCATGCAC (SEQ ID NO: 68)
1480 I08	AAATATGGCATGCAC (SEQ ID NO: 68)
Consensus	AAATATGGCATGCAC (SEQ ID NO: 68)

CDR1 (chothia):

1443 C16	TCTGGATTACGTTTCACAAA (SEQ ID NO: 69)
1469 M23	TCTGGATTACCTTTCACAAA (SEQ ID NO: 70)
1456 A12	TCTGGATTACGTTTCACAAA (SEQ ID NO: 69)
1503 H05	TCTGGATTACCTTTCACAAA (SEQ ID NO: 70)
1489 I13	TCTGGATTACGTTTCACAAA (SEQ ID NO: 69)
1480 I08	TCTGGATTACGTTTCACAAA (SEQ ID NO: 69)
Consensus*	TCTGGATTACXTTTCACAAA (SEQ ID NO: 71)
Variation1	TCTGGATTACGTTTCACAAA (SEQ ID NO: 69)
Variation2	TCTGGATTACCTTTCACAAA (SEQ ID NO: 70)

* Wherein X is C or G.

CDR2:

1443 C16	CTCATCTCAGATGACGGAATGAGGAAATATCATTTCAGACTCCATGTG GGGC (SEQ ID NO: 72)
1469 M23	CTCATCTCAGATGACGGAATGAGGAAATATCATTTCAGACTCCATGTG GGGC (SEQ ID NO: 72)
1456 A12	CTCATCTCAGATGACGGAATGAGGAAATATCATTTCAGACTCCATGTG GGGC (SEQ ID NO: 72)
1503 H05	CTCATCTCAGATGACGGAATGAGGAAATATCATTTCAGACTCCATGTG GGGC (SEQ ID NO: 72)
1489 I13	CTCATCTCAGATGACGGAATGAGGAAATATCATTCAAACCTCCATGTG GGGC (SEQ ID NO: 73)
1480 I08	CTCATCTCAGATGACGGAATGAGGAAATATCATTTCAGACTCCATGTG GGGC (SEQ ID NO: 72)
Consensus*	CTCATCTCAGATGACGGAATGAGGAAATATCATTTCAXACTCCATGTG GGGC (SEQ ID NO: 74)
Variation1	CTCATCTCAGATGACGGAATGAGGAAATATCATTTCAGACTCCATGTG GGGC (SEQ ID NO: 72)
Variation2	CTCATCTCAGATGACGGAATGAGGAAATATCATTCAAACCTCCATGTG GGGC (SEQ ID NO: 73)

* Wherein X is A or G.

CDR3:

1443 C16 (SEQ ID NO: 75)

GAGGCTGGTGGGCCAATCTGGCATGACGACGTCAAATATTACGATTTTAATGACGG
CTACTACAACCTACCACTACATGGACGTC

1469 M23 (SEQ ID NO: 75)

GAGGCTGGTGGGCCAATCTGGCATGACGACGTCAAATATTACGATTTTAATGACGG
CTACTACAACCTACCACTACATGGACGTC

1456 A12 (SEQ ID NO: 77)

GAGGCCGGTGGGCCAATCTGGCATGACGACGTCAAATATTACGATTTTAATGACGG
CTACTACAACCTATCACTACATGGACGTC

1503 H05 (SEQ ID NO: 79)

GAGGCTGGTGGGCCAATCTGGCATGACGACGTCAAATATTACGATTTTAATGACGG
CTACTACAATTACCACTACATGGACGTC

1489 I13 (SEQ ID NO: 75)

GAGGCTGGTGGGCCAATCTGGCATGACGACGTCAAATATTACGATTTTAATGACGG
CTACTACAACCTACCACTACATGGACGTC

1480 I08 (SEQ ID NO: 75)

GAGGCTGGTGGGCCAATCTGGCATGACGACGTCAAATATTACGATTTTAATGACGG
CTACTACAACCTACCACTACATGGACGTC

Consensus (SEQ ID NO: 76)

GAGGCXGGTGGGCCAATCTGGCATGACGACGTCAAATATTACGATTTTAATGACGG
CTACTACAACCTATCACTACATGGACGTC

Variation1 (SEQ ID NO: 78)

GAGGCCGGTGGGCCAATCTGGCATGACGACGTCAAATATTACGATTTTAATGACGG
CTACTACAACCTATCACTACATGGACGTC

Variation2 (SEQ ID NO: 77)

GAGGCCGGTGGGCCAATCTGGCATGACGACGTCAAATATTACGATTTTAATGACGG
CTACTACAACCTATCACTACATGGACGTC

* Wherein X is T, C or G.

Table 12. Consensus nucleotide sequences of Kabat CDRs of light chains of 1443 PG16 sister clones.CDR1:1443 C16 AATGGAACCAGCAGTGACGTTGGTGGATTTGACTCTGTCTCC (SEQ
ID NO: 80)1469 M23 AATGGAACCAGAAGTGACGTTGGTGGATTTGACTCTGTCTCC (SEQ
ID NO: 82)1456 A12 AATGGAACCAGCCGTGACGTTGGTGGATTTGACTCTGTCTCC (SEQ
ID NO: 83)1503 H05 AATGGAACCAGAAGTGACGTTGGTGGATTTGACTCTGTCTCC (SEQ
ID NO: 82)1489 I13 AATGGAACCAGCAGTGACGTTGGTGGATTTGACTCTGTCTCC (SEQ
ID NO: 80)1480 I08 AATGGAACCAGCAGTGACGTTGGTGGATTTGACTCTGTCTCC (SEQ
ID NO: 80)Consensus* AATGGAACCAGX₁X₂GTGACGTTGGTGGATTTGACTCTGTCTCC (SEQ

	ID NO: 81)
Variation1	AATGGAACCAGCAGTGACGTTGGTGGATTTGACTCTGTCTCC (SEQ ID NO: 80)
Variation2	AATGGAACCAGAAAGTGACGTTGGTGGATTTGACTCTGTCTCC (SEQ ID NO: 82)
Variation2	AATGGAACCAGCCGTGACGTTGGTGGATTTGACTCTGTCTCC (SEQ ID NO: 83)

* Wherein X₁ is C or A. Wherein X₂ is C or A.

CDR2:

1443 C16	GATGTCAGTCATCGGCCCTCA (SEQ ID NO: 84)
1469 M23	GATGTCAGTCATCGGCCCTCA (SEQ ID NO: 84)
1456 A12	GATGTCAGTCATCGGCCCTCA (SEQ ID NO: 84)
1503 H05	GATGTCAGTCATCGGCCCTCA (SEQ ID NO: 84)
1489 I13	GATGTCAGTCATCGGCCCTCA (SEQ ID NO: 84)
1480 I08	GATGTCAGTCATCGGCCCTCA (SEQ ID NO: 84)
Consensus	GATGTCAGTCATCGGCCCTCA (SEQ ID NO: 84)

CDR3:

1443 C16	TCTTCACTGACAGACAGAAGCCATCGCATA (SEQ ID NO: 85)
1469 M23	TCTTCACTGACAGACAGAAGCCATCGCATA (SEQ ID NO: 85)
1456 A12	TCTTCATTGACAGACAGAAGCCATCGCATA (SEQ ID NO: 86)
1503 H05	TCTTCACTGACAGACAGAAGCCATCGCATA (SEQ ID NO: 85)
1489 I13	TCTTCACTGACAGACAGAAGCCATCGCATA (SEQ ID NO: 85)
1480 I08	TCTTCACTGACAGACAGAAGCCATCGCATA (SEQ ID NO: 85)
Consensus*	TCTTCAXTGACAGACAGAAGCCATCGCATA (SEQ ID NO: 87)
Variation1	TCTTCACTGACAGACAGAAGCCATCGCATA (SEQ ID NO: 85)
Variation2	TCTTCATTGACAGACAGAAGCCATCGCATA (SEQ ID NO: 86)

* Wherein X₁ is C or T and wherein X₂ is C or T.

Table 13. Consensus protein sequences of Kabat CDRs of Heavy chains of 1443 PG16 sister clones.

CDR1:

1443 C16	KYGMH (SEQ ID NO: 88)
1469 M23	KYGMH (SEQ ID NO: 88)
1456 A12	KYGMH (SEQ ID NO: 88)
1503 H05	KYGMH (SEQ ID NO: 88)
1489 I13	KYGMH (SEQ ID NO: 88)
1480 I08	KYGMH (SEQ ID NO: 88)
Consensus	KYGMH (SEQ ID NO: 88)

CDR2:

1443 C16	LISDDGMRKYHSDSMWG (SEQ ID NO: 89)
1469 M23	LISDDGMRKYHSDSMWG (SEQ ID NO: 89)

1456 A12	LISDDGMRKYHSDSMWG (SEQ ID NO: 89)
1503 H05	LISDDGMRKYHSDSMWG (SEQ ID NO: 89)
1489 I13	LISDDGMRKYHSNSMWG (SEQ ID NO: 98)
1480 I08	LISDDGMRKYHSDSMWG (SEQ ID NO: 89)
Consensus*	LISDDGMRKYHSXSMWG (SEQ ID NO: 91)
Variation1	LISDDGMRKYHSDSMWG (SEQ ID NO: 89)
Variation2	LISDDGMRKYHSNSMWG (SEQ ID NO: 98)

* Wherein X is D or N, or wherein X is an amino acid with similar physical properties to either D or N.

CDR3:

1443 C16	EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6)
1469 M23	EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6)
1456 A12	EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6)
1503 H05	EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6)
1489 I13	EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6)
1480 I08	EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6)
Consensus	EAGGPIWHDDVKYYDFNDGYNYHYMDV (SEQ ID NO: 6)

Table 14. Consensus protein sequences of Kabat CDRs of light chains of 1443 PG16 sister clones.

CDR1:

1443 C16	NGTSSDVGGFDSVS (SEQ ID NO: 97)
1469 M23	NGTRSDVGGFDSVS (SEQ ID NO: 92)
1456 A12	NGTSRDVGGFDSVS (SEQ ID NO: 93)
1503 H05	NGTRSDVGGFDSVS (SEQ ID NO: 92)
1489 I13	NGTSSDVGGFDSVS (SEQ ID NO: 97)
1480 I08	NGTSSDVGGFDSVS (SEQ ID NO: 97)
Consensus*	NGTX ₁ X ₂ DVGGFDSVS (SEQ ID NO: 94)
Variation1	NGTSSDVGGFDSVS (SEQ ID NO: 97)
Variation2	NGTRSDVGGFDSVS (SEQ ID NO: 92)
Variation3	NGTSRDVGGFDSVS (SEQ ID NO: 93)

* Wherein X₁ is S or R, or wherein X₁ is an amino acid with similar physical properties to either S or R. Wherein X₂ is S or R, or wherein X₂ is an amino acid with similar physical properties to either S or R.

CDR2:

1443 C16	DVSHRPS (SEQ ID NO: 95)
1469 M23	DVSHRPS (SEQ ID NO: 95)
1456 A12	DVSHRPS (SEQ ID NO: 95)
1503 H05	DVSHRPS (SEQ ID NO: 95)
1489 I13	DVSHRPS (SEQ ID NO: 95)
1408 I08	DVSHRPS (SEQ ID NO: 95)
Consensus	DVSHRPS (SEQ ID NO: 95)

CDR3:

1443 C16	SSLTDRSHRI (SEQ ID NO: 41)
1469 M23	SSLTDRSHRI (SEQ ID NO: 41)
1456 A12	SSLTDRSHRI (SEQ ID NO: 41)
1503 H05	SSLTDRSHRI (SEQ ID NO: 41)
1489 I13	SSLTDRSHRI (SEQ ID NO: 41)
1480 I08	SSLTDRSHRI (SEQ ID NO: 41)
Consensus	SSLTDRSHRI (SEQ ID NO: 41)

[0890] Monoclonal and recombinant antibodies are particularly useful in identification and purification of the individual polypeptides or other antigens against which they are directed. The antibodies of the invention have additional utility in that they may be employed as reagents in immunoassays, radioimmunoassays (RIA) or enzyme-linked immunosorbent assays (ELISA). In these applications, the antibodies can be labeled with an analytically-detectable reagent such as a radioisotope, a fluorescent molecule or an enzyme. The antibodies may also be used for the molecular identification and characterization (epitope mapping) of antigens.

[0891] As mentioned above, the antibodies of the invention can be used to map the epitopes to which they bind. Applicants have discovered that the antibodies 1443_C16 (PG16) (TCN-116), 1503 H05 (PG16) (TCN-119), 1456 A12 (PG16) (TCN-117), 1469 M23 (PG16) (TCN-118), 1489_I13 (PG16) (TCN-120), 1480_I08 (PG16), 1456_P20 (PG20), 1460_G14 (PGG14), 1495_C14 (PGC14), 1496_C09 (PG9) (TCN-109), 4838_L06 (PGT-121), 4873_E03 (PGT-121), 4877_D15 (PGT-122), 4858_P08 (PGT-123), 6123_A06 (PGT-125), 5141_B17 (PGT-126), 5145_B14 (PGT-127), 5114_A19 (PGT-128), 5147_N06 (PGT-130), 5136_H01 (PGT-131), 5343_B08 (PGT-135), 5344_E16 (PGT-135), 5329_C19 (PGT-136), 5366_P21 (PGT-136), 4964_G22 (PGT-141), 5345_I01 (PGT-137), 4993_K13 (PGT-141), 4995_E20 (PGT-142), 4980_N08 (PGT-143), 4970_K22 (PGT-144), 4995_P16 (PGT-145), 4835_F12 (PGT-124), 4869_K15 (PGT-133), 4876_M06 (PGT-134), 5131_A17 (PGT-132), 5138_G07 (PGT-138), 5120_N10 (PGT-139), 6831_A21 (PGT-151), 6889_I17 (PGT-152), 6891_F06 (PGT-153), 6843_G20 (PGT-154), 6892_D19 (PGT-155), 6808_B09 (PGT-156), 6892_C23 (PGT-157), and/or 6881_N05 (PGT-158) neutralize HIV. Although the Applicant does not wish to be bound by this theory, it is postulated that the antibodies 1443_C16 (PG16) (TCN-116), 1503 H05 (PG16) (TCN-119), 1456 A12 (PG16) (TCN-117), 1469 M23 (PG16) (TCN-118), 1489_I13 (PG16) (TCN-120), 1480_I08 (PG16), 1456_P20 (PG20), 1460_G14 (PGG14), 1495_C14 (PGC14), 1496_C09 (PG9) (TCN-109), 4838_L06 (PGT-121), 4873_E03 (PGT-121), 4877_D15

(PGT-122), 4858_P08 (PGT-123), 6123_A06 (PGT-125), 5141_B17 (PGT-126), 5145_B14 (PGT-127), 5114_A19 (PGT-128), 5147_N06 (PGT-130), 5136_H01 (PGT-131), 5343_B08 (PGT-135), 5344_E16 (PGT-135), 5329_C19 (PGT-136), 5366_P21 (PGT-136), 4964_G22 (PGT-141), 5345_I01 (PGT-137), 4993_K13 (PGT-141), 4995_E20 (PGT-142), 4980_N08 (PGT-143), 4970_K22 (PGT-144), 4995_P16 (PGT-145), 4835_F12 (PGT-124), 4869_K15 (PGT-133), 4876_M06 (PGT-134), 5131_A17 (PGT-132), 5138_G07 (PGT-138), 5120_N10 (PGT-139), 6831_A21 (PGT-151), 6889_I17 (PGT-152), 6891_F06 (PGT-153), 6843_G20 (PGT-154), 6892_D19 (PGT-155), 6808_B09 (PGT-156), 6892_C23 (PGT-157), and/or 6881_N05 (PGT-158) bind to one or more conformational epitopes formed by HIV1-encoded proteins.

[0892] Neutralization activity of human monoclonal antibodies was tested against HIV-1 strains SF162 and JR-CSF. HIV-1 strains SF162 and JR-CSF both belong to HIV clade B. Each clonal monoclonal antibody was screened for neutralization activity and for anti-gp120, anti-gp41 and total IgG in quantitative ELISA. For the monoclonal antibodies 1456_P20, 1495_C14, and 1460_G14 anti-gp120 antigen-specific binding was detected. Neutralizing activity against SF162, but not JR-CSF was detected for 1456_P20 (PG20), 1495_C14 (PGC14), and 1460_G14 (PGG14). For the two monoclonal antibody preparations that did not show binding to gp120 in the ELISA assay, 1443_C16 (PG16) and 1496_C09 (PG9), high quantities of human IgG were determined to be present in the assay. However, 1443_C16 (PG16) and 1496_C09 (PG9) both were found to exhibit neutralizing activity against HIV-1 strain JR-CSF, but not against strain SF162. 1443_C16 (PG16) and 1496_C09 (PG9) also were found to lack gp41 binding activity in the ELISA assay.

[0893] The epitopes recognized by these antibodies may have a number of uses. The epitopes and mimotopes in purified or synthetic form can be used to raise immune responses (i.e. as a vaccine, or for the production of antibodies for other uses) or for screening patient serum for antibodies that immunoreact with the epitopes or mimotopes. Preferably, such an epitope or mimotope, or antigen comprising such an epitope or mimotope is used as a vaccine for raising an immune response. The antibodies of the invention can also be used in a method to monitor the quality of vaccines in particular to check that the antigen in a vaccine contains the correct immunogenic epitope in the correct conformation.

[0894] The epitopes may also be useful in screening for ligands that bind to said epitopes. Such ligands preferably block the epitopes and thus prevent infection. Such ligands are encompassed within the scope of the invention.

[0895] Standard techniques of molecular biology may be used to prepare DNA sequences coding for the antibodies or fragments of the antibodies of the present invention. Desired DNA sequences may be synthesized completely or in part using oligonucleotide synthesis techniques. Site-directed mutagenesis and polymerase chain reaction (PCR) techniques may be used as appropriate.

[0896] Any suitable host cell/vector system may be used for expression of the DNA sequences encoding the antibody molecules of the present invention or fragments thereof. Bacterial, for example *E. coli*, and other microbial systems may be used, in part, for expression of antibody fragments such as Fab and F(ab')₂ fragments, and especially Fv fragments and single chain antibody fragments, for example, single chain Fvs. Eukaryotic, e.g. mammalian, host cell expression systems may be used for production of larger antibody molecules, including complete antibody molecules. Suitable mammalian host cells include CHO, HEK293T, PER.C6, myeloma or hybridoma cells.

[0897] The present invention also provides a process for the production of an antibody molecule according to the present invention comprising culturing a host cell comprising a vector of the present invention under conditions suitable for leading to expression of protein from DNA encoding the antibody molecule of the present invention, and isolating the antibody molecule. The antibody molecule may comprise only a heavy or light chain polypeptide, in which case only a heavy chain or light chain polypeptide coding sequence needs to be used to transfect the host cells. For production of products comprising both heavy and light chains, the cell line may be transfected with two vectors, a first vector encoding a light chain polypeptide and a second vector encoding a heavy chain polypeptide. Alternatively, a single vector may be used, the vector including sequences encoding light chain and heavy chain polypeptides.

[0898] Alternatively, antibodies according to the invention may be produced by i) expressing a nucleic acid sequence according to the invention in a cell, and ii) isolating the expressed antibody product. Additionally, the method may include iii) purifying the antibody. Transformed B cells are screened for those producing antibodies of the desired antigen specificity, and individual B cell clones can then be produced from the positive cells. The

screening step may be carried out by ELISA, by staining of tissues or cells (including transfected cells), a neutralization assay or one of a number of other methods known in the art for identifying desired antigen specificity. The assay may select on the basis of simple antigen recognition, or may select on the additional basis of a desired function e.g. to select neutralizing antibodies rather than just antigen-binding antibodies, to select antibodies that can change characteristics of targeted cells, such as their signaling cascades, their shape, their growth rate, their capability of influencing other cells, their response to the influence by other cells or by other reagents or by a change in conditions, their differentiation status, etc.

[0899] The cloning step for separating individual clones from the mixture of positive cells may be carried out using limiting dilution, micromanipulation, single cell deposition by cell sorting or another method known in the art. Preferably the cloning is carried out using limiting dilution.

[0900] The immortalized B cell clones of the invention can be used in various ways e.g. as a source of monoclonal antibodies, as a source of nucleic acid (DNA or mRNA) encoding a monoclonal antibody of interest, for research, etc.

[0901] Unless otherwise defined, scientific and technical terms used in connection with the present invention shall have the meanings that are commonly understood by those of ordinary skill in the art. Further, unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular. Generally, nomenclatures utilized in connection with, and techniques of, cell and tissue culture, molecular biology, and protein and oligo- or polynucleotide chemistry and hybridization described herein are those well known and commonly used in the art. Standard techniques are used for recombinant DNA, oligonucleotide synthesis, and tissue culture and transformation (*e.g.*, electroporation, lipofection). Enzymatic reactions and purification techniques are performed according to manufacturer's specifications or as commonly accomplished in the art or as described herein. The practice of the present invention will employ, unless indicated specifically to the contrary, conventional methods of virology, immunology, microbiology, molecular biology and recombinant DNA techniques within the skill of the art, many of which are described below for the purpose of illustration. Such techniques are explained fully in the literature. See, *e.g.*, Sambrook, *et al.* Molecular Cloning: A Laboratory Manual (2nd Edition, 1989); Maniatis *et al.* Molecular Cloning: A Laboratory Manual (1982); DNA Cloning: A Practical Approach, vol. I & II (D. Glover, ed.);

Oligonucleotide Synthesis (N. Gait, ed., 1984); Nucleic Acid Hybridization (B. Hames & S. Higgins, eds., 1985); Transcription and Translation (B. Hames & S. Higgins, eds., 1984); Animal Cell Culture (R. Freshney, ed., 1986); Perbal, A Practical Guide to Molecular Cloning (1984). The nomenclatures utilized in connection with, and the laboratory procedures and techniques of, analytical chemistry, synthetic organic chemistry, and medicinal and pharmaceutical chemistry described herein are those well known and commonly used in the art. Standard techniques are used for chemical syntheses, chemical analyses, pharmaceutical preparation, formulation, and delivery, and treatment of patients.

[0902] The following definitions are useful in understanding the present invention: The term “antibody” (Ab) as used herein includes monoclonal antibodies, polyclonal antibodies, multispecific antibodies (*e.g.*, bispecific antibodies), and antibody fragments, as long as they exhibit the desired biological activity. The term “immunoglobulin” (Ig) is used interchangeably with “antibody” herein.

[0903] A “neutralizing antibody” may inhibit the entry of HIV-1 virus for example SF162 and/or JR-CSF with a neutralization index >1.5 or >2.0 . (Kostrikis LG et al. *J Virol.* 1996; 70(1): 445–458.) By “broad and potent neutralizing antibodies” are meant antibodies that neutralize more than one HIV-1 virus species (from diverse clades and different strains within a clade) in a neutralization assay. A broad neutralizing antibody may neutralize at least 2, 3, 4, 5, 6, 7, 8, 9 or more different strains of HIV-1, the strains belonging to the same or different clades. A broad neutralizing antibody may neutralize multiple HIV-1 species belonging to at least 2, 3, 4, 5, or 6 different clades. The inhibitory concentration of the monoclonal antibody may be less than about 25 mg/ml to neutralize about 50% of the input virus in the neutralization assay.

[0904] An “isolated antibody” is one that has been separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody is purified: (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight; (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator; or (3) to homogeneity by SDS-PAGE under reducing or non-reducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the

antibody *in situ* within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

[0905] The basic four-chain antibody unit is a heterotetrameric glycoprotein composed of two identical light (L) chains and two identical heavy (H) chains. An IgM antibody consists of 5 basic heterotetramer units along with an additional polypeptide called J chain, and therefore contain 10 antigen binding sites, while secreted IgA antibodies can polymerize to form polyvalent assemblages comprising 2-5 of the basic 4-chain units along with J chain. In the case of IgGs, the 4-chain unit is generally about 150,000 daltons. Each L chain is linked to an H chain by one covalent disulfide bond, while the two H chains are linked to each other by one or more disulfide bonds depending on the H chain isotype. Each H and L chain also has regularly spaced intrachain disulfide bridges. Each H chain has at the N-terminus, a variable region (V_H) followed by three constant domains (C_H) for each of the α and γ chains and four C_H domains for μ and ϵ isotypes. Each L chain has at the N-terminus, a variable region (V_L) followed by a constant domain (C_L) at its other end. The V_L is aligned with the V_H and the C_L is aligned with the first constant domain of the heavy chain (C_{H1}). Particular amino acid residues are believed to form an interface between the light chain and heavy chain variable regions. The pairing of a V_H and V_L together forms a single antigen-binding site. For the structure and properties of the different classes of antibodies, see, *e.g.*, Basic and Clinical Immunology, 8th edition, Daniel P. Stites, Abba I. Terr and Tristram G. Parslow (eds.), Appleton & Lange, Norwalk, Conn., 1994, page 71, and Chapter 6.

[0906] The L chain from any vertebrate species can be assigned to one of two clearly distinct types, called kappa (κ) and lambda (λ), based on the amino acid sequences of their constant domains (C_L). Depending on the amino acid sequence of the constant domain of their heavy chains (C_H), immunoglobulins can be assigned to different classes or isotypes. There are five classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, having heavy chains designated alpha (α), delta (δ), epsilon (ϵ), gamma (γ) and mu (μ), respectively. The γ and α classes are further divided into subclasses on the basis of relatively minor differences in C_H sequence and function, *e.g.*, humans express the following subclasses: IgG1, IgG2, IgG3, IgG4, IgA1, and IgA2.

[0907] The term "variable" refers to the fact that certain segments of the V domains differ extensively in sequence among antibodies. The V domain mediates antigen binding and defines

specificity of a particular antibody for its particular antigen. However, the variability is not evenly distributed across the 110-amino acid span of the variable regions. Instead, the V regions consist of relatively invariant stretches called framework regions (FRs) of 15-30 amino acids separated by shorter regions of extreme variability called “hypervariable regions” that are each 9-12 amino acids long. The variable regions of native heavy and light chains each comprise four FRs, largely adopting a β -sheet configuration, connected by three hypervariable regions, which form loops connecting, and in some cases forming part of, the β -sheet structure. The hypervariable regions in each chain are held together in close proximity by the FRs and, with the hypervariable regions from the other chain, contribute to the formation of the antigen-binding site of antibodies (see Kabat *et al.*, Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md. (1991)). The constant domains are not involved directly in binding an antibody to an antigen, but exhibit various effector functions, such as participation of the antibody in antibody dependent cellular cytotoxicity (ADCC).

[0908] The term “hypervariable region” when used herein refers to the amino acid residues of an antibody that are responsible for antigen binding. The hypervariable region generally comprises amino acid residues from a “complementarity determining region” or “CDR” (*e.g.*, around about residues 24-34 (L1), 50-56 (L2) and 89-97 (L3) in the V_L , and around about 31-35 (H1), 50-65 (H2) and 95-102 (H3) in the V_H when numbered in accordance with the Kabat numbering system; Kabat *et al.*, Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md. (1991)); and/or those residues from a “hypervariable loop” (*e.g.*, residues 24-34 (L1), 50-56 (L2) and 89-97 (L3) in the V_L , and 26-32 (H1), 52-56 (H2) and 95-101 (H3) in the V_H when numbered in accordance with the Chothia numbering system; Chothia and Lesk, J. Mol. Biol. 196:901-917 (1987)); and/or those residues from a “hypervariable loop”/CDR (*e.g.*, residues 27-38 (L1), 56-65 (L2) and 105-120 (L3) in the V_L , and 27-38 (H1), 56-65 (H2) and 105-120 (H3) in the V_H when numbered in accordance with the IMGT numbering system; Lefranc, M.P. et al. Nucl. Acids Res. 27:209-212 (1999), Ruiz, M. et al. Nucl. Acids Res. 28:219-221 (2000)). Optionally the antibody has symmetrical insertions at one or more of the following points 28, 36 (L1), 63, 74-75 (L2) and 123 (L3) in the V_L , and 28, 36 (H1), 63, 74-75 (H2) and 123 (H3) in the V_H when numbered in accordance with AHO; Honneger, A. and Plunkthun, A. J. Mol. Biol. 309:657-670 (2001)).

