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(54) Titre : ANTICORPS NEUTRALISANTS ANTI-VIRUS DE L'IMMUNODEFICIENCE HUMAINE (VIH)

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

(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 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-HIV bNabs are also provided. Furthermore, methods for vaccination using suitable epitopes are provided.

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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-HIV bNAbs are also provided. Furthermore, methods for vaccination using suitable epitopes are provided.

DEMANDE OU BREVET VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET COMPREND PLUS D'UN TOME.

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HUMAN IMMUNODEFICIENCY VIRUS (HIV)-NEUTRALIZING ANTIBODIES

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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 EAGGPIWHDDVKYYDFNDGYINYHYMDV (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 EAGGPIWHDDVKYYDFNDGYINYHYMDV (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 EAGGPIWHDDVKYYDFNDGYINYHYMDV (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 EAGGPIWHDDVKYYDFNDGYINYHYMDV (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 EAGGPIWHDDVKYYDFNDGYINYHYMDV (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 EAGGPIWHDDVKYYDFNDGYINYHYMDV (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 EAGGPIWHDDVKYYDFNDGYINYHYMDV (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), MVTPIFGEAKYSQRFEG (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), MVTPIFGEAK (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 DRRVVPMATDNWLDP (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), DRRVVPMATDNWLDP (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), LIDPENGARYAEKFQG (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), LIDPENGAR (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), YVHKSGDTNYSPSLKS (SEQ ID NO: 265), TLHGRRYGVAFNEWFTYFYMDV (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), TLHGRRYGVAFNEWFTYFYMDV (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), YVHDSGDTNYPNPSLKS (SEQ ID NO: 157), 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), 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 TKHGRRIYGVVAFKEWFTYFYMDV (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), YVHSGDTNYPNPSLKR (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), YVHSGDTN (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), SLSHCQSFWSGWTGFHNPSLKS (SEQ ID NO: 186), and FDGEVLVYNHWPKPAPVDL (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),

SLSHCQSFWSGWTG (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), HHHYTTAVLHNPSLKS (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 SSLFGRWDV (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), HHHYTTAVL (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 GGEWGDKDYHWG (SEQ ID NO: 233), SIHWRGTTHYKESLRR (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 GDSIRGGEWGDKD (SEQ ID NO: 236), SIHWRGTTH (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), WMSHEGDKTESAQRFGK (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), WMSHEGDKTESAQRFGK (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),

IIHHYNTAVLHNPALKS (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), IIHHYNTAVL (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 GGEWGDSDYHWG (SEQ ID NO: 364), SIHWRGTTHYNAPFRG (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 GGSIRGGEWGSD (SEQ ID NO: 367), SIHWRGTTH (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 NYYYWT (SEQ ID NO: 406); a V_H CDR2 region which may comprise the amino acid sequence of YISDRETTTYPNSLNS (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 HIHYNTAVLHNPALKS (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 KSSESLRQSNGKTSLY (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 AISADAWHVYSGSVQG (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 EASNRFS (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), DRRVVPMTDNWLDP (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), TLHGRRYIGIVAFNEWFTYFYMDV (SEQ ID NO: 143), DNYWS (SEQ ID NO: 261), YVHDSGDTNYPNPSLKS (SEQ ID NO: 157), TKHGRRYIGVVAFKEWFTYFYMDV (SEQ ID NO: 262), DAYWS (SEQ ID NO: 169), YVHHSGDTNYPNPSLKR (SEQ ID NO: 170), ALHGKRIYGIVALGELFTYFYMDV (SEQ ID NO: 171), ACTYFWG (SEQ ID NO: 185), SLSHCQSFWSGWTGTFHNPSLKS (SEQ ID NO: 186), FDGEVLVYNHWPKEAWVDL (SEQ ID NO: 187), ACDYFWG (SEQ ID NO: 201), GLSHCAGYYNTGWTYHNPSLKS (SEQ ID NO: 202), FDGEVLVYHDWPKPAWVDL

(SEQ ID NO: 203), TGHYYWG (SEQ ID NO: 217), HIHYTTAVLHNPSLKS (SEQ ID NO: 218), SGGDILYYYEWQKPHWFSP (SEQ ID NO: 219), GGEWGDKDYHWG (SEQ ID NO: 233), SIHWRGTTHYKESLRR (SEQ ID NO: 234), HRHHDVFMVLPIAGWFDV (SEQ ID NO: 235), GTDWGENDFHYG (SEQ ID NO: 250), SIHWRGRITTHYKTSFRS (SEQ ID NO: 251), HKYHDI FRVVPVAGWFDV (SEQ ID NO: 252), KYDVH (SEQ ID NO: 277), WMSHEGDKTESAQRFKG (SEQ ID NO: 278), GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (SEQ ID NO: 279), WISHERDKTESAQRFKG (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), QAWETTTTTFVF (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), QQSFTPT (SEQ ID NO: 42), RASQTIHTYLN (SEQ ID NO: 113), GASTLQS (SEQ ID NO: 114), QQSYSTPT (SEQ ID NO: 43), SGSKLGDKYVS (SEQ ID NO: 120), ENDRRPS (SEQ ID NO: 121), QAWETTTTTFVF (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), 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 DRRAVPIATDNWLDP (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), TLHGRRYIGIVAFNEWFTYFYMDV (SEQ ID NO: 143), GTLVRD (SEQ ID NO: 263), YVHDSGDTN (SEQ ID NO: 264), TKHGRRYIGVAVFKEWFTYFYMDV (SEQ ID NO:

262), GASIND (SEQ ID NO: 172), YVHHSGLDN (SEQ ID NO: 173), ALHGKRIYGI VALGELFTYFYMDV (SEQ ID NO: 171), GESTGACT (SEQ ID NO: 188), SLSHCQSFWGSGWTF (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), HIHYTTAVL (SEQ ID NO: 221), SGGDILYYYEWQKPHWFSP (SEQ ID NO: 219), GDSIRGGEGWDKD (SEQ ID NO: 236), SIHWRGTH (SEQ ID NO: 237), HRHHDVFM LVPIAGWFDV (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), GNTFRK (SEQ ID NO: 309), and GSKHRLRDYVLYDDYGLINQEWNDYLEFLDV (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), QQSFTSPRT (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), QAWETTTTTFVF (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).

[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 includes: (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 (bNAb) 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 (bNAb) wherein the bNAb 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", "comprising", "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 bNAbs 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 IGV ^L ^a	Germline IGV ^H ^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)	ARDRRVPIATDNWL 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)	QAWETTTT 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	94UG103	>50	0.17	0.300	>50	>50
	92RW020	20.60	0.06	0.004*	>50	>50
	93UG077	>50	>50	>50	>50	>50
Clade B	92BR020	0.04	>50	>50	>50	>50
	APV.13	>50	>50	>50	>50	>50
	JRC5F	>50	<0.0025	<0.0025	>50	>50
	APV.17	>50	26.45	>50	>50	>50
	APV.6	7.47	0.09	0.004*	>50	22.770
Clade C	93IN905	>50	N/A	0.104	>50	>50
	IAVI-C18	>50	0.48	0.007	>50	>50
	IAVI-C22	>50	N/A	0.004*	>50	>50
	IAVI-C3	0.50	12.01	14.80	>50	>50
Clade D	92UG024	>50	10.06	>50	>50	>50
	92UG085	>50	>50	>50	>50	>50
CRF01_AE	92TH021	>50	0.11	0.15*	>50	>50
	CMU02	>50	>50	>50	>50	>50
negative control	amx.v	>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	0.02	0.08	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 Δ VI/ Δ 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 NABs 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 γ 3 coding sequence (variable region in bold)

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ATGGAGTTTGGGCTGAGCTGGGTTTTCTCGCAACTCTGTTAAGAGTTGTG
AAGTGTCAGGAACAACCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCC
GGGGGGGTCCCTGAGACTCTCCTGTTTAGCGTCTGGATTACGTTTC
ACAAATATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGCCTG
GAGTGGGTGGCACTCATCTCAGATGACGGAATGAGGAAATATCATTC
AGACTCCATGTGGGGCCGAGTCACCATCTCCAGAGACAATTCCAAGA
ACACTCTTTATCTGCAATTCAGCAGCCTGAAAGTCAAGACACGGCT
ATGTTCTTCTGTGCGAGAGAGGCTGGTGGGCCAATCTGGCATGACGA
CGTCAAATATTACGATTTTAATGACGGCTACTACAACTACCACTACAT
GGACGTCTGGGGCAAGGGGACCACGGTCACCGTCTCGAGCGCCTCCA
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CCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCT
 GGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACC
 GGTGACGGTGTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCT
 TCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGA
 CCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
 CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTT
 GTGACAAAACCTCACACATGCCACCGTGCCCAGCACCTGAACTCCTGGGG
 GGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGAT
 CTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAG
 ACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT
 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
 TCAGCGTCCTACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
 AAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCAICGAGAAAACCAT
 CTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCC
 CCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGT
 CAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG
 CAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCTGGACTCCGACG
 GCTCCTTCTTCTCTATAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAG
 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA
 CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:
 11)

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

CAGGAACAACCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCGGGGGGGT
 CCCTGAGACTCTCCTGTTTAGCGTCTGGATTACGTTTACAAATATGGCA
 TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGCCTGGAGTGGGTGGCACTC
 ATCTCAGATGACGGAATGAGGAAATATCATTACAGACTCCATGTGGGGCCG
 AGTCAACCATCTCCAGAGACAATTCCAAGAACACTCTTTATCTGCAATTCA
 GCAGCCTGAAAGTCGAAGACACGGCTATGTTCTTCTGTCCGAGAGAGGCT
 GGTGGGCCAATCTGGCATGACGACGTCAAATATTACGATTTTAATGACGG
 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
AREAGGPIWHDDV**KYYDF**NDGYNYHYMDVWG**KGTTVT**VSSASTKGPS
 VFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP
 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
 KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG

QPENNYKTTTPVLDSGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY
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***GFTHKYGMH***WVRQAPGKGLEWVAL
ISDDGMRKYHSDSMWGRVTISRDNSKNTLYLQFSSLKVEDTAMFFCARE***EAG***
GPIWHDDVKYYDFNDGYINYHYMDVWGKGTTVTVSS (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: EAGGPIWHDDVKYYDFNDGYINYHYMDV (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: EAGGPIWHDDVKYYDFNDGYINYHYMDV (SEQ ID NO: 6)

[0210] 1443_C16 (PG16) (TCN-116) lambda light chain nucleotide sequence: 1443_C16 λ2 coding sequence (variable region in bold)

ATGGCCTGGGCTCTGCTATTCTCCTCACCTCTTCACTCAGGGCACAGGGTCC
TGGGGCCAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCT
GGACAGACGATCACCATCTCCTGCAATGGAACCAGCAGTGACGTTGG
TGGATTTGACTCTGTCTCCTGGTACCAACAATCCCCAGGGAAAGCCC
CCAAAGTCATGGTTTTTGATGTCAGTCATCGGCCCTCAGGTATCTCTA
ATCGCTTCTCTGGCTCCAAGTCCGGCAACACGGCCTCCCTGACCATC
TCTGGGCTCCACATTGAGGACGAGGGCGATTATTTCTGCTCTTCACT
GACAGACAGAAGCCATCGCATATTTCGGCGGCGGGACCAAGGTGACC
GTTCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTC
CTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTG
ACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCC
GTCAAGGCGGGAGTGGAGACCACCACACCCTCCAACAAAGCAACAACA
AGTACCGCGCCAGCAGCTACCTGAGCCTGACGCC

TGAGCAGTGGAAGTCCCACAAAAGCTACAGCTGCCAGGTCACGCATGAA
GGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTTCATAG (SEQ
ID NO: 13)

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

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGACG
 ATCACCATCTCCTGCAATGGAACCAGCAGTGACGTTGGTGGATTTGACTC
 TGTCTCCTGGTACCAACAATCCCCAGGGAAAGCCCCCAAAGTCATGGTTT
 TTGATGTCAGTCATCGGCCCTCAGGTATCTCTAATCGCTTCTCTGGCTCCA
 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
ADSSPVKAGVETTTTPSKQSNKYAASSYLSLTPEQWKSHKSYSCQVTHEGST
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*NGTSSDVGGFDSV*SWYQQSPGKAPKVMVFD**
VSHRPS**GISNRFSGSKSGNTASLTISGLHIEDEGDYFC****SSLTDRSHRI****FGG****GTK**
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)

ATGGACTGGATTGGAGGTTCTCTTTGTGGTGGCAGCAGCTACAGGTGT
 CCAGTCCCAGGTCCGCCTGGTACAGTCTGGGCCTGAGGTGAAGAAGC
 CTGGGTCTCGGTGACGGTCTCCTGCCAGGCTTCTGGAGGCACCTTC
 AGCAGTTATGCTTTCACCTGGGTGCGCCAGGCCCCCGGACAAGGTCT
 TGAGTGGTTGGGCATGGTCACCCCAATCTTTGGTGAGGCCAAGTACT
 CACAAAGATTTCGAGGGCAGAGTCACCATCACCGCGGACGAATCCACG
 AGCACAAACCTCCATAGAATTGAGAGGCCTGACATCCGAAGACACGGC
 CATTTATTACTGTGCGCGAGATCGGCGCGCGGTTCCAATTGCCACGG

ACAACTGGTTAGACCCCTGGGGCCAGGGGACCCTGGTCACCGTCTCG
AGCGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAA
GAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACT
TCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGGC
GTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG
CAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAG
CCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGA
ACTCTGGGGGGACCGTCAGTCTTCTCTTCCCCCCTTCCCAAGGACA
CCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG
AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
AGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAC
GTACCGTGTGGTACGCGTCTCACCCTGCTGACCAGGACTGGCTGAATG
GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATC
GAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
ACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCT
GACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
AGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCTCCCGTGCT
GGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGA
GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT
CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATG
A (SEQ ID NO: 15)

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

CAGGTCCGCTGGTACAGTCTGGGCCTGAGGTGAAGAAGCCTGGGTCTCT
GGTGACGGTCTCCTGCCAGGCTTCTGGAGGCACCTTCAGCAGTTATGCTTT
CACCTGGGTGCGCCAGGCCCCCGGACAAGGTCTTGAGTGGTTGGGCATGG
TCACCCCAATCTTTGGTGAGGCCAAGTACTCACAAAGATTTCGAGGGCAGA
GTCACCATCACCGCGGACGAATCCACGAGCACAACCTCCATAGAATTGAG
AGGCCTGACATCCGAAGACACGGCCATTTATTACTGTGCGCGAGATCGGC
GCGCGGTTCCAATTGCCACGGACAACCTGGTTAGACCCCTGGGGCCAGGGG
ACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 101)

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

QVRLVQSGPEVKKPGSSVTVSCQASGGTFSSYAFTWVRQAPGQGLEWL
GMVTPIFGEAKYSQRFEGRVTITADESTSTTSIELRGLTSEDTAIYYCARD
RRAVPIATDNWLDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALG
CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQ
TYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKD
TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLF
PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF
FLYSKLTVDKSRWQQGNVFCFVSMHEALHNHYTQKSLSLSPGK (SEQ ID
NO: 16)

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

QVRLVQSGPEVKKPGSSVTVSCQASGGTFSSYAFTWVRQAPGQGLEWLGMV
*TPIFGEAKYSQRFEG*RVTTITADESTSTTSIELRGLTSEDTAIYYCAR*DRRAVPIA*
*TDNWLD*WPWGQGLVTVSS (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
CCGAGGTGCCAGATGTGACATCCAGTTGACCCAGTCTCCATCCTCCCT
GTCTGCATCTGTTGGCGACAGAGTCTCCATCACTTGCCGGGCGAGTC
AGACCATTAACAACTACTTAAATTGGTATCAACAGACACCCGGGAAA
GCCCCTAAACTCCTGATCTATGGTGCCTCCAATTTGCAAAATGGGGT
CCCATCAAGGTT**CAGCGGCAGTGGCTCTGGGACAGACTTCACTCTCA**
CCATCAGCAGTCTGCAACCTGAGGATTTTGCAACTTACTACTGTCAAC
AGAGTTTCAGTACTCCGAGGACCTTCGGCCAAGGGACACGACTGGAT
ATTAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGAT
GAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTC
TATCCAGAGAGGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAAT
CGGGTA**ACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCAC**
CTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAA
CACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGT
CACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO: 17)

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

GACATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTTGGCGAC
AGAGTCTCCATCACTTGCCGGGCGAGTCAGACCATTAACA**ACTACTTAAA**
TTGGTATCAACAGACACCCGGGAAAGCCCCTAAACTCCTGATCTATGGTG
CCTCCAATTTGCAAAATGGGGTCCCATCAAGGTTCAGCGGCAGTGGCTCT
GGGACAGACTTCACTCTACCATCAGCAGTCTGCAACCTGAGGATTTGC
AACTTACTACTGTCAACAGAGTTTCAGTACTCCGAGGACCTTCGGCCAAG
GGACACGACTGGATATTAAA (SEQ ID NO: 106)

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

DIQLTQSPSSLSASVGDRVSITCRASQTINNYLNWYQQTPGKAPKLLIYGA
SNLQNGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSFSTPRTFGQGT
RLDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVT
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
QNGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSFSTPRTFGQGTRLDIK
(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: QQSFSPTPT (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: QQSFSPTPT (SEQ ID NO: 42)

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

ATGGACTGGATTTGGAGGTTCTCTTGGTGGTGGCAGCAGCTACAGGTGT
CCAGTCCCAGGTCCTGCTGGTGCACTCTGGGACTGAGGTGAAGAAGC
CTGGGTCCTCGGTGAAGGTCTCCTGTCAGGCTTCTGGAGGCGCCTTC
AGTAGTTATGCTTTCAGCTGGGTGCGACAGGCCCTGGACAGGGGCT
TGAATGGATGGGCATGATCACCCCTGTCTTTGGTGAGACTAAATATG
CACCGAGGTTCCAGGGCAGACTCACACTTACCGCGGAAGAATCCTTG
AGCACCACTACATGGAATTGAGAAGCCTGACATCTGATGACACGGC
CTTTTATTATTGTACGAGAGATCGGCGCGTAGTTCCAATGGCCACAG
ACAACCTGGTTAGACCCCTGGGGCCAGGGGACGCTGGTCACCGTCTCG
AGCGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCTCCAA
GAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACT
TCCCCGAACCGGTGACGGTGTCGTGGAACCTCAGGCGCCCTGACCAGCGGC
GTGCACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG
CAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAG
CCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGA

ACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCC AAAACCCAAGGACA
 CCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTG
 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
 AGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAC
 GTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG
 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCCTCCAGCCCCCATC
 GAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
 ACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTACGCCT
 GACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
 AGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCT
 GGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGA
 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT
 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATG
 A (SEQ ID NO: 19)

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

CAGGTCCTGCTGGTGCAGTCTGGGACTGAGGTGAAGAAGCCTGGGTCCTC
 GGTGAAGGTCTCCTGTCAGGCTTCTGGAGGCGCCTTCAGTAGTTATGCTTT
 CAGCTGGGTGCGACAGGCCCTGGACAGGGGCTTGAATGGATGGGCATG
 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
 GMITPVFGETKYAPRFQGR~~LT~~LTAEESLSTTYMELRSLTSDDTAFYYCTR
 DRRVVP~~MA~~TDNWLD~~PWG~~QGT~~LV~~TVSSASTKGPSVFPLAPSSKSTSGGTAA
 LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLG
 TQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP
 KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
 LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG
 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID
 NO: 20)

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

QVLLVQSGTEVKKPGSSVKVSCQASGGAFSSYAFSWVRQAPGQGLEWMGM
ITPVFGETKYAPRFQGR~~LT~~LTAEESLSTTYMELRSLTSDDTAFYYCTRDRRVV
PMA~~TDNWLD~~PWGQGT~~LV~~TVSS (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: GGAFSS (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
 GACCATAACACACCTATTTAAATTGGTATCAGCAAATTCAGGAAAAGC
 CCCTAAGCTCCTGATCTATGGTGCCTCCACCTTGCAAAGTGGGGTCC
 CGTCAAGGTTCAAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACC
 ATCAACAGTCTCCAACCTGAGGACTTTGCAACTTACTACTGTCAACAG
 AGTTACAGTACCCCAAGGACCTTCGGCCAAGGGACACGACTGGATAT
 TAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGA
 GCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTA
 TCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCG
 GGTAACCTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCT
 ACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACA
 CAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCA
 CAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO: 21)
- [0235] 1460_G14 (PGG14) kappa light chain variable region nucleotide sequence:
- GACATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGAC
 AGGGTCACCGTCACTTGCCGGGCGAGTCAGACCATAACACCTATTTAAA
 TTGGTATCAGCAAATTCAGGAAAAGCCCTAAGCTCCTGATCTATGGTG
 CCTCCACCTTGCAAAGTGGGGTCCCGTCAAGGTTCAAGTGGCAGTGGATCT
 GGGACAGATTTCACTCTCACCATCAACAGTCTCCAACCTGAGGACTTTGC
 AACTTACTACTGTCAACAGAGTTACAGTACCCCAAGGACCTTCGGCCAAG
 GGACACGACTGGATATTAAA (SEQ ID NO: 112)
- [0236] 1460_G14 kappa light chain amino acid sequence: expressed protein with variable region in bold.
- DIQLTQSPSSLSASVGDRVTVTCRASQTIHTYLNWYQQIPGKAPKLLIYG
 ASTLQSGVPSRFSGSGSGTDFLTINSLPEDFATYYCQSYSTPRTFGQG

TRLDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPV
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***WYQQIPGKAPKLLIY***GASTL***
QSGVPSRFSSGSGGTDFLTINSLQPEDFATYYC***QQSYSTPRT***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: QQSYSTPRT (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: QQSYSTPRT (SEQ ID NO: 43)

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

ATGGACTGGATTGAGGATCCTCCTCTTGGTGGCAGCAGCTACAGGCAC
CCTCGCCGACGGCCACCTGGTTCAGTCTGGGGTTGAGGTGAAGAAGA
CTGGGGCTACAGTCAAAATCTCCTGCAAGGTTTCTGGATACAGCTTC
ATCGACTACTACCTTCATTGGGTGCAACGGGCCCCCTGGAAAAGGCCT
TGAGTGGGTGGGACTTATTGATCCTGAAAATGGTGAGGCTCGATATG
CAGAGAAGTTCCAGGGCAGAGTCACCATAATCGCGGACACGTCTATA
GATACAGGCTACATGGAAATGAGGAGCCTGAAATCTGAGGACACGGC
CGTGATTTCTGTGCAGCAGGTGCCGTGGGGGCTGATTCCGGGAGCT
GGTTCGACCCCTGGGGCCAGGGAACCTCTGGTCACCGTCTCGAGCGCC
TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCAC
CTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG
AACCGGTGACGGTGTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGAC
ACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTG
GTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGT
GAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAA
TCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAACTCCT
GGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCTCA
TGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCAC
GAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGAGGTGC
ATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCG
TGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGG

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

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

GACGGCCACCTGGTTCAAGTCTGGGGTTGAGGTGAAGAAGACTGGGGCTAC
 AGTCAAAATCTCCTGCAAGGTTTCTGGATACAGCTTCATCGACTACTACCT
 TCATTGGGTGCAACGGGGCCCTGGAAAAGGCC'TTGAGTGGGTGGGACTTA
 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
GLIDPENGGEARYAEKFQGRVTIIADTSIDTGYMEMRSLKSEDTAVYFCAA
GAVGADSGSWFDPWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGC
 LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQT
 YICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT
 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
 VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFF
 LYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
 24)

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

DGHLVQSGVEVKKTGATVKISCKVSGYSFIDYYLHWVQRAPGKGLEWV***GLI***
DPENGGEARYAEKFQGRVTIIADTSIDTGYMEMRSLKSEDTAVYFCAAGAV***G***
DSGSWFDPWGQGTTLTVSS (SEQ ID NO: 37)

[0244] 1495_C14 gamma heavy chain Kabat CDRs:

CDR 1: DYYLH (SEQ ID NO: 116)

CDR 2: LIDPENGGEARYAEKFQG (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: LIDPENGGEAR (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
GTAGTCTCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCA
GGACAGACAGCCAGCATCACCTGTTCTGGATCTAAATTGGGGGATAA
ATATGTTTCCTGGTATCAACTGAGGCCAGGCCAGTCCCCCATACTGG
TCATGTATGAAAATGACAGGCGGCCCTCCGGGATCCCTGAGCGATT
TCCGGTTCCAATTCTGGCGACACTGCCACTCTGACCATCAGCGGGAC
CCAGGCTTTGGATGAGGCTGACTTCTACTGTGAGGCGTGGGAGACCA
CCACCACCACTTTTGTTCCTTCGGCGGAGGGACCCAGCTGACCGTT
CTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCT
GAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTT
CTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTC
AAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGT
ACGCGGCCAGCAGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCAC
AAAAGCTACAGCTGCCAGGTACGCATGAAGGGAGCACCGTGGAGAAGA
CAGTGGCCCCCTACAGAAATGTTTCATAG (SEQ ID NO: 25)

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

TCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGAC
AGCCAGCATCACCTGTTCTGGATCTAAATTGGGGGATAAATATGTTTCCTG
GTATCAACTGAGGCCAGGCCAGTCCCCCATACTGGTCATGTATGAAAATG
ACAGGCGGCCCTCCGGGATCCCTGAGCGATTCTCCGGTTCCAATTCTGGC
GACACTGCCACTCTGACCATCAGCGGGACCCAGGCTTTGGATGAGGCTGA
CTTCTACTGTGAGGCGTGGGAGACCACCACCACCTTTTGTTCCTTCGG
CGGAGGGACCCAGCTGACCGTTCTA (SEQ ID NO: 119)

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

SYELTQPPSVSVSPGQTASITCSGSKLGDKYVSWYQLRPGQSPILVMYEN
DRRPSGIPERFSGSNSGDTATLTISGTQALDEADFYCQAWETTTTTFVFFG
GGTQLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKA
DSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTV
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)

SYELTQPPSVSVSPGQTASITCSGSKLGDKYVSWYQLRPGQSPILVMYENDRR
PSGIPERFSGSNSGDTATLTISGTQALDEADFYCQAWETTTTTFVFFGGGTQL
 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 γ3
 coding sequence (variable region in bold)

ATGGAGTTTGGGCTGAGCTGGGTTTTCCTCGTTGCTTTCTTAAGAGGTGTC
 CAGTGTCAGCGATTAGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGG
 GTCGTCCCTGAGACTCTCCTGTGCAGCGTCCGGATTGCACTTCAGTA
 GACAAGGCATGCACTGGGTCCGCCAGGCTCCAGGCCAGGGGCTGGA
 GTGGGTGGCATTATTAATAATGATGGAAGTGAGAAATATCATGCTG
 ACTCCGTATGGGGCCGACTCAGCATCTCCAGAGACAATTCCAAGGAT
 ACGCTTTATCTCCAAATGAATAGCCTGAGAGTCGAGGACACGGCTAC
 ATATTTTGTGTGAGAGAGGCTGGTGGGCCCGACTACCGTAATGGGT
 ACAACTATTACGATTCTATGATGGTTATTATAACTACCACTATATGG
 ACGTCTGGGGCAAAGGGACCACGGTCACCGTCTCGAGCGCCTCCACC
 AAGGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGG
 GGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGG
 TGACGGTGTCTGGAAGTCAAGGCGCCCTGACCAGCGGCGTGACACCTTC
 CCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAC
 CGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATC
 ACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTG
 TGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGG
 GACCGTCAGTCTTCTCTTCCCCCAAACCAAGGACACCTCATGATCT
 CCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGA
 CCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG
 CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGT
 CAGCGTCTCACCCTGTCACCAGGACTGGCTGAATGGCAAGGAGTACA
 AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATC
 TCCAAGCCAAAGGGCAGCCCCGAGAACACAGGTGTACACCCTGCCCC
 CATCCCCGGGAGGAGATGACCAAGAACCAGGTACGCTGACCTGCCTGGTC
 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGC
 AGCCGGAGAACAACTACAAGACCACGCCCTCCCGTGTGGACTCCGACGG
 CTCCTTCTTCTCTATAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAGC

AGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 27)

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

CAGCGATTAGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGTCTCCCT
GAGACTCTCCTGTGCAGCGTCCGGATTGACTTCAGTAGACAAGGCATGC
ACTGGGTCCGCCAGGCTCCAGGCCAGGGGCTGGAGTGGGTGGCATTATT
AAATATGATGGAAGTGAGAAATATCATGCTGACTCCGTATGGGGCCGACT
CAGCATCTCCAGAGACAATTCCAAGGATACGCTTTATCTCCAAATGAATA
GCCTGAGAGTCGAGGACACGGCTACATATTTTGTGTGAGAGAGGCTGGT
GGGCCCCGACTACCGTAATGGGTACAATACTATTACGATTTCTATGATGGTTAT
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.

QRLVESGGGVVQPGSSRLRLSCAASGFD~~FS~~RQGMHWVRQAPGQGLEWVAFIK
YDGSEKYHADSVWGRLSISRDN~~SK~~DTLYLQMNSLRVEDTATYFCVREAGGP
DYRNGYNYYDFYDGYNYHYMDVWGKGTTVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV
VTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGP
SVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT
KPREEQYNSTYRVSVLT~~VL~~HQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
TPPVLDSDGSFFLYSKLTVDKSRWQQGNV~~F~~SCSV~~M~~HEALHNHYTQKSLSLSP
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)

QRLVESGGGVVQPGSSRLRLSCAASGFD~~FS~~**RQGMHWVRQAPGQGLEWVAFI**
KYDGSEKYHADSVWGRLSISRDN~~SK~~DTLYLQMNSLRVEDTATYFCVRE**AGG**
PDYRNGYNYYDFYDGYNYHYMDVWGKGTTVTVSS (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: EAGGPDYRNGYNYYDFYDGYNYHYMDV (SEQ ID NO: 7)

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

CDR 1: GFD~~FS~~R (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 λ2 coding sequence (variable region in bold)

ATGGCCTGGGCTCTGCTTTTCCTCACCCCTCCTCACTCAGGGCACAGGGTCC
TGGGCCCAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCT
GGACAGTCGATCACCATCTCCTGCAATGGAACCAGCAATGATGTTGG
TGGCTATGAATCTGTCTCCTGGTACCAACAACATCCCGGCAAAGCCC
CCAAAGTCGTGATTTATGATGTCAGTAAACGGCCCTCAGGGGTTTCT
AATCGCTTCTCTGGCTCCAAGTCCGGCAACACGGCCTCCCTGACCAT
CTCTGGGCTCCAGGCTGAGGACGAGGGTGACTATTACTGCAAGTCTC
TGACAAGCACGAGACGTCGGGTTTTCGGCACTGGGACCAAGCTGACC
GTTCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCTCGCCCTC
CTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTG
ACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCC
GTCAAGGCGGGAGTGGAGACCACCACACCTCCAAACAAGCAACAACA
AGTACGCGGCCAGCAGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCC
CACAAAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGA
AGACAGTGGCCCTACAGAATGTTTCATAG (SEQ ID NO: 29)

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

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCG
ATCACCATCTCCTGCAATGGAACCAGCAATGATGTTGGTGGCTATGAATC
TGTCTCCTGGTACCAACAACATCCCGGCAAAGCCCCCAAAGTCGTGATTT
ATGATGTCAGTAAACGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTCCA
AGTCCGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGAC
GAGGGTGACTATTACTGCAAGTCTCTGACAAGCACGAGACGTCGGGTTT
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
KADSSPVKAGVETTPSKQSNKYAASSYLSLTPEQWKSHKSYSCQVTHEGS
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**NGTSNDVGGYESV**SWYQQHPGKAPKVVI**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), MVTPIFGEAKYSQRFEG (SEQ ID NO: 105), and DRRAVPLATDNWLDP (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 QQSFSTPRT (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 DRRAVPIATDNWLDP (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 DRRVVPMATDNWLDP (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), QQSYSTPTPT (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), DRRVVPMATDNWLDP (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), QQSYSTPTPT (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), LIDPENGEARYAEKFQG (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 QAWETTTTTTFVF (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), LIDPENGEAR (SEQ ID NO:

103), GAVGADSGSWFDP (SEQ ID NO: 10). The light chain CDRs of the 1495_C14 (PGC14) antibody have the following sequences per Chothia definition: SGSKLGDKYVS (SEQ ID NO: 120), ENDRRPS (SEQ ID NO: 121), and QAWETTTTTFVF (SEQ ID NO: 44).

Table 6A. Heavy Chain Variable Region Protein Alignment

Table 6B. Light Chain Variable Region Protein Alignment

[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)

ATGGAGTTTGGGCTGAGCTGGGTTTTCCTCGCAACTCTGTTAAGAGTTGTG
AAGTGTCAGGAAAACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCC
GGGGGGGTCCCTGAGACTCTCCTGTTTAGCGTCTGGATTACCTTTC
ACAAATATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGCCTG
GAGTGGGTGGCACTCATCTCAGATGACGGAATGAGGAAATATCATTC
AGACTCCATGTGGGGCCGAGTCACCATCTCCAGAGACAATTCCAAGA
ACACTCTATATCTGCAATTCaGCAGCCTGAAAAGTCGAAGACACGGCTA
TGTTCTTCTGTGCGAGAGAGGCTGGTGGGGCCAATCTGGCATGACGAC
GTCAAATATTACGATTTTAATGACGGCTACTACAACCTACCACTACATG
GACGTCTGGGGCAAGGGGACCAACGGTCACCGiCTCCTCAGCGTCGACC
AAGGGCCCATCGGTCTTCCCTCTGGCACCATCATCCAAGTCGACCTCTGG
GGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGG
TGACGGTGTCTGGAAGTCAAGGCGCCCTGACCAGCGGCGTGCACACCTTC
CCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAC
CGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATC
ACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTG
TGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGG
GACCGTCAGTCTTCTCTTCCCCC AAAACCCAAGGACACCCTCATGATCT
CCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGA
CCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG
CCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCACGTACCGTGTGGT
CAGCGTCCTCACCGTCTTGCACCAAGGACTGGCTGAATGGCAAGGAGTACA
AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATC
TCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTTGCCCC
CATCCCGGGAGGAGATGACCAAGAACCAGGTACGCCTGACCTGCCTGGTC
AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGC
AGCCGGAGAACAACTACAAGACCACGCCCTCCCGTGCTGGACTCCGACGG
CTCCTTCTTCTCTATAGCAAGCTACCGTGGACAAGAGCAGGTGGCAGC
AGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 138)

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

CAGGAAAACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCGGGGGGGT
 CCCTGAGACTCTCCTGTTTAGCGTCTGGATTACCTTTACAAATATGGCA
 TGCCTGGGTCCGCCAGGCTCCAGGCAAGGGCCTGGAGTGGGTGGCACTC
 ATCTCAGATGACGGAATGAGGAAATATCATTACAGACTCCATGTGGGGCCG
 AGTCACCATCTCCAGAGACAATTCCAAGAACAACCTCTATATCTGCAATTCaG
 CAGCCTGAAAGTCGAAGACACGGCTATGTTCTTCTGTGCGAGAGAGGCTG
 GTGGGGCCAATCTGGCATGACGACGTCAAATATTACGATTTTAATGACGGC
 TACTACAACCTACCACTACATGGACGTCTGGGGCAAGGGGACCACGGTCAC
 CGtCTCCTCA (SEQ ID NO: 128)

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

QEKLVESGGGVVQPGGSLRLSCLASGFT**FKYGMH**WVRQAPGKGLEW
 VALISDDGMRKYHSDSMWGRVTISRDN**SKNTLYLQFSSLKVEDTAMFFC**
AREAGGPIWHDDVKYYDFNDGYNYHYMDVWVGKGT**TVTVSS**ASTKGPS
 VFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
 GLYSLSSVTVPS**SSLGTQTYICNVNHKPSNTKVDKRVEPK**SCDKTHTCPPCP
 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGV
 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
 KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV**FSCSV**MHEALHNHY
 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***GFTFKYGMH***WVRQAPGKGLEW***VAL***
ISDDGMRKYHSDSMWGRVTISRDN***SKNTLYLQFSSLKVEDTAMFFCAREAG***
GPIWHDDVKYYDFNDGYNYHYMDVWVGKGT***TVTVSS*** (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: GFTFK (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
 GACAGACAGAAGCCATCGCATATTTCGGCGGCGGGACCAAGCTGACC
 GTTCTAGGTTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTC
 CTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTG
 ACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCC
 GTCAAGGCGGGAGTGGAGACCACACACCTCCAAACAAGCAACAACA
 AGTACGCGGCCAGCAGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCC
 CACAAAAGCTACAGCTGCCAGGTACGCATGAAGGGAGCACCGTGGAGA
 AGACAGTGGCCCCCTACAGAATGTTTCATAG (SEQ ID NO: 141)

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

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGACG
 ATCACCATCTCCTGCAATGGAACCAGAAGTGACGTTGGTGGATTTGACTC
 TGTCTCTTGGTACCAACAATCCCCAGGGAGAGCCCCCAAAGTCATGGTTT
 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
FDVSHRPSGISNRFSSGSKSGNTASLTISGLHIEDEGDYFCSSLTDRSHRIFG
 GGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKA
 DSSPVKAGVETTTPSKQSNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTV
 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***
VSHRPSGISNRFS***SGSKSGNTASLTISGLHIEDEGDYFC******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)

ATGGAGTTTGGGCTGAGCTGGGTTTTCTCGCAACTCTGTTAAGAGTTGTG
AAGTGTCACGAACAACTGGTGGAGGCCGGGGGAGGCGTGTTCCAGC
CGGGGGGGTCCCTGAGACTCTCTGTTTAGCGTCTGGATTACGTTT
CACAAATATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGCCT
GGAGTGGGTGGCACTCATCTCAGATGACGGAATGAGGAAATATCATT
CAGACTCCATGTGGGGCCGAGTCACCATCTCCAGAGACAATTCCAAG
AACTCTTTATCTGCAATTCAGCAGCCTGAGAGTCGAAGACACGGC
TATGTTCTTCTGTGCGAGAGAGGCCGGTGGGCCAATCTGGCATGACG
ACGTCAAATATTACGATTTTAATGACGGCTACTACAACTATCACTACA
TGGACGTCTGGGGCAAGGGGACCAAGGTCACCGTCTCCTCAGCGTCG
ACCAAGGGCCCATCGGTCTTCCCTCTGGCACCATCATCCAAGTCGACCTCT
GGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACC
GGTGACGGTGTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCT
TCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGA
CCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTT
GTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAACCTCCTGGGG
GGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGAT
CTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAG
ACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGAGGTGCATAAT
GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
TCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
AAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCAT
CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCC
CCATCCCGGGAGGAGATGACCAAGAACCAGGTACGCTGACCTGCCTGGT
CAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG
CAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCTGGACTCCGACG
GCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA
CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:
46)