[0909] By “germline nucleic acid residue” is meant the nucleic acid residue that naturally occurs in a germline gene encoding a constant or variable region. “Germline gene” is the DNA found in a germ cell (*i.e.*, a cell destined to become an egg or in the sperm). A “germline mutation” refers to a heritable change in a particular DNA that has occurred in a germ cell or the zygote at the single-cell stage, and when transmitted to offspring, such a mutation is incorporated in every cell of the body. A germline mutation is in contrast to a somatic mutation which is acquired in a single body cell. In some cases, nucleotides in a germline DNA sequence encoding for a variable region are mutated (*i.e.*, a somatic mutation) and replaced with a different nucleotide.

[0910] The term “monoclonal antibody” as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, *i.e.*, the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic site. Furthermore, in contrast to polyclonal antibody preparations that include different antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen. In addition to their specificity, the monoclonal antibodies are advantageous in that they may be synthesized uncontaminated by other antibodies. The modifier “monoclonal” is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies useful in the present invention may be prepared by the hybridoma methodology first described by Kohler *et al.*, *Nature*, 256:495 (1975), or may be made using recombinant DNA methods in bacterial, eukaryotic animal or plant cells (see, *e.g.*, U.S. Pat. No. 4,816,567). The “monoclonal antibodies” may also be isolated from phage antibody libraries using the techniques described in Clackson *et al.*, *Nature*, 352:624-628 (1991) and Marks *et al.*, *J. Mol. Biol.*, 222:581-597 (1991), for example.

[0911] In some aspects, the alternative EBV immortalization method described in WO2004/076677 is used. Using this method, B-cells producing the antibody of the invention can be transformed with EBV in the presence of a polyclonal B cell activator. Transformation with EBV is a standard technique and can easily be adapted to include polyclonal B cell activators. Additional stimulants of cellular growth and differentiation may be added during the transformation step to further enhance the efficiency. These stimulants may be cytokines such as

IL-2 and IL-15. In a particularly preferred aspect, IL-2 is added during the immortalization step to further improve the efficiency of immortalization, but its use is not essential.

[0912] The monoclonal antibodies herein include “chimeric” antibodies in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired biological activity (see U.S. Pat. No. 4,816,567; and Morrison *et al.*, Proc. Natl. Acad. Sci. USA, 81:6851-6855 (1984)). The present invention provides variable region antigen-binding sequences derived from human antibodies. Accordingly, chimeric antibodies of primary interest herein include antibodies having one or more human antigen binding sequences (*e.g.*, CDRs) and containing one or more sequences derived from a non-human antibody, *e.g.*, an FR or C region sequence. In addition, chimeric antibodies of primary interest herein include those comprising a human variable region antigen binding sequence of one antibody class or subclass and another sequence, *e.g.*, FR or C region sequence, derived from another antibody class or subclass. Chimeric antibodies of interest herein also include those containing variable region antigen-binding sequences related to those described herein or derived from a different species, such as a non-human primate (*e.g.*, Old World Monkey, Ape, etc). Chimeric antibodies also include primatized and humanized antibodies.

[0913] Furthermore, chimeric antibodies may comprise residues that are not found in the recipient antibody or in the donor antibody. These modifications are made to further refine antibody performance. For further details, see Jones *et al.*, Nature 321:522-525 (1986); Reichmann *et al.*, Nature 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol. 2:593-596 (1992).

[0914] A “humanized antibody” is generally considered to be a human antibody that has one or more amino acid residues introduced into it from a source that is non-human. These non-human amino acid residues are often referred to as “import” residues, which are typically taken from an “import” variable region. Humanization is traditionally performed following the method of Winter and co-workers (Jones *et al.*, Nature, 321:522-525 (1986); Reichmann *et al.*, Nature, 332:323-327 (1988); Verhoeven *et al.*, Science, 239:1534-1536 (1988)), by substituting import

hypervariable region sequences for the corresponding sequences of a human antibody. Accordingly, such “humanized” antibodies are chimeric antibodies (U.S. Pat. No. 4,816,567), wherein substantially less than an intact human variable region has been substituted by the corresponding sequence from a non-human species.

[0915] A “human antibody” is an antibody containing only sequences present in an antibody naturally produced by a human. However, as used herein, human antibodies may comprise residues or modifications not found in a naturally occurring human antibody, including those modifications and variant sequences described herein. These are typically made to further refine or enhance antibody performance.

[0916] An “intact” antibody is one that comprises an antigen-binding site as well as a C_L and at least heavy chain constant domains, C_H 1, C_H 2 and C_H 3. The constant domains may be native sequence constant domains (*e.g.*, human native sequence constant domains) or amino acid sequence variant thereof. Preferably, the intact antibody has one or more effector functions.

[0917] An “antibody fragment” comprises a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', F(ab')₂, and Fv fragments; diabodies; linear antibodies (see U.S. Pat. No. 5,641,870; Zapata *et al.*, Protein Eng. 8(10): 1057-1062 [1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

[0918] The phrase “functional fragment or analog” of an antibody is a compound having qualitative biological activity in common with a full-length antibody. For example, a functional fragment or analog of an anti-IgE antibody is one that can bind to an IgE immunoglobulin in such a manner so as to prevent or substantially reduce the ability of such molecule from having the ability to bind to the high affinity receptor, Fc RI.

[0919] Papain digestion of antibodies produces two identical antigen-binding fragments, called “Fab” fragments, and a residual “Fc” fragment, a designation reflecting the ability to crystallize readily. The Fab fragment consists of an entire L chain along with the variable region domain of the H chain (V_H), and the first constant domain of one heavy chain (C_H 1). Each Fab fragment is monovalent with respect to antigen binding, *i.e.*, it has a single antigen-binding site. Pepsin treatment of an antibody yields a single large F(ab')₂ fragment that roughly corresponds to two disulfide linked Fab fragments having divalent antigen-binding activity and is still capable of cross-linking antigen. Fab' fragments differ from Fab fragments by having additional few

residues at the carboxy terminus of the C_H1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab')₂ antibody fragments originally were produced as pairs of Fab' fragments that have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

[0920] The “Fc” fragment comprises the carboxy-terminal portions of both H chains held together by disulfides. The effector functions of antibodies are determined by sequences in the Fc region, which region is also the part recognized by Fc receptors (FcR) found on certain types of cells.

[0921] “Fv” is the minimum antibody fragment that contains a complete antigen-recognition and -binding site. This fragment consists of a dimer of one heavy- and one light-chain variable region domain in tight, non-covalent association. From the folding of these two domains emanate six hypervariable loops (three loops each from the H and L chain) that contribute the amino acid residues for antigen binding and confer antigen binding specificity to the antibody. However, even a single variable region (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

[0922] “Single-chain Fv” also abbreviated as “sFv” or “scFv” are antibody fragments that comprise the V_H and V_L antibody domains connected into a single polypeptide chain. Preferably, the sFv polypeptide further comprises a polypeptide linker between the V_H and V_L domains that enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun in *The Pharmacology of Monoclonal Antibodies*, vol. 113, Rosenberg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994); Borrebaeck 1995, *infra*.

[0923] The term “diabodies” refers to small antibody fragments prepared by constructing sFv fragments (see preceding paragraph) with short linkers (about 5-10 residues) between the V_H and V_L domains such that inter-chain but not intra-chain pairing of the V domains is achieved, resulting in a bivalent fragment, *i.e.*, fragment having two antigen-binding sites. Bispecific diabodies are heterodimers of two “crossover” sFv fragments in which the V_H and V_L domains of the two antibodies are present on different polypeptide chains. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger *et al.*, *Proc. Natl. Acad. Sci. USA*, 90:6444-6448 (1993).

[0924] Domain antibodies (dAbs), which can be produced in fully human form, are the smallest known antigen-binding fragments of antibodies, ranging from 11 kDa to 15 kDa. dAbs are the robust variable regions of the heavy and light chains of immunoglobulins (VH and VL respectively). They are highly expressed in microbial cell culture, show favourable biophysical properties including solubility and temperature stability, and are well suited to selection and affinity maturation by in vitro selection systems such as phage display. dAbs are bioactive as monomers and, owing to their small size and inherent stability, can be formatted into larger molecules to create drugs with prolonged serum half-lives or other pharmacological activities. Examples of this technology have been described in WO9425591 for antibodies derived from *Camelidae* heavy chain Ig, as well in US20030130496 describing the isolation of single domain fully human antibodies from phage libraries.

[0925] As used herein, an antibody that “internalizes” is one that is taken up by (*i.e.*, enters) the cell upon binding to an antigen on a mammalian cell (*e.g.*, a cell surface polypeptide or receptor). The internalizing antibody will of course include antibody fragments, human or chimeric antibody, and antibody conjugates. For certain therapeutic applications, internalization *in vivo* is contemplated. The number of antibody molecules internalized will be sufficient or adequate to kill a cell or inhibit its growth, especially an infected cell. Depending on the potency of the antibody or antibody conjugate, in some instances, the uptake of a single antibody molecule into the cell is sufficient to kill the target cell to which the antibody binds. For example, certain toxins are highly potent in killing such that internalization of one molecule of the toxin conjugated to the antibody is sufficient to kill the infected cell.

[0926] As used herein, an antibody is said to be “immunospecific,” “specific for” or to “specifically bind” an antigen if it reacts at a detectable level with the antigen, preferably with an affinity constant, K_a , of greater than or equal to about 10^4 M^{-1} , or greater than or equal to about 10^5 M^{-1} , greater than or equal to about 10^6 M^{-1} , greater than or equal to about 10^7 M^{-1} , or greater than or equal to 10^8 M^{-1} . Affinity of an antibody for its cognate antigen is also commonly expressed as a dissociation constant K_D , and in certain embodiments, HIV1 antibody specifically binds to an HIV1 polypeptide if it binds with a K_D of less than or equal to 10^{-4} M , less than or equal to about 10^{-5} M , less than or equal to about 10^{-6} M , less than or equal to 10^{-7} M , or less than or equal to 10^{-8} M . Affinities of antibodies can be readily determined using conventional

techniques, for example, those described by Scatchard *et al.* (*Ann. N.Y. Acad. Sci. USA* 51:660 (1949)).

[0927] Binding properties of an antibody to antigens, cells or tissues thereof may generally be determined and assessed using immunodetection methods including, for example, immunofluorescence-based assays, such as immuno-histochemistry (IHC) and/or fluorescence-activated cell sorting (FACS).

[0928] An antibody having a “biological characteristic” of a designated antibody is one that possesses one or more of the biological characteristics of that antibody which distinguish it from other antibodies. For example, in certain embodiments, an antibody with a biological characteristic of a designated antibody will bind the same epitope as that bound by the designated antibody and/or have a common effector function as the designated antibody.

[0929] The term “antagonist” antibody is used in the broadest sense, and includes an antibody that partially or fully blocks, inhibits, or neutralizes a biological activity of an epitope, polypeptide, or cell that it specifically binds. Methods for identifying antagonist antibodies may comprise contacting a polypeptide or cell specifically bound by a candidate antagonist antibody with the candidate antagonist antibody and measuring a detectable change in one or more biological activities normally associated with the polypeptide or cell.

[0930] An “antibody that inhibits the growth of infected cells” or a “growth inhibitory” antibody is one that binds to and results in measurable growth inhibition of infected cells expressing or capable of expressing an HIV1 epitope bound by an antibody. Preferred growth inhibitory antibodies inhibit growth of infected cells by greater than 20%, preferably from about 20% to about 50%, and even more preferably, by greater than 50% (*e.g.*, from about 50% to about 100%) as compared to the appropriate control, the control typically being infected cells not treated with the antibody being tested. Growth inhibition can be measured at an antibody concentration of about 0.1 to 30 µg/ml or about 0.5 nM to 200 nM in cell culture, where the growth inhibition is determined 1-10 days after exposure of the infected cells to the antibody. Growth inhibition of infected cells *in vivo* can be determined in various ways known in the art.

[0931] The antibody is growth inhibitory *in vivo* if administration of the antibody at about 1 µg/kg to about 100 mg/kg body weight results in reduction the percent of infected cells or total number of infected cells within about 5 days to 3 months from the first administration of the antibody, preferably within about 5 to 30 days.

[0932] An antibody that “induces apoptosis” is one which induces programmed cell death as determined by binding of annexin V, fragmentation of DNA, cell shrinkage, dilation of endoplasmic reticulum, cell fragmentation, and/or formation of membrane vesicles (called apoptotic bodies). Preferably the cell is an infected cell. Various methods are available for evaluating the cellular events associated with apoptosis. For example, phosphatidyl serine (PS) translocation can be measured by annexin binding; DNA fragmentation can be evaluated through DNA laddering; and nuclear/chromatin condensation along with DNA fragmentation can be evaluated by any increase in hypodiploid cells. Preferably, the antibody that induces apoptosis is one that results in about 2 to 50 fold, preferably about 5 to 50 fold, and most preferably about 10 to 50 fold, induction of annexin binding relative to untreated cell in an annexin binding assay.

[0933] Antibody “effector functions” refer to those biological activities attributable to the Fc region (a native sequence Fc region or amino acid sequence variant Fc region) of an antibody, and vary with the antibody isotype. Examples of antibody effector functions include: C1q binding and complement dependent cytotoxicity; Fc receptor binding; antibody-dependent cell-mediated cytotoxicity (ADCC); phagocytosis; down regulation of cell surface receptors (*e.g.*, B cell receptor); and B cell activation.

[0934] “Antibody-dependent cell-mediated cytotoxicity” or “ADCC” refers to a form of cytotoxicity in which secreted Ig bound to Fc receptors (FcRs) present on certain cytotoxic cells (*e.g.*, Natural Killer (NK) cells, neutrophils, and macrophages) enable these cytotoxic effector cells to bind specifically to an antigen-bearing target cell and subsequently kill the target cell with cytotoxins. The antibodies “arm” the cytotoxic cells and are required for such killing. The primary cells for mediating ADCC, NK cells, express FcγRIII only, whereas monocytes express FcγRI, FcγRII and FcγRIII. FcR expression on hematopoietic cells is summarized in Table 4 on page 464 of Ravetch and Kinet, *Annu. Rev. Immunol* 9:457-92 (1991). To assess ADCC activity of a molecule of interest, an *in vitro* ADCC assay, such as that described in U.S. Pat. No. 5,500,362 or U.S. Pat. No. 5,821,337 may be performed. Useful effector cells for such assays include peripheral blood mononuclear cells (PBMC) and Natural Killer (NK) cells.

[0935] Alternatively, or additionally, ADCC activity of the molecule of interest may be assessed *in vivo*, *e.g.*, in a animal model such as that disclosed in Clynes *et al.*, *Proc. Natl. Acad. Sci. (USA)* 95:652-656 (1998).

DEMANDE OU BREVET VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET COMPREND PLUS D'UN TOME.

CECI EST LE TOME 1 DE 2
CONTENANT LES PAGES 1 À 249

NOTE : Pour les tomes additionels, veuillez contacter le Bureau canadien des brevets

JUMBO APPLICATIONS/PATENTS

THIS SECTION OF THE APPLICATION/PATENT CONTAINS MORE THAN ONE VOLUME

THIS IS VOLUME 1 OF 2
CONTAINING PAGES 1 TO 249

NOTE: For additional volumes, please contact the Canadian Patent Office

NOM DU FICHIER / FILE NAME :

NOTE POUR LE TOME / VOLUME NOTE:

THE EMBODIMENTS OF THE INVENTION FOR WHICH AN EXCLUSIVE PROPERTY OR PRIVILEGE ARE CLAIMED ARE DEFINED AS FOLLOWS:

1. An antibody, comprising a heavy chain with a CDR 1 comprising the amino acid sequence DSYWS (SEQ ID NO: 90), a CDR 2 comprising the amino acid sequence YVHKSGDTNYSPSLKS (SEQ ID NO: 265), and a CDR 3 comprising the amino acid sequence TLHGRRYIGIVAFNEWFTYFYMDV (SEQ ID NO: 143), and a light chain with a CDR 1 comprising the amino acid sequences of GEKSLGSRAVQ (SEQ ID NO: 150), a CDR 2 comprising the amino acid sequence NNQDRPS (SEQ ID NO: 151), and a CDR 3 comprising the amino acid sequence HIWDSRVPTKWV (SEQ ID NO: 152).
2. An antibody comprising a heavy chain with a CDR 1 comprising the amino acid sequence GASISD (SEQ ID NO: 144), a CDR 2 comprising the amino acid sequence YVHKSGDTN (SEQ ID NO: 145), and a CDR 3 comprising the amino acid sequence TLHGRRYIGIVAFNEWFTYFYMDV (SEQ ID NO: 143), and a light chain with a CDR 1 comprising the amino acid sequence GEKSLGSRAVQ (SEQ ID NO: 150), a CDR 2 comprising the amino acid sequence NNQDRPS (SEQ ID NO: 151), and a CDR 3 comprising the amino acid sequence HIWDSRVPTKWV (SEQ ID NO: 152).
3. An isolated fully human monoclonal antibody comprising a heavy chain sequence comprising the amino acid sequence of SEQ ID NO: 79 and a light chain sequence comprising amino acid sequence of SEQ ID NO: 149.
4. The antibody of claim 3, wherein heavy chain variable sequence comprises the amino acid sequence of SEQ ID NO: 79 and light chain variable sequence comprises the amino acid sequence of SEQ ID NO: 149.
5. The antibody according to any one of claims 1 to 4, wherein the antibody neutralizes HIV-1 species belonging to two or more clades, wherein the clades are selected from Clade A, Clade B, Clade C, Clade D and Clade AE.

6. A fragment of the antibody of any one of claims 1 to 5, wherein the fragment has the same binding specificity as the antibody of any one of claims 1 to 5.
7. The fragment of claim 6, which is selected from the group consisting of the Fab, Fab', F(ab')₂, Fv, single chain Fv, diabody and domain antibody (dAb) fragments.
8. An isolated nucleic acid molecule encoding the antibody of any one of claims 1 to 3, or the fragment thereof of claim 6 or 7.
9. The nucleic acid molecule of claim 8, wherein the nucleic acid molecule comprises the nucleotide sequence of SEQ ID NO: 63 encoding a heavy chain variable sequence and the nucleotide sequence of SEQ ID NO: 147 encoding a light chain variable sequence.
10. The nucleic acid molecule of claim 8, wherein the nucleic acid molecule comprises the nucleotide sequence of SEQ ID NO: 62 encoding a heavy chain sequence and the nucleotide sequence of SEQ ID NO: 146 encoding a light chain sequence.
11. The nucleic acid molecule according to claim 8, 9 or 10, which is selected from the group consisting of cDNA, hnRNA and mRNA.
12. A vector comprising the nucleic acid molecule of any one of claims 8 to 11.
13. A cell comprising the vector of any one of claims 8 to 11.
14. An immortalized B cell clone expressing the antibody of any one of claims 1 to 5.
15. A pharmaceutical composition comprising a pharmaceutically acceptable carrier and the antibody of any one of claims 1 to 5, or the fragment of claim 6 or 7 or the nucleic acid molecule as recited in any one of claims 8 to 11.

16. Use of a therapeutically effective amount of the antibody as recited in any one of claims 1 to 5 or the fragment of claim 6 or 7 or the nucleic acid molecule as recited in any one of claims 8 to 11 for immunization against HIV or to reduce the effect of an HIV infection.
17. The use according to claim 16, additionally comprising the use of a second therapeutic agent.
18. The use as recited in claim 17, wherein said second therapeutic agent is an anti-viral agent.
19. Use of an effective amount of the pharmaceutical composition of claim 15 to treat an individual infected with HIV-1.
20. Use of an effective amount of an antibody according to any one of claims 1 to 5 or the fragment of claim 6 or 7 or the nucleic acid molecule as recited in any one of claims 8 to 11 as an adjuvant therapy to treat an individual infected with HIV-1.
21. The use according to claim 20, wherein the use comprises multiple doses of said antibody.
22. Use of an immunotherapeutically effective amount of the antibody according to claims 1 to 5 or the fragment of claim 6 or 7 or the nucleic acid molecule as recited in any one of claims 8 to 11 for treatment of HIV-1 infection in an individual, or post-exposure prophylaxis of an individual.
23. Use of the antibody as recited in any one of claims 1 to 5 or the fragment of claim 4 or 5 in the manufacture of a medicament for immunization against HIV or to reduce the effect of an HIV infection.
24. Use of the pharmaceutical composition of claim 15 in the manufacture of a medicament to treat an individual infected with HIV-1.

25. Use of the antibody according to any one of claims 1 to 5 or the fragment of claim 6 or 7 in the manufacture of a medicament for use as an adjuvant therapy to treat an individual infected with HIV-1.
26. Use of the antibody according to any one of claims 1 to 5 or the fragment of claim 6 or 7 in the manufacture of a medicament for treatment of HIV-1 infection in an individual, or post-exposure prophylaxis of an individual.
27. Use of the antibody according to any one of claims 1 to 5 or the fragment of claim 6 or 7 or the nucleic acid molecule as recited in any one of claims 8 to 11 in the manufacture of a medicament for use as an adjuvant therapy to treat an individual against a plurality of HIV-1 species.
28. A method for producing the antibody to any one of claims 1 to 5 or the fragment according of claim 6 or 7 comprising (i) culturing an immortalized B cell clone expressing the antibody to any one of claims 1 to 5 or the fragment according of claim 6 or 7 and (ii) isolating the antibody or fragment.

FIG. 1A Heavy Chain Tree

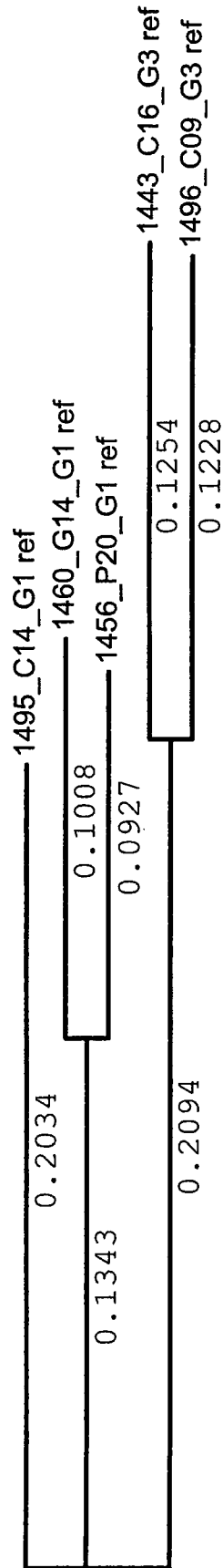


FIG. 1B Light Chain Tree

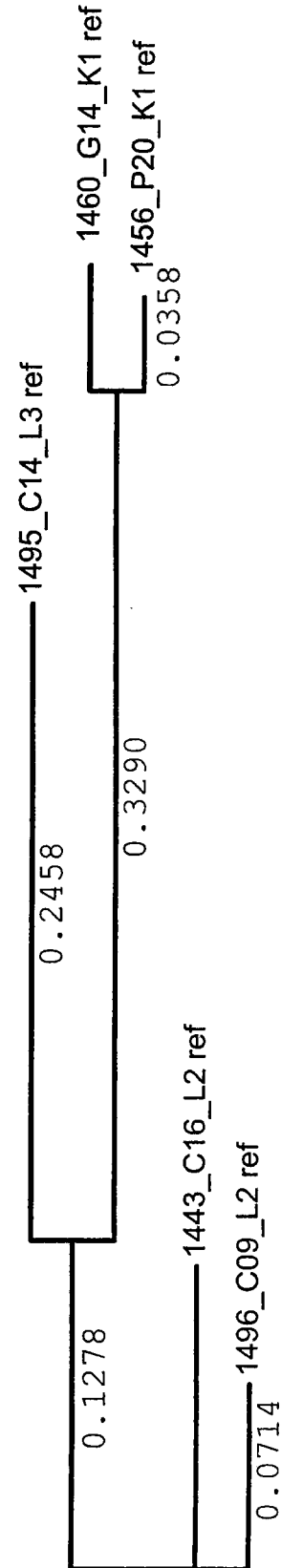


FIG. 2

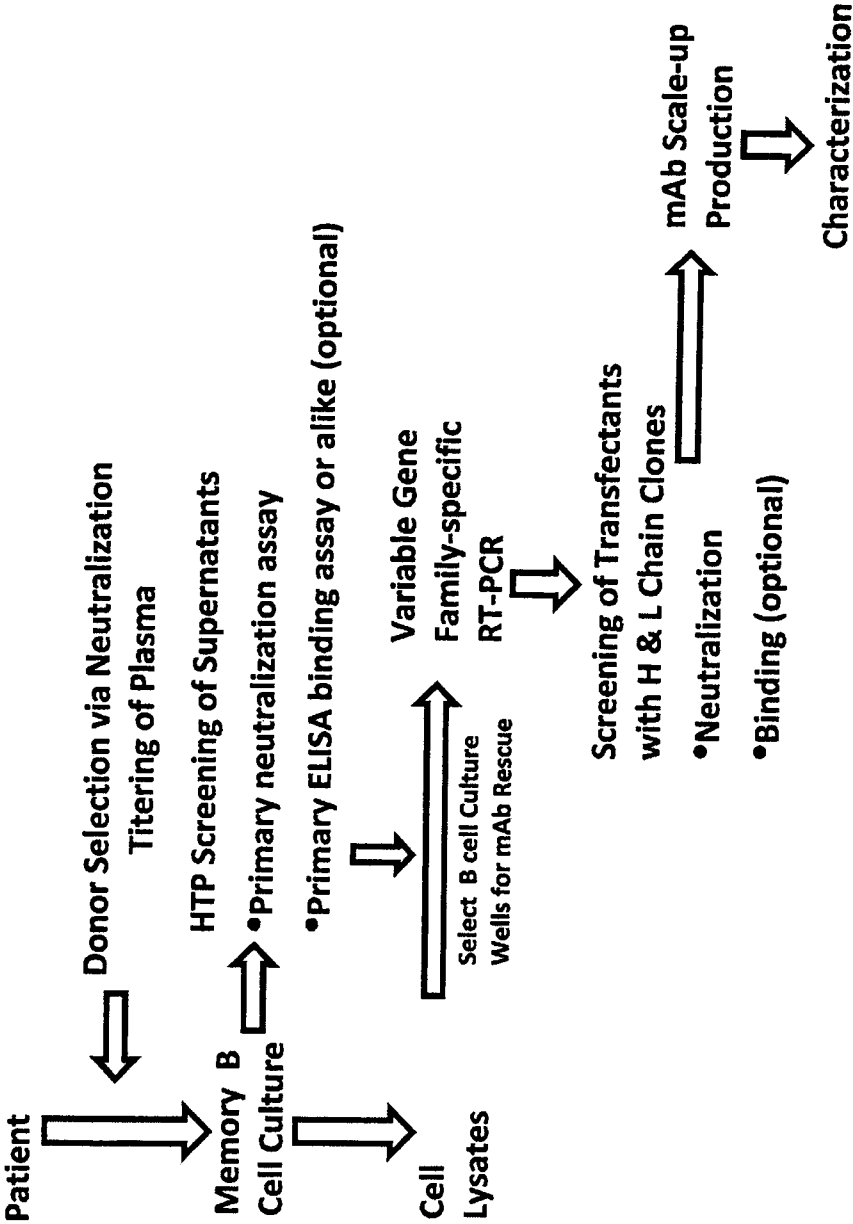
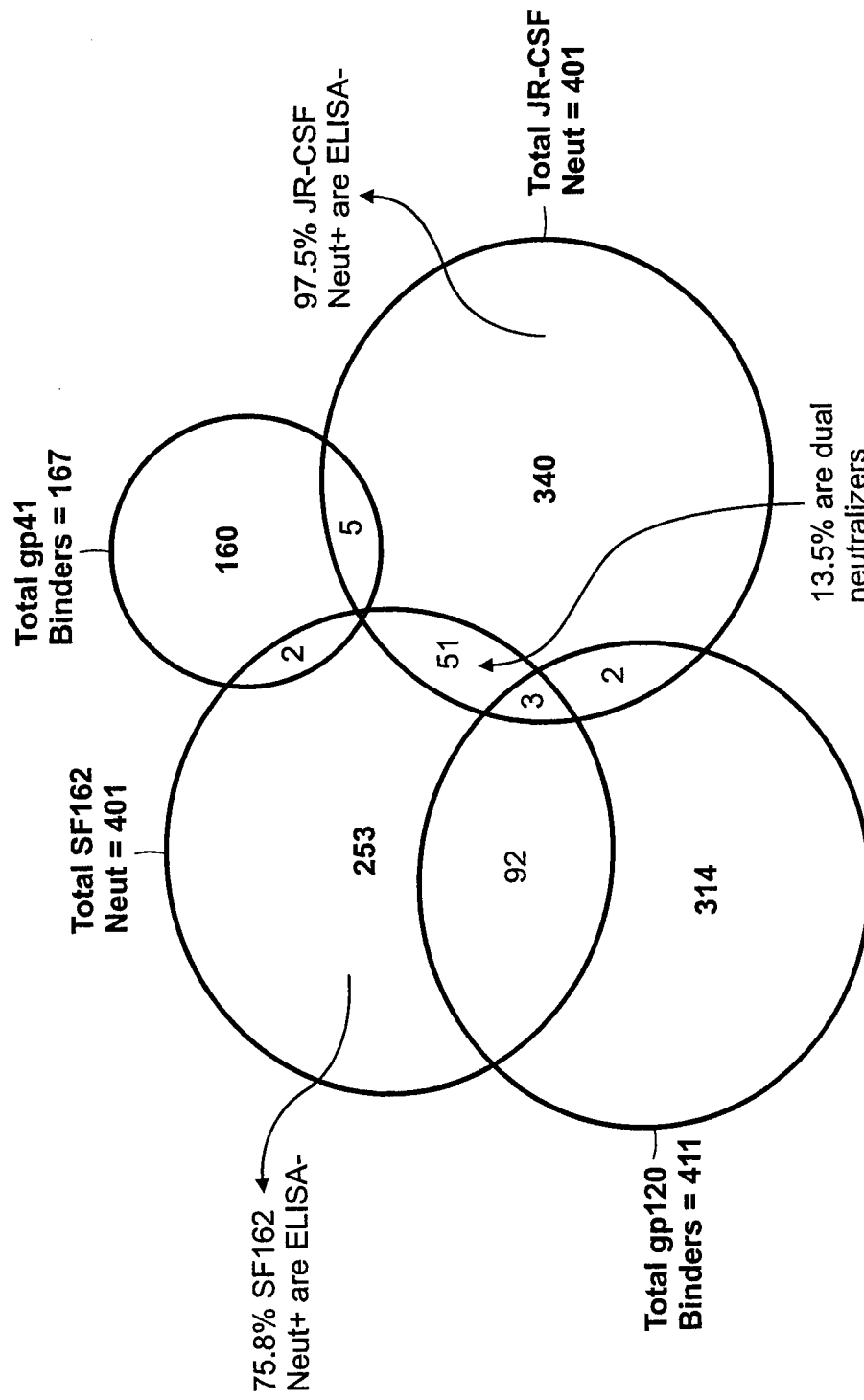


FIG. 3A



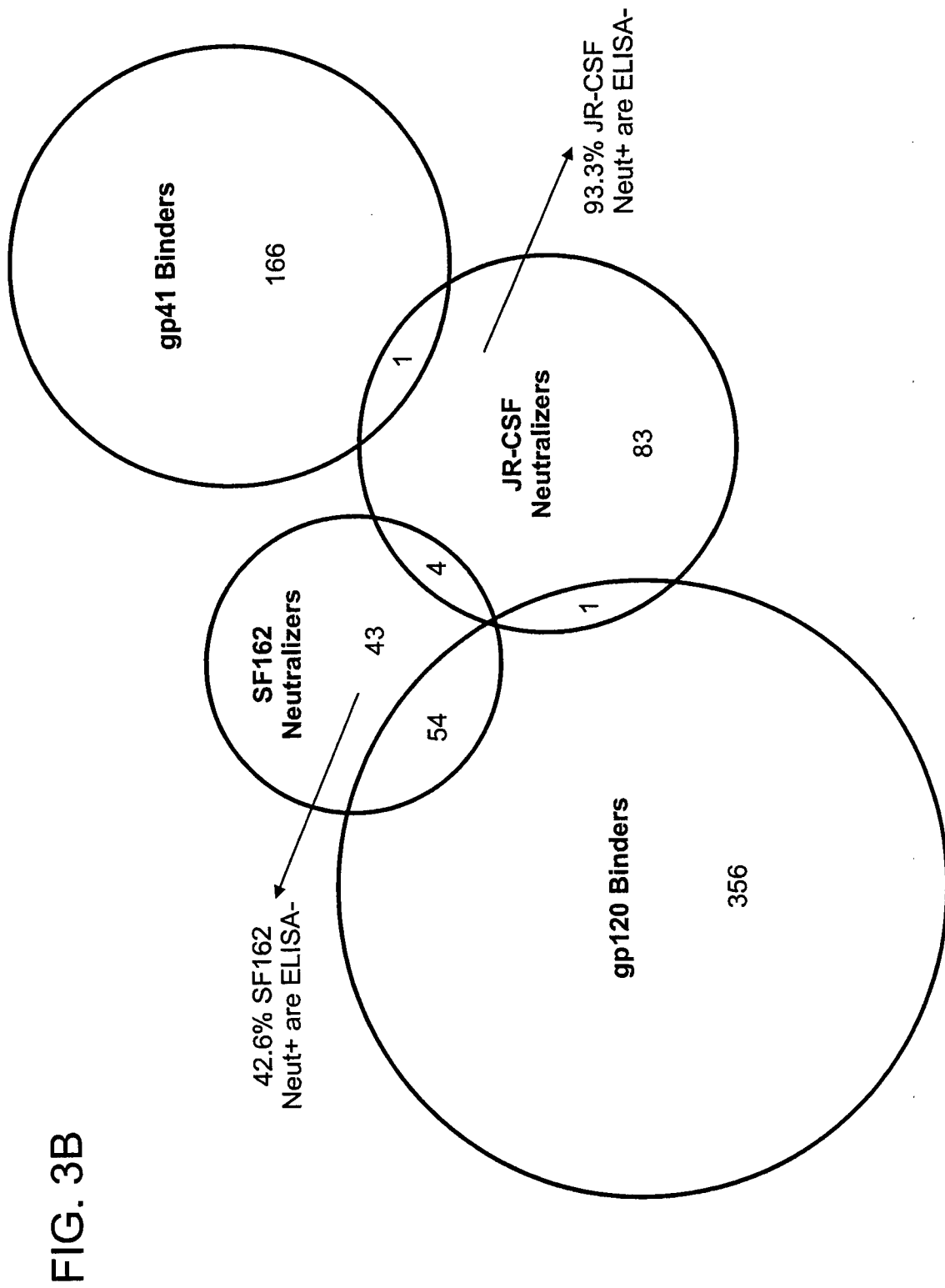


FIG. 4 PG9 and PG16 Neutralization Assays

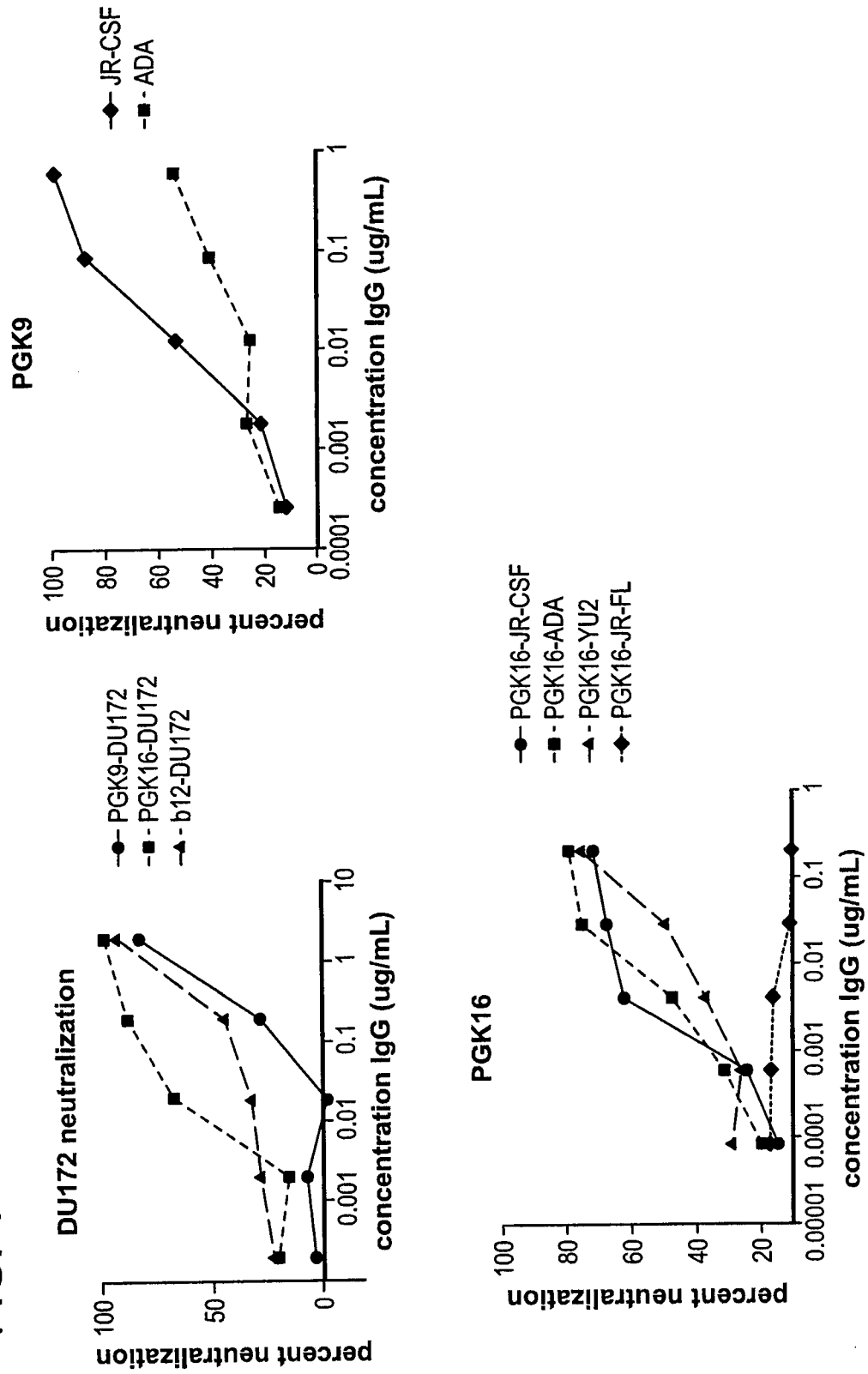
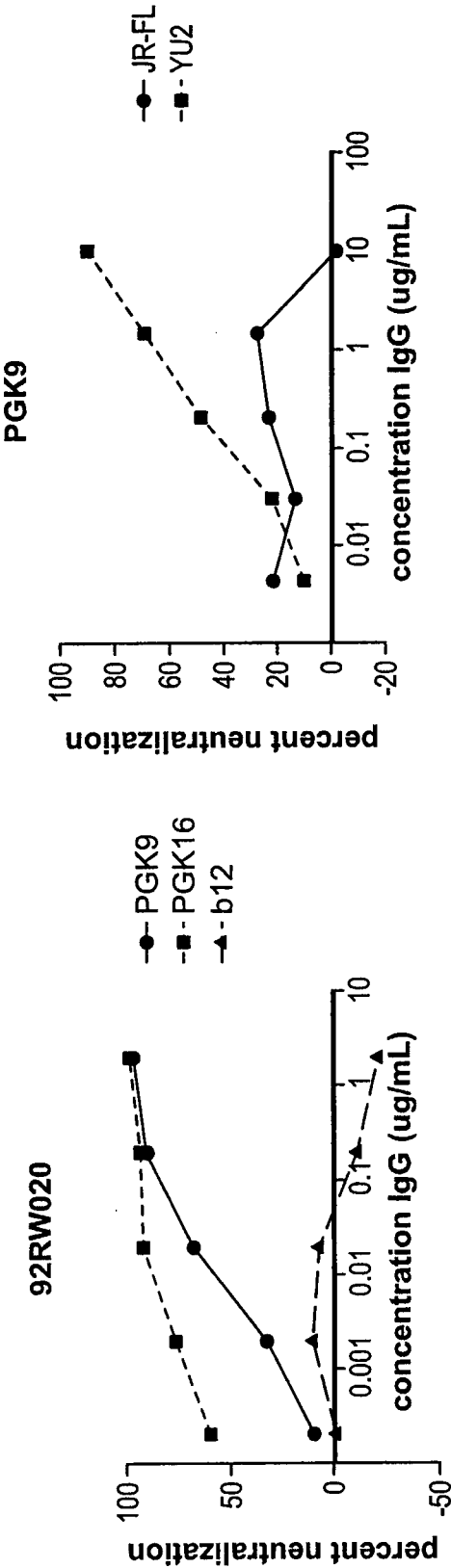


FIG. 4 (continued)



Virus Strain					
Virus Strain	clade B			clade C	
	YU2	JR -FL	JR -CSF	ADA	DU172
	92RW20	ZM214	0.004	0.4	0.6
	PGK9	0.4	0.004	0.4	0.6
	PGK16	<0.1	0.002	<0.1	0.008

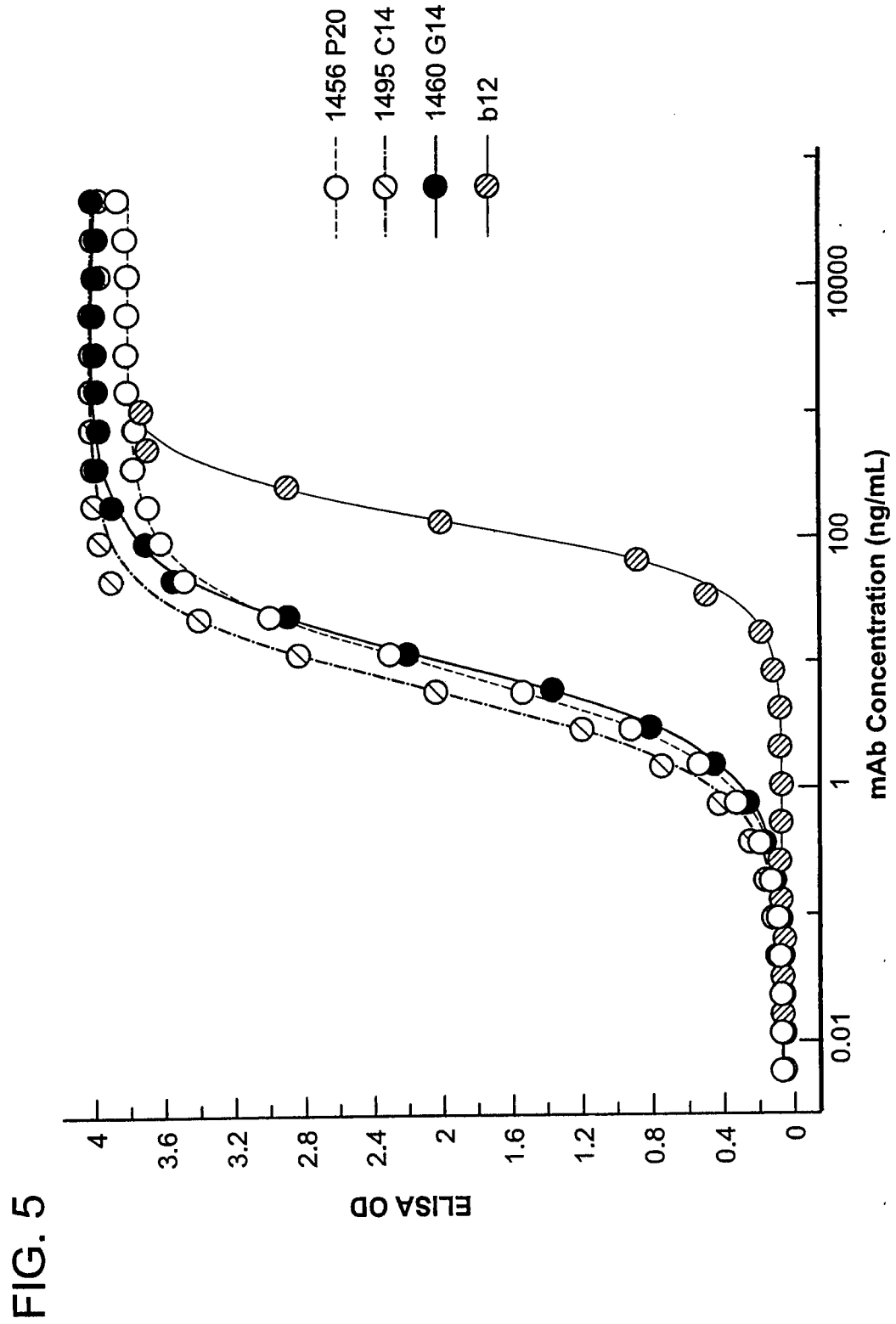


FIG. 6

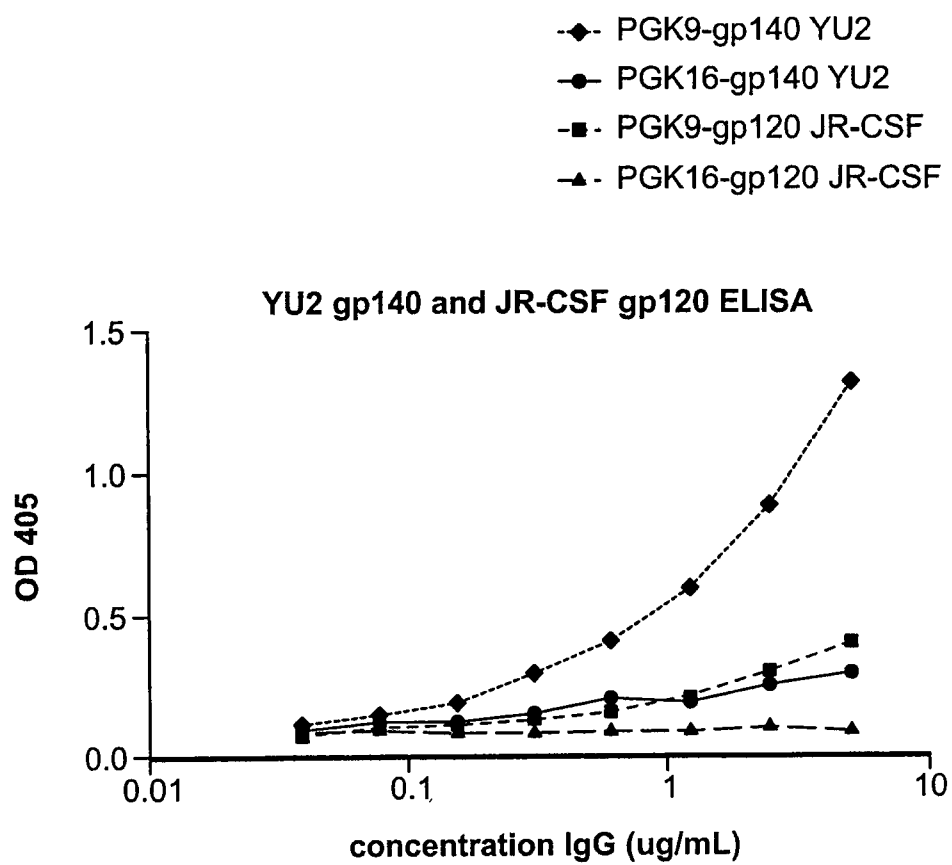


FIG. 6 (continued)

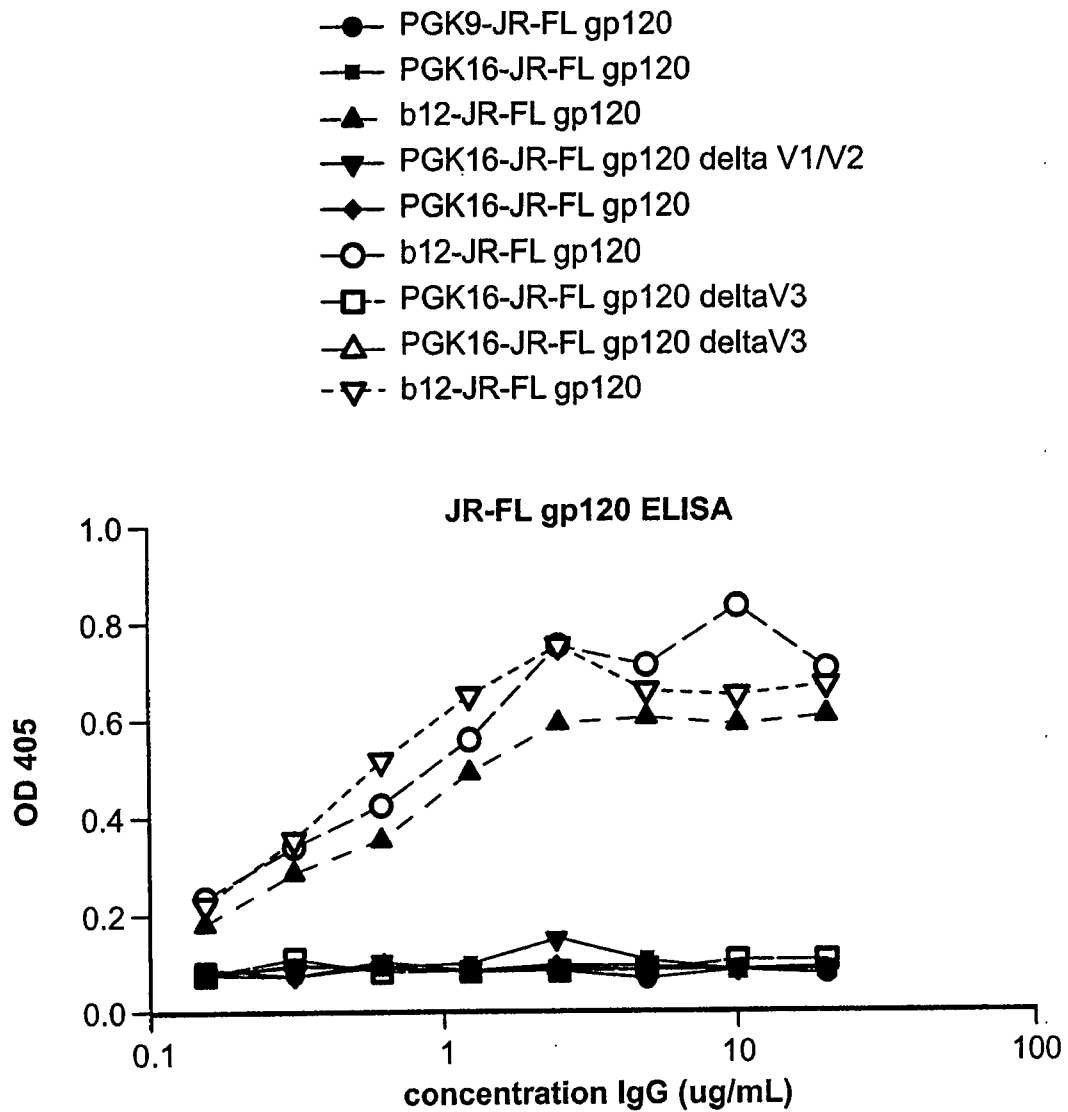


FIG. 6 (continued)

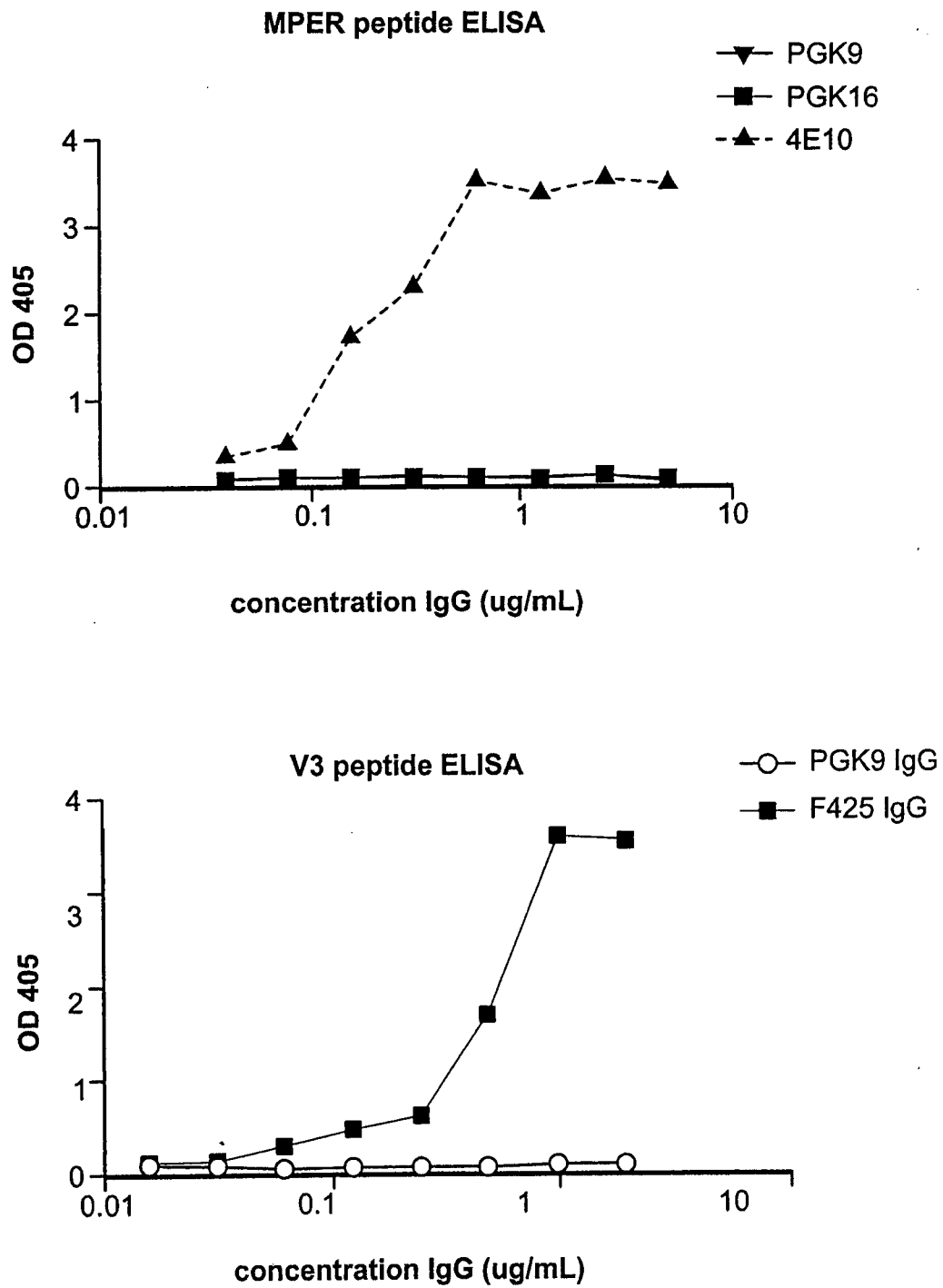


FIG. 7

Binding of PG16 and PG9 to HIV-1YU2 gp160 expressed on Cell Surface
in the presence and absence of sCD4