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

CACGAACAACCTGGTGGAGGCCGGGGGAGGCGTGGTCCAGCCGGGGGGGT
 CCCTGAGACTCTCCTGTTTAGCGTCTGGATTCACGTTTCACAAATATGGCA
 TGCAGTGGGTCCGCCAGGCTCCAGGCAAGGGCCTGGAGTGGGTGGCACTC
 ATCTCAGATGACGGAATGAGGAAATATCATTACAGACTCCATGTGGGGCCG
 AGTCACCATCTCCAGAGACAATTCCAAGAACAACACTCTTTATCTGCAATTCA
 GCAGCCTGAGAGTCGAAGACACGGCTATGTTCTTCTGTGCGAGAGAGGCC
 GGTGGGCCAATCTGGCATGACGACGTCAAATATTACGATTTAATGACGG
 CTACTACAACTATCACTACATGGACGTCTGGGGCAAGGGGACCAAGGTCA
 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
VALISDDGMRKYHSDSMWGRVTISRDNKNTLYLQFSSLRVEDTAMFFC
AREAGGPIWHDDVKYYDFNDGYINYHYMDVWGKGTKVTVSSASTKGPS
 VFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
 GLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP
 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGV
 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
 KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY
 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)

HEQLVEAGGGVVQPGGSLRLSCLASGFTFHKYGMHWVRQAPGKGLEWVAL
ISDDGMRKYHSDSMWGRVTISRDNKNTLYLQFSSLRVEDTAMFFCAREAG
GPIWHDDVKYYDFNDGYINYHYMDVWGKGTKVTVSS (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: EAGGPIWHDDVKYYDFNDGYINYHYMDV (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: EAGGPIWHDDVKYYDFNDGYINYHYMDV (SEQ ID NO: 6)

[0298] 1456_A12 (PG16) (TCN-117) lambda light chain nucleotide sequence: 1456_A12 λ2 coding sequence (variable region in bold)

ATGGCCTGGGCTTGCTATTCCTCACCTCTTCACTCAGGGCACAGGGTCCT
 GGGGCCAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCT
 GGACAGACGATCACCATCTCCTGCAATGGAACCAGCCGTGACGTTGG
 TGGATTTGACTCTGTCTCCTGGTATCAACAATCCCCAGGGAAAGCCC
 CCAAAGTCATGGTTTTTGTATGTCAGTCATCGGCCCTCAGGTATGTCTA
 ATCGCTTCTCTGGCTCCAAGTCCGGCAACACGGCCTCCCTGACCATT
 TCTGGGCTCCACATTGAGGACGAGGGCGATTATTTCTGCTCTTCATT
 GACAGACAGAAGCCATCGCATATTCGGCGGCGGGACCAAGCTGACC
 GTTCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTC
 CTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTG
 ACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCC
 GTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACA
 AGTACGCGGCCAGCAGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCC
 CAAAAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGA
 AGACAGTGGCCCCCTACAGAATGTTTCATAG (SEQ ID NO: 49)

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

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGACG
 ATCACCATCTCCTGCAATGGAACCAGCCGTGACGTTGGTGGATTTGACTCT
 GTCTCCTGGTATCAACAATCCCCAGGGAAAGCCCCCAAAGTCATGGTTTT
 TGATGTCAGTCATCGGCCCTCAGGTATGTCTAATCGCTTCTCTGGCTCCAA
 GTCCGGCAACACGGCCTCCCTGACCATTCTGGGCTCCACATTGAGGACG
 AGGGCGATTATTTCTGCTCTTCATTGACAGACAGAAGCCATCGCATATTCG
 GCGGCGGGACCAAGCTGACCGTTCTA (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
 KADSSPVKAGVETTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGS
 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**NGTSRDVGGFDSVS**WYQQSPGKAPKVMV**FD**
VSHRPSGMSNRFSGSKSGNTASLTISGLHIEDEGDYFC**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)

ATGGAGTTTGGCTGAGCTGGGTTTTCCTCGCAACTCTGTAAAGAGTTGTGA
AGTGTCAAGGAAAACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCG
GGGGGGTCCCTGAGACTCTCCTGTTTAGCGTCTGGATTACCTTTCA
CAAATATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGCCTGG
AGTGGGTGGCACTCATCTCAGATGACGGAATGAGGAAATATCATTCA
GACTCCATGTGGGGCCGAGTCACCATCTCCAGAGACAATTCCAAGAA
CACTTTATATCTGCAATTCAGCAGCCTGAAAGTCGAAGACACGGCTA
TGTTCTTCTGTGCGAGAGAGGCTGGTGGGCCAATCTGGCATGACGAC
GTCAAATATTACGATTTTAATGACGGCTACTACAATTACCACTACATG
GACGTCTGGGGCAAGGGGACCATTGTCAACCGTCTCCTCAGCGTCGAC
CAAGGGCCCATCGGTCTTCCCTCTGGCACCATCATCCAAGTCGACCTCTG
GGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG
GTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTT
CCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGA
CCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCCAAATCTT
GTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAACCTCTGGGG
GGACCGTCAGTCTTCCCTCTTCCCCCAAAACCCAAGGACACCCTCATGAT
CTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAG
ACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT
GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
TCAGCGTCCCTACCGTCTGCAACCAGGACTGGCTGAATGGCAAGGAGTAC
AAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCAT
CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCC
CCATCCCGGGAGGAGATGACCAAGAACCAGGTGACCTGACCTGCCTGGT
CAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG
CAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG
GCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA
CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:
52)

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

CAGGAAAACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCGGGGGGGT
 CCCTGAGACTCTCCTGTTTAGCGTCTGGATTACCTTTCACAAATATGGCA
 TGCCTGGGTCCGCCAGGCTCCAGGCAAGGGCCTGGAGTGGGTGGCACTC
 ATCTCAGATGACGGAATGAGGAAATATCATTACAGACTCCATGTGGGGCCG
 AGTCACCATCTCCAGAGACAATTCCAAGAACACTTTATATCTGCAATTCA
 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.

QEKLVESGGGVVQPGGSLRLSCLASGFT**FKYGMH**WVRQAPGKGLEW
 VALISDDGMRKYHSDSMWGRVTISRDN**SKNTLYLQFSSLKVEDTAMFFC**
AREAGGPIWHDDVKYYDFNDGYNYHYMDVWGKG**TIVTVSS**ASTKGPS
 VFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRV**EPKSCDKTHTCPPCP**
 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
 EVHNAKTK**PREEQYN**STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
 KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
 QPENNYK**TTTPVLDSDGSFFLYSKLTV**DKSRWQQGNVFSCSV**MHEALHNHY**
 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**GFTFKYGMH**WVRQAPGKGLEW**VAL**
ISDDGMRKYHSDSMWGRVTISRDN**SKNTLYLQFSSLKVEDTAMFFCAREAG**
GPIWHDDVKYYDFNDGYNYHYMDVWGKG**TIVTVSS** (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: GFTFKH (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)

ATGGCCTGGGCTTGCTATTCCCTCACCTCTTCACTCAGGGCACAGGGTCCT
 GGGGCCAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCT
 GGACAGACGATCACCATCTCCTGCAATGGAACCAGAAGTGACGTTGG
 TGGATTTGACTCTGTCTCCTGGTACCAACAATCCCCAGGGAAAAGCCC
 CCAAAGTCATGGTTTTTTGATGTCAGTTCATCGGCCCTCAGGTATCTCTA
 ATCGCTTCTCTGGCTCCAAGTCCGGCAACACGGCCTCCCTGACCATC
 TCTGGGCTCCACATTGAGGACGAGGGCGATTATTTCTGCTCTTCACT
 GACAGACAGAAGCCATCGCATATTTCGGCGGCGGGACCAAGGTGACC
 GTTCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTC
 CTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTG
 ACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCC
 GTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACA
 AGTACGCGGCCAGCAGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCC
 CACAAAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGA
 AGACAGTGGCCCCTACAGAATGTTTCATAG (SEQ ID NO: 55)

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

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGACG
 ATCACCATCTCCTGCAATGGAACCAGAAGTGACGTTGGTGGATTTGACTC
 TGTCTCCTGGTACCAACAATCCCCAGGGAAAGCCCCCAAAGTCATGGTTT
 TTGATGTCAGTTCATCGGCCCTCAGGTATCTCTAATCGCTTCTCTGGCTCCA
 AGTCCGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCACATTGAGGAC
 GAGGGCGATTATTTCTGCTCTTCACTGACAGACAGAAGCCATCGCATATT
 CGGCGCGGGACCAAGGTGACCGTTCTA (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
 ADSSPVKAGVETTTPSKQSNKYAASSYLSLTPEQWKSHKSYSCQVTHEGST
 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*SSLTDRSHRI*FGGGTK
 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)

ATGGAGTTTGGGCTGAGCTGGGTTTTCTCGCAACTCTGTTAAGAGTTGTG
AAGTGTCAGGAACAACCTGTTGGAGTCTGGGGGAGGCGTGGTCCAGCC
GGGGGGGTCCCTGAGACTCTCCTGTTTAGCGTCTGGATTACGTTTC
ACAAATATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGCCTG
GAGTGGGTGGCACTCATCTCAGATGACGGAATGAGGAAATATCATTC
AAACTCCATGTGGGGCCGAGTCAACATCTCCAGAGACAATTCGAAGA
ACACTCTTTATCTGCAATTCAGCAGCCTGAAAGTCGAAGACACGGCT
ATGTTCTTCTGTGCGAGAGAGGCTGGTGGGCCAATCTGGCATGACGA
CGTCAAATATTACGATTTTAATGACGGCTACTACAACCTACCACTACAT
GGACGTCTGGGGCAAGGGGACCACGGTCACCGTCTCCTCAGCGTCGA
CCAAGGGCCCATCGGTCTTCCCTCTGGCACCATCATCCAAGTCGACCTCTG
GGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG
GTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGCACACCTT
CCCGGCTGTCTTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGA
CCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTT
GTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGG
GGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGAT
CTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAG
ACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT
GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
TCAGCGTCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT
CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCC
CCATCCCCGGGAGGAGATGACCAAGAACCAGGTACGCTGACCTGCCTGGT
CAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG
CAGCCGGAGAACTACAAGACCACGCTCCCGTGCTGGACTCCGACG
GCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA
CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:
58)

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

CAGGAACAACCTGTTGGAGTCTGGGGGAGGCGTGGTCCAGCCGGGGGGGT
 CCCTGAGACTCTCCTGTTTAGCGTCTGGATTACGTTTCACAAATATGGCA
 TGCAGTGGGTCCGCCAGGCTCCAGGCAAGGGCCTGGAGTGGGTGGCACTC
 ATCTCAGATGACGGAATGAGGAAATATCATTCAAACCTCCATGTGGGGCCG
 AGTCACCATCTCCAGAGACAATTCCAAGAACACTCTTTATCTGCAATTCA
 GCAGCCTGAAAGTCGAAGACACGGCTATGTTCTTCTGTGCGAGAGAGGCT
 GGTGGGCCAATCTGGCATGACGACGTCAAATATTACGATTTTAATGACGG
 CTACTACAACTACCACTACATGGACGTCTGGGGCAAGGGGACCACGGTCA
 CCGTCTCCTCA (SEQ ID NO: 134)

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

QEQLLESGGGVVQPGGSLRLSCLASGFTFHKYGMHWVRQAPGKGLEW
 VALISDDGMRKYHSNSMWGRVTISRDNKNTLYLQFSSLKVEDTAMFFC
AREAGGPIWHDDVKYYDFNDGYNNYHYMDVWVGKGTTVTVSSASTKGPS
 VFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
 GLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP
 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGV
 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
 KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY
 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)

QEQLLESGGGVVQPGGSLRLSCLASG***FTFHKYGMHWVRQAPGKGLEWVAL***
ISDDGMRKYHSNSMWGRVTISRDNKNTLYLQFSSLKVEDTAMFFCAREAG
GPIWHDDVKYYDFNDGYNNYHYMDVWVGKGTTVTVSS (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: EAGGPIWHDDVKYYDFNDGYNNYHYMDV (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: EAGGPIWHDDVKYYDFNDGYNNYHYMDV (SEQ ID NO: 6)

[0322] 1489_I13 (PG16) (TCN-120) lambda light chain nucleotide sequence: 1489_I13 λ2 coding sequence (variable region in bold)

ATGGCCTGGGCTCTGCTATTCCTCACCTCTTCACTCAGGGCACAGGGTCC
 CGGGGCCAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCT
 GGACAGACGATCACCATCTCCTGCAATGGAACCAGCAGTGACGTTGG
 TGGATTTGACTCTGTCTCCTGGTATCAACAATCCCCAGGGAAAGCCC
 CCAAAGTCATGGTTTTTGTATGTCAGTCATCGGCCCTCAGGTATCTCTA
 ATCGTTCTCTGGCTCCAAGTCCGGCAACACGGCCTCCCTGACCATC
 TCTGGGCTCCACATTGAGGACGAGGGCGATTATTTCTGCTCTTCACT
 GACAGACAGAAGCCATCGCATATTCGGCGGCGGGACCAAGGTGACC
 GTTCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTC
 CTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTG
 ACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCC
 GTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACA
 AGTACGCGGCCAGCAGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCC
 CACAAAAGCTACAGCTGCCAGGTACGCATGAAGGGAGCACCGTGGAGA
 AGACAGTGGCCCCCTACAGAATGTTTCATAG (SEQ ID NO: 61)

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

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGACG
 ATCACCATCTCCTGCAATGGAACCAGCAGTGACGTTGGTGGATTTGACTC
 TGTCTCCTGGTATCAACAATCCCCAGGGAAAGCCCCCAAAGTCATGGTTT
 TTGATGTCAGTCATCGGCCCTCAGGTATCTCTAATCGCTTCTCTGGCTCCA
 AGTCCGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCACATTGAGGAC
 GAGGGCGATTATTTCTGCTCTTCACTGACAGACAGAAGCCATCGCATATT
 CGGCGGGCGGGACCAAGGTGACCGTTCTA (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
 GGTKVTVLGGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWK
 ADSSPVKAGVETTTPSKQSNKYAASSYLSTPEQWKSHKSYSCQVTHEGST
 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)

ATGGAGTTTGGCTGAGCTGGGTTTTCCTCGCAACTCTGTTAAGAGTTGTGA
AGTGTCTCAGGAACAACCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCC
GGGGGGTCCCTGAGACTCTCCTGTTTAGCGTCTGGATTACGTTTCA
CAAATATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGCCTGG
AGTGGGTGGCACTCATCTCAGATGACGGAATGAGGAAATATCATTCA
GACTCCATGTGGGGCCGAGTCACCATCTCCAGAGACAATTCCAAGAA
CACTCTTTATCTGCAATTCAGCAGCCTGAAAGTCGAAGACACGGCTA
TGTTCTTCTGTGCGAGAGAGGCTGGTGGGCCAATCTGGCATGACGAC
GTCAAATATTACGATTTTAATGACGGCTACTACAACCTACCACTACATG
GACGTCTGGGGCAAGGGGACCACGGTCACCGTCTCCTCAGCGTCGAC
CAAGGGCCCATCGGTCTTCCCTCTGGCACCATCATCCAAGTCGACCTCTG
GGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG
GTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGCACACCTT
CCCGGCTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGA
CCGTGCCCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTT
GTGACAAAACCTCACACATGCCACCCGTGCCAGCACCTGAACTCCTGGGG
GGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGAT
CTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAG
ACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT
GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
TCAGCGTCTCTACCGTCTTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
AAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCAT
CTCCAAGCCAAAGGGCAGCCCCGAGAACCAACAGGTGTACACCCTGCCC
CCATCCCCGGGAGGAGATGACCAAGAACCAGGTACGCCTGACCTGCCTGGT
CAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG
CAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG
GCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA
CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:
64)

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

CAGGAACAACCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCGGGGGGGT
CCCTGAGACTCTCCTGTTTAGCGTCTGGATTACGTTTCAAAATATGGCA
TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGCCTGGAGTGGGTGGCACTC
ATCTCAGATGACGGAATGAGGAAATATCATTCAGACTCCATGTGGGGCCG

AGTCACCATCTCCAGAGACAATTCCAAGAACTCTTTATCTGCAATTCA
GCAGCCTGAAAGTCGAAGACACGGCTATGTTCTTCTGTGCGAGAGAGGCT
GGTGGGCCAATCTGGCATGACGACGTCAAATATTACGATTTTAATGACGG
CTACTACAACTACCACTACATGGACGTCTGGGGCAAGGGGACCACGGTCA
CCGTCTCCTCA (SEQ ID NO: 136)

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

**QEQLVESGGGVVQPGGSLRLSCLASGFTFHKYGMHWVRQAPGKGLEW
VALISDDGMRKYHSDSMWGRVTISRDN SKNTLYLQFSSLKVEDTAMFFC
AREAGGPIWHDDVKYYDFNDGYNNYHYMDVWGKGTTVTVSSASTKGPS
VFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP
APPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGV
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)

**QEQLVESGGGVVQPGGSLRLSCLASGFTFHKYGMHWVRQAPGKGLEWVAL
ISDDGMRKYHSDSMWGRVTISRDN SKNTLYLQFSSLKVEDTAMFFCAREAG
GPIWHDDVKYYDFNDGYNNYHYMDVWGKGTTVTVSS (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: EAGGPIWHDDVKYYDFNDGYNNYHYMDV (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: EAGGPIWHDDVKYYDFNDGYNNYHYMDV (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
GACAGACAGAAGCCATCGCATATTCGGCGGCGGGACCAAGGTGACC
GTTCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTC
CTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTG
ACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCC
GTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACA
AGTACGCGGCCAGCAGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCC
CACAAAAGCTACAGCTGCCAGGTACGCATGAAGGGAGCACCGTGGAGA
AGACAGTGGCCCCCTACAGAATGTTCATAG (SEQ ID NO: 67)

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

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGACG
ATCACCATCTCCTGCAATGGAACCAGCAGTGACGTTGGTGGATTTGACTC
TGTCTCCTGGTATCAACAATCCCCAGGGAAAGCCCCCAAAGTCATGGTTT
TTGATGTCAAGTCATCGGCCCTCAGGTATCTCTAATCGCTTCTCTGGCTCCA
AGTCCGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCACATTGAGGAC
GAGGGCGATTATTTCTGCTCTTCACTGACAGACAGAAGCCATCGCATATT
CGCGGGCGGGACCAAGGTGACCGTTCTA (SEQ ID NO: 137)

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

QSALTQPASVSGSPGQTITISCNGTSSDVGGFDSVSWYQQSPGKAPKVMV
FDVSHRPSGISNRFSGSKSGNTASLTISGLHIEDEGDYFCSSLTDRSHRIFG
GGTKVTVLGGPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWK
ADSSPVKAGVETTTPSKQSNKYAASSYLSLTPEQWKSHKSYSCQVTHEGST
VEKTVAPTECS (SEQ ID NO: 14)

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

QSALTQPASVSGSPGQTITISCNGTSSDVGGFDSVSWYQQSPGKAPKVMVFD
VSHRPSGISNRFSGSKSGNTASLTISGLHIEDEGDYFCSSLTDRSHRIFGGGTK
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 EAGGPIWHDDVKYYDFNDGYINYHYMDV (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 EAGGPIWHDDVKYYDFNDGYINYHYMDV (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 EAGGPIWHDDVKYYDFNDGYINYHYMDV (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)

ATGAAACACCTGTGGTTCTTCCTTCTCCTGGTGGCAGCTCCCAGATGGGTC
 CTGTACAGATGCAGTTACAGGAGTCGGGCCCCGGACTGGTGAAGCC
TTCGGAACCCGTGCCCTCACGTGCAGTGTGTCTGGTGCCTCCATAA
GTGACAGTTACTGGAGCTGGATCCGGCGGTCCCCAGGGAAGGGACTT
GAGTGGATTGGGTATGTCCACAAAAGCGGCGACACAAATTACAGCCC
CTCCCTCAAGAGTCGAGTCAACTTGTCTGTTAGACACGTCCAAAAATC
AGGTGTCCCTGAGCCTTGTGGCCGCGACCGCTGCGGACTCGGGCAAA
TATTATTGCGCGAGAACACTGCACGGGAGGAGAATTTATGGAATCGT
TGCCTTCAATGAGTGGTTCACCTACTTCTACATGGACGTCTGGGGCA
ATGGGACTCAGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCCATCGG
TCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCC
CTGGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGT
GAACTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCGGCTGTCTTAC
AGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC
AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAA
CACCAAGGTGGACAAGAGAGTTGAGCCCCAAATCTTGTGACAAAATCAG
ACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTT
CCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTG
AGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA
GTTCAACTGGTACGTGGACGGCGTGAGGTGCATAATGCCAAGACAAAG
CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCTAC
CGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCT
CCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA
GGGAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCGGGAGG
AGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGAGCCCGGAGAAC
ACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCT
ATAGCAAGCTACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTT
CTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGA
GCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 62)

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

CAGATGCAGTTACAGGAGTCGGGCCCCGGACTGGTGAAGCCTTTCGGAAA
 CCCTGTCCCTCACGTGCAGTGTGTCTGGTGCCTCCATAAGTGACAGTTACT
 GGAGCTGGATCCGGCGGTCCCCAGGGAAGGGACTTGAGTGGATTGGGTAT
 GTCCACAAAAGCGGCGACACAAATTACAGCCCCTCCCTCAAGAGTCGAGT
 CAACTTGTCTGTTAGACACGTCCAAAAATCAGGTGTCCCTGAGCCTTGTGG
 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 GDTNYSPLKSRVNLSDTSKNQVSLSLVAATAADSGKYCARTLH
 GRRIYGIVAFNEWFTYFYMDVWGNGTQVTVSSASTKGPSVFPLAPSSKSTS
 GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTV
 PSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCDKTHTCPPCPAPELLGGPSVF
 LFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
 EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP
 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***VHK***
*SGDTNYSPLKSRVNLSDTSKNQVSLSLVAATAADSGKYCART****TLHGRR******Y***
*GIVAFNEWFTYFYMDV*WGNGTQVTVSS (SEQ ID NO: 79)

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

CDR 1: DSYWS (SEQ ID NO: 90)

CDR 2: YVHKSGDTNYSPLKS (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
 GTGACCTCCGATATATCTGTGGCCCCAGGAGAGACGGCCAGGATTTT
 CTGTGGGGAAAAGAGCCTTGGAAGTAGAGCTGTACAATGGTATCAAC
 ACAGGGCCGGCCAGGCCCCCTCTTTAATCATATATAATAATCAGGAC
 CGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCCTGACTCCCC
 TTTTGGGACCACGGCCACCCTGACCATCACCAGTGTCGAAGCCGGGG
 ATGAGGCCGACTATTACTGTCATATATGGGATAGTAGAGTTCCCACC
 AAATGGGTCTTCGGCGGAGGGACCACGCTGACCGTGTTAGGTCAGCC
 CAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCA
 AGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAG
 CCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTC AAGGCGGGAGT
 GGAGACCACACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGC
 AGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCACAAAAGCTACA

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
ERFSGSPDSPFGTTATLTITSVEAGDEADYYCHIWDSPVPTKWVFGGGTT
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
SGSPDSPFGTTATLTITSVEAGDEADYYCHIWDSRVPTKWVFGGGTTTLTVL
(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
 TCCCTCAAGAGTCGAGTCAACTTGTCTGTAGACACGTCCAAAAATCA
 GGTGTCCCTGAGCCTTGTGGCCGCGACCGCTGCGGACTCGGGCAAAT
 ATTATTGCGCGAGAACACTGCACGGGAGGAGAATTTATGGAATCGTT
 GCCTTCAATGAGTGGTTCACCTACTTCTACATGGACGTCTGGGGCAA
 TGGGACTCAGGTCAACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTC
 TTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGACACAGCGGCCCT
 GGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGA
 ACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTTACAG
 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAG
 CTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACA
 CCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACAC
 ATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCC
 TCTTCCCCCCTAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTT
 CAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG
 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTTACCCGT
 CCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCC
 AACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAG
 GGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA
 GATGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGCTTCTATC
 CCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAA
 CTACAAGACCACGCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTA
 TAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC
 TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAG
 CCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 62)

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

CAGATGCAGTTACAGGAGTCGGGCCCCGGACTGGTGAAGCCTTCGGAAA
 CCCTGTCCCTCACGTGCAGTGTGTCTGGTGCCTCCATAAGTGACAGTTACT
 GGAGCTGGATCCGGCGGTCCCCAGGGAAGGGACTTGAGTGGATTGGGTAT
 GTCCACAAAAGCGGCGACACAAATTACAGCCCCCTCCCTCAAGAGTCGAGT
 CAACTTGTCTGTAGACACGTCCAAAAATCAGGTGTCCCTGAGCCTTGTGG
 CCGCGACCGCTGCGGACTCGGGCAAATATTATTGCGCGAGAACACTGCAC
 GGGAGGAGAATTTATGGAATCGTTGCCTTCAATGAGTGGTTCACCTACTT
 CTACATGGACGTCTGGGGCAATGGGACTCAGGTCACCGTCTCTCTCA (SEQ
 ID NO: 63)

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

MKHLWFFLLLVAAPRWVLSQMQLQESGPGLVKPSETLSLTCSVSGASIS
 DSYWSWIRRSPGKGLEWIGYVHKSGDTNYIPSLKSRVNLSDTSKNQVSL
 SLVAATAADSGKYCARTLHGRRIYGIVAFNEWFTYFYMDVWNGTQV
 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG

VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHHKPSNTKVDKRVEPKS
 CDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE
 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
 KVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
 SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS
 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)

QMQLQESGPGLVKPSETLSLTCSVSGASISDSYWSWIRRS PGKGLEWIGYVHK
SGDTNYSPSLKSRVNLSDT SKNQVSLSLVAATAADSGKYCARTLHGRRY
GIVAFNEWFTYFYMDVWGNGTQVTVSS (SEQ ID NO: 79)

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

CDR 1: DSYWS (SEQ ID NO: 90)

CDR 2: YVHKSGDTNYSPLKS (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
 GTGACCTCCGATATATCTGTGGCCCCAGGAGAGACGGCCAGGATTTCT
 CTGTGGGGGAAAAGAGCCTTGGAAGTAGAGCTGTACAATGGTATCAAC
 ACAGGGCCCGGCCAGGCCCCCTCTTAATCATATATAATAATCAGGAC
 CGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCCTGACTCCCC
 TTTTGGGACCACGGCCACCCTGACCATCACCAGTGTCGAAGCCGGGG
 ATGAGGCCGACTATTACTGTCATATATGGGATAGTAGAGTTCCCACC
 AAATGGGTCTTCGGCGGAGGGACCACGCTGACCGTGTTAGGTCAGCC
 CAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCA
 AGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAG
 CCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTC AAGGCGGGAGT
 GGAGACCACCACACCCTCCAAACAAGCAACAACAAGTACGCGGCCAGC
 AGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCAAAAAGCTACA
 GCTGCCAGGTACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCC
 TACAGAATGTTTCATAG (SEQ ID NO: 146)

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

TCCGATATATCTGTGGCCCCAGGAGAGACGGCCAGGATTTTCCTGTGGGGA
AAAGAGCCTTGGAAGTAGAGCTGTACAATGGTATCAACACAGGGCCGGC
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.

MAWTFLLGLLSHCTASVTS~~DISVAPGETARISC~~**GEKSLGSRAVQWYQH**
RAGQAPSLIIYNNQDRPSGIPERFSGSPDSPFGTTATLTITTSVEAGDEADYY
CHIWDSRVPTKWVFGGGTTLTVLGQPKAAPSVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADSSPVKAGVETTTTPSKQSNKYAASSYLSLTPEQWK
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**WYQH**RAGQAPSLIIYNNQDRPSGIPERF**
SGSPDSPFGTTATLTITTSVEAGDEADYY**CHIWD**SRVPTKWVFGGGTTLTVL
(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: HIWD

[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: HIWD

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

ATGAAACACCTGTGGTTCTTCCCTTCTCCTGGTGGCAGCTCCCAGATGGGTC
CTGTCCCAGGTTTCATCTGCAGGAGTCGGGCCCCGGACTGGTGAAGCC
TTCGGAGACCCTGTCCCTCACGTGCAATGTGTCTGGGACCCTCGTGC
GTGATAACTACTGGAGCTGGATCAGACAACCCCTCGGGAAGCAACCT
GAGTGGATTGGCTATGTCCATGACAGCGGGGACACGAATTACAACCC
CTCCCTGAAGAGTCGAGTCCACTTATCGTTGGACAAGTCCAAAAACC
TGGTGTCCCTGAGGCTGACCGGCGTGACCGCCGCGGACTCGGCCATA
TATTATTGCGCGACAACAAAACACGGGAGGAGGATTTATGGCGTCGT

TGCCTTCAAAGAGTGGTTACCTATTTCTACATGGACGTCTGGGGCA
AAGGGACTTCGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGG
TCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCC
CTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGT
GAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTAC
AGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC
AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAA
CACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCAC
ACATGCCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTT
CCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTG
AGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA
GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG
CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCAC
CGTCTGCAACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCT
CCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA
GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGG
AGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAA
ACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTCCTCT
ATAGCAAGCTACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTT
CTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGA
GCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 153)

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

CAGGTTCATCTGCAGGAGTCGGGCCCCGGACTGGTGAAGCCTTCGGAGAC
CCTGTCCCTCACGTGCAATGTGTCTGGGACCCTCGTGCGTGATAACTACTG
GAGCTGGATCAGACAACCCCTCGGGAAGCAACCTGAGTGGATTGGCTATG
TCCATGACAGCGGGGACACGAATTACAACCCCTCCCTGAAGAGTCGAGTC
CACTTATCGTTGGACAAGTCCAAAAACCTGGTGTCCCTGAGGCTGACCGG
CGTGACCGCCGCGGACTCGGCCATATATTATTGCGCGACAACAAAACACG
GGAGGAGGATTTATGGCGTCTGTCCTTCAAAGAGTGGTTACCTATTTCT
ACATGGACGTCTGGGGCAAAGGGACTTCGGTCACCGTCTCCTCA (SEQ ID
NO: 154)

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

MKHLWFFLLLVAAPRWVLSQVHLQESGPGLVKPSETLSLTCNVSGTLVR
DNYWSWIRQPLGKQPEWIGYVHDSGDTNYPNPSLKSRVHLSLDKSKNLVS
LRLTGVTAADSAIYYCATT**KHGRRIYGVVAFKEWFTYFYMDVWGK**TS
VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPK
SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
KVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP

SDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
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)

QVHLQESGPGLVKPSETLSLTCNV***SGTLVRD***NYWSWIRQPLGKQPEWIGYVH
DSGDTNYNPSLKSRVHLSLDKSKNLVSLRLTGVTAADSAIYYCAT***TKHGRRI***
YGVVAFKEWFTYFYMDVWGKGTSTVSS (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: TKHGRRIYGVVAFKEWFTYFYMDV (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: TKHGRRIYGVVAFKEWFTYFYMDV (SEQ ID NO: 262)

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

ATGGCCTGGACCGTTCTCCTCCTCGGCCTCCTCTCTCACTGCACAGGCGCG
GTGTCTACCTTTGTGTCACTGGCCCCAGGACAGACGGCCAGGATTACT
TGTGGGGAAGAGAGCCTTGGAAGTAGATCTGTTATTTGGTATCAACA
GAGGCCAGGCCAGGCCCTTCATTAATCATCTATAATAATAATGACC
GGCCCTCAGGGATTCCTGACCGATTTTCTGGGTCCCCTGGCTCCACT
TTTGGGACCACGGCCACCCTGACCATCACCAAGTGTCTGAAGCCGGGGA
TGAGGCCGACTATTATTGTCTATCTGGGATAGTAGACGACCAACCA
ATTGGGTCTTCGGCGAAGGGACCACTGATCGTGTTAGCTCAGCCCA
AGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAG
CCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCC
GTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAGGCGGGAGTGG
AGACCACACACCTCCAAACAAGCAACAACAAGTACGCGGCCAGCAG
CTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAAAAGCTACAGCT
GCCAGGTACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCCTAC
AGAATGTTTCATAG (SEQ ID NO: 158)

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

ACCTTTGTGTCACTGGCCCCAGGACAGACGGCCAGGATTACTTGTGGGGA
AGAGAGCCTTGGAAGTAGATCTGTTATTTGGTATCAACAGAGGCCAGGCC
AGGCCCTTCATTAATCATCTATAATAATAATGACCGGCCCTCAGGGATTC
CTGACCGATTTTCTGGGTCCCCTGGCTCCACTTTTGGGACCACGGCCACCC

TGACCATCACCAAGTGTCTGAAGCCGGGGATGAGGCCGACTATTATTGTCAT
ATCTGGGATAGTAGACGACCAACCAATTGGGTCTTCGGCGAAGGGACCAC
ACTGATCGTGTTA (SEQ ID NO: 159)

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

MAWTVLLLGLLSHCTGAVSTFVSVAPGQTARITCGEESLGSRSVIWIYQQ
RPGQAPSLIIYNNDRPSGIPDRFSGSPGSTFGTTATLTITSVEAGDEADYY
CHIWDSSRRPTNWWVFEGGTTLIVLGOPKAAPSVTLFPPSSEELQANKATLVC
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***WYQQRPGQAPSLIIY***NNDRPS***GIPDRF
SGSPGSTFGTTATLTITSVEAGDEADYY***CHIWDSSRRPTNWWVFEGGTTLIVL***
(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: HIWDSSRRPTNWW (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: HIWDSSRRPTNWW (SEQ ID NO: 164)

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

ATGAAACACCTGTGGATCTTCCTTCTCCTGGTGGCAACTCCCAGATGGGTC
GAGTCCCAGCTGCACCTGCAGGAGTCGGGCCAGGGCTGGTGAAGCC
TCCGGAGACCCTGTCCCTCACGTGTAGTGTGTCTGGCGCCTCCATCA
ATGATGCCTATTGGAGTTGGATTTCGGCAGTCCCCAGGGAAGCGGCCT
GAGTGGGTTGGATATGTCCATCACAGCGGTGACACAAATTATAATCC
CTCACTCAAGAGGCGCGTCACGTTTTTCATTAGACACGGCCAAGAATG
AAGTGTCCCTGAAATTAGTAGACCTGACCGCTGCGGACTCGGCCACA
TATTTTTGTGCGCGAGCACTTCACGGGAAGAGGATTTATGGGATAGT
TGCCCTCGGAGAGTTGTTACCTACTTCTACATGGACGTCTGGGGCA
AGGGGACTGCGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGG
TCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCC
CTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTG

GAAGTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTTAC
 AGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC
 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAA
 CACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCAC
 ACATGCCCACCGTGCCAGCACCTGAACCTCTGGGGGGACCGTCAGTCTT
 CCTCTTCCCCCAAAACCCAAGGACACCCCTCATGATCTCCCGGACCCCTG
 AGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA
 GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG
 CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCAC
 CGTCTGCAACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCT
 CCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA
 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGG
 AGATGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTAT
 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGACA
 ACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCT
 ATAGCAAGCTACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTT
 CTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGA
 GCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 165)

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

CAGCTGCACCTGCAGGAGTCGGGCCCAGGGCTGGTGAAGCCTCCGGAGA
 CCCTGTCCCTCACGTGTAGTGTGTCTGGCGCTCCATCAATGATGCCTATT
 GGAGTTGGATTCGGCAGTCCCCAGGGAAGCGGCCTGAGTGGGTGGATAT
 GTCCATCACAGCGGTGACACAAATTATAATCCCTCACTCAAGAGGCGCGT
 CACGTTTTTCATTAGACACGGCCAAGAATGAAGTGTCCCTGAAATTAGTAG
 ACCTGACCGCTGCGGACTCGGCCACATATTTTGTGCGCGAGCACTTAC
 GGGAAGAGGATTTATGGGATAGTTGCCCTCGGAGAGTTGTTACCTACTT
 CTACATGGACGTCTGGGGCAAGGGGACTGCGGTACCGTCTCTCTCA (SEQ
 ID NO: 166)

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

MKHLWIFLLLVATPRWVESQLHLQESGPGLVKPPETLSLTCSVSGASIND
AYWSWIRQSPGKRPEWVGYYVHSGDTNYPNPSLKRRVTFSLDTAKNEVS
LKLVDLTAADSATYFCARALHGKRIYGIVALGELFTYFYMDVWGKGTA
VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRV
EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS
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**
HSGDTNYPNPSLKRRVTFSLDTAKNEVSLKLVDLTAADSATYFCAR**ALHGKRI**
YGIVALGELFTYFYMDVVWGKGTA VTVSS (SEQ ID NO: 168)

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

CDR 1: DAYWS (SEQ ID NO: 169)

CDR 2: YVHHS GDTNYPNPSLKR (SEQ ID NO: 170)

CDR 3: ALHGKRIY GIVALGELFTYFYMDV (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: ALHGKRIY GIVALGELFTYFYMDV (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
ATGAGGCCGACTATTACTGTCTATATATATGATGCTAGAGGTGGCACC
AATTGGGTCTTCGACAGAGGGACCACACTGACCGTCTTAGGTCAGCCC
AAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTICAA
GCCAACAAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGC
CGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTG
GAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCA
GCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAAAAGCTACAGC
TGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCCTA
CAGAAATGTTTCATAG (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
KPGQPPSLIYNNQDRPAGVPERFSASPD~~FRPGTTATLTITNVDAEDEADY~~
YCHIDARGGTNWVFD~~RGTTTLTVLGQPKAAPSVTLFPPSSEELQANKATLV~~
CLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQW
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***GKESIGSRAVQ***WYQQKPGQPPSLIY***NNQDRPA***GVPER
FSASPD~~FRPGTTATLTITNVDAEDEADY~~YC***HIYDARGGTNWV***FD~~RGTTTLTVL~~
(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
TTTCACTCGACACGCCCAAGAATCAGGTCTTCCTCAAGCTCACTTCTC
TGA CTGCCGCGGACACGGCCACTTACTACTGTGCGCGATTTCGACGGC
GAAGTCTTGGTCTATAATCATTGGCCAAAGCCGGCCTGGGTGGACCT
CTGGGGCCCGCGGAATACCGGTACCGTCTCCTCAGCCTCCACCAAGGG
CCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCA
CAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACG
GTGTCTGTGGA ACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGC
TGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC
CTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC
CCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAA
AACTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGT
CAGTCTTCCTCTTCCCCCAAACCCAAGGACACCTCATGATCTCCCGGA
CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAG

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

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

CAGTCGCAGCTGCAGGAGTCGGGCCCCACGACTGGTGGAGGCCTCGGAGA
CCCTGTCACTACGTGCAATGTGTCCGGCGAGTCCACTGGTGCCTGTACTT
ATTTCTGGGGCTGGGTCCGGCAGGCCCCAGGGAAGGGGCTGGAGTGGATC
GGGAGTTTGTCCCATTGTCTCAGAGTTTCTGGGGTTCCGGTTGGACCTTCCAC
AACCCGTCTCTCAAGAGTCGACTCACGATTTCACTCGACACGCCCAAGAA
TCAGGTCTTCTCAAGCTCACTTCTCTGACTGCCGCGGACACGGCCACTTA
CTACTGTGCGCGATTCGACGGCGAAGTCTTGGTCTATAATCATTGGCCAA
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
LDTPKNQVFLKLTS**LAADTATYYCARFDGEVLVYNHWPKPAWVDLW**
GRGIPVT**VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT****SVNS**
GALTS**GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK**
RVEPK**SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS**
HEDPEV**KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK**
EYCKV**SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK**
GFYPSD**IAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNV**
FSCSV**MHEALHNHYTQKSLSLSPGK** (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)

QSQLQESGPRLVEASETSLSLTCNVSGEST***ACTYFWGWVRQAPGKGLEWIGS***
LSHCQSFWGSWTFHNPSLKSRLTIS***LDTPKNQVFLKLTS******LAADTATYYCA***
RFDGEVLVYNHWPKPAWVDL***WGRGIPVT******VSS*** (SEQ ID NO: 184)

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

CDR 1: ACTYFWG (SEQ ID NO: 185)

CDR 2: SLSHCQSFWGSWTFHNPSLKS (SEQ ID NO: 186)

CDR 3: FDGEVLVYNHWPKPAWVDL (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: FDGEVLVYNHWPKPAWVDL (SEQ ID NO: 187)

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

ATGGCCTGGGCTCTGCTCCTCCTCACCCCTCCTCACTCAGGGCACAGGGGC
CTGGGCCCAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCC
TGGACAGTCAATCACCATCTCCTGCAATGGAACCGCCACTAACTTTGT
CTCCTGGTACCAACAATTCCCAGACAAGGCCCCCAAACATCATTTTT
TGGGGTTCGATAAGCGCCCCCCCCGGTGTCCCCGATCGTTTCTCTGGCT
CCCGGTCTGGCACGACGGCCTCCCTTACCGTCTCCCGACTCCAGACT
GACGATGAGGCTGTCTATTATTGCGGTTCACTTGTCGGCAACTGGGA
TGTGATTTTCGGCGGAGGGACCACCTTGACCGTCCTAGGTCAGCCCAA
GGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGC
CAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCG
TGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGA
GACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGC
TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCACAAAAGCTACAGCTG
CCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACA
GAATGTTTCATAG (SEQ ID NO: 190)

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

CAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCCTGGACAGTCA
ATCACCATCTCCTGCAATGGAACCGCCACTAACTTTGTCTCCTGGTACCAA
CAATTCCCAGACAAGGCCCCCAAACATCATTTTTTGGGGTCGATAAGCG
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
WYQQFPDKAPKLIIFGVDKRPPGVDRFSGSRSGTTASLTVSRLQTDDEA
VYYCGSLVGNWDVIFGGGTTLTVLGQPKAAPSVTLFPPSSEELQANKATLV
CLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNKYYAASSYLSLTPEQW
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**NGTATNFVS**WYQQFPDKAPKLIIF**GVDKRPPG**
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
CTGTCCCAGCCGAGCTGCAGGAGTCGGGGCCAGGACTGGTGGAGGC
TTCGGAGACCCTGTCCCTCACCTGCACTGTGTCCGGCGACTCCACTG
CTGCTTGTGACTATTTCTGGGGCTGGGTCCGGCAGCCCCCAGGGAAG
GGCCTGGAGTGGATTGGGGGTTTGTCAATTGTGCAGGTTACTACAA
TACTGGCTGGACCTACCACAACCCGTCCTCTCAAGAGTCGGCTCACGA
TTTCACTCGACACCCCAAGAATCAGGTCTTCCTGAAGTTAAATTCTG
TGACCGCCGCGGACACGGCCATTTACTACTGTGCGCGATTTCGACGGC
GAAGTTTTGGTGTAACACGATTGGCCAAAGCCGGCCTGGGTGACCT
CTGGGGCCCGGGGAACCTTGGTCAACCGTCTCCTCAGCCTCCACCAAGGG
CCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCA
CAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACG
GTGTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCGGC
TGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC
CTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC
CCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAA
AACTCACACATGCCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGT
CAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA
CCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAG
GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGAC
AAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTACGCGTC
CTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA
GGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAG
CCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
GAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCT

TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA
 GAACAACCTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCT
 TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA
 CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC
 AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 197)

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

CAGCCGCAGCTGCAGGAGTCGGGGCCAGGACTGGTGGAGGCTTCGGAGA
 CCCTGTCCCTCACCTGCACTGTGTCCGGCGACTCCACTGCTGCTTGTGACT
 ATTTCTGGGGCTGGGTCCGGCAGCCCCCAGGGAAGGGCCTGGAGTGGATT
 GGGGGTTTGTACATTGTGCAGGTTACTACAATACTGGCTGGACCTACCA
 CAACCCGTCTCTCAAGAGTCGGCTCACGATTTCACTCGACACCCCAAGA
 ATCAGGTCTTCTGAAGTTAAATTCTGTGACCGCCGCGGACACGGCCATT
 ACTACTGTGCGCGATTTCGACGGCGAAGTTTTGGTGTACCACGATTGGCCA
 AAGCCGGCCTGGGTTCGACCTCTGGGGCCGGGGAACCTTTGGTCACCGTCTC
 CTCA (SEQ ID NO: 198)

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

MKHLWFFLLLVAAPRWVLSQPQLQESGPGLVEASETSLTCTVSGDSTA
 ACDYFWGWVRQPPGKGLEWIGGLSHCAGYYNTGWTYHNPSLKSRLTIS
 LDTPKNQVFLKLNSVTAADTAIYYCARFDGEVLVYHDWPKPAWVDLWG
 RGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS
 GALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK
 RVEPKSCDKTHHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
 EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
 GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV
 FSCSVMEALHNHYTQKSLSLSPGK (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)

QPQLQESGPGLVEASETSLTCTVSGDSTA***ACDYFWGWVRQPPGKGLEWIGG***
LSHCAGYYNTGWTYHNPSLKSRLTISLDTPKNQVFLKLNSVTAADTAIYYCAR
FDGEVLVYHDWPKPAWVDLWGRGTLLTVSS (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
TCTCCTGGTACCAGCAACACCCAGGCAAGGCCCCCAAACCTCGTCATT
TATGGGGTCAATAAGCGCCCCCTCAGGTGTCCCTGATCGTTTTTCTGG
CTCCAAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGGCTCCAGA
CTGACGATGAGGCTGTCTATTACTGCAGCTCACTTGTAGGCAACTGG
GATGTGATTTTCGGCGGAGGGACCAAGTTGACCGTCTCTGGGTACGCC
CAAGGCTGCCCCCTCGGTCACTCTGTTCGCCCTCCTCTGAGGAGCTTCA
AGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGAAGTCTACCCGGGAG
CCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGT
GGAGACCACACACCTCCAAACAAAGCAACAACAAGTACGCGGCCAGC
AGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAAAAGCTACA
GCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCC
TACAGAATGTTTCATAG (SEQ ID NO: 206)

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

CAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCCTGGACAGTCA
ATCTCCATCTCCTGCACTGGAACCAGCAATAGGTTGTCTCCTGGTACCAG
CAACACCCAGGCAAGGCCCCCAAACCTCGTCATTTATGGGGTCAATAAGCG
CCCCCTCAGGTGTCCCTGATCGTTTTTCTGGCTCCAAGTCTGGCAACACGGC
CTCCCTGACCGTCTCTGGGCTCCAGACTGACGATGAGGCTGTCTATTACTG
CAGCTCACTTGTAGGCAACTGGGATGTGATTTTCGGCGGAGGGACCAAGT
TGACCGTCTCTG (SEQ ID NO: 207)

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

MAWALLLLTLLTQGTGAWAQSALTQPPSASGSPGQSSISCTGTSNRFVS
WYQQHPGKAPKLVIYGVNKRPSGVPDRFSGSKSGNTASLTVSGLQTDDE
AVYYCSSLVGNWDVIFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATL
VCLISDFYPGAVTVAWKADSSPVKAGVETTPSKQSNNKYAASSYLSLTPEQ
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)

QSALTQPPSASGSPGQSSISCT***GTGSNRFVS***WYQQHPGKAPKLVIY***GVNKRPS***
GVPDRFSGSKSGNTASLTVSGLQTDDEAVYYC***SSLVGNWDVIF***GGGTKLTVL
(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
 GCCGTCTATCACTGCGTACGATCCGGCGGGCAGACATCTTATATTATTAT
 GAGTGGCAAAAGCCGCACTGGTTCTCTCCCTGGGGCCCGGGAATCCA
 CGTCAACCGTCTCGAGCGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG
 GCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT
 GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAAGTCAAGGCG
 CCCTGACCAGCGGCGTGACACCTTCCCGGCTGTCCTACAGTCCTCAGGA
 CTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGAC
 CCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG
 GACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCAC
 GTGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCTCTTCCCCC
 AAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCG
 TGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTAC
 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC
 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG
 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC
 TCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCG
 AGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG
 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACAT
 CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACC
 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTC
 ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGT
 GATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGT
 CTCCGGGTAAATGA (SEQ ID NO: 213)
- [0424] 5147_N06 (PGT-130) gamma heavy chain variable region nucleotide sequence:

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTGCGGAGA
 CCCTGTCCCTCACCTGCAGTGTCTCTGGAGAATCTATCAATACTGGTCATT
 ACTACTGGGGCTGGGTCCGTCAGGTCCCAGGGAAGGGACTTGAGTGGATA
 GGTCAATATCCATTATACGACGGCTGTCTGCACAACCCGTCCCTCAAGAG
 TCGACTCACCATCAAAATTACACGTTGAGAAACCAGATTACCCTGAGGC
 TCAGTAATGTGACGGCCGCGGACACGGCCGTCTATCACTGCGTACGATCC
 GGCGGCGACATCTTATATTATTATGAGTGGCAAAGCCGCACTGGTTCTC
 TCCCTGGGGCCCCGGAATCCACGTCAACGTCTCGAGC (SEQ ID NO:214)

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

MKHLWFFLLVAAPRWVLSQVQLQESGPGLVKPAETLSLTCSVSGESIN
 TGHYYWGWVRQVPGKGLEWIGHIHYTTAVLHNPSLKSRLTIKIYTLRN
QITLRLSNVTAADTAVYHCVRSGGDILYYYEWQKPHWFSPWGPGIHVTV
 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
 TFPAYLQSSGLYSLSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCD
 KHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
 NWWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV
 NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI
 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*
*YYYEWQKPHWFSPWGP*GIHVTVSS (SEQ ID NO: 216)

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

CDR 1: TGHYYWG (SEQ ID NO: 217)

CDR 2: HHIHYTTAVLHNPSLKS (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: HHIHYTTAVL (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)

ATGGCCTGGGCTCTGCTCCTCCTCACCTCCTCACTCAGGGCACAGGGTCC
 TGGGCCCAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCTT

GGACAGTCAGTCACCATCTCCTGCAATGGAACCAGCAGTGACATTGG
 CGGTTGGAATTTTGTCTCCTGGTATCAACAGTTCCCGGGCAGAGCCC
 CCAGACTCATTATTTTGTAGGTCAATAAGCGGCCCTCAGGGGTCCCT
 GGTCGCTTCTCTGGCTCCAAGTCGGGCAATTCGGCCTCCCTGACCGT
 CTCTGGGCTCCAGTCTGACGATGAGGGTCAATATTTCTGCAGTTCAC
 TTTTCGGCAGGTGGGATGTTGTTTTTGGCGGGGGGACCAAGCTGACC
 GTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTC
 CTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTG
 ACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCC
 GTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACA
 AGTACGCGGCCAGCAGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCC
 CACAAAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGA
 AGACAGTGGCCCCCTACAGAATGTTCATAG (SEQ ID NO: 222)

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

CAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCTTGGACAGTCA
 GTCACCATCTCCTGCAATGGAACCAGCAGTGACATTGGCGGTGGAATTT
 TGTCTCCTGGTATCAACAGTTCCCGGGCAGAGCCCCCAGACTCATTATTT
 TGAGGTCAATAAGCGGCCCTCAGGGGTCCCTGGTCGCTTCTCTGGCTCCA
 AGTCGGGCAATTCGGCCTCCCTGACCGTCTCTGGGCTCCAGTCTGACGAT
 GAGGGTCAATATTTCTGCAGTTCATTTTCGGCAGGTGGGATGTTGTTTTT
 GGCGGGGGGACCAAGCTGACCGTCCTA (SEQ ID NO: 223)

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

MAWALLLLTLLTQGTGSWAQSALTQPPSASGSLGQSVTISCNGTSSDIGG
 WNFVSWYQQFPGRAPRLIIFEVNKRPSGVPGRFSGSKSGNSASLTVSGLQ
 SDDEGQYFCSSLFGRWDVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQAN
 KATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNKYYASSYLSL
 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***NGTSSDIGGWNFVSWYQQFPGRAPRLIIFEVN***
KRPSGVPGRFSGSKSGNSASLTVSGLQSDDEGQYFC***SSLFGRWDVVFGGGTK***
 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
TTCGGAGACCTGTCTCTGAGTTGCACTGTCTCTGGTGAATCCATAA
GGGGTGGCGAGTGGGGCGATAAAGATTATCATTGGGGCTGGGTCCG
CCACTCAGCAGGAAAGGGCCTGGAGTGGATTGGGAGTATCCATTGGA
GGGGGACCACCCACTACAAAGAGTCCCTCAGGAGAAGAGTGAGTATG
TCGATCGACACGTCCAGGAATTGGTTCTCCCTGAGGCTGGCCTCTGT
GACCGCCGCGGACACGGCCGTCTACTTTTGTGCGAGACACCGACATC
ATGATGTTTTTCATGTTGGTCCCTATTGCGGGCTGGTTCGACGTCTGG
GGCCCGGGAGTCCAGGTACCGTCTCGAGCGCCTCCACCAAGGGCCCA
TCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGT
CGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTC
CTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC
AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCCAG
CAACACCAAGGTGGACAAGAGAGTTGAGCCCAATCTTGTGACAAAACCT
CACACATGCCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGGACCGTCACT
CTTCCTCTTCCCCCCTAAACCAAGGACACCCCTCATGATCTCCCGGACCCC
TGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCA
AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAA
GCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCCTC
ACCGTCTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGG
TCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAGCC
AAAGGGCAGCCCCGAGAACACAGGTGTACACCCTGCCCCCATCCCGGG
AGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTC
TATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGA
ACAACCTACAAGACCACGCCTCCCGTGGTGGACTCCGACGGCTCCTTCTTC
CTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACG
TCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
AAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 229)

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

CAGTTGCAGATGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGA
CCCTGTCTCTGAGTTGCACTGTCTCTGGTGAATCCATAAGGGGTGGCGAGT
GGGGCGATAAAGATTATCATTGGGGCTGGGTCCGCCACTCAGCAGGAAA
GGGCCTGGAGTGGATTGGGAGTATCCATTGGAGGGGGACCCCACTACA
AAGAGTCCCTCAGGAGAAGAGTGAGTATGTCGATCGACACGTCCAGGAA
TGGTTCTCCCTGAGGCTGGCCTCTGTGACCGCCGCGGACACGGCCGTCT
ACTTTTGTGCGAGACACCGACATCATGATGTTTTTCATGTTGGTCCCTATTG

CGGGCTGGTTCGACGTCTGGGGCCCCGGGAGTCCAGGTCACCGTCTCGAGC
(SEQ ID NO: 230)

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

MKHLWFFLLLVAAPRWVLSQLQMQUESGPGLVKPSETLSLSCTVSGDSIR
GGEWGDKDYHWGWVRHSAGKGLEWIGSIHWRGTTHYKESLRRRVSM
SIDTSRNWFSRLASVTAADTAVYFCARHRHHDVFMLVPIAGWFDVWGP
GVQVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSG
ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKR
VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNV
FSCSVMHREALHNHYTQKSLSLSPGK (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)

QLQMQUESGPGLVKPSETLSLSCTVSGDSIR***GGEWGDKDYHWGWVRHSAGK***
GLEWIG***SIHWRGTTHYKESLRRRVSM***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)

ATGGAAACCCAGCTCAGCTTCTCTTCCTCCTGCTACTCTGGCTCCCAGAT
ACCACTGGAGAAATTGTGATGACGCAGTCTCCCGACACCCTGTCTGTC
TCTCCAGGGGAGACAGTCACACTCTCCTGCAGGGCCAGTCAGAATAT
TAACAAGAATTTAGCCTGGTACCAATACAAACCTGGCCAGTCTCCA
GGCTCGTAATTTTGAACATATAGCAAGATCGCTGCTTTCCCTGCCA
GGTTCGTTGCCAGTGGTTCTGGGACAGAGTTCACTCTCACCATCAAC
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
 CCTGGTACCAATACAAACCTGGCCAGTCTCCCAGGCTCGTAATTTTGA
 ACATATAGCAAGATCGCTGCTTCCCTGCCAGGTTCGTTGCCAGTGTTCT
 GGGACAGAGTTCACTCTCACCATCAACAACATGCAGTCTGAAGATGTTGC
 AGTTTATTACTGTCAACAATATGAAGAGTGGCCTCGGACGTTCCGGGCAAG
 GGACCAAGGTGGATATCAAA (SEQ ID NO: 239)

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

METPAQLLFLLLWLPDTTGEIVMTQSPDTLSVSPGETVTLSCRASQNIN
KNLAWYQYKPGQSPRLVIFETYSKIAAFPARFVASGSGTEFTLTINNMQS
EDVAVYYCQQYEEWPRTFGQG**TKVDIKRTVAAPS**VFIFPPSDEQLKSGTAS
 VVCLLN**FYPREAKVQWKVDNALQSGNSQESVTEQDSK**STYLSSTLTL**SK**
 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)

EIVMTQSPDTLSVSPGETVTLSC***RASONINKNLA***WYQYKPGQSPRLVIF***ETYS***
KIAAFPARFVASGSGTEFTLTINNMQSE***DVAVYYCQQYEEWPRT***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: QQYEEWPRT (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: QQYEEWPRT (SEQ ID NO: 245)