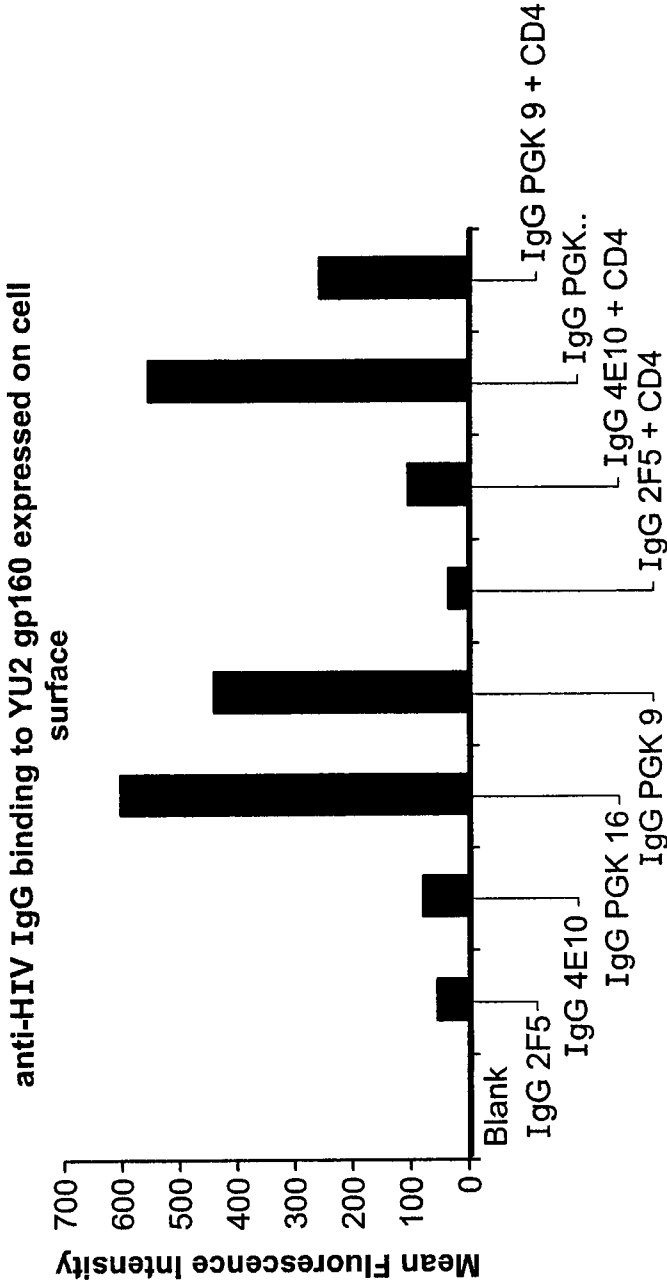


FIG. 8

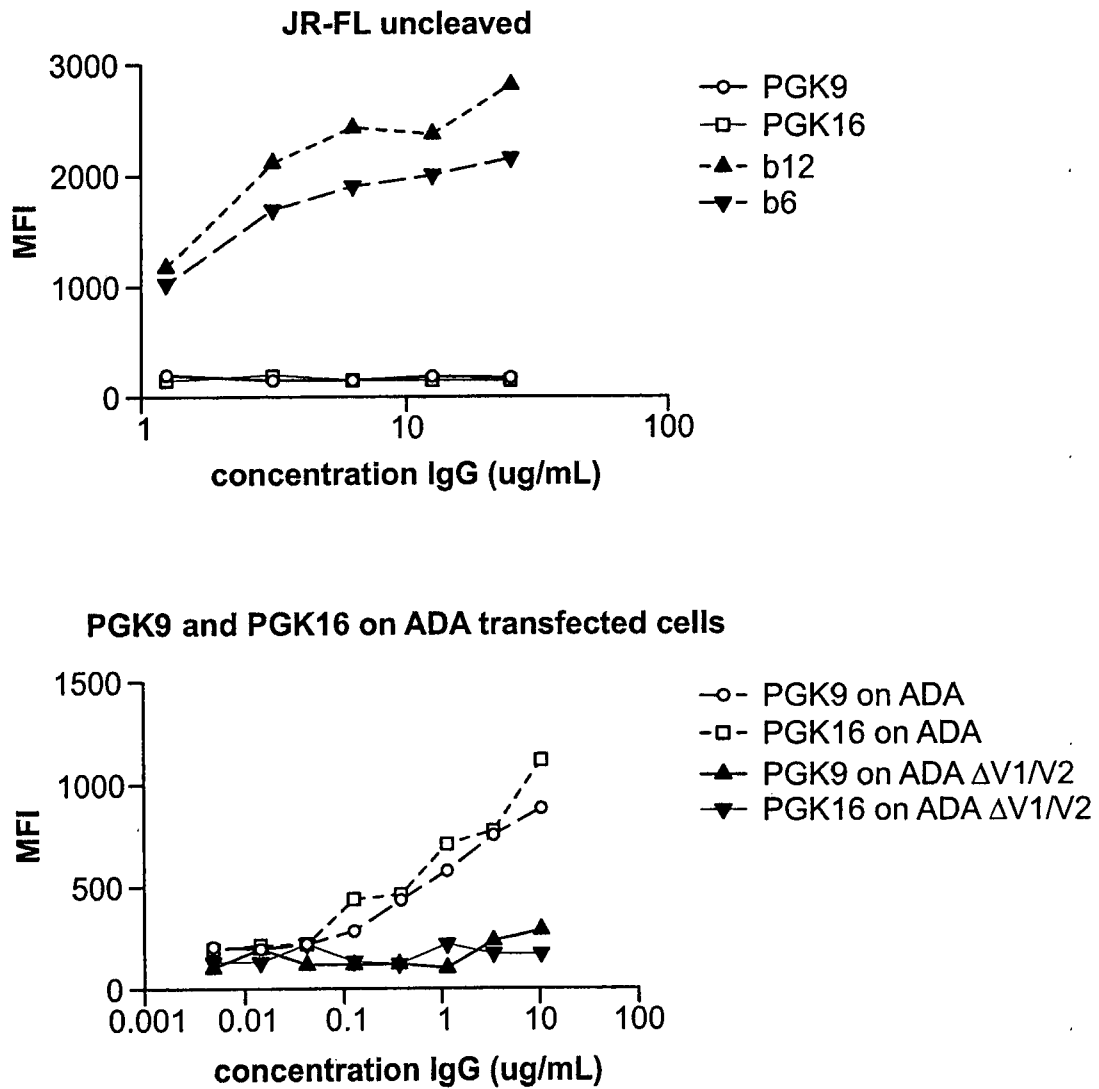
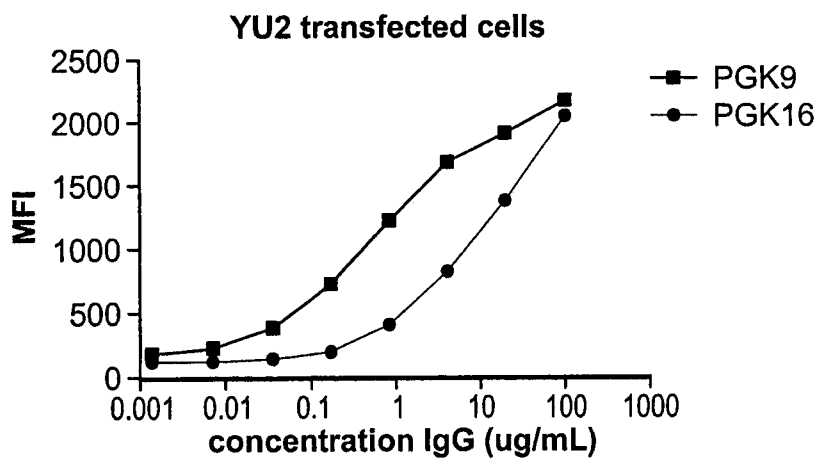
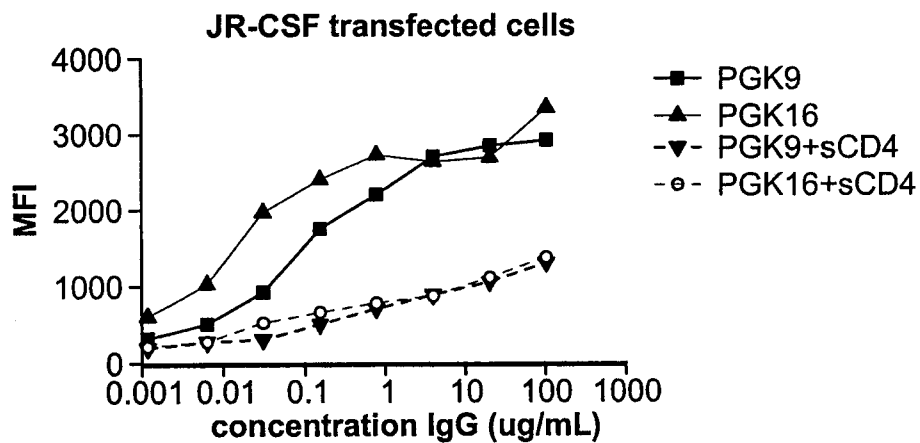
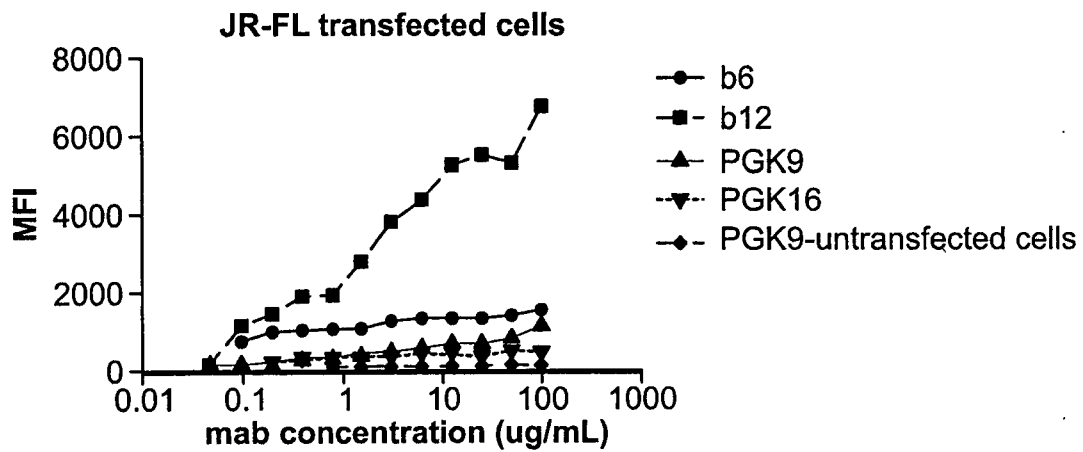


FIG. 8 (continued)



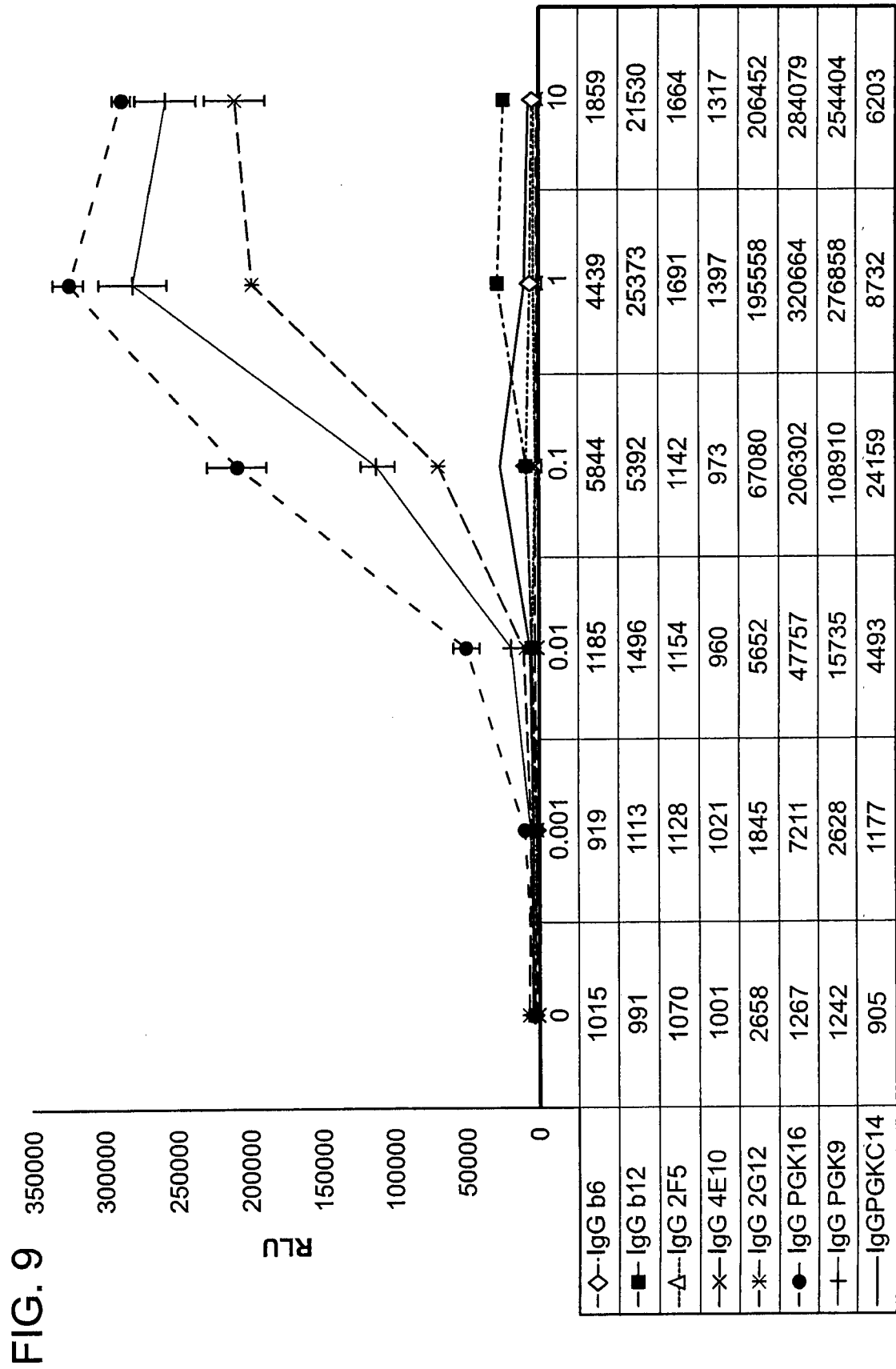


FIG. 10A

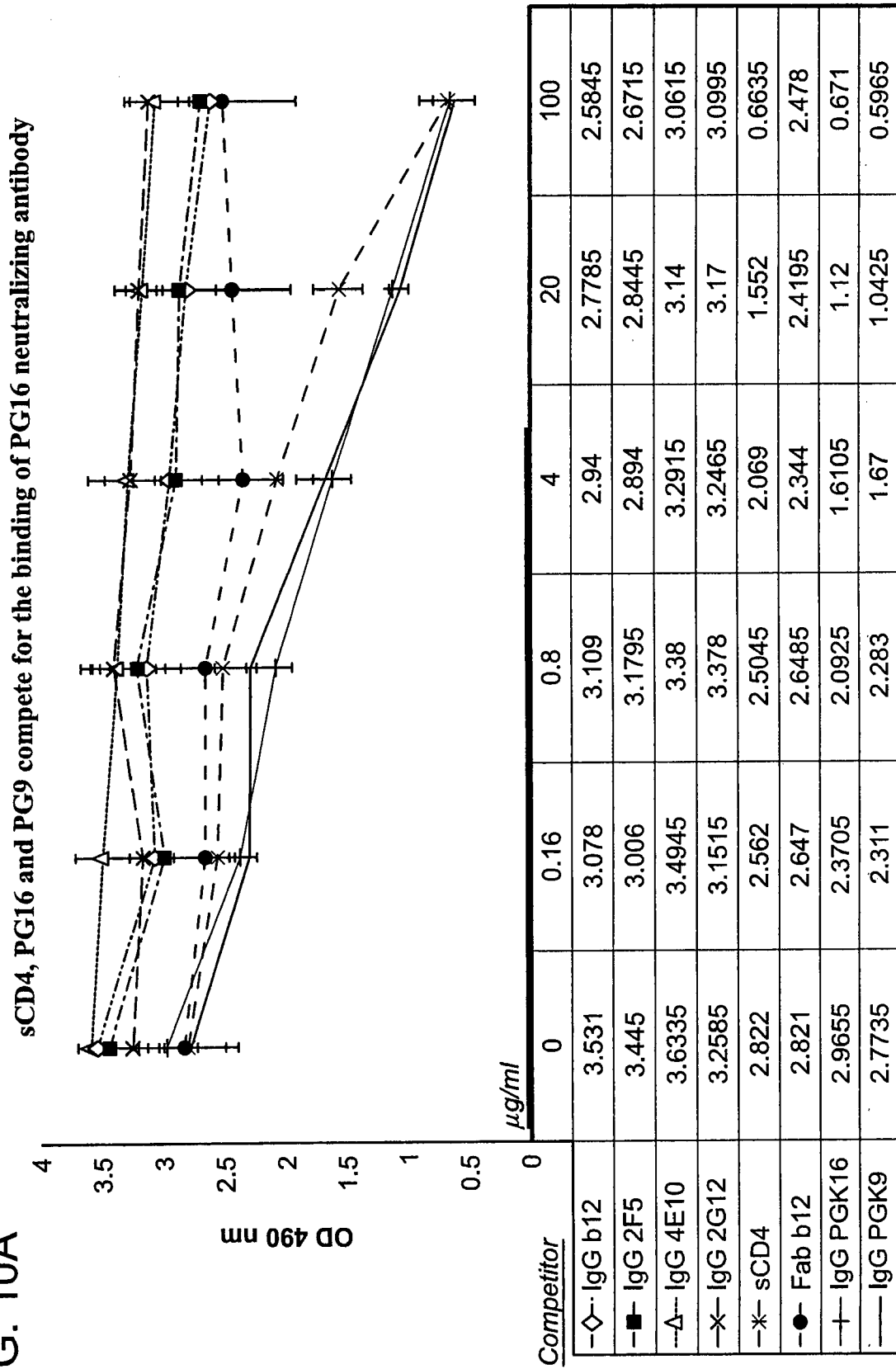
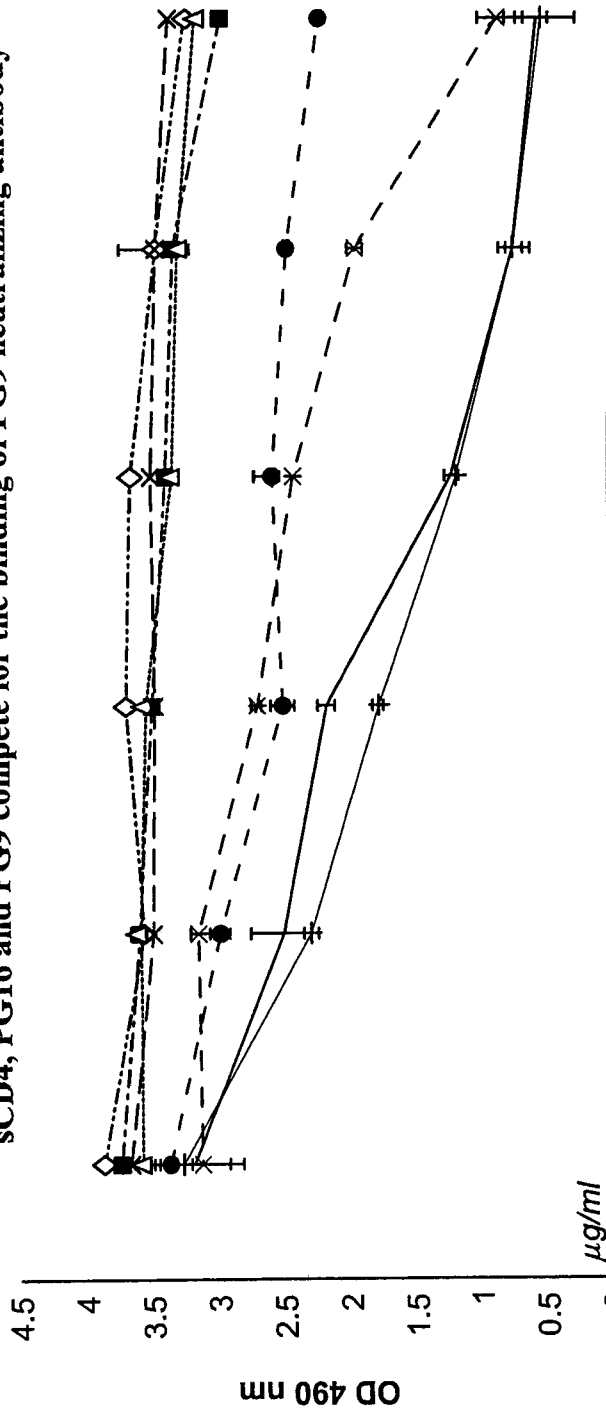


FIG. 10B

sCD4, PG16 and PG9 compete for the binding of PG9 neutralizing antibody



Competitor	0	0.16	0.8	4	20	100
—◇— IgG b12	3.834	3.522	3.6425	3.6095	3.417	3.1835
—■— IgG 2F5	3.7115	3.5455	3.476	3.338	3.278	2.923
—△— IgG 4E10	3.5755	3.513	3.505	3.3065	3.277	3.123
—×— IgG 2G12	3.647	3.4715	3.4425	3.4575	3.411	3.31
—*— sCD4	3.112	3.106	2.672	2.4035	1.9395	0.8495
—●— Fab b12	3.3325	2.963	2.481	2.5565	2.4585	2.202
—+— IgG PGK16	3.248	2.271	1.763	1.1625	0.734	0.526
— — IgG PGK9	3.154	2.4825	2.1545	1.2055	0.7345	0.5615

FIG. 11A

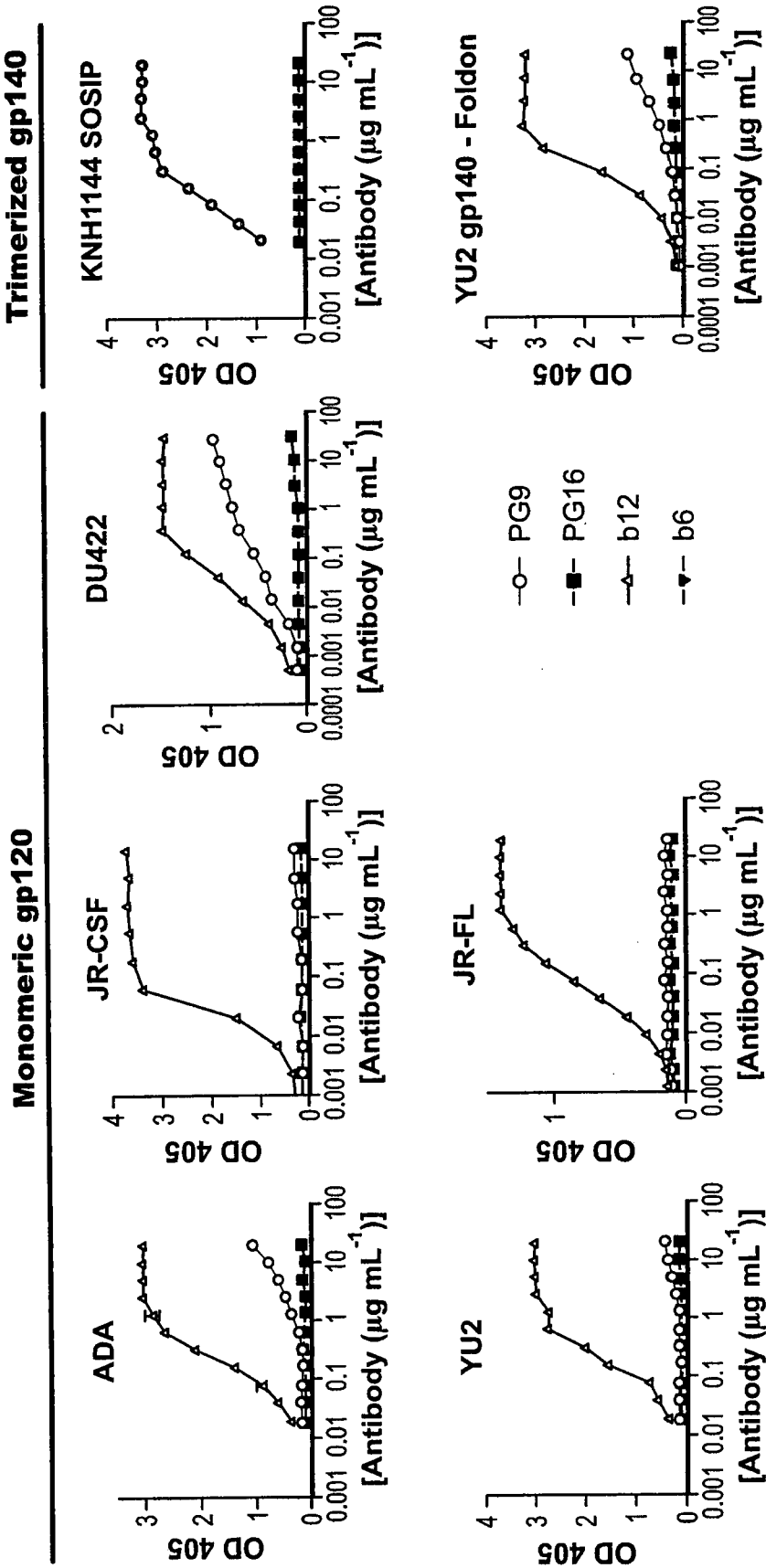


FIG. 11B

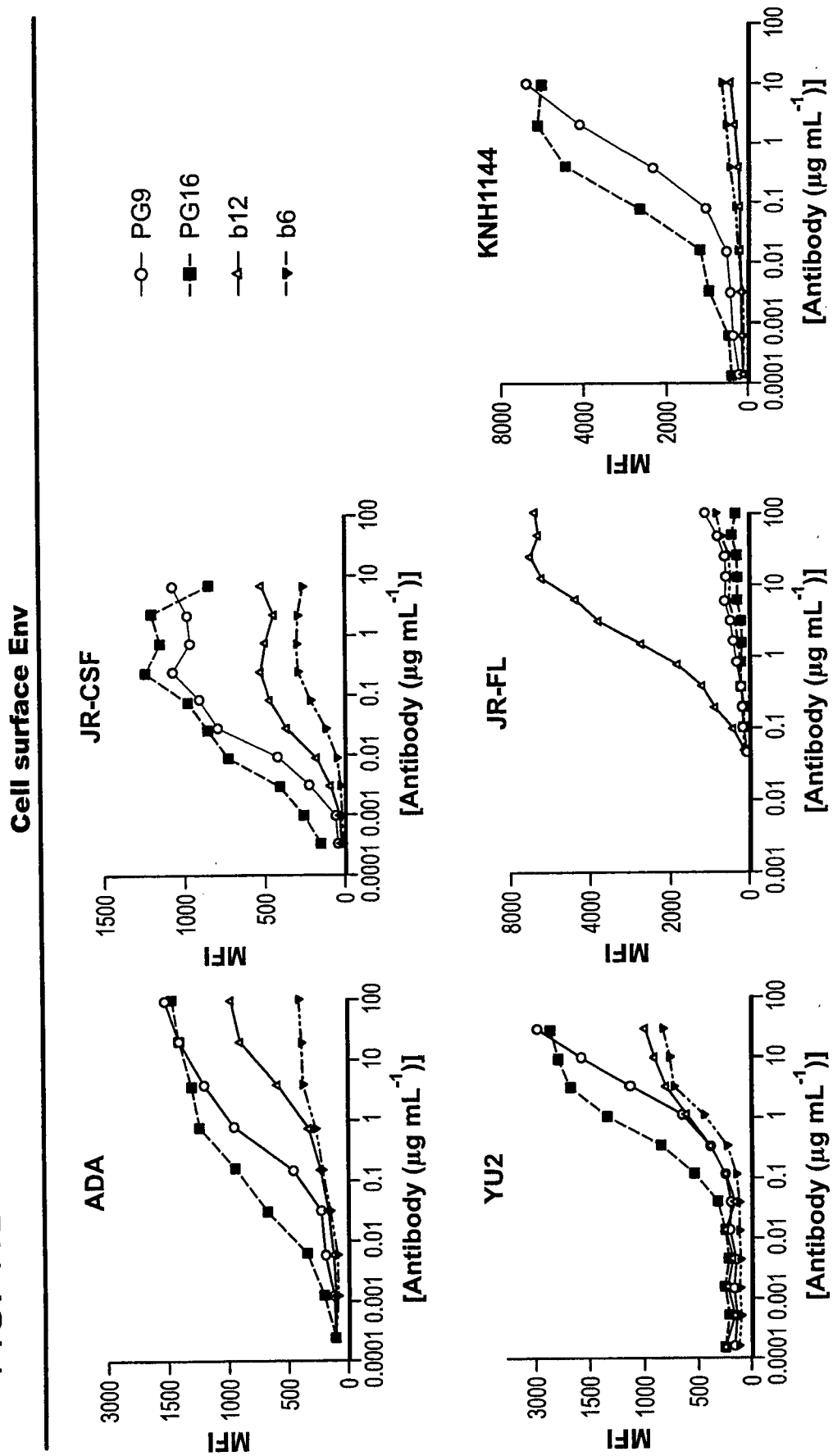


FIG. 12

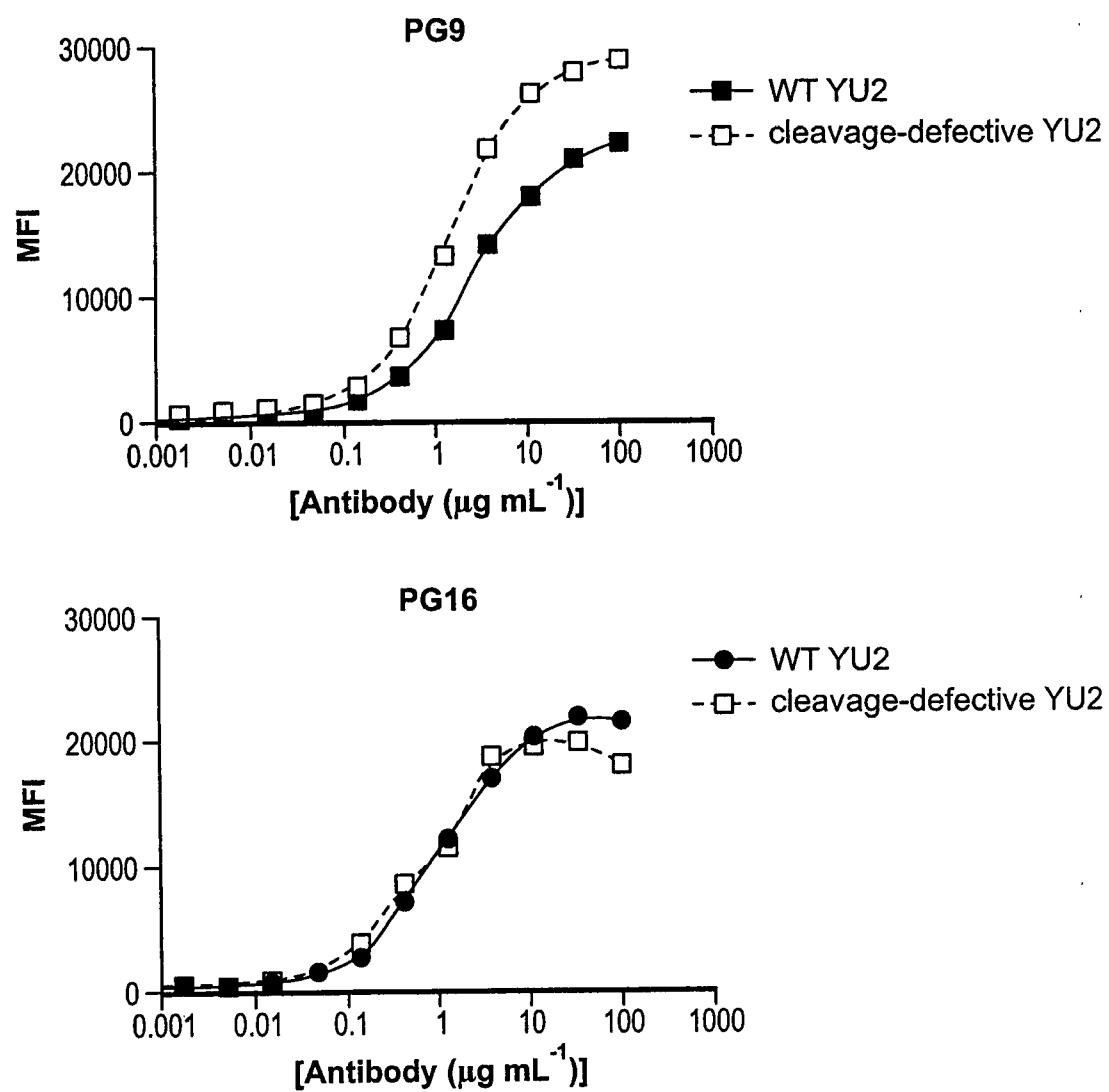


FIG. 13A

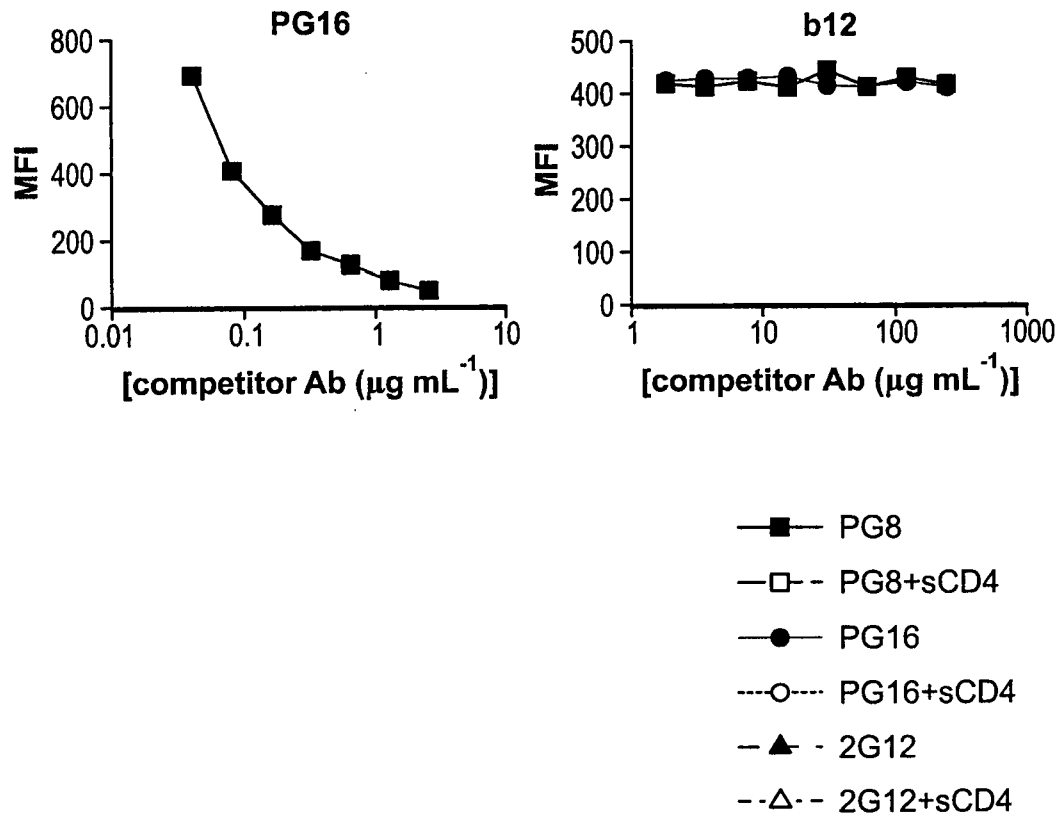


FIG. 13B

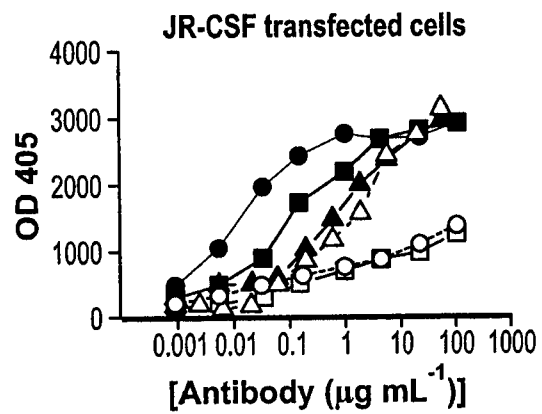
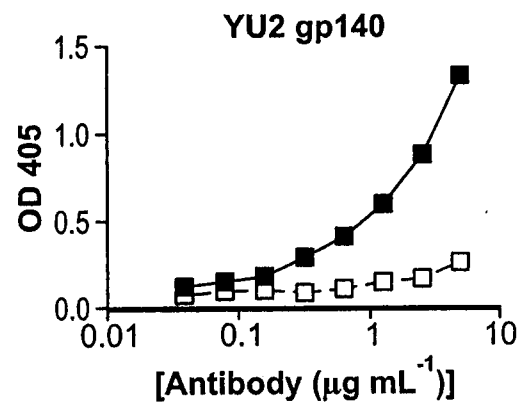


FIG. 13C



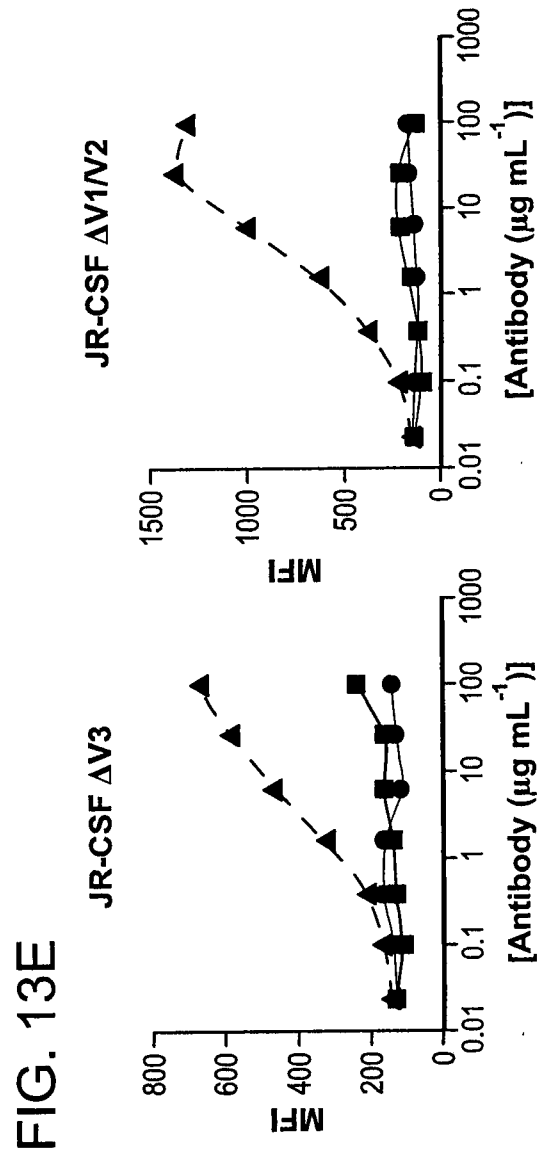
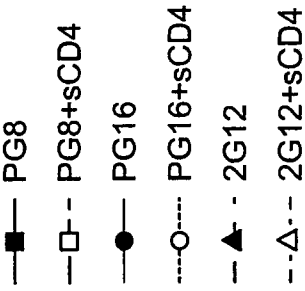
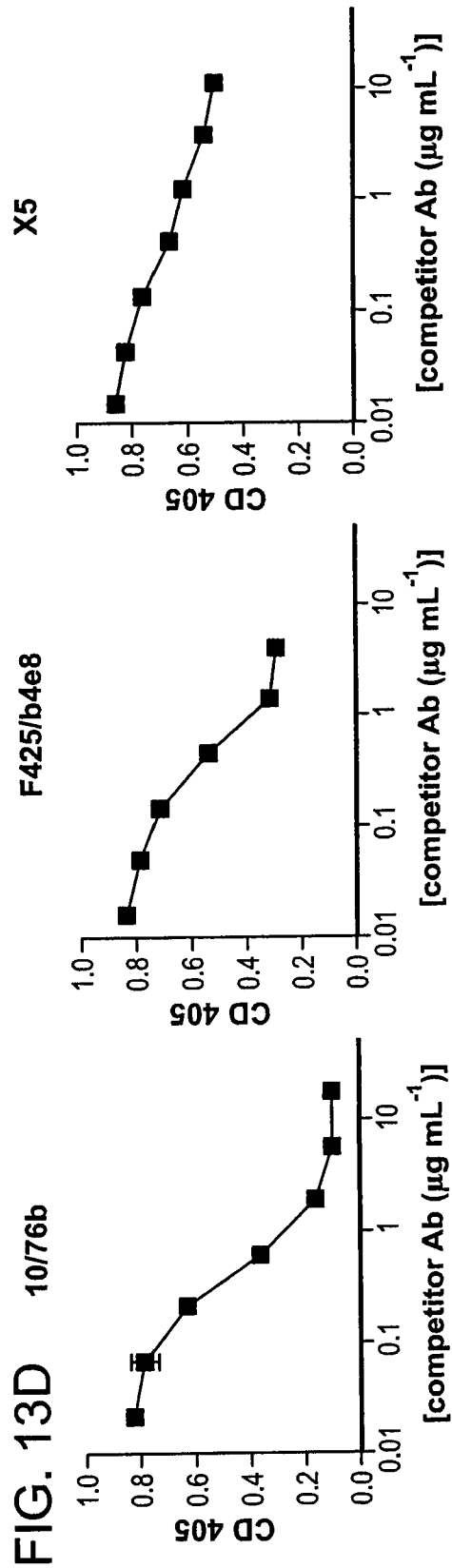


FIG. 14

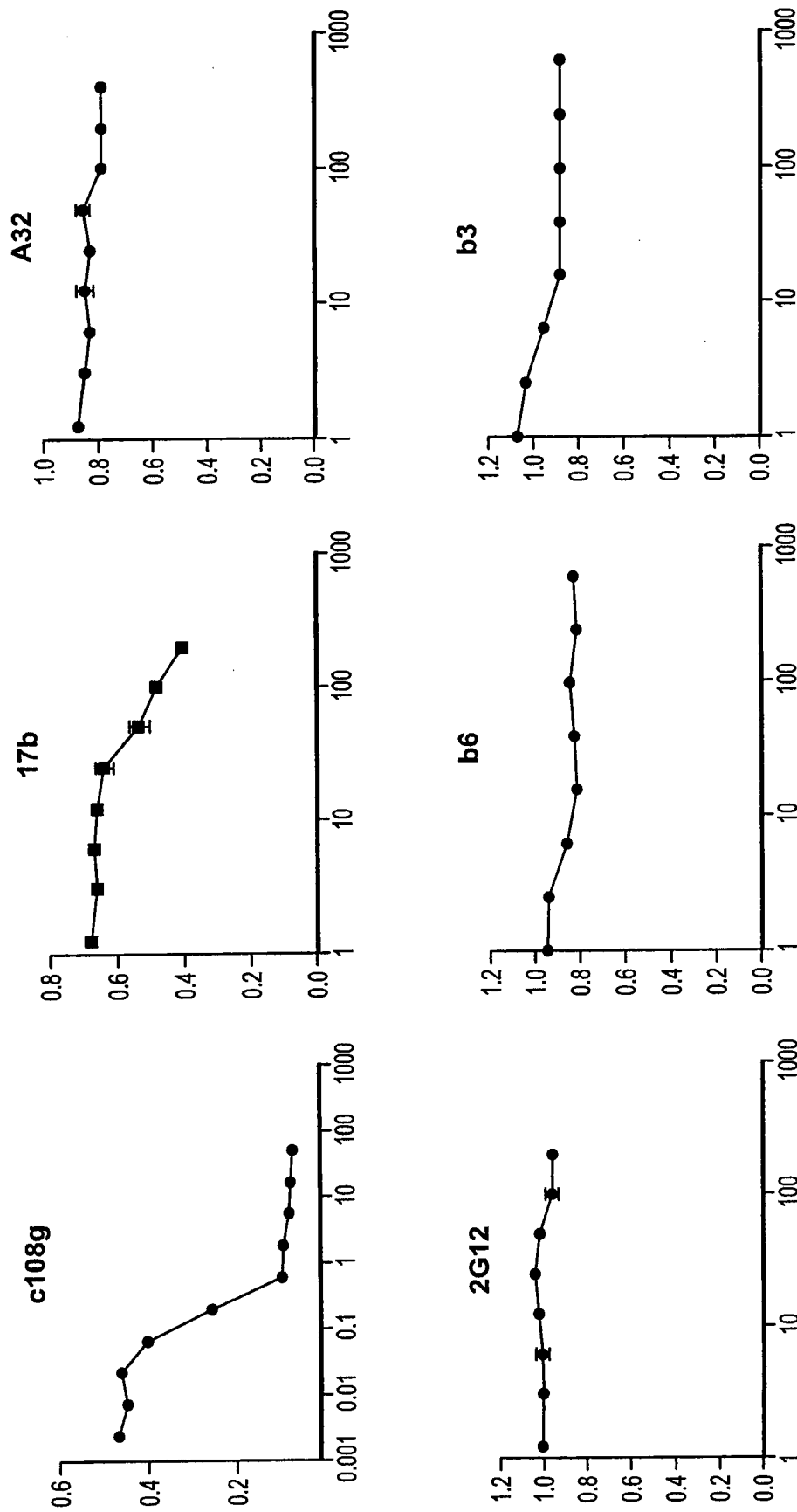


FIG. 15

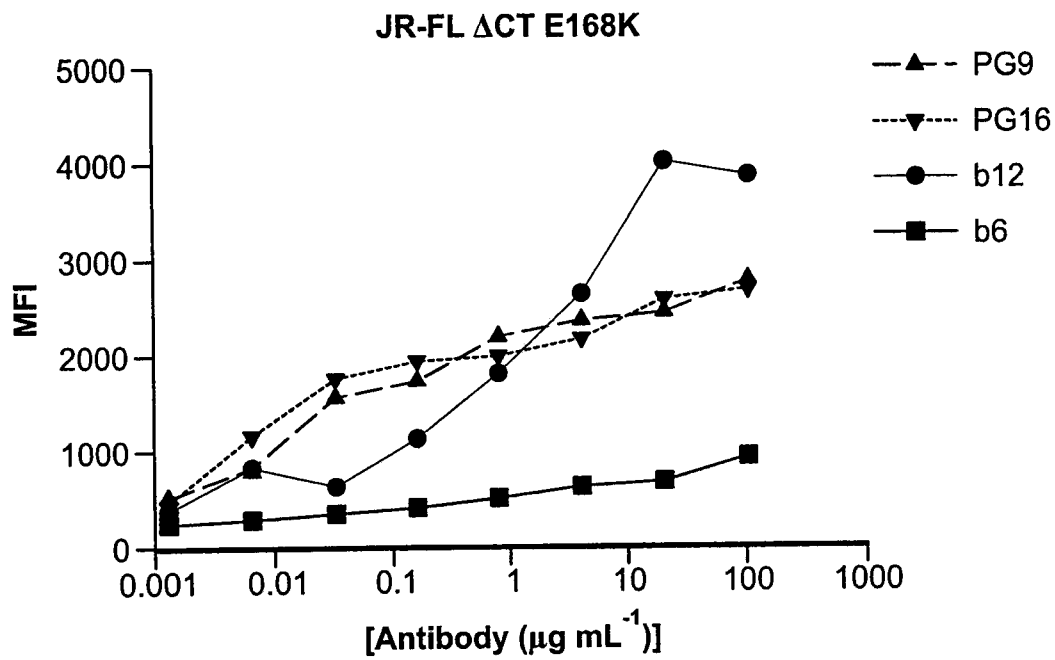


FIG. 16

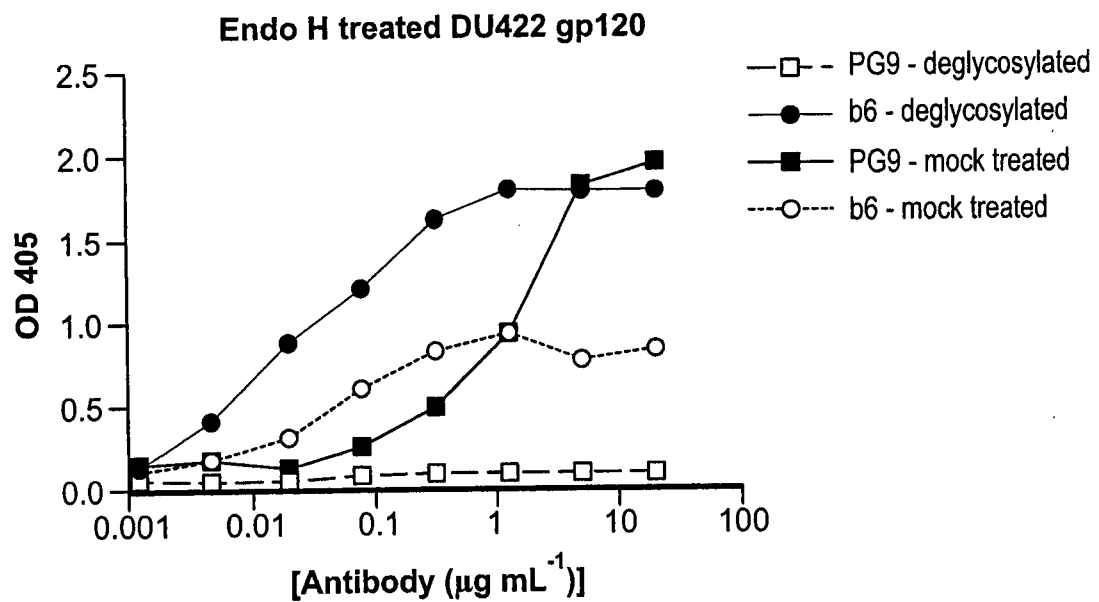


FIG. 17

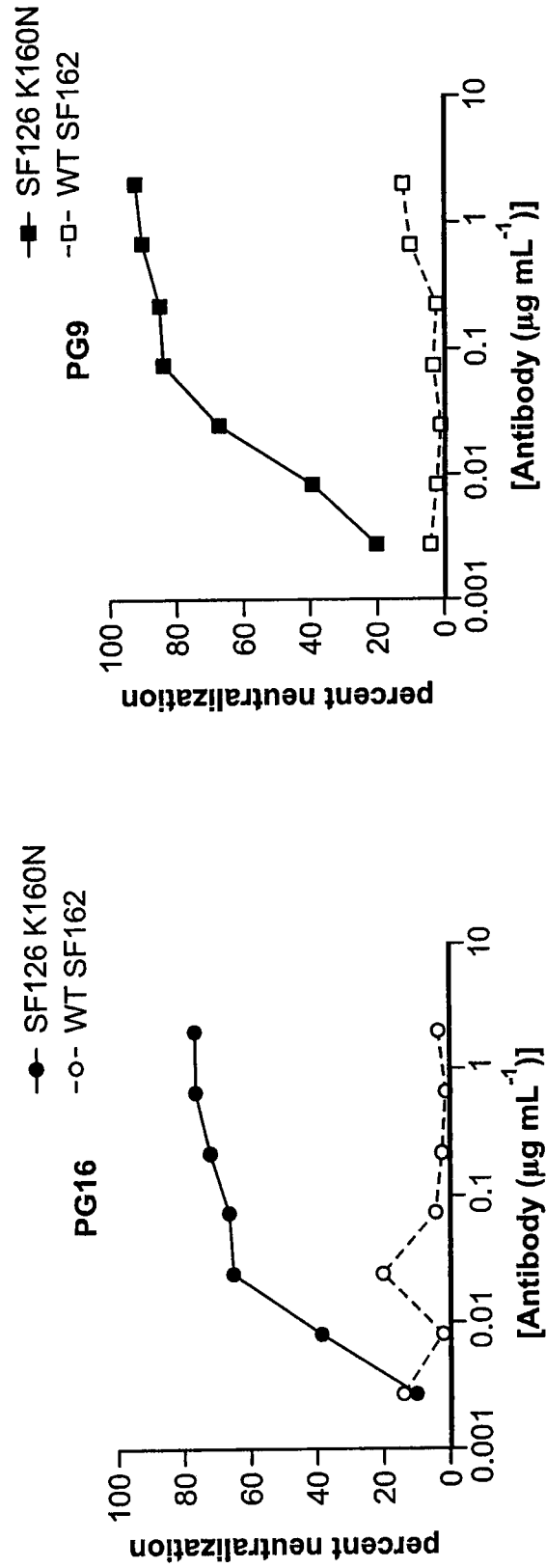


FIG. 18

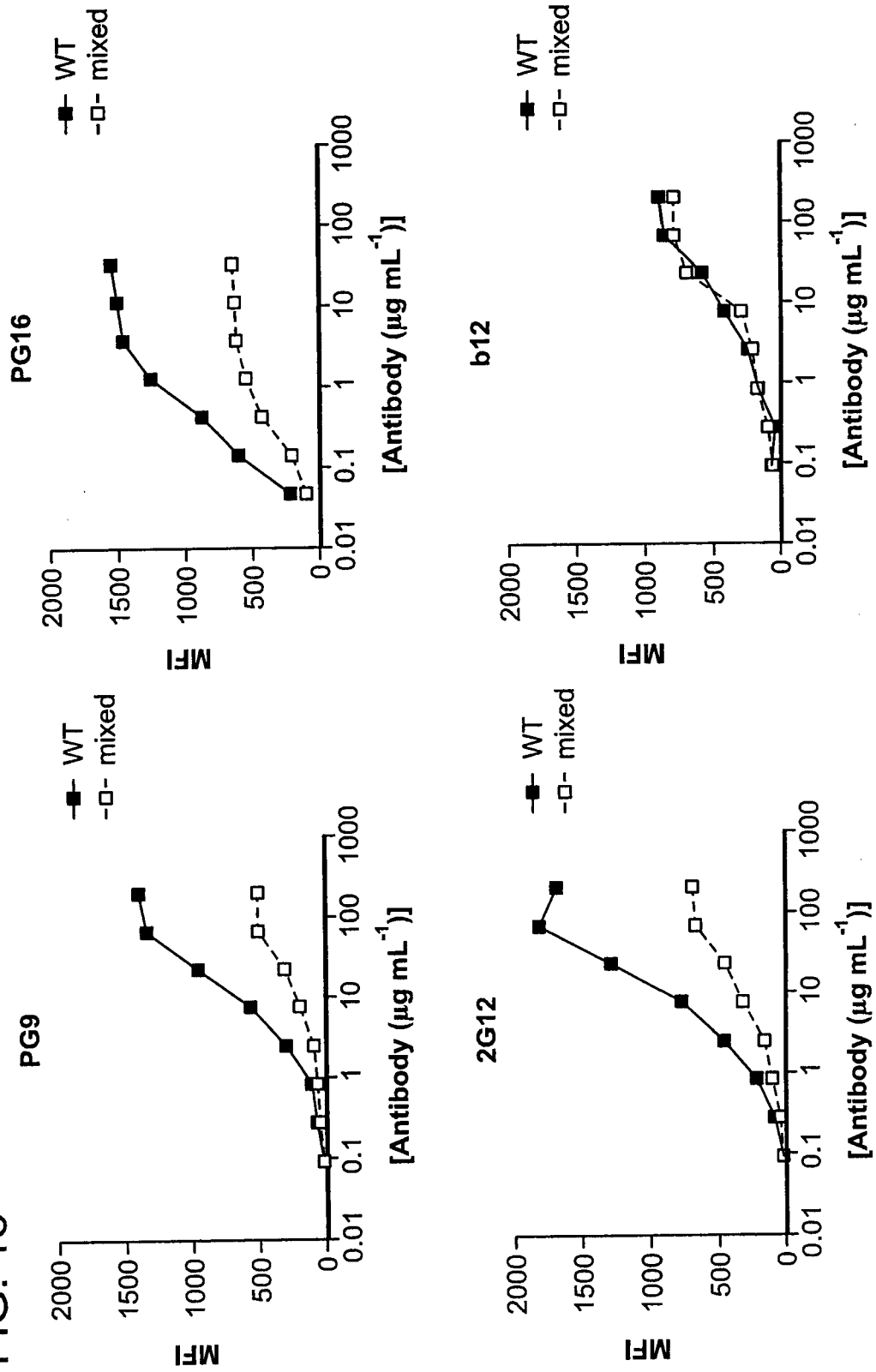


FIG. 19

VH

	1443 C16	1456 A12	1408 I08	1503 H05	1489 I13	1469 M23
1443 C16	0	4	0	2	2	1
1456 A12	3	0	4	5	6	5
1408 I08	0	3	0	2	2	1
1503 H05	1	3	1	0	4	1
1489 I13	0	3	0	1	0	3
1469 M23	3	4	3	2	3	0