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

ATGAAACACCTGTGGTTCTTCCTCTTGCTGGTGGCGGCTCCCAGATGGGTC
CTGTCCCAGTTGCAGATGCAGGAGTCGGGCCCAGGACTGGTGAAGCC
TTCGGAGACCCGTGTCTCTGAGTTGCACTGTCTCTGGTGA CTCCATAA
GGGGTGGCGAGTGGGGCGATAAAGATTATCATTGGGGCTGGGTCCG
CCACTCAGCAGGAAAGGGCCTGGAGTGGATTGGGAGTATCCATTGGA
GGGGGACCACCCACTACAAAGAGTCCCTCAGGAGAAGAGTGAGTATG
TCGATCGACACGTCCAGGAATTGGTTCTCCCTGAGGCTGGCCTCTGT
GACCGCCGCGGACACGGCCGTCTACTTTTGTGCGAGACACCGACATC
ATGATGTTTTTCATGTTGGTCCCTATTGCGGGCTGGTTCGACGTCTGG
GGCCCCGGGAGTCCAGGTACCGTCTCGAGCGCCTCCACCAAGGGCCCCA
TCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGACACAGC
GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGT
CGTGGA ACTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCGCTGTC
CTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC
AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCAG
CAACACCAAGGTGGACAAGAGAGTTGAGCCCCAAATCTTGTGACAAA CT
CACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTCAGT
CTTCCTCTTCCCCCCCCAAAACCCAAGGACACCCCTCATGATCTCCCGGACCCC
TGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCA
AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAA
GCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCT
ACCGTCTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGG
TCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAGCC
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG
AGGAGATGACCAAGAACCAGGTACGCCTGACCTGCCTGGTCAAAGGCTTC
TATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGA
ACA ACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTC
CTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACG
TCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
AAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 229)

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

CAGTTGCAGATGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCCGGAGA
CCCTGTCTCTGAGTTGCACTGTCTCTGGTGA CTCCATAAGGGGTGGCGAGT
GGGGCGATAAAGATTATCATTGGGGCTGGGTCCGCCACTCAGCAGGAAA
GGGCCTGGAGTGGATTGGGAGTATCCATTGGAGGGGGACCACTACTACA
AAGAGTCCCTCAGGAGAAGAGTGAGTATGTCGATCGACACGTCCAGGAA
TTGGTTCTCCCTGAGGCTGGCCTCTGTGACCGCCGCGGACACGGCCGTCT
ACTTTTGTGCGAGACACCGACATCATGATGTTTTTCATGTTGGTCCCTATTG
CGGGCTGGTTTCGACGTCTGGGGCCCCGGGAGTCCAGGTACCGTCTCGAGC
(SEQ ID NO: 230)

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

MKHLWFFLLLVAAAPRWVLSQLQMQUESGPGLVKPSETLSLSCTVSGDSIR
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)

QLQMQUESGPGLVKPSETLSLSCTVSGDSIRGGEWGDKDYHWGWVRHSAGK
GLEWIGSIHWRGTTHYKESLRRRVSMSIDTSRNWFSRLASVTAADTAVYFC
ARHRHHDVFMLVPIAGWFDVWGPVQVTVSS (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
GGCTCGTAATTTTTGAAACATATAGCAAGATCGCTGCTTTCCCTGCCA
GGTTCGTTGCCAGTGGTTCTGGGACAGAGTTCACTCTCACCATCAAC
AACATGCAGTCTGAAGATGTTGCAGTTTATTACTGTCAACAATATGAA
GAGTGGCCTCGGACGTTCCGGGCAAGGGACCAAGGTGGATATCAAACG
TACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT
GAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAG
AGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAAC

TCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCC
 TCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGT
 CTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGA
 GCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO: 238)

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

GAAATTGTGATGACGCAGTCTCCCGACACCCTGTCTGTCTCTCCAGGGGA
 GACAGTCACACTCTCCTGCAGGGCCAGTCAGAATATTAACAAGAATTTAG
 CCTGGTACCAATACAAACCTGGCCAGTCTCCAGGCTCGTAATTTTTGAA
 ACATATAGCAAGATCGCTGCTTTCCCTGCCAGGTTGTTGCCAGTGGTTCT
 GGGACAGAGTTCACTCTCACCATCAACAACATGCAGTCTGAAGATGTTGC
 AGTTTATTACTGTCAACAATATGAAGAGTGGCCTCGGACGTTCCGGGCAAG
 GGACCAAGGTGGATATCAAA (SEQ ID NO: 239)

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

METPAQLLFLLLLWLPDTTGEIVMTQSPDTLSVSPGETVTLSCRASQNIN
 KNLAWYQYKPGQSPRLVIFETYSKIAAFPARFVASGSGTEFTLTINMQS
 EDVAVYYCQQYEEWPRTFGQGTKVDIKRTVAAPSVFIFPPSDEQLKSGTAS
 VVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTLTLSK
 ADYEKHKVYACEVTHQGLSPVTKSFNRGEC (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)

EIVMTQSPDTLSVSPGETVTLSCRASONINKNLAWYQYKPGQSPRLVIFETYS
KIAAFPARFVASGSGTEFTLTINMQSEDVAVYYCQQYEEWPRTFGQGTKVD
 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
CTGTGCGAGCTGCAGTTGCAGGAATCGGGCCCAGGACTGGTGAAGCC
TTCGGAGACCCTGTCCCTGACTTGACAGTTTCTGGTGGCTCCATGA
GGGGCACCGACTGGGGCGAGAATGACTTCCACTACGGCTGGATCCG
CCAGTCTCCGCAAAGGGGCTGGAGTGGATTGGGAGCATCCATTGGA
GGGGGAGGACCACCACTACAAGACGTCCTTCAGGAGTCGGGGCCAC
CTTGTCGATAGACACGTCCAATAATCGCTTCTCCCTGACGTTTAGTTT
TGTGACCGCCGCGGACACGGCCGTCTACTATTGTGCGAGACATAAAT
ATCATGATATTTTCAGGGTGGTCCCTGTTGCGGGCTGGTTCGACCCC
TGGGGCCAGGGATTACTGGTCAACCGTCTCGAGCGCCTCCACCAAGGGC
CCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCAC
AGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG
TGTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCGGT
GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC
CTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC
CCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAA
AACTCACACATGCCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGT
CAGTCTTCTCTTCCCCC AAAACCCAAGGACACCCTCATGATCTCCCGGA
CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAG
GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGAC
AAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTACGCGTC
CTCACCGTCTGCAACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA
GGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
CCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
GAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCT
TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA
GAACAACACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCT
TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA
CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC
AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 246)

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

CAGCTGCAGTTGCAGGAATCGGGCCCAGGACTGGTGAAGCCTTCGGAGA
CCCTGTCCCTGACTTGACAGTTTCTGGTGGCTCCATGAGGGGCACCGACT
GGGGCGAGAATGACTTCCACTACGGCTGGATCCGCCAGTCTCCGCAAAG
GGGCTGGAGTGGATTGGGAGCATCCATTGGAGGGGGAGGACCACCCACT
ACAAGACGTCCTTCAGGAGTCGGGCCACCTTGTCGATAGACACGTCCAAT
AATCGCTTCTCCCTGACGTTTAGTTTTGTGACCGCCGCGGACACGGCCGTC
TACTATTGTGCGAGACATAAATATCATGATATTTTCAGGGTGGTCCCTGTT
GCGGGCTGGTTCGACCCCTGGGGCCAGGGATTACTGGTCAACCGTCTCGAG
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
 IDTSNNRFSLTFSFVTAADTAVYYCARHKYHDIFRVVPVAGWFDPWGQG
 LLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL
 TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRV
 PKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHE
 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
 KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
 YPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
 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)

QLQLQESGPGLVKPSETLSLTCTVSGGSMRGTDWGENDFYHGWIRQSSAKG
 LEWIGSIHWRGRTHYKTSFRSRATLSIDTSNNRFSLTFSFVTAADTAVYYCA
 RHKYHDIFRVVPVAGWFDPWGQGLLVTVSS (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: HKYHDIFRVVPVAGWFDP (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: HKYHDIFRVVPVAGWFDP (SEQ ID NO: 252)

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

ATGGAACCCAGCTCAGCTTCTCTTCCTCCTGCTACTCTGGCTCCCAGAT
 AGCACTGGAGAAATAGTGATGACGCAGTCTCCACCCACCCTGTCTGTG
 TCTCCAGGGGAAACAGCCACACTCTCCTGTAGGGCCAGTCAGAATGT
 TAAGAATAATTTAGCCTGGTACCAGCTGAAACCTGGCCAGGCTCCCA
 GGCTCCTCATCTTTGATGCGTCCAGCAGGGCCGGTGGTATTCCTGAC
 AGGTTCAGTGGCAGCGGTTATGGGACAGACTTCACTCTCACCGTCAA
 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
GAGATTATTTTGTGAGCAATATGAAGAGTGGCCTCGGACGTTCCGGCCAA
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
ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (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)

EIVMTQSPPTLSVSPGETATLSCR***ASONVKNNLAWYQLKPGQAPRLLIFDASS***
RAGGIPDRFSGSGYGTDFTLTVNSVQSE***DFGDYFCQQYEEWPRTFGQG***TKVD
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
CTGTGCGCAGCTGCAGTTGCAGGAATCGGGCCCAGGACTGGTGAAGCC
TTCGGAGACCCTGTCCCTGACTTGACAGTTTCTGGTGGCTCCATGA

GGGGCACCGACTGGGGCGAGAATGACTTCCACTACGGCTGGATCCG
 CCAGTCCTCCGCAAAGGGGCTGGAGTGGATTGGGAGCATCCATTGGA
 GGGGGAGGACCACCCACTACAAGACGTCCTTCAGGAGTCGGGCCAC
 CTTGTGATAGACACGTCCAATAATCGCTTCTCCCTGACGTTTAGTTT
 TGTGACCGCCGCGGACACGGCCGTCTACTATTGTGCGAGACATAAAT
 ATCATGATATTTTCAGGGTGGTCCCTGTTGCGGGCTGGTTCGACCCC
 TGGGGCCAGGGATTACTGGTCACCGTCTCGAGCGCCTCCACCAAGGGC
 CCATCGGTCTTCCCCCTGGCACCCCTCTCCAAGAGCACCTCTGGGGGCAC
 AGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG
 TGTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCCGGCT
 GTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC
 CTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC
 CCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAA
 AACTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGT
 CAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA
 CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAG
 GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGAC
 AAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
 CTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA
 GGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAG
 CCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
 GAGGAGATGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGCT
 TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA
 GAACAACCTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCT
 TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA
 CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC
 AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 246)

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

CAGCTGCAGTTGCAGGAATCGGGCCCAGGACTGGTGAAGCCTTCGGAGA
 CCCTGTCCCTGACTTGCACAGTTTCTGGTGGCTCCATGAGGGGCACCGACT
 GGGGCGAGAATGACTTCCACTACGGCTGGATCCGCCAGTCCTCCGCAAAG
 GGGCTGGAGTGGATTGGGAGCATCCATTGGAGGGGGAGGACCACCCACT
 ACAAGACGTCTTCAGGAGTCGGGCCACCTTGTCGATAGACACGTCCAAT
 AATCGCTTCTCCCTGACGTTTAGTTTTGTGACCGCCGCGGACACGGCCGTC
 TACTATTGTGCGAGACATAAATATCATGATATTTTCAGGGTGGTCCCTGTT
 GCGGGCTGGTTTCGACCCCTGGGGCCAGGGATTACTGGTCACCGTCTCGAG
 C (SEQ ID NO: 247)

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

MKHLWFFLLVAAPRWVLSQLQLQESGPGLVKPSETLSLTCTVSGGSM
RGTDWGENDFHYGWIRQSSAKGLEWIGSIHWRGRTHYKTSFRSRATLS
IDTSNNRFSLTFSFVTAADTAVYYCARHKYHDI**FRVVPVAGWFD****WPWGQ**
LLVT**VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP****VT****VS****WNSGAL**

TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKRVE
PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPVYTLPPSREEMTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
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)

QLQLQESGPGLVKPSETLSLTCTVSGG***SMRGTDWGEND***FHYGWIRQSSAKG
LEWIG***SIHWRGR***TTHYKTSFRSRATLSIDTSNNRFSLTFSFVTAADTAVYYCA
RHKYHDIFRVVPVAGWFDPWGQGLLVTVSS (SEQ ID NO: 249)

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

CDR 1: GTDWGENDFHYG (SEQ ID NO: 250)

CDR 2: SIHWRGR***TTHYKTSFRS*** (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: SIHWRGR***TTH*** (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
AGCACTGGAGAAATAGTGATGACGCAGTCTCCACCCACCCTGTCTGTG
TCTCCAGGGGAAACAGCCACACTCTCCTGTAGGGCCAGTCAGAATGT
TAAGAATAATTTAGCCTGGTACCAGCTGAAACCTGGCCAGGCTCCCA
GGCTCCTCATCTTTGATGCGTCCAGCAGGGCCGGTGGTATTCTGAC
AGGTTCACTGGCAGCGGTTATGGGACAGACTTCACTCTCACCGTCAA
CAGTGTGCAGTCCGAAGATTTTGGAGATTATTTTGTGTCAGCAATATGA
AGAGTGGCCTCGGACGTTCCGGCCAAGGGACCAAGGTGGATATCAAAC
GTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGT
TGAAATCTGGAACTGCCTCTGTTGTGTGCTGCTGAATAACTTCTATCCCA
GAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAA
CTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGC
CTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAG
TCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAG
AGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO: 255)

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

GAAATAGTGATGACGCAGTCTCCACCCACCCTGTCTGTGTCTCCAGGGGA
AACAGCCACACTCTCCTGTAGGGCCAGTCAGAAATGTTAAGAATAATTTAG
CCTGGTACCAGCTGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTTTGAT
GCGTCCAGCAGGGCCGGTGGTATTCTGACAGGTTTCAGTGGCAGCGGTTA
TGGGACAGACTTCACTCTCACCGTCAACAGTGTGCAGTCCGAAGATTTTG
GAGATTATTTTGTGTCAGCAATATGAAGAGTGGCCTCGGACGTTCCGGCCAA
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
VVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSK
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)

EIVMTQSPPTLSVSPGETATLSCRASQNVKNNLAWYQLKPGQAPRLLIFDASS
RAGGIPDRFSGSGYGTDFTLTVNSVQSEDFGDYFCQQYEEWPRTFGQGTKVD
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)

ATGGACTGGATTGGAGGATCCTCTTCTTGGTGGCAGCAGTTGCAAGTGC
CCACTCGCAGGTGCAGCTGGTGCAGTCTGGGCCGGAGGTGAAGAAGC
CTGGGTCTCAGTGAAGGTCTCCTGCAAGGCCTCTGGAAACACCTTC
AGTAAATATGATGTCCACTGGGTACGACAGGCCACTGGACAGGGGCT
TGAATGGGTGGGATGGATGAGTCATGAGGGTGATAAGACAGAATCTG
CACAGAGATTAAAGGGCCGAGTCACCTTCACGAGGGACACTTCCGCA
AGCACAGCCTACATGGAAGTGC GCGGCCTGACATCTGACGACACGGC
CATCTATTATTGTACGAGAGGCTCAAAACATCGTTTGCGAGACTACGT

TCTCTACGATGACTACGGCTTAATTAATTATCAAGAGTGGAATGACTA
CCTTGAATTTTTGGACGTCTGGGGCCATGGAACCGCGGTACCGTCT
CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCC
AAGAGCACCTCTGGGGGACAGCGGCCCTGGGCTGCCTGGTCAAGGACT
ACTTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCCTGACCAGC
GGCGTGACACCTTCCCGGTGTCTACAGTCTCAGGACTCTACTCCCTC
AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
CTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTT
GAGCCCAAATCTTGTGACAAACTCACACATGCCCACCGTGCCCAGCACC
TGAACCTCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCCAAGG
ACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGAC
GTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT
GGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
ACGTACCGTGTGGTCAGCGTCCTCACCCTGTCACCAGGACTGGGTGAA
TGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCA
TCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
GTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTGAGC
CTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTG
GGAGAGCAATGGGCAGCCGGAGAACAATAAGACCACGCCTCCCGTG
CTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAA
GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGG
CTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
TGA (SEQ ID NO: 273)

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

CAGGTGCAGCTGGTGCAGTCTGGGCCGGAGGTGAAGAAGCCTGGGT
CCTCAGTGAAGGTCTCCTGCAAGGCCTCTGGAAACACCTTCAGTAAA
TATGATGTCCACTGGGTACGACAGGCCACTGGACAGGGGGCTTGAATG
GGTGGGATGGATGAGTCATGAGGGTGATAAGACAGAATCTGCACAGA
GATTTAAGGGCCGAGTCACCTTCACGAGGGACACTTCCGCAAGCACA
GCCTACATGGAACCTGCGCGGCCTGACATCTGACGACACGGCCATCTA
TTATTGTACGAGAGGCTCAAAACATCGTTTTCGAGACTACGTTCTCTA
CGATGACTACGGCTTAATTAATTATCAAGAGTGGAATGACTACCTTGA
ATTTTTGGACGTCTGGGGCCATGGAACCGCGGTACCGTCTCCTCA
(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*SQVQLVQSGPEVKKPGSSVKVSKKASGNTFSKY
DVHWVRQATGQGLEWVGWMSHEGDKTESAQRFKGRVTFTRDTSASTA
YMELRGLTSDDTAIYYCTRGSKHRLRDYVLYDDYGLINYQEWNDYLEFL
DVWGHGTA VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTV
SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT
KVDKRVEPKCDKTHTCPPCAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD

WLNQKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS
 LTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSR
 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)

QVQLVQSGPEVKKPGSSVKVSCKASGNTFSKYDVHWVRQATGQGLEWVG
WMSHEGDKTESAQRFKGRVTFTRDTSASTAYMELRGLTSDDTAIYYCTRGS
KHRLRDYVLYDDYGLINYQEWNDYLEFLDVWGHGTA VTVSS (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
 TCCAGTGCGGATACTGTCGTGACTCAGTCTCCACTCTCCCTGCCCCGTC
 ACCCTGGAGAGGCGGCCTCCATGTCTGTTCTGTCGACTCAGAGCCT
 CCGGCATAGTAATGGAGCCAACTATTTGGCTTGGTATCAGCACAAAC
 CGGGGCAGTCTCCACGACTCCTAATCCGTTTAGGTTCTCAACGGGCC
 TCCGGGGTCCCTGACAGATTCACTGGCAGTGGATCAGGCACTCATT
 TACACTGAAAATCAGTAGAGTGGAGGCTGAAGATGCTGCAATTTATT
 ATTGCATGCAAGGTCTGAACCGTCCCTGGACGTTCCGCAAGGGGACC
 AAGTTGGAAATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCC
 GCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCT
 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAAC
 GCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCA
 AGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGA
 CTACGAGAAACACAAAGTCTACGCTGCGAAGTCACCCATCAGGGCCTGA
 GCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:
 282)

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

GATACTGTCGTGACTCAGTCTCCACTCTCCCTGCCCCGTCACCCCTGG
 AGAGGCGGCCTCCATGTCCTGTTCTGTCGACTCAGAGCCTCCGGGCATA
 GTAATGGAGCCAACTATTTGGCTTGGTATCAGCACAACCGGGGCAG
 TCTCCACGACTCCTAATCCGTTTAGGTTCTCAACGGGCCTCCGGGGT
 CCCTGACAGATTCAAGTGGCAGTGGATCAGGCACTCATTTTACACTGA
 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.

*MRLPAQLLGLLMLWVSGSSADTVVTQSPLSLPVT*PGEAASMSCSSTQSLRHS
 NGANYLAWYQHKPGQSPRLILRLGSQRASGVPDRFSGSGSGTHFTLKISR
 VEAEDAAIYYCMQGLNRPWTFGKGTKLEIKRTVAAPSVFIFPPSDEQLKSG
 TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLT
 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (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)

DTVVTQSPLSLPVT*PGEAASMSCSSTQSLRHS*NGANYLAWYQHKPGQSPRLIL
RLGSQRASGVPDRFSGSGSGTHFTLKISRVEAEDAAIYYCMQGLNRPWTFGK
 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)

ATGGACTGGATTGGAGGATCCTCTTCTTGGTGGCAGCAGTTGCAAGTGC
 CCACTCGCAGGTGCAGCTGGTGCAGTCTGGGCCTGAGGTGAAGAAGC
 CTGGGTCCTCAGTGAAGGTCTCCTGCAAGGCCTCTGGAAACACCTTC
 AGTAAATATGATGTCCACTGGGTACGGCAGGCCACTGGACAGGGGCT
 TGAATGGGTGGGATGGATGAGTCATGAGGGTGATAAGACAGAATCTG
 CACAGAGATTTAAGGGCCGAGTCACCTTCACGAGGGACACTTCCGCA
 AGCACAGCCTACATGGAACGCGCGGCCTGACATCTGACGACACGGC

CATTTATTATTGTACGAGAGGCTCAAAACATCGCTTGCGAGACTATGT
TCTCTACGATGACTACGGCTTAATTAATTATCAAGAGTGGAATGACTA
CCTTGAATTTTTGGACGTCTGGGGCCATGGAACCGCGGTACCGTCT
CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCC
AAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACT
ACTTCCCCGAACCGGTGACGGTGTCGTGGAACCTCAGGCGCCCTGACCAGC
GGCGTGACACCTTCCCGGTGTCTTACAGTCTCAGGACTCTACTCCCTC
AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
CTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTT
GAGCCCAAATCTTGTGACAAACTCACACATGCCACCGTGCCAGCACC
TGAATCCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGG
ACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGAC
GTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT
GGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
ACGTACCGTGTGGTCAGCGTCTCACCCTGCTGACCCAGGACTGGCTGAA
TGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCA
TCGAGAAAACCATCTCCAAGCCAAAGGCGAGCCCCGAGAACCACAGGT
GTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTACGC
CTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTG
GGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTG
CTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAA
GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGG
CTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
TGA (SEQ ID NO: 289)

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

CAGGTGCAGCTGGTGCAGTCTGGGCCTGAGGTGAAGAAGCCTGGGT
CCTCAGTGAAGGTCTCCTGCAAGGCCTCTGGAAACACCTTCAGTAAA
TATGATGTCCACTGGGTACGGCAGGCCACTGGACAGGGGGCTTGAATG
GGTGGGATGGATGAGTCATGAGGGTGATAAGACAGAATCTGCACAGA
GATTTAAGGGCCGAGTCACCTTCACGAGGGACACTTCCGCAAGCACA
GCCTACATGGAACTGCGCGGCCTGACATCTGACGACACGGCCATTTA
TTATTGTACGAGAGGCTCAAAACATCGCTTGCGAGACTATGTTCTCTA
CGATGACTACGGCTTAATTAATTATCAAGAGTGGAATGACTACCTTGA
ATTTTGGACGTCTGGGGCCATGGAACCGCGGTACCGTCTCCTCA(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.

*MDWIWRILFLVAAVASAHSQVQLVQSGPEVKKPGSSVKV***SCKASGNTFSKY**
DVHWVRQATGQGLEWVGWMSHEGDKTESAQR**FKGRVTFTRDTSASTA**
YMELRGLTSDDTAIYYCTRGS**KHRLRDYVLYDDYGLINYQEWNDYLEFL**
DVWGHGTA**VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV**
SWNSGALTSGVHTFPAVLQSSGLYSLSSV**TVPSSSLGTQTYICNVNHKPSNT**
KVDKR**VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV**

VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
 WLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS
 LTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR
 WQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (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)

QVQLVQSGPEVKKPGSSVKVSCKASGNTFSKYDVHWVRQATGQGLEWVG
WMSHEGDKTESAQRFKGRVTFTRDTSASTAYMELRGLTSDDTAIYYCTRGS
KHRLRDYVLYDDYGLINYQEWNDYLEFLDVWGHGTAVTVSS (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: GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (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: GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (SEQ ID NO: 279)

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

ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGGTCTCTGGA
 TCCAGTGCGGATACTGTCGTGACTCAGTCTCCACTCTCCCTGCCCCTC
 ACCCCTGGAGAGGCGGCCTCCATGTCCTGTTTCGTCGACTCAGAGCCT
 CCGGCATAGTAATGGAGCCAACTATTTGGCTTGGTATCAGCACAAAC
 CGGGGCAGTCTCCACGACTCCTAATCCGTTTAGGTTCTCAACGGGGCC
 TCCGGGGTCCCTGACAGATTGAGTGGCAGTGGATCAGGCACTCATTT
 TAACTGAAAATCAGTAGAGTGGAGGCTGAAGATGCTGCAATTTATT
 ATTGCATGCAAGGTCTGAACCGTCCCTGGACGTTTCGGCAAGGGGACC
 AAGTTGGAAATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCC
 GCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCT
 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAAC
 GCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCA
 AGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGA
 CTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGA
 GCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG(SEQ ID NO:
 282)

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

GATACTGTCGTGACTCAGTCTCCACTCTCCCTGCCCCGTCACCCCTGG
 AGAGGCGGCCTCCATGTCCTGTTCTGTCGACTCAGAGCCTCCGGGCATA
 GTAATGGAGCCAACTATTTGGCTTGGTATCAGCACAAACCGGGGCAG
 TCTCCACGACTCCTAATCCGTTTAGGTTCTCAACGGGCCTCCGGGGT
 CCCTGACAGATTCAAGTGGCAGTGGATCAGGCACTCATTTTACACTGA
 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.

MRLPAQLLGLMLWVSGSSADTVVTQSPLSLPVTGPGEAASMSCSSTQSLRHS
*NGANYLA***WYQHKPGQSPRL***LIRLGSQRASGVPDRFSGSGSGTHFTLKISR*
VEAEDAAIYYCMQGLNRPWTFGKGTKLEIK*RTVAAPSVFIFPPSDEQLKSG*
TASVVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLT
LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (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)

*DTVVTQSPLSLPVTGPGEAASMSC***SSTQSLRHS***NGANYLA***WYQHKPGQSPRL***LIRLGSQRASGVPDRFSGSGSGTHFTLKISR***VEAEDAAIYYCMQGLNRPWTFGK***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
 CTGGGTCCTCAGTGAAGGTCTCCTGCAAGGCCTCTGGAAACACCTTC
 AGTAAATATGATGTCCACTGGGTACGACAGGCCACTGGACAGGGGCT
TGAATGGGTGGGATGGATTAGTCATGAGCGTGATAAGACAGAATCTG
CACAGAGATTTAAGGGCCGAGTCACCTTCACGAGGGACACTTCCGCA
ACCACAGCCTACATGGA**ACTGCGCGGCCTGACATCTGACGACACGGC**

CATTTATTATTGTACGAGAGGCTCAAAACATCGCTTGCGAGACTACGT
TCTCTACGATGACTACGGCTTAATTAATTATCAAGAGTGGAATGACTA
CCTTGAATTTTTGGACGTCTGGGGCCATGGAACCGCGGTACCGTCT
CCTCAGCCTCCACCAAGGGGCCATCGGTCTTCCCCCTGGCACCCCTCCTCC
AAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACT
ACTTCCCCGAACCGGTGACGGTGTCGTGGAACCTCAGGCGCCCTGACCAGC
GGCGTGACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTC
AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
CTGCAACGTGAATCACAAGCCCCAGCAACACCAAGGTGGACAAGAGAGTT
GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACC
TGAACCTCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCCAAGG
ACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGAC
GTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT
GGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
ACGTACCGTGTGGTCAGCGTCTCACCCTGTCACCGTGGTGGTGGAC
TGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCA
TCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
GTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTGAGC
CTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTG
GGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTG
CTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAA
GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGG
CTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
TGA (SEQ ID NO: 314)

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

CAGGTGCAGCTGGTGCAGTCTGGGCCTGAGGTGAAGAAGCCTGGGT
CCTCAGTGAAGGTCTCCTGCAAGGCCTCTGGAAACACCTTCAGTAAA
TATGATGTCCACTGGGTACGACAGGCCACTGGACAGGGGGCTTGAATG
GGTGGGATGGATTAGTCATGAGCGTGATAAGACAGAATCTGCACAGA
GATTTAAGGGCCGAGTCACCTTCACGAGGGACACTTCCGCAACCACA
GCCTACATGGAACTGCGCGGCCTGACATCTGACGACACGGCCATTTA
TTATTGTACGAGAGGCTCAAAACATCGCTTGCGAGACTACGTTCTCTA
CGATGACTACGGCTTAATTAATTATCAAGAGTGGAATGACTACCTTGA
ATTTTTGGACGTCTGGGGCCATGGAACCGCGGTACCGTCTCCTCA
(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*AVASAHSQVQLVQSGPEVKKPGSSVKVSCKASGNTFSKY
DVHWVRQATGQGLEWVGWISHERDKTESAQRFKGRVTFTTRDTSATTAY
MELRGLTSDDTAIYYCTRGSKHRLRDYVLYDDYGLINYQEWNDYLEFLD
VWGHGTA~~VT~~VSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTK
VDKRVEPKSCDKHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV

VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
 LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
 CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
 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)

QVQLVQSGPEVKKPGSSVKVSCASGNTFSKYDVHWVRQATGQGLEWVG
WISHERDKTESAQRFKGRVTFTRDTSATTAYMELRGLTSDDTAIYYCTRGSK
HRLRDYVLYDDYGLINYQEWNDYLEFLDVWGHGTAVTVSS (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: GSKHRLRDYVLYDDYGLINYQEWDYLEFLDV (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: GSKHRLRDYVLYDDYGLINYQEWDYLEFLDV (SEQ ID NO: 279)

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

ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGGTCTCTGGA
 TCCAGTGCGGATACTGTCGTGACTCAGTCTCCACTCTCCCTGCCCGTC
 ACCCTGGAGAGGCGGCCTCCATGTCCTGTTCTGTCGACTCAGAGCCT
 CCGGCATAGTAATGGAGCCAACTATTTGGCTTGGTATCAGCACAAAC
 CGGGGCAGTCTCCACGACTCCTAATCCGTTTAGGTTCTCAACGGGCC
 TCCGGGGTCCCTGACAGATTCAGTGGCAGTGGATCAGGCACTCATTT
 TACACTGAAAATCAGTAGAGTGGAGGCTGAAGATGCTGCAATTTATT
 ATTGCATGCAAGGTCTGAACCGTCCCTGGACGTTCCGGCAAGGGGACC
 AAGTTGGAAATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCC
 GCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCT
 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAAC
 GCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCA
 AGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGA
 CTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGA
 GCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:
 282)

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

GATACTGTCGTGACTCAGTCTCCACTCTCCCTGCCCCGTCACCCCTGG
 AGAGGCGGCCTCCATGTCCTGTTCTGTCGACTCAGAGCCTCCGGCATA
 GTAATGGAGCCAACTATTTGGCTTGGTATCAGCACAACCGGGGCAG
 TCTCCACGACTCCTAATCCGTTTAGGTTCTCAACGGGCCTCCGGGGT
 CCCTGACAGATTCAGTGGCAGTGGATCAGGCACTCATTTTACACTGA
 AATCAGTAGAGTGGAGGCTGAAGATGCTGCAATTTATTATTGCATG
 CAAGGTCTGAACCGTCCCTGGACGTTCCGCAAGGGGACCAAGTTGGA
 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.

MRLPAQLLGLLMLWVSGSSADTVVTQSPLSLPVTGPGEAASMSCSSTQSLRHS
*NGANYLA*WYQHKGQSPRLILRLGSQRASGVPDRFSGSGSGTHFTLKISR
 VEAEDAAIYYCMQGLNRPWTFGKGTKLEIKRTVAAPSVFIFPPSDEQLKSG
 TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLT
 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (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)

DTVVTQSPLSLPVTGPGEAASMSC*SSTQSLRHS**NGANYLA*WYQHKGQSPRLIL
*RLGSQRAS*GVPDRFSGSGSGTHFTLKISRVEAEDAAIYYC*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
 CACAGAGATTTAAGGGGCGAGTCACCTTCACGAGGGACACTTCCGCA
 AGCACAGCCTACATGGAAGTGC GCGGCCTGACATCTGACGACACGGC

CATTTATTATTGTACGAGAGGTTCAAAACATCGCTTGCGAGACTACGT
TCTCTACGATGACTACGGCTTAATTAATTATCAAGAGTGGAATGACTA
CCTTGAATTTTTGGACGTCTGGGGCCATGGAACCGCGGTACCGTCT
CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCCTCC
AAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACT
ACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAGC
GGCGTGACACCTTCCCGGTGTCTTACAGTCCTCAGGACTCTACTCCCTC
AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
CTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTT
GAGCCCAAATCTTGTGACAAAACTCACACATGCCACCGTGCCACGACC
TGAACCTCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGG
ACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGAC
GTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT
GGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
ACGTACCGTGTGGTCAGCGTCCTACCGTCCTGCACCAGGACTGGCTGAA
TGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCA
TCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
GTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTACGC
CTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTG
GGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTG
CTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAA
GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGG
CTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
TGA (SEQ ID NO: 295)

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

CAGGTGCAGCTGGAGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGT
CCTCAGTGAAGGTCTCCTGCAAGGCCTCTGGAAACACCTTCAGTAAA
TATGATGTCCACTGGGTACGACAGGCCACTGGACAGGGGGCTTGAATG
GGTGGGATGGATGAGTCATGAGGGTGATAAGACAGAATCTGCACAGA
GATTTAAGGGGCGAGTCACCTTCACGAGGGACACTTCCGCAAGCACA
GCCTACATGGAACTGCGCGGCCTGACATCTGACGACACGGCCATTTA
TTATTGTACGAGAGGTTCAAAACATCGCTTGCGAGACTACGTTCTCTA
CGATGACTACGGCTTAATTAATTATCAAGAGTGGAATGACTACCTTGA
ATTTTTGGACGTCTGGGGCCATGGAACCGCGGTACCGTCTCCTCA
(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**.

*MDWIWRILFLVAAVASAHAQVQLEQSGAEVKKPGSSVKV***SCKASGNTFSKY**
*DVHWVRQATGQGLEWVGWMSHEGDKTESAQR***FKGRVTFTRDTSASTA**
*Y***MELRGLTSDDTAIYYCTRGS***KHRLRDYVLYDDYGLINYQE***W***NDYLEFL*
*DVWGHGTA***VT***VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV*
*SWNSGALTSGVHTFPAVLQSSGLYSLSSVTV***PSS***SLGTQTYICNVNHKPSNT*
*KVDKR***VEPKSCDK***TH***TCPPCPAPELLG***GPSVFLFPPKPKDTLMISRTPEV***TCV**

VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
WLNQKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS
LTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSR
WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (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
WMSHEGDKTESAQR***FKGRV***TFTRDTSASTAYMELRGLTSDDTAIYYCTR***GS***
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: WMSHEGDKTESAQR***FKG*** (SEQ ID NO: 278)

CDR 3: GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (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: GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (SEQ ID NO: 279)

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

ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGGTCTCTGGA
TCCAGTGCGGATACTGTCGTGACTCAGTCTCCACTCTCCCTGCCCCGTC
ACCCCTGGAGAGGCGGCCTCCATGTCCTGTACGTCGACTCAGAGCCT
CCGTCATAGTAATGGAGCCAACTATTTGGCTTGGTACCAGCACAAAC
CAGGGCAGTCTCCACGACTCCTAATCCGTTTAGGTTCTCAACGGGGCC
TCCGGGGTCCCTGACAGATTCAGTGGCAGTGGATCAGGCACTCATTT
TACACTGAAAATCAGTCGAGTGGAGCCTGAAGATGCTGCAATTTATT
ATTGCATGCAAGGTCTGAACCGTCCCTGGACGTTCCGCAAGGGGACC
AAGTTGGAAATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCC
GCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCT
GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAAC
GCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCA
AGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGA
CTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGA
GCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:
299)

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

GATACTGTCGTGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGG
 AGAGGCGGCCTCCATGTCTGTACGTCGACTCAGAGCCTCCGTCATA
 GTAATGGAGCCAACTATTTGGCTTGGTACCAGCACAAACCAGGGCAG
 TCTCCACGACTCCTAATCCGTTTAGGTTCTCAACGGGCCTCCGGGGT
 CCCTGACAGATTCAGTGGCAGTGGATCAGGCACTCATTTTACACTGA
 AAATCAGTCGAGTGGAGCCTGAAGATGCTGCAATTTATTATTGCATG
 CAAGGTCTGAACCGTCCCTGGACGTTCCGGCAAGGGGACCAAGTTGGA
 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.