Protein

VL

	1443 C16	1456 A12	1408 I08	1503 H05	1489 I13	1469 M23
1443 C16	0	7	0	7	2	3
1456 A12	6	0	7	13	9	10
1408 I08	1	5	0	7	2	3
1503 H05	1	7	2	0	9	4
1489 I13	1	5	0	2	0	5
1469 M23	3	7	4	2	4	0

Nucleotide

VH

VL

FIG. 20A

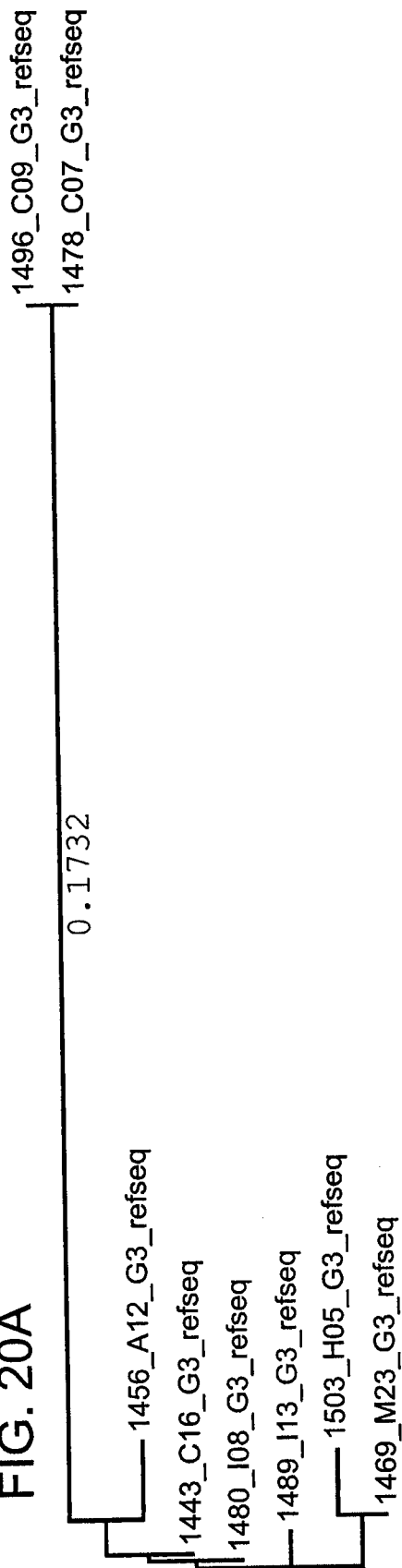


FIG. 20B

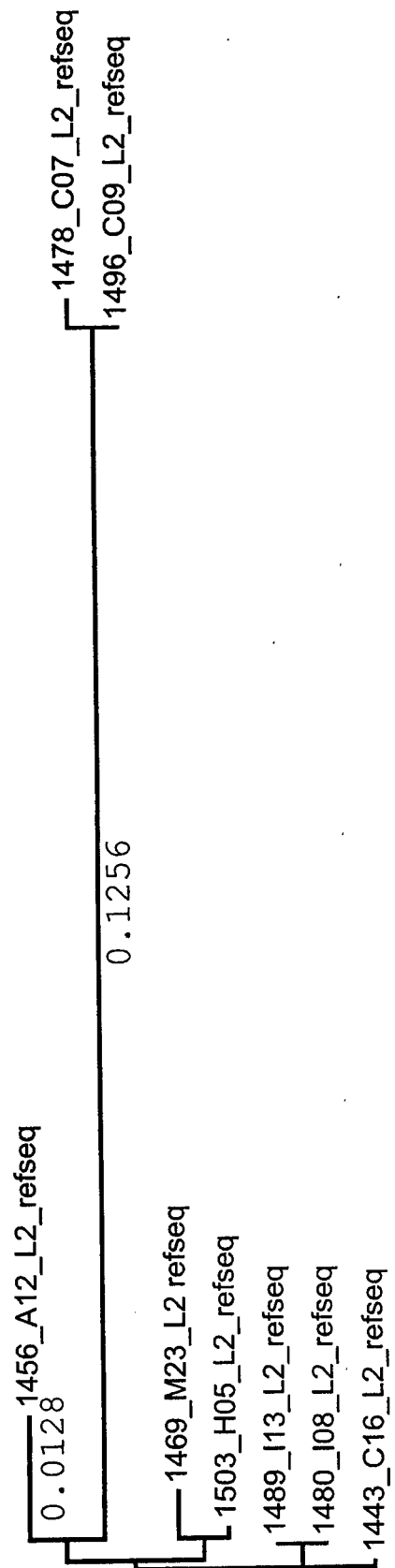


FIG. 21A

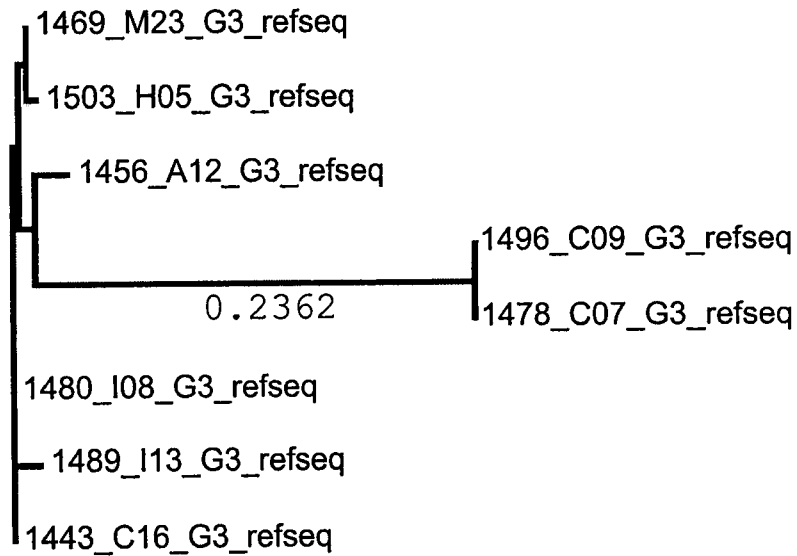


FIG. 21B

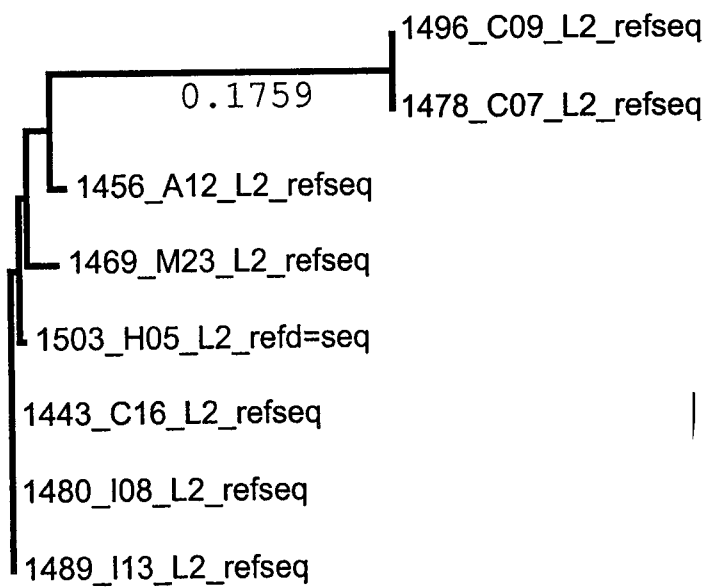


FIGURE 22

Number of HIV-Neutralizing Hits Detected
in Primary Screening

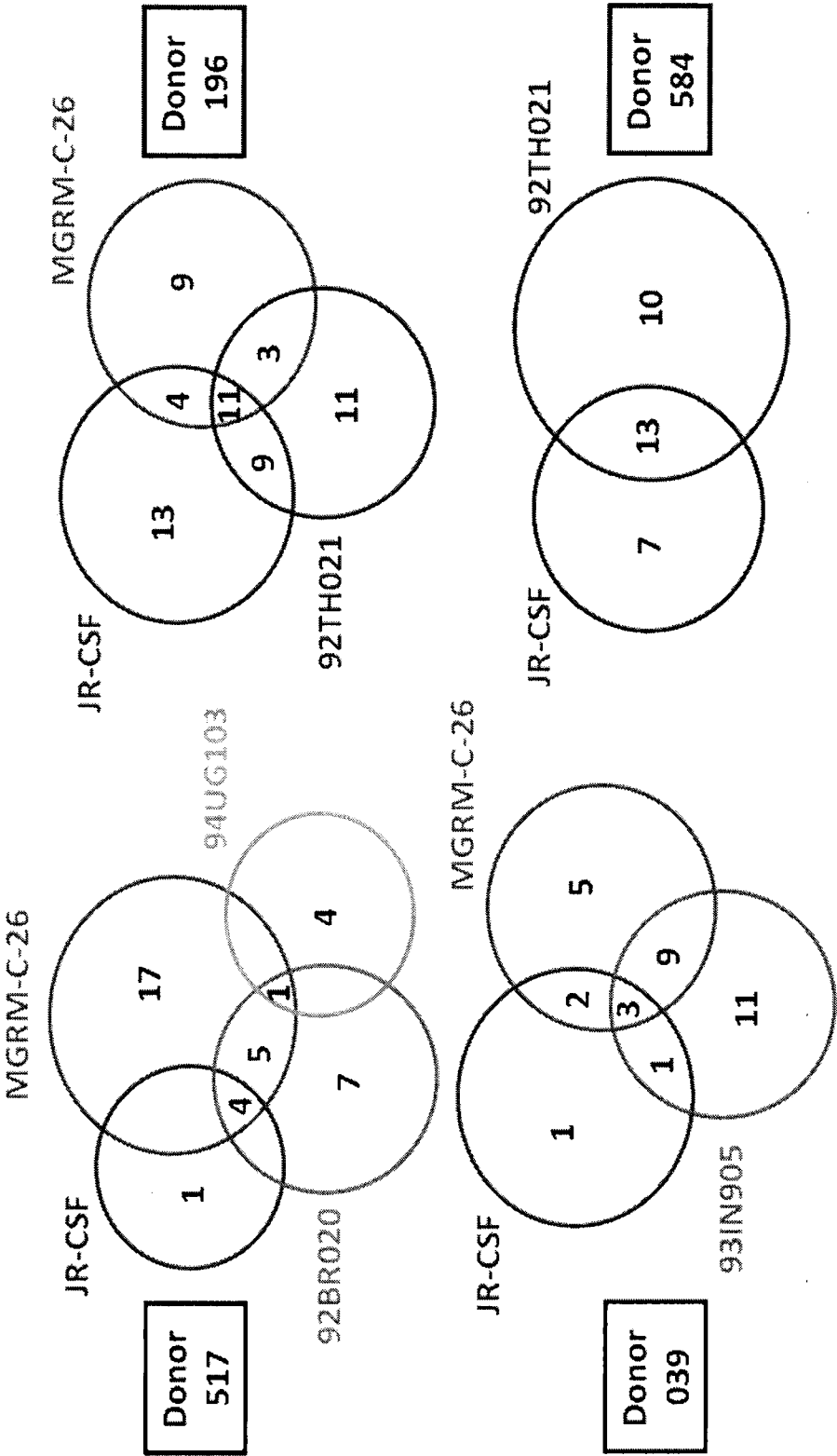
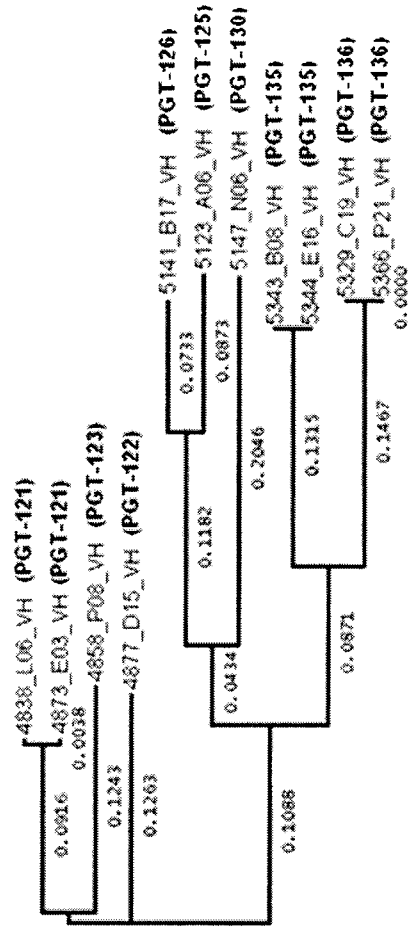


FIGURE 23

Heavy Chain Variable Gene Relationship Tree



0.03

FIGURE 24

Light Chain Variable Gene Relationship Tree

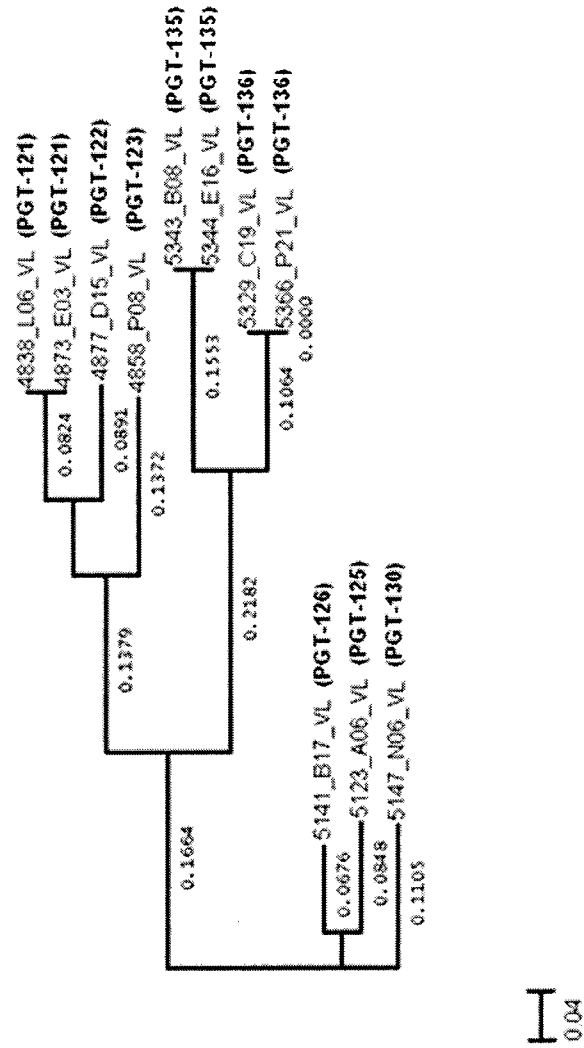


FIGURE 25

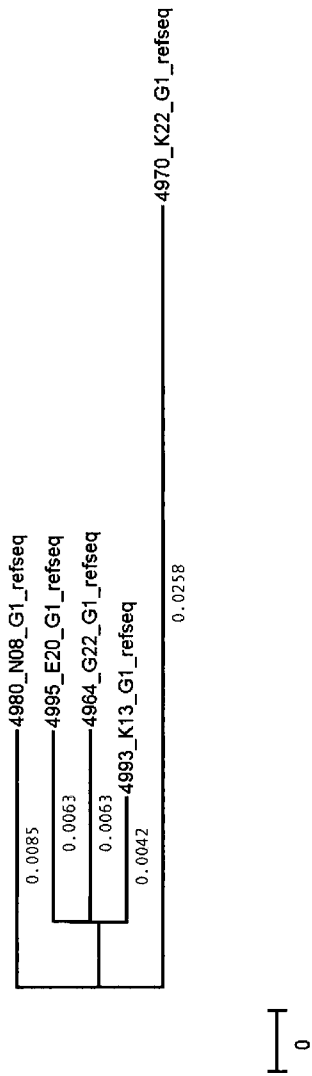


FIGURE 26

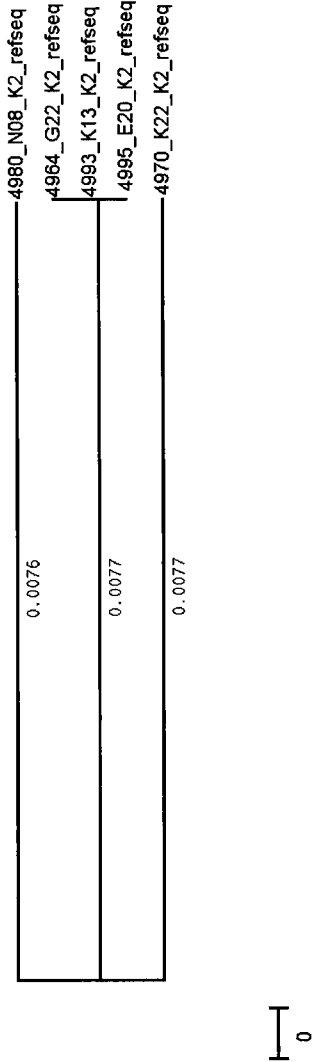


FIGURE 27

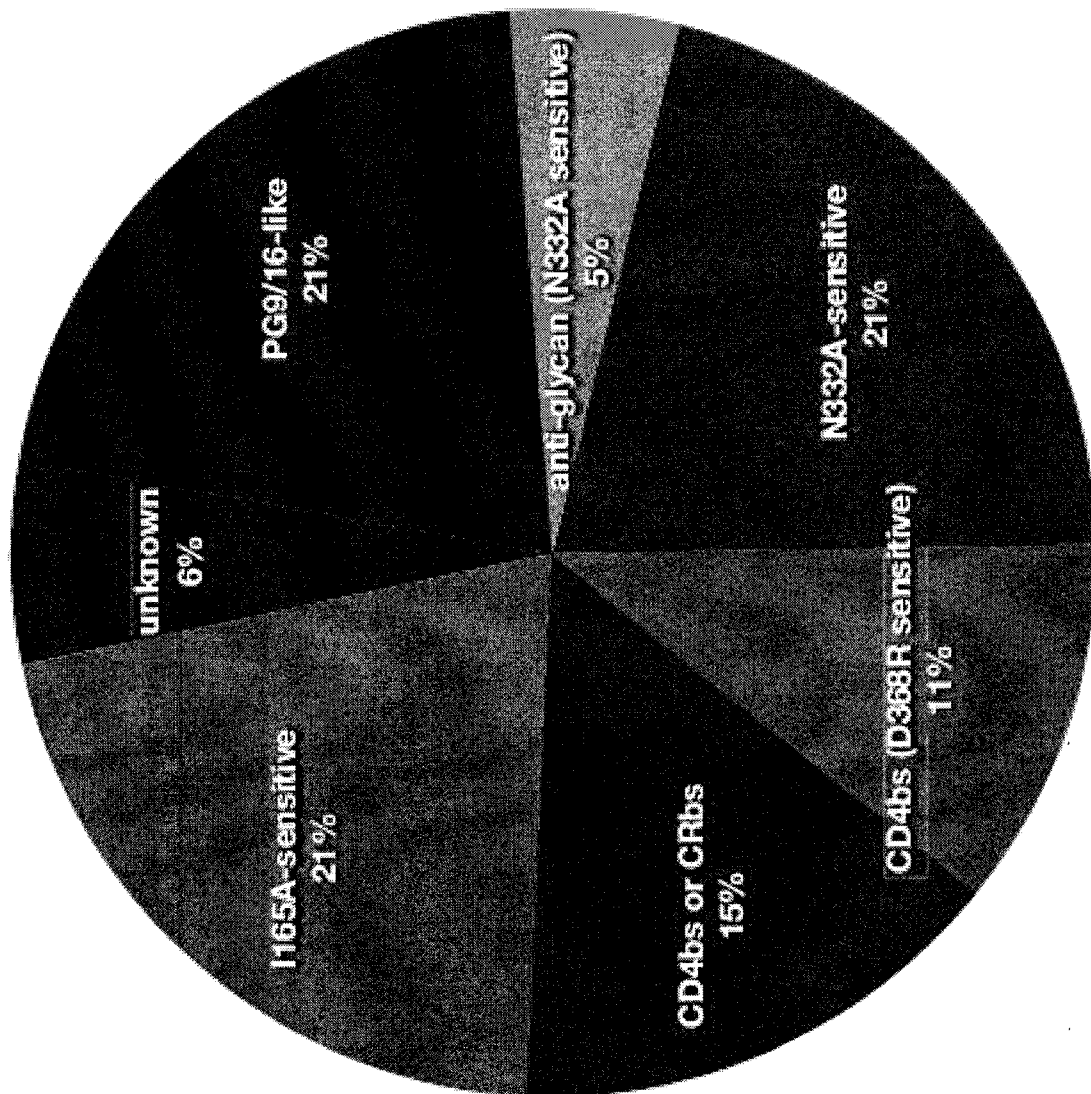


FIGURE 28

I-STAR™ Human bNAb Discovery Platform

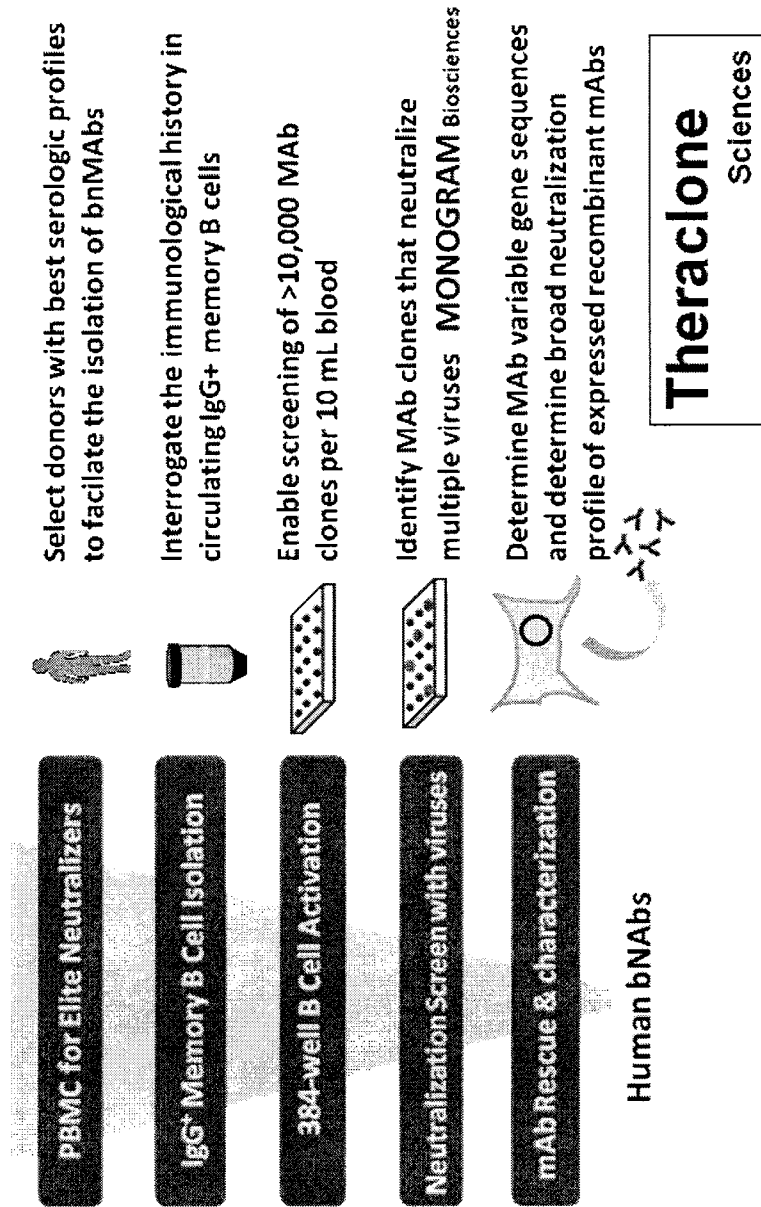


FIGURE 29

bnMAb Isolation from IgG⁺ Memory B Cells

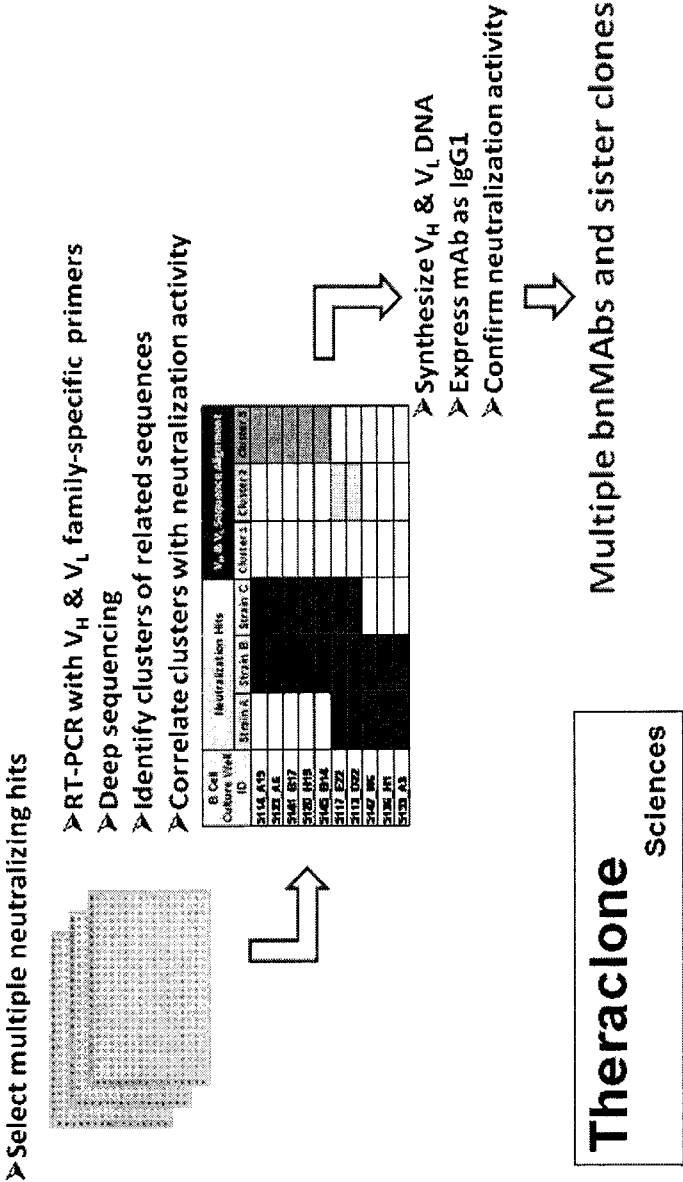


FIGURE 30

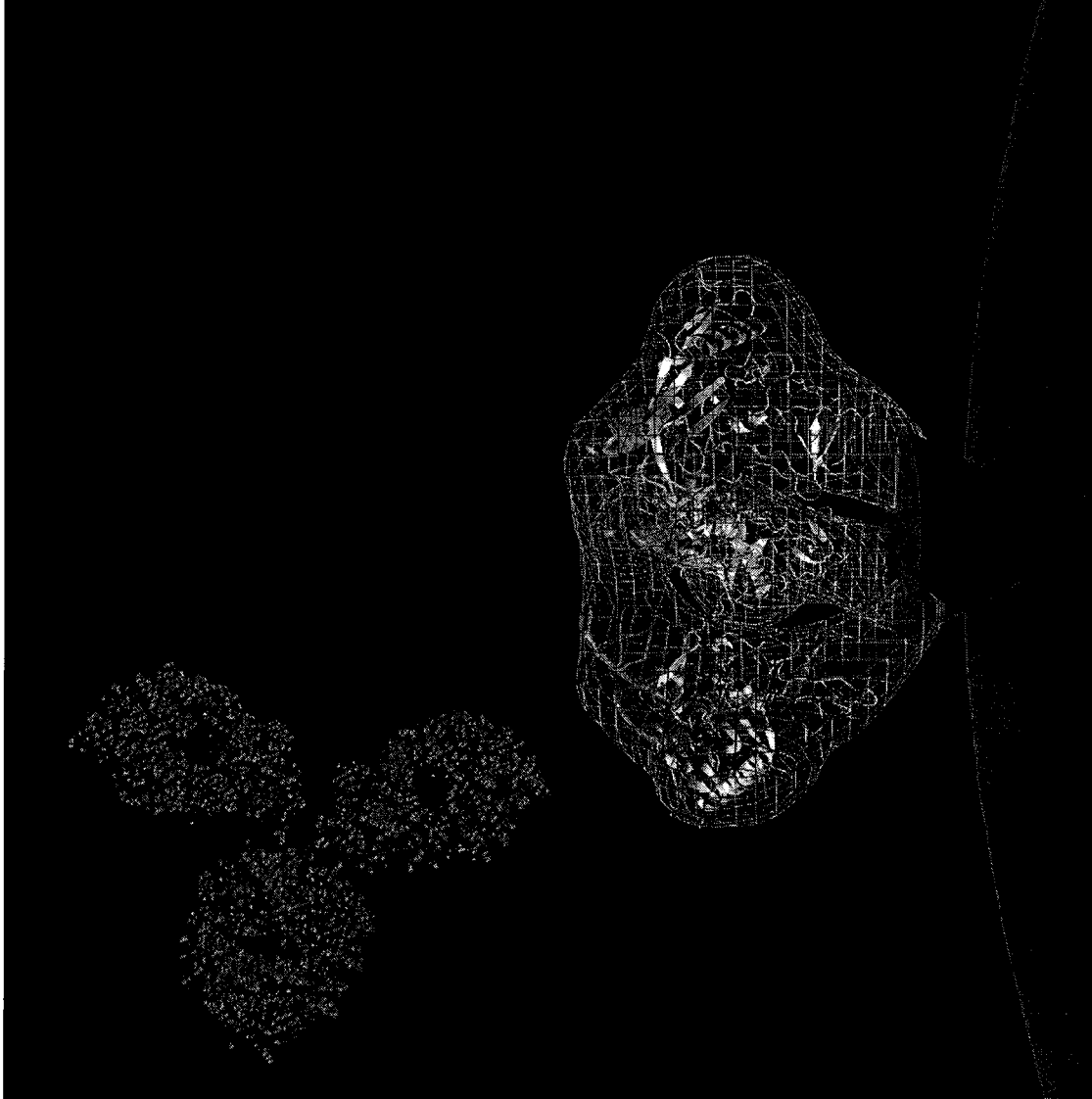


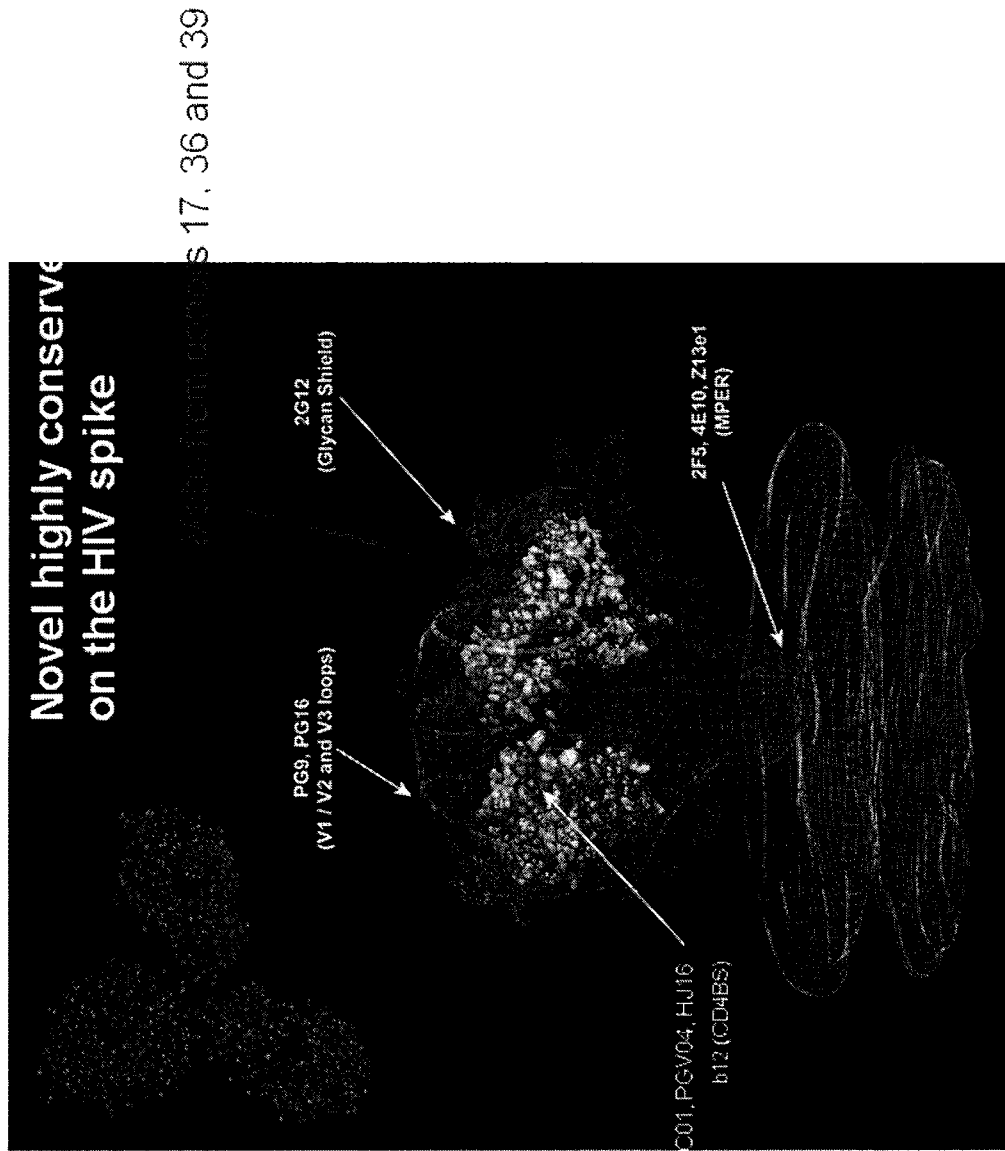
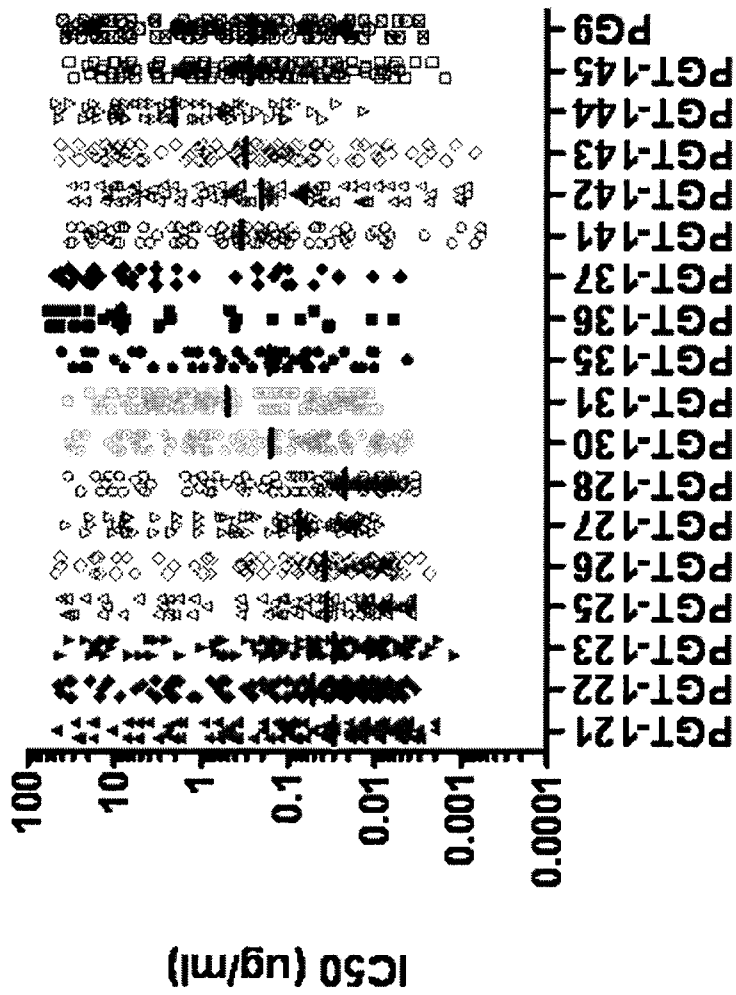
FIGURE 31

FIGURE 32



A

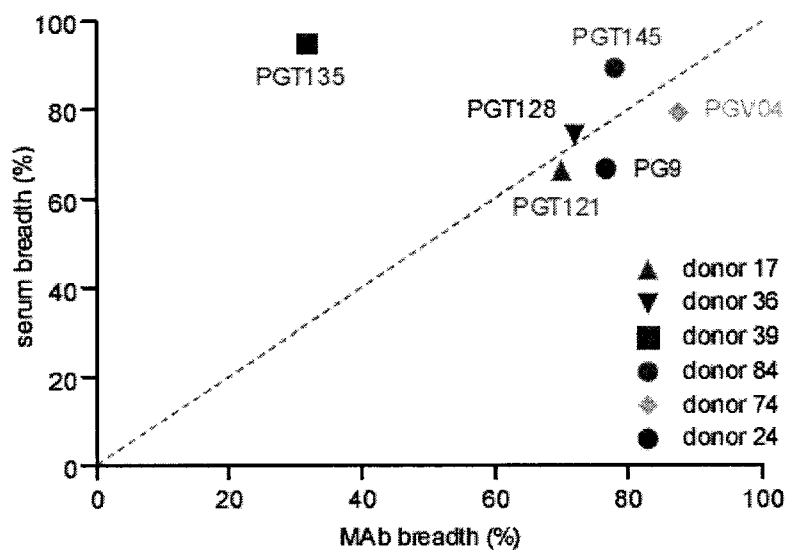
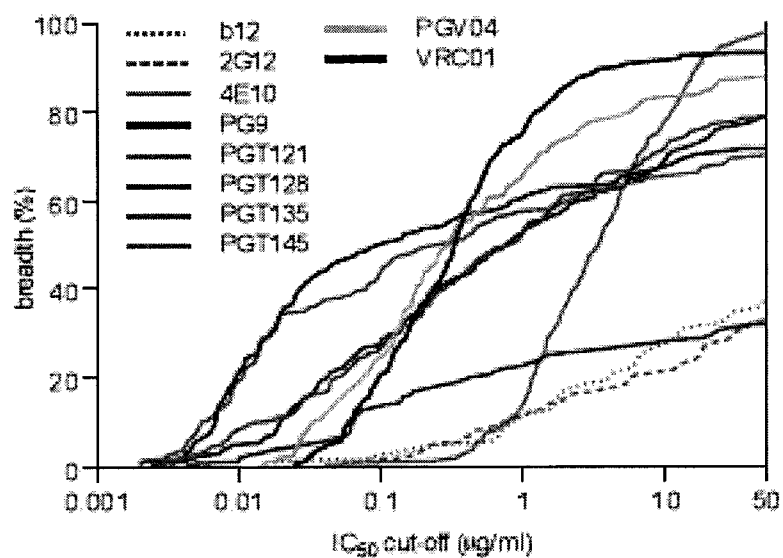
**B**

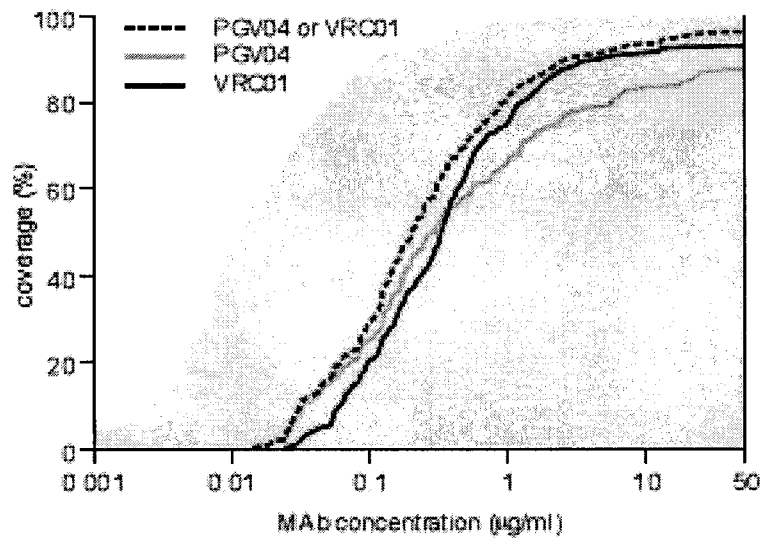
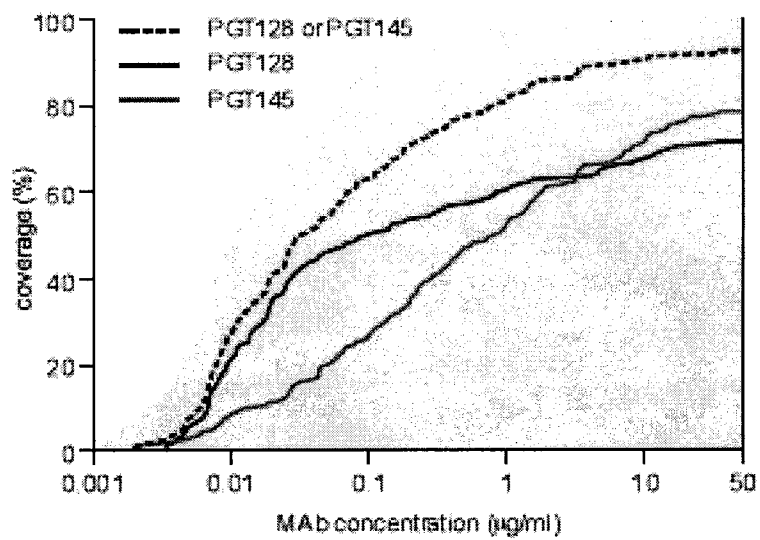
FIGURE 33**C****D**