MRLPAQLLGLLMLWVSGSSADTVVTQSPLSLPVTGPGEAASMSCTSTQSLRHS
NGANYLAWYQHKPGQSPRLILRLGSQRASGVPDRFSGSGSGTHFTLKISR
VEPEDAAIYYCMQGLNRPWTFGKGTKLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLT
LSKADYEEKHKVYACEVTHQGLSSPVTKSFNRGEC (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)

*DTVVTQSPLSLPVTGPGEAASMSCT****TSTQSLRHS****NGANYLAWYQHKPGQSPRLIL*
*RLGSQRAS**GVPDRFSGSGSGTHFTLKISR**VEPEDAAIYYCM****QGLNRPWT****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
 CTGGGTCCTCAGTGAAGGTCTCCTGCAAGGCCTCTGGAAACACCTTC
 AGGAAATATGATGTCCACTGGGTACGACAGGCCACTGGACAGGGGGCT
 TGAATGGGTGGGATGGATGAGTCATGAGGGTGATAAGACAGAATCTG
 CACAGAGATTTAAGGGCCGAGTCTCTTTCACGAGGGGACAATCCGCA
 AGCACAGCCTACATTGAACTGCGCGGCCTGACATCTGACGACACGGC

CATTTATTATTGTACCGGAGGCTCAAAACATCGCTTGCGAGACTACGT
TCTCTACGATGATTACGGCCTAATAAATCAGCAAGAGTGGAATGACT
ACCTTGAATTTTGGACGTCTGGGGCCATGGAACCGCGGTACCGTC
TCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCCTC
CAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACT
ACTTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCCTGACCAGC
GGCGTGACACCTTCCCGGTGTCTACAGTCTCAGGACTCTACTCCCTC
AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
CTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTT
GAGCCCAAATCTTGTGACAAACTCACACATGCCCACCGTGCCCAGCACC
TGAATCCTGGGGGGACCGTCAGTCTTCTTCTTCCCCCAAACCCAAGG
ACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGAC
GTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT
GGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
ACGTACCGTGTGGTCAGCGTCCTACCGTCCTGCACCAGGACTGGCTGAA
TGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCA
TCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
GTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGC
CTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTG
GGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTG
CTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAA
GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGG
CTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
TGA (SEQ ID NO: 304)

[0532] 4970_K22 (PGT-144) gamma heavy chain variable region nucleotide sequence:

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGT
CCTCAGTGAAGGTCTCCTGCAAGGCCTCTGGAAACACCTTCAGGAAA
TATGATGTCCACTGGGTACGACAGGCCACTGGACAGGGGCTTGAATG
GGTGGGATGGATGAGTCATGAGGGTGATAAGACAGAATCTGCACAGA
GATTTAAGGGCCGAGTCTCTTTCACGAGGGACAATTCCGCAAGCACA
GCCTACATTGAACTGCGCGGCCTGACATCTGACGACACGGCCATTTA
TTATTGTACCGGAGGCTCAAAACATCGCTTGCGAGACTACGTTCTCTA
CGATGATTACGGCCTAATAAATCAGCAAGAGTGGAATGACTACCTTG
AATTTTGGACGTCTGGGGCCATGGAACCGCGGTACCGTCTCCTCA
(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**SKASGN**TFRKY**
DVHWVRQATGQGLEWVGWMSHEGDKTESAQRFKGRV**SFTRDNSASTA**
YIELRGLTSDDTAIYYCTGGSKHRLRDYVLYDDYGLIN**Q**QEWNDY**LEFL**
DVWGHGTAVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV
SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS**SSLGTQTYICNVNHKPSNT**
KVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV**TCV**

VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
 WLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS
 LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (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***VRQATGQGLEWVG
WMSHEGDKTESAQRFKGRVSFTRDNSASTAYIELRGLTSDDTAIYYCTG***GSK***
HRLRDYVLYDDYGLINQ***QEWNDYLEFLDV***WGHGTAFTVSS (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: GSKHRLRDYVLYDDYGLINQ***QEWNDYLEFLDV*** (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: GSKHRLRDYVLYDDYGLINQ***QEWNDYLEFLDV*** (SEQ ID NO: 308)

[0537] 4970_K22 (PGT-144) kappa light chain nucleotide sequence: coding sequence
 (variable region in bold)

ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGGTCTCTGGA
 TCCAGTGCGGATACTGTCGTGACTCAGTCTCCACTCTCCCTGTCCGTC
 ACCCCTGGAGAGGCGGCCTCCATGTCCTGTACGTCGACTCAGAGCCT
 CCGGCATAGTAATGGAGCCAACTATTTGGCTTGGTACCAGCACAAAC
 CAGGGCAGTCTCCACGACTCCTAATCCGTTTAGGTTCTCAACGGGCC
 TCCGGGGTCCCTGACAGATTCAGTGGCAGTGGATCAGGCACTCATTT
 TACACTGAAAATCAGTAGAGTGGAGGCTGACGATGCTGCAATTTATT
 ATTGCATGCAAGGTCTGAACCGTCCCTGGACGTTCCGCAAGGGGACC
 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
 CTCCACGACTCCTAATCCGTTTGGTTCTCAACGGGCCTCCGGGGTC
 CCTGACAGATTCAGTGGCAGTGGATCAGGCACTCATTTTACACTGAA
 AATCAGTAGAGTGGAGGCTGACGATGCTGCAATTTATTATTGCATGC
 AAGGTCTGAACCGTCCCTGGACGTTCCGCAAGGGGACCAAGTTGGAG
 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**.

MRLPAQLLGLLMLWVSGSSADTVVTQSPLSLSVTPGEAASMSCTSTQSLRHS
NGANYLAWYQHKPGQSPRLLIRLGSQRASGVDPDRFSGSGSGTHFTLKISR
VEADDAIYYCMQGLNRPWTFGKGTKLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLT
LSKADYEEKHKVYACEVTHQGLSSPVTKSFNRGEC (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****WYQHKPGQSPRLLI*
RLGSQRAS*GVDPDRFSGSGSGTHFTLKISRVEADDAIYYCM****MQGLNRPWTFGK***
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 TLHGRRYIGIVAFNEWFTYFYMDV (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), YVHKSGDTNYSPSLKS (SEQ ID NO: 265), and TLHGRRYIGIVAFNEWFTYFYMDV (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 TLHGRRYIGIVAFNEWFTYFYMDV (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), ALHGKRIYGIVALGELFTYFYMDV (SEQ ID NO: 171). The light chain CDRs of the 4858_P08 (PGT-123) antibody have the following sequences per Kabat definition: GKESIGSRVAVQ (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), ALHGKRIYGIVALGELFTYFYMDV (SEQ ID NO: 171). The light chain CDRs of the 4858_P08 (PGT-123) antibody have the following sequences per Chothia definition: GKESIGSRVAVQ (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), SLSHCQSFWGSGWTFHNPSLKS (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), SLSHCQSFWGSGWTF (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), HIHYTTAVLHNPSLKS (SEQ ID NO: 218), and SGGDILYYYEWQKPHWFSP (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), HIHYTTAVL (SEQ ID NO: 221), and SGGDILYYYEWQKPHWFSP (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: GGEWGD KDYHWG (SEQ ID NO: 233), SIHWRTTTHYKESLRR (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: GDSIRGGEWGD KD (SEQ ID NO: 236), SIHWRTTTH (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: GGEWGDYHWG (SEQ ID NO: 233), SIHWRGTHYKESLRR (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), SIHWRGTH (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 GSKHRLRDYVLYDDYGLINQEWNDYLEFLDV (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
CTGTCCCAGCCGAGCTGCAGGAGTCGGGCCAGGACTGGTGGAGGC
TTCGGAGACCCTGTCCCTCACGTGCACTGTGTCCGGCGACTCCACTG
GTCGTTGTAATTATTTCTGGGGCTGGGTCCGGCAGCCCCCAGGGAAG
GGGCTGGAGTGGATTGGGAGTTTGTCCCACTGTAGAAGTTACTACAA
TACTGACTGGACCTACCACAACCCGTCTCTCAAGAGTCGACTCACTAT
TTCACTCGACACGCCCAAGAATCAGGTCTTCCTGAGATTGACCTCTGT
GACCGCCGCGGACACGGCCACTTATTACTGTGCGCGATTCCGGCGGCG
AAGTTCTAGTGTACAGAGATTGGCCAAAGCCGGCCTGGGTCCGACCTC
TGGGGCCGGGGAACGCTGGTCGTCACCGTCTCGAGCGCCTCCACCAA
GGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGG
GCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTG
ACGGTGTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCC
GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG
TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCAC
AAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTG TG
ACAAAACCTCACACATGCCCACCGTGCCCAGCACCTGAACCTCTGGGGGGA
CCGTCACTCTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCC
CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACC
CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCC
AAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCA
GCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG
TGCAAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTC
CAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA

TCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCA
AAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCA
GCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCT
CCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTA
CACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 316)

[0593] 5145_B14 (PGT-127) gamma heavy chain variable region nucleotide sequence:

CAGCCGCAGCTGCAGGAGTCGGGCCCCAGGACTGGTGGAGGCTTCGGAGA
CCCTGTCCCTCACGTGCACTGTGTCCGGCGACTCCACTGGTCGTTGTAATT
ATTTCTGGGGCTGGGTCCGGCAGCCCCAGGGAAGGGGCTGGAGTGGATT
GGGAGTTTGTCCCACTGTAGAAGTTACTACAATACTGACTGGACCTACCA
CAACCCGTCTCTCAAGAGTCGACTCACTATTTCACTCGACACGCCCAAGA
ATCAGGTCTTCCTGAGATTGACCTCTGTGACCGCCGCGGACACGGCCACT
TATTACTGTGCGCGATTTCGGCGGCGAAGTTCTAGTGACAGAGATTGGCC
AAAGCCGGCCTGGGTTCGACCTCTGGGGCCGGGGAACGCTGGTCGTACCG
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.

MKHLWFFLLVAAPRWVLSQPQLQESGPGLVEASETSLTCTVSGDSTGRC
NYFWGWVRQPPGKGLEWIGSLSHCRSYNTDWTYHNPSLKSRLTISLDT
PKNQVFLRLTSVTAADTATYYCARFGGEVLVYRDWPKPAWVDLWGRG
TLVVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG
ALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKR
VEPKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNV
FSCSVMEALHNHYTQKSLSLSPGK (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)

QPQLQESGPGLVEASETSLTCTVSGDSTGRC***NYFWGWVRQPPGKGLEWIGS***
LSHCRSYNTDWTYHNPSLKSRLTISLDT***PKNQVFLRLTSVTAADTATYYCAR***
FGGEVLVYRDWPKPAWVDL***WGRGTLVVTVSS*** (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)

ATGGCCTGGGCTCTGCTCCTCCTCACCTCCTCACTCAGGGCACAGGGGC
CTGGGCCCAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCC
TGGACAGTCAATCACCATCTCCTGCACTGGAACCAGCAATAACTTTGT
CTCCTGGTACCAACAATACCCAGGCAAGGCCCCCAAACCTCGTCATTT
ATGAGGTCAATAAGCGCCCCCTCAGGTGTCCCTGATCGTTTCTCTGGC
TCCAAGTCTGGCAGCACGGCCTCCCTGACCGTCTCTGGACTCCAGGC
TGACGATGAGGGTGTCTATTATTGTAGTTCACTTGTAGGCAACTGGG
ATGTGATTTTCGGCGGAGGGACCAAGTTGACCGTCTTAGGTACAGCCCA
AGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAG
CCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCC
GTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAGGCGGGAGTGG
AGACCACACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAG
CTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCT
GCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCCTAC
AGAATGTTTCATAG (SEQ ID NO:327)

[0599] 5145_B14 (PGT-127) lambda light chain variable region nucleotide sequence:

CAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCCTGGACAGTCA
ATCACCATCTCCTGCACTGGAACCAGCAATAACTTTGTCTCCTGGTACCAA
CAATACCCAGGCAAGGCCCCCAAACCTCGTCATTTATGAGGTCAATAAGCG
CCCCCTCAGGTGTCCCTGATCGTTTCTCTGGCTCCAAGTCTGGCAGCACGGC
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.

MAWALLLLLLTQGTGAWAQSALTQPPSASGSPGQSITISCTGTSNNFVSWY
QQYPGKAPKLVIYEVNKRPSGVPDRFSGSKSGSTASLTVSGLQADDEGVY
YCSSLVGNWDVIFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTPSKQSNNKYAASSYLSLTPEQWKS
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)

QSALTQPPSASGSPGQSITISCT**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
CTGTCCCAGCCGAGCTGCAGGAGTCGGGCCCAACACTGGTGGAGGC
TTCGGAGACTCTGTCCCTCACCTGCGCTGTGTCCGGCGACTCCACTG
CTGCATGTAATTCTTTCTGGGGCTGGGTCCGGCAGCCCCCAGGGAAG
GGGCTGGAGTGGGTTGGGAGTTTGTCCCATTTGTGCAAGCTATTGGAA
TCGTGGGTGGACCTACCACAACCCGTCTCTCAAGAGTCGGCTCACGC
TTGCTCTCGACACACCAAGAATCTGGTCTTCCTCAAATTAATTTCTG
TGACTGCCGCGGACACGGCCACTTACTACTGTGCGCGATTCCGGCGGC
GAAGTTTTACGCTACACGGATTGGCCAAAGCCGGCCTGGGTGACCT
CTGGGGCCCGGGAACGCTGGTCAACCGTCTCGAGCGCCTCCACCAAGG
GCCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGC
ACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGAC
GGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGCGCTGCACACCTTCCCCG
CTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGC
CCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAG
CCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACA
AAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCG
TCAGTCTTCCTCTTCCCCCCTTCCCAAGGACACCCCTCATGATCTCCCGG
ACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
GGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA
CAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGT
CCTCACCGTCTGCAACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCA
AGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCG
GGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC
TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG
AGAACAATAACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC
TTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGA

ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACG
CAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 331)

[0605] 5114_A19 (PGT-128) gamma heavy chain variable region nucleotide sequence:

CAGCCGCAGCTGCAGGAGTCGGGCCCAACACTGGTGGAGGCTTCGGAGA
CTCTGTCCCTCACCTGCGCTGTGTCCGGCGACTCCACTGCTGCATGTAATT
CTTTCTGGGGCTGGGTCCGGCAGCCCCCAGGGAAGGGGCTGGAGTGGGTT
GGGAGTTTGTCCCATTTGTGCAAGCTATTGGAATCGTGGGTGGACCTACCA
CAACCCGTCTCTCAAGAGTCGGCTCACGCTTGCTCTCGACACACCCAAGA
ATCTGGTCTTCTCAAATTAATTCTGTGACTGCCGCGGACACGGCCACTT
ACTACTGTGCGCGATTTCGGCGGCGAAGTTTTACGCTACACGGATTGGCCA
AAGCCGGCCTGGGTTCGACCTCTGGGGCCGGGAACGCTGGTCACCGTCTC
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.

MKHLWFFLLVAAPRWVLSQPQLQESGPTLVEASETSLTCAVSGDSTAAC
NSFWGWVRQPPGKGLEWVGSLSHCASYWNRGWTYHNPSLKSRLTLAL
DTPKNLVFLKLNSVTAADTATYYCARFGGEVRLRYTDWPKPAWVDLWG
RGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNS
GALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK
RVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV
FSCSVMEALHNHYTQKSLSLSPGK (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)

QPQLQESGPTLVEASETSLTCAVSGDSTAACNSFWGWVRQPPGKGLEWVG
SLSHCASYWNRGWTYHNPSLKSRLTLALDTPKNLVFLKLNSVTAADTATYYC
*ARFGGEVRLRYTDWPKPAWVDL*WGRGTTLTVSS (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: FGGEVRLRYTDWPKPAWVDL (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: FGGEVRLRYTDWPKPAWVDL (SEQ ID NO: 336)

[0610] 5114_A19 (PGT-128) lambda light chain nucleotide sequence: coding sequence
(variable region in bold)

ATGGCCTGGGCTCTGCTCCTCCTCACCTCCTCACTCAGGGCACAGGGGC
CTGGGCCCAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCC
TGGACAGTCAATCACCATCTCCTGCACTGGAACCAGCAATAACTTTGT
CTCCTGGTACCAGCAACACGCAGGCAAGGCCCCCAAGCTCGTCATTT
ATGACGTCAATAAGCGCCCCTCAGGTGTCCCTGATCGTTTCTCTGGC
TCCAAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGACTCCAGAC
TGACGATGAGGCTGTCTATTACTGCGGCTCACTTGAGGCAACTGGG
ATGTGATTTTTCGGCGGAGGGACCAAGTTGACCGTCCTAGGTCAGCCCA
AGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAG
CCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCC
GTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGG
AGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAG
CTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCACAGAAGCTACAGCT
GCCAGGTCACGCATGAAGGGAGACCGTGGAGAAGACAGTGGCCCCTAC
AGAATGTTTCATAG(SEQ ID NO: 390)

[0611] 5114_A19 (PGT-128) lambda light chain variable region nucleotide sequence:

CAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCCTGGACAGTCA
ATCACCATCTCCTGCACTGGAACCAGCAATAACTTTGTCTCCTGGTACCAG
CAACACGCAGGCAAGGCCCCCAAGCTCGTCATTTATGACGTCAATAAGCG
CCCCTCAGGTGTCCCTGATCGTTTCTCTGGCTCCAAGTCTGGCAACACGGC
CTCCCTGACCGTCTCTGGACTCCAGACTGACGATGAGGCTGTCTATTACTG
CGGCTCACTTGAGGCAACTGGGATGTGATTTTCGGCGGAGGGACCAAGT
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
LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWK
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***TGTSNNFVS***WYQQHAGKAPKLVIY***DVNKRPS***
GVPDRFSGSKSGNTASLTVSGLQTDDEAVYYC***GS******SLVGNWDVIF***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
CTTTCCCAGGTGCAACTACAGGAGTCGGGCCCAGGACTGGTGAAGCC
TTCGGAGACCCTTTCCCTCACCTGCACTGTCTCTGGTGACTCCATCAA
CACTGGTCATCACTACTGGGGCTGGGTCCGTCAGGTCCCAGGGAAGG
GACCGGAATGGATTGCTCACATCCACTATAATACGGCTGTCTTACAC
AATCCGGCCCTCAAGAGTCGAGTCACCATTTTCGATTTTACCCCTGAA
GAATCTGATTACCTGAGCCTCAGTAATGTGACCGCCGCGGACACGG
CCGTCTATTTCTGCGTTCGATCCGGCGGCGACATTTTATACTATATTG
AGTGGCAAAAACCCCACTGGTTCTATCCCTGGGGCCCGGGAATTTTG
GTCACCGTCTCGAGCGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGG
CACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTG
GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC
CCTGACCAGCGGCGTGACACCTTCCCGGCTGTCCTACAGTCCTCAGGAC
TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGG
ACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCCG
TGCCCAGCACCTGAACTCCTGGGGGGGACCGTCAGTCTTCTCTTCCCCCA
AAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGT
GGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACG
TGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCA
GTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGG
ACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCT
CCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA
GAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGA
ACCAGGTACGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATC
GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCA
CGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCA
CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG
ATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTC
TCCGGGTAAATGA (SEQ ID NO: 344)

[0617] 5136_H01 (PGT-131) gamma heavy chain variable region nucleotide sequence:

CAGGTGCAACTACAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCCGAGA
CCCTTTCCCTCACCTGCACTGTCTCTGGTGACTCCATCAACACTGGTCATC

ACTACTGGGGCTGGGTCCGTCAGGTCCCAGGGAAGGGACCGGAATGGATT
 GCTCACATCCACTATAATACGGCTGTCTTACACAATCCGGCCCTCAAGAG
 TCGAGTCACCATTTTCGATTTTCACCCTGAAGAATCTGATTACCCTGAGCCT
 CAGTAATGTGACCGCCGCGGACACGGCCGTCTATTTCTGCGTTCGATCCG
 GCGGCGACATTTTATACTATATTGAGTGGCAAAAACCCCACTGGTTCTATC
 CCTGGGGCCCGGGAATTTTGGTCACCGTCTCGAGC(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.

MKHLWFFLLVAAPRWVLSQVQLQESGPGLVKPSSETLSLTCTVSGDSINTGH
HYWGWVRQVPGKGPEWIAHHYNTAVLHNPALKSRVTISIFTLKNLITLS
LSNVTAADTAVYFCVRSGGDILYYIEWQKPHWFYPWGPILVTVSSASTK
 GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
 QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCP
 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
 PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES
 NGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVSMHEALHN
 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)

QVQLQESGPGLVKPSSETLSLTCTVSGDSINTGH***HYWGWVRQVPGKGPEWIA***
HHYNTAVLHNPALKSRVTISIFTLKNLITLSLSNVTAADTAVYFCVRS***GGDIL***
YYIEWQKPHWFYPWGPILVTVSS (SEQ ID NO: 347)

[0620] 5136_H01 (PGT-131) gamma heavy chain Kabat CDRs:

CDR 1: TGHHYWG (SEQ ID NO: 348)

CDR 2: HHYNTAVLHNPALKS (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: HHYNTAVL (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
 TGGGCCCAGTCTGCCCTGACTCAGCCTCCTCCGCGTCCGGGTCTCTT
 GGACAGTCACTACCATCTCCTGCAGTGGAAACCGGCAGTGACATTGG
 CAGTTGGAATTTTGTCTCCTGGTATCAACAATTCCCAGGCAGAGCCC

CCAACCTCATTATTTTTGAGGTCAATAGGCGGCGATCAGGGGTCCCT
 GATCGCTTCTCTGGTTCCAAGTCGGGCAATACGGCCTCCCTGACCGT
 CTCTGGGCTCCGGTCTGAGGATGAGGCTGAATATTTTTGCAGTTCCC
 TTTCAGGCAGGTGGGACATTGTTTTTGGCGGAGGGACCAAGGTGACC
 GTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTC
 CTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTG
 