FIGURE 34

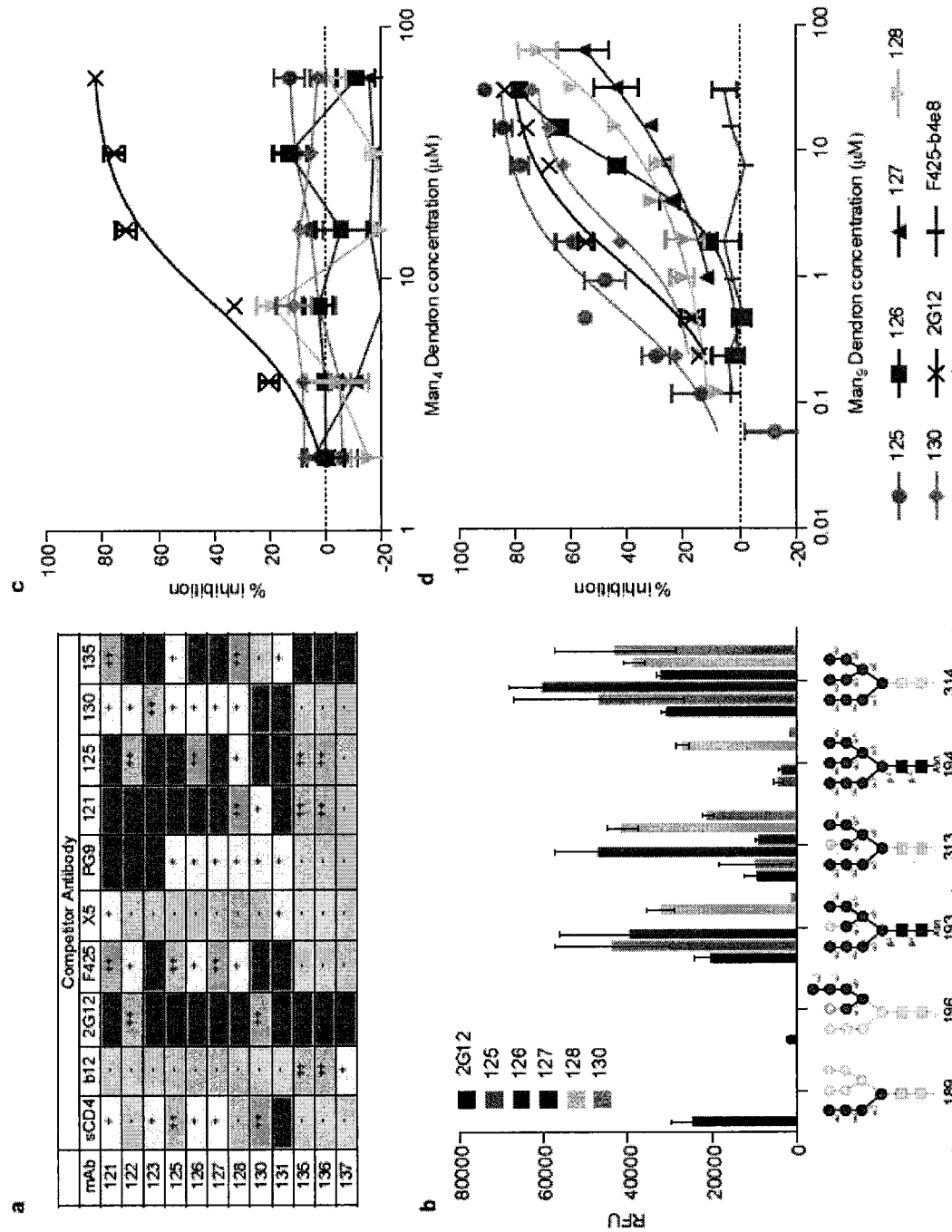


FIGURE 35

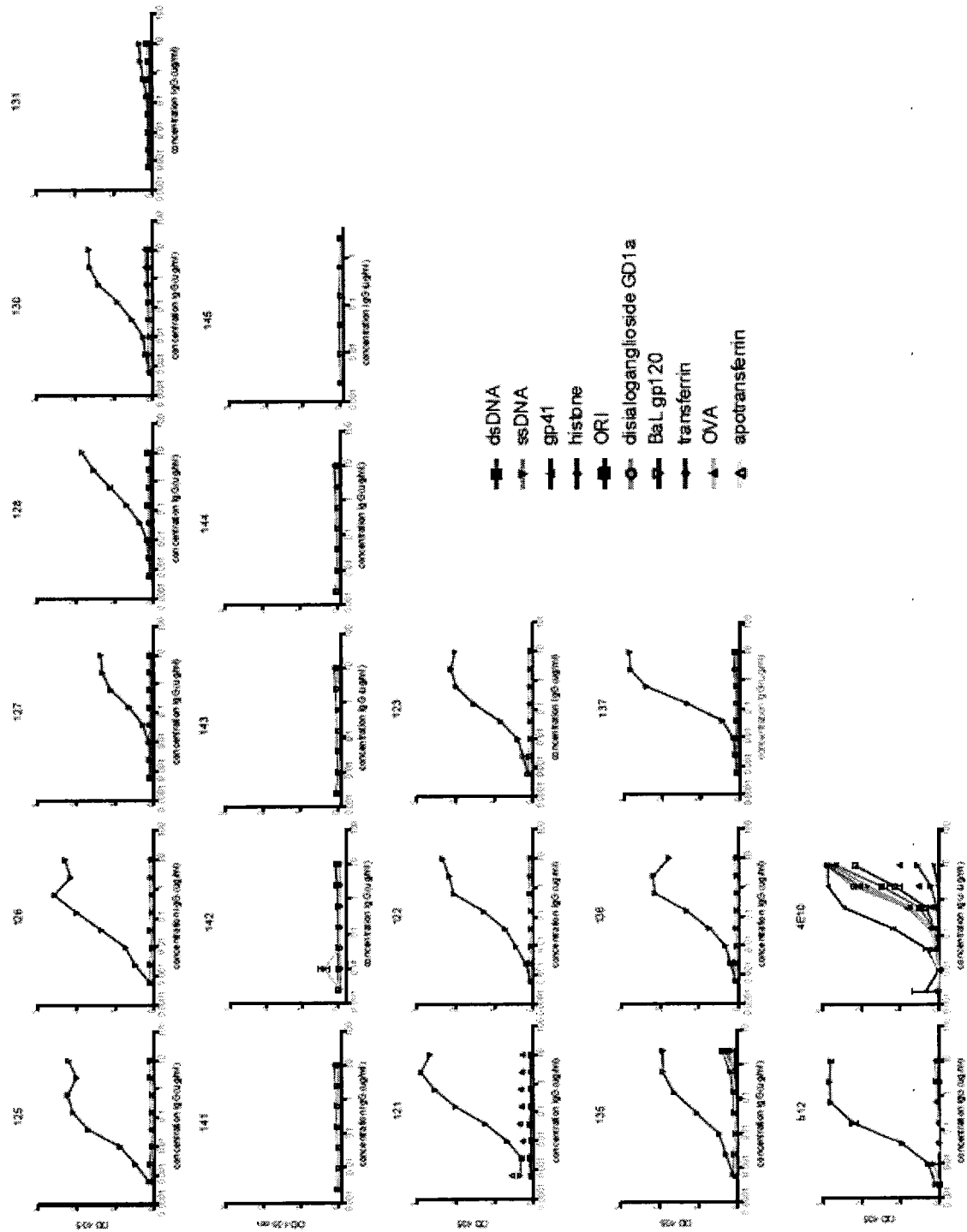


FIGURE 36

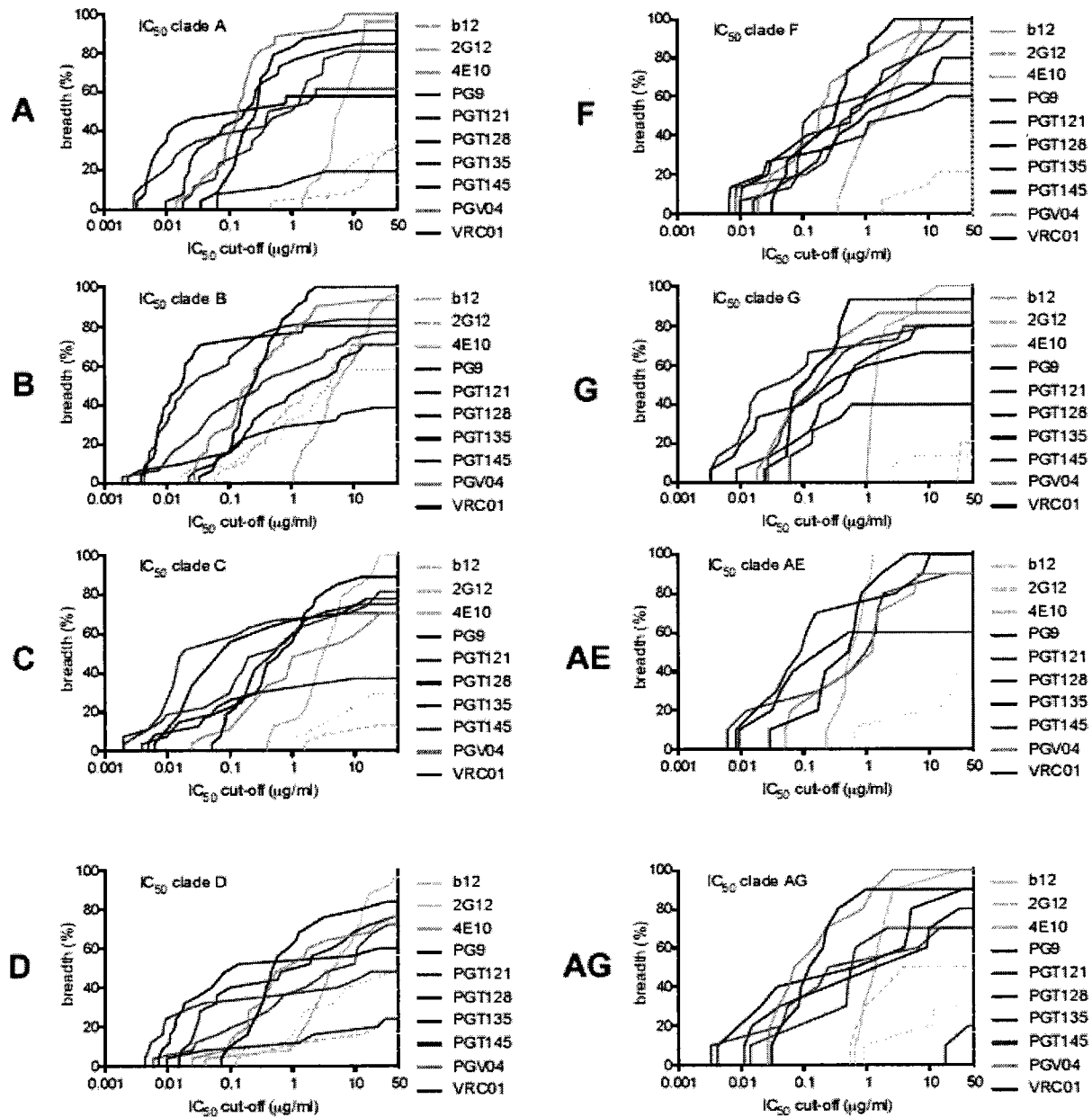


FIGURE 37

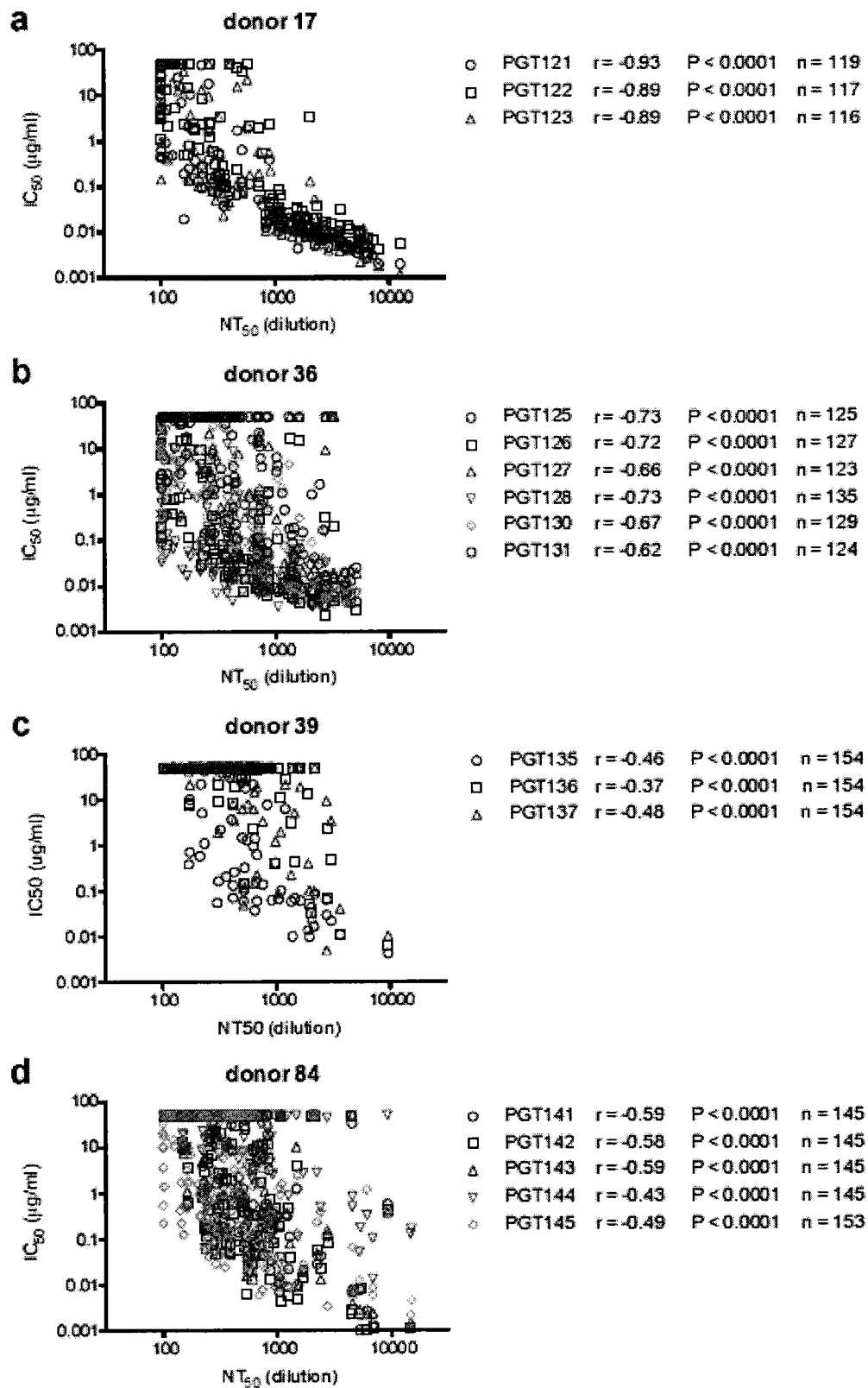


FIGURE 38

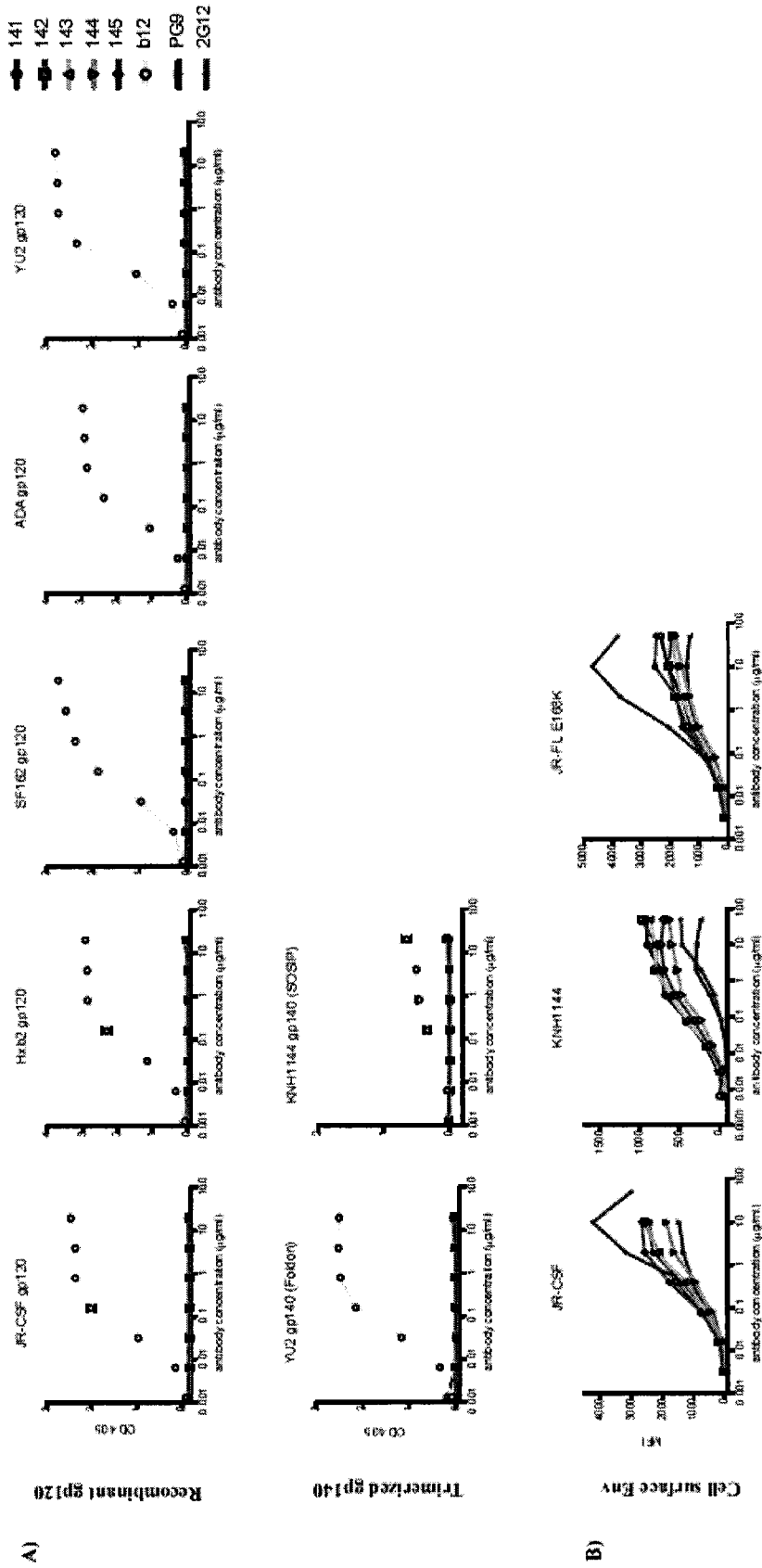


FIGURE 39

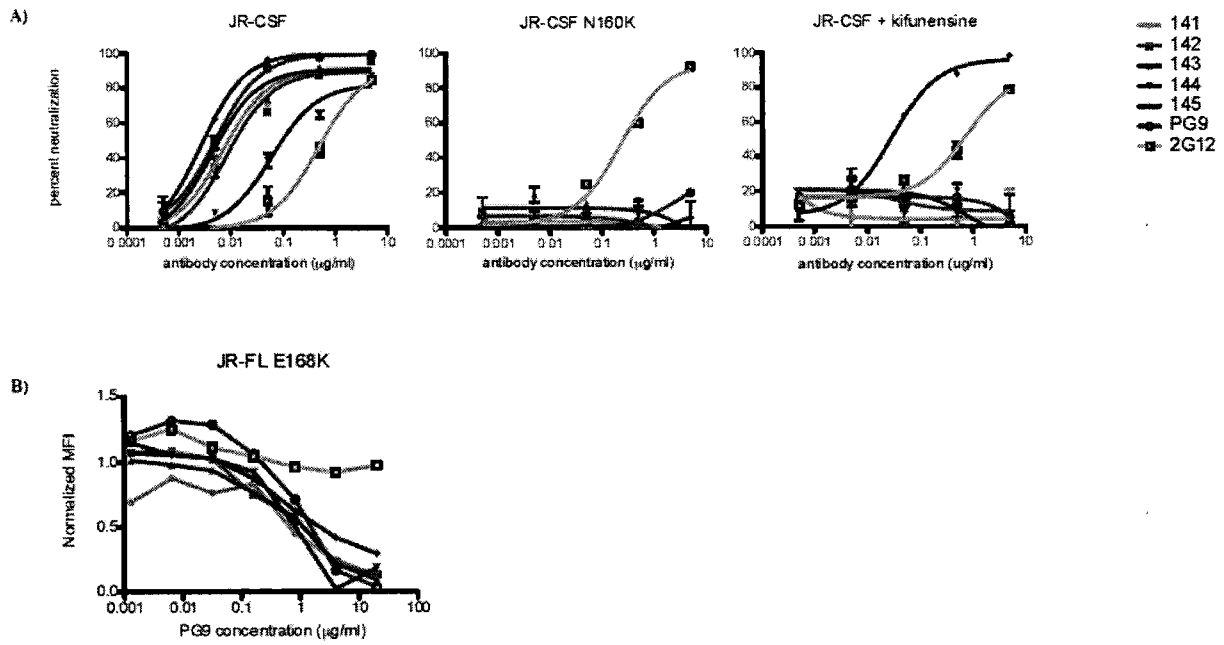


FIGURE 40

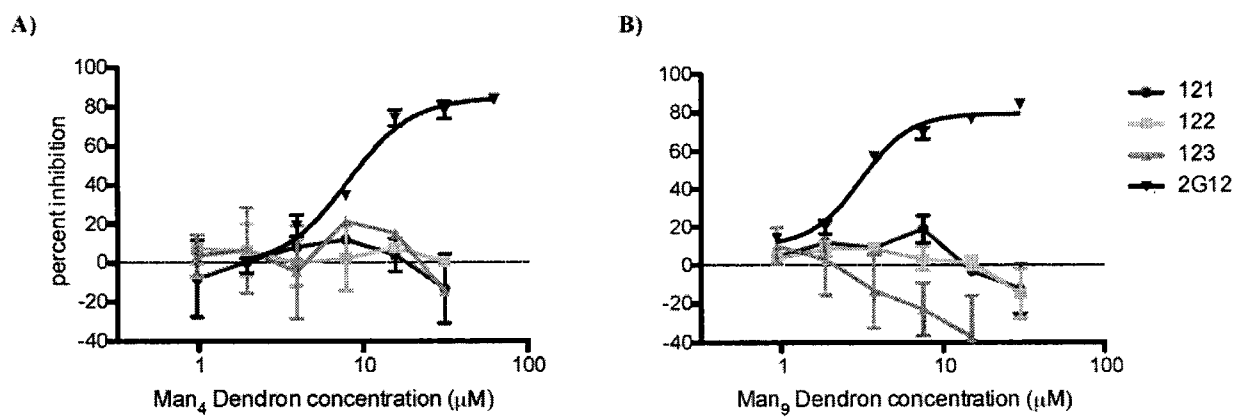


FIGURE 41

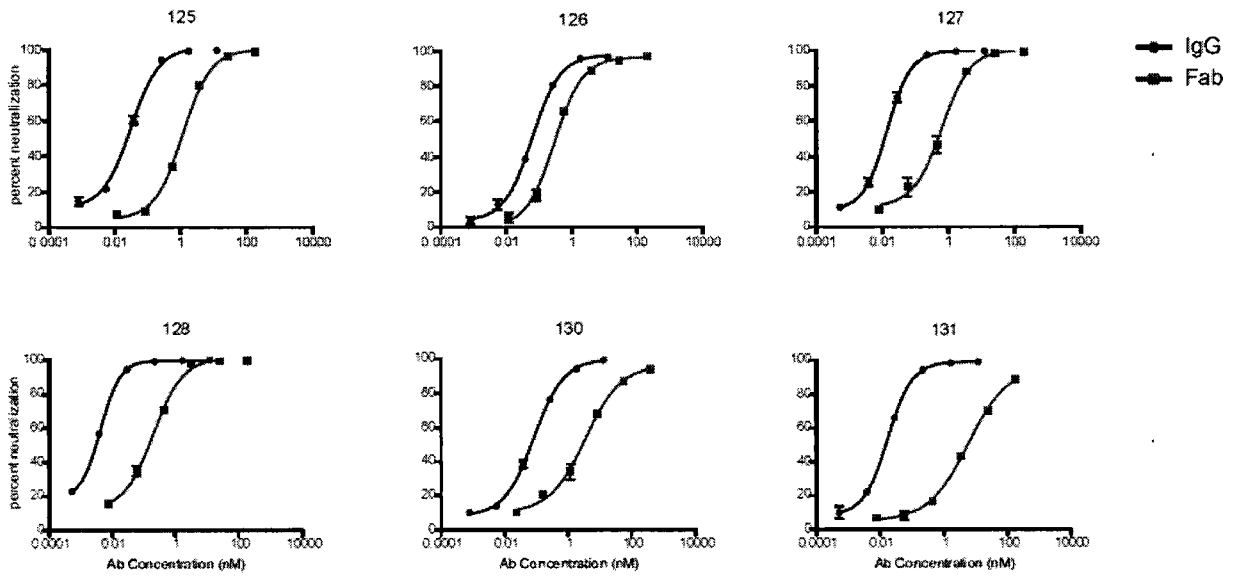


FIGURE 42

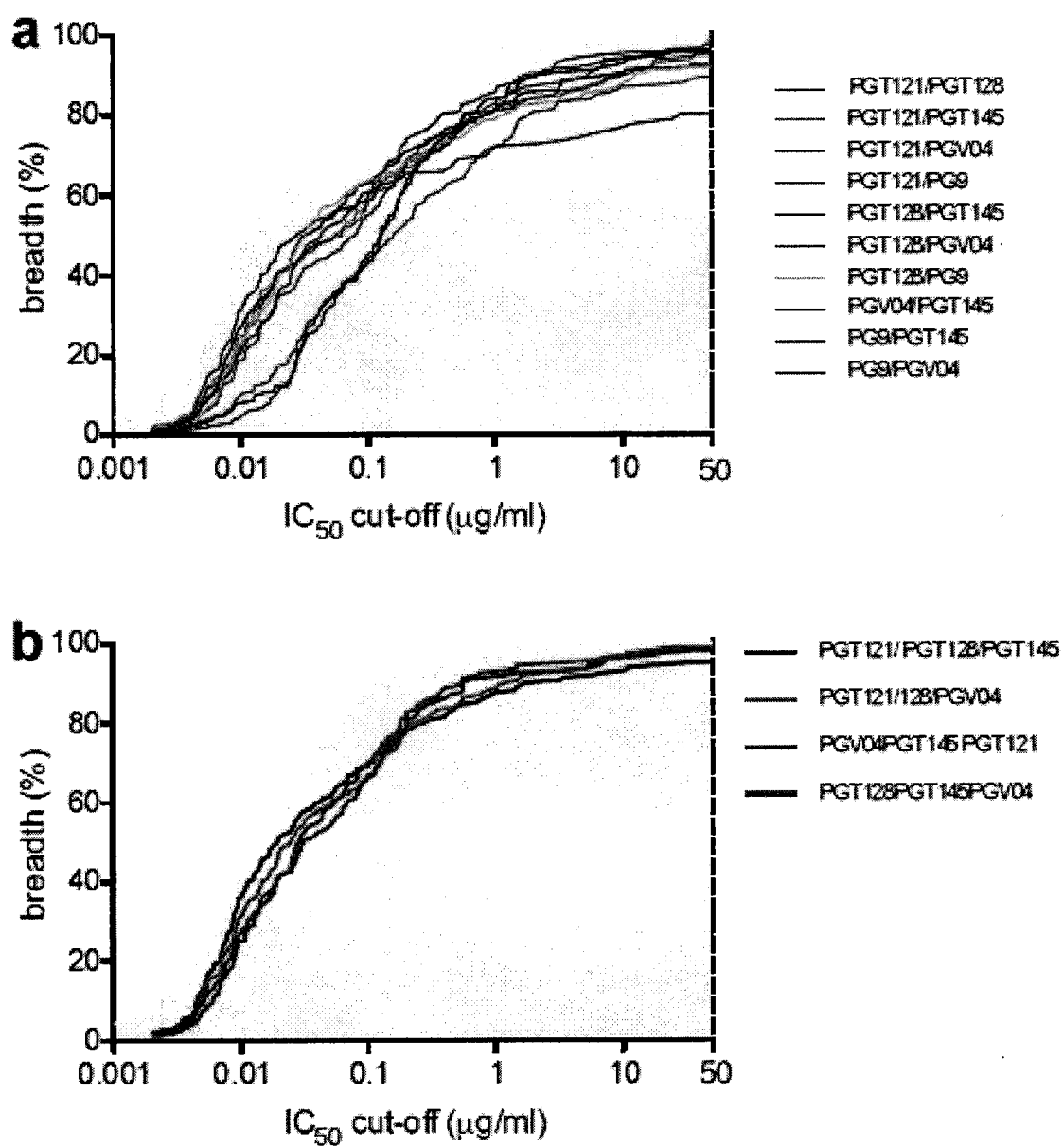


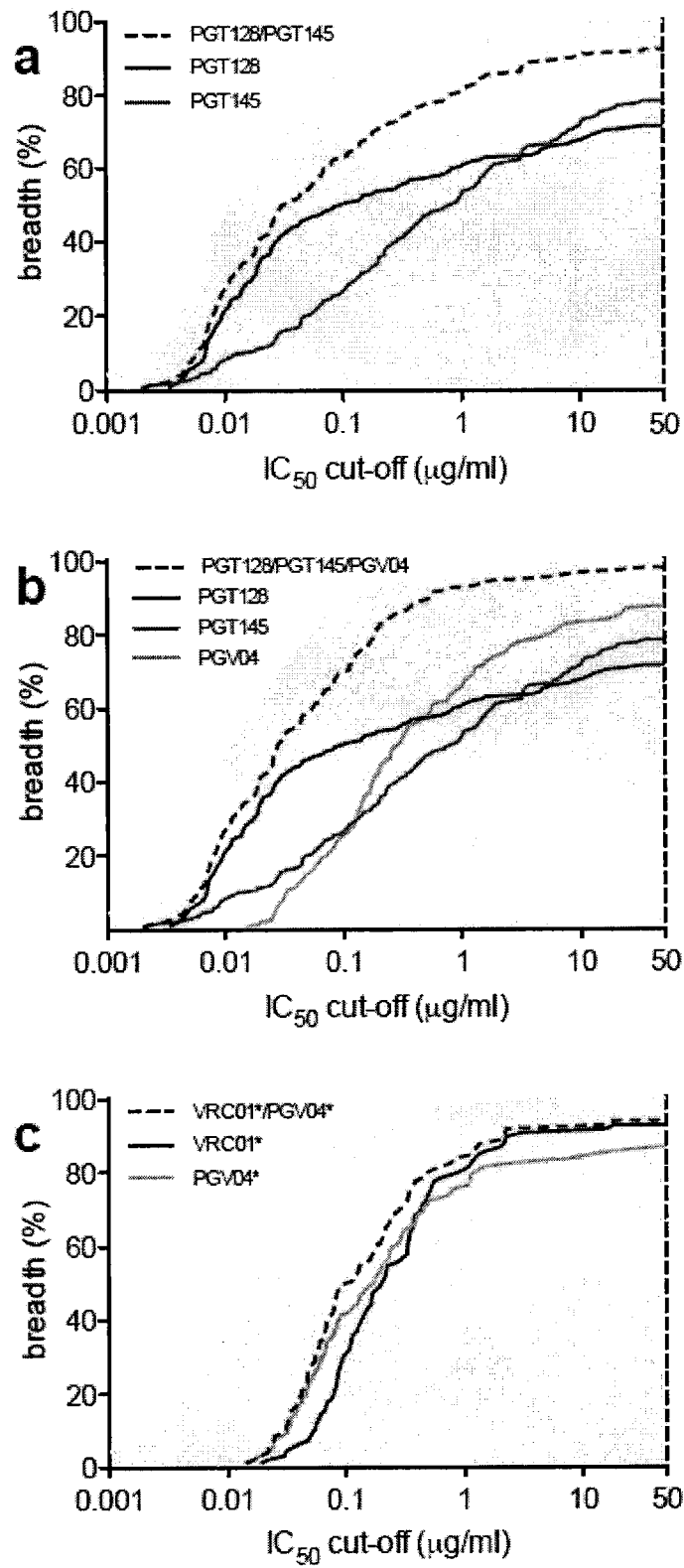
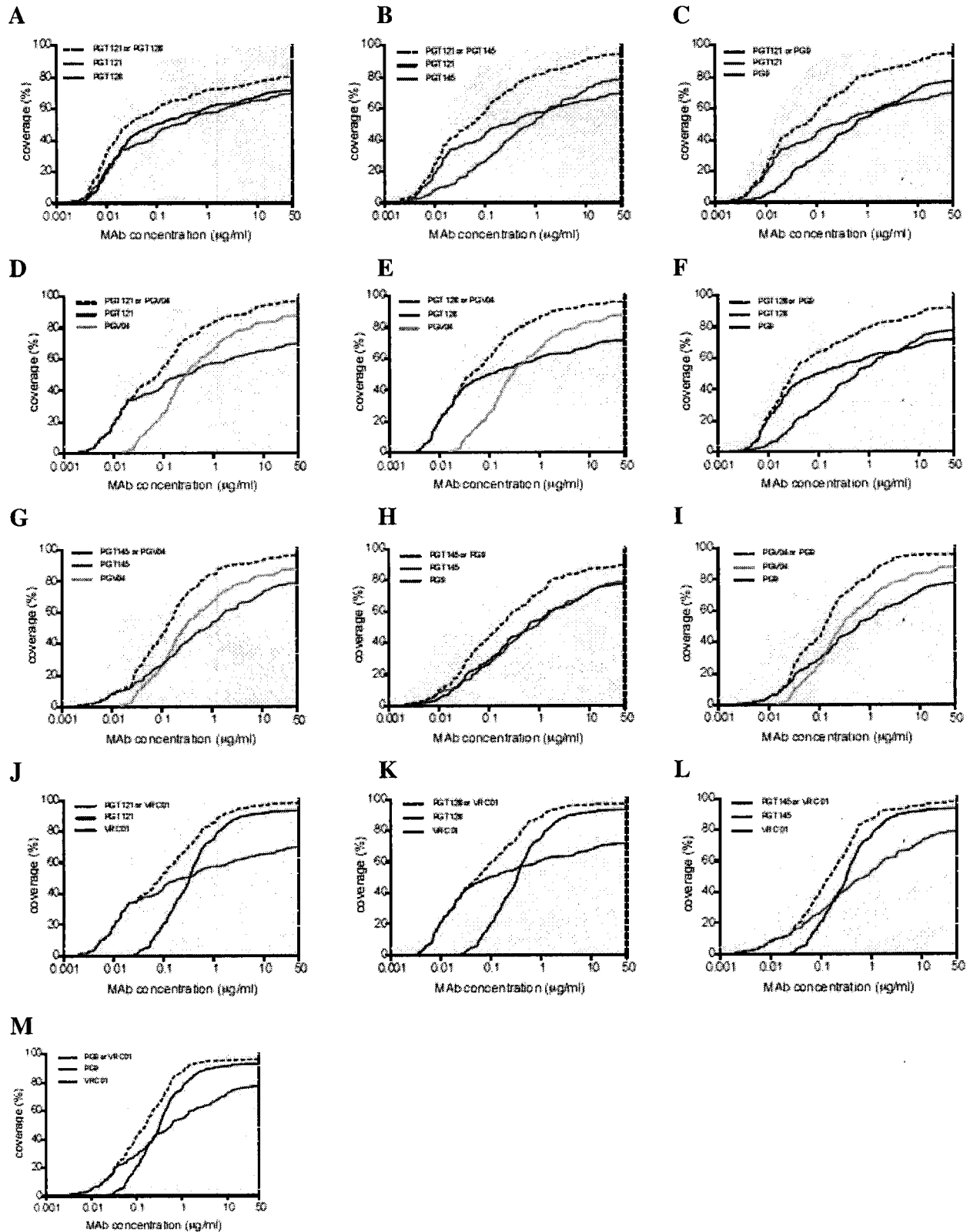
FIGURE 43

FIGURE 44



Number of HIV-Neutralizing Hits Detected in Primary Screening

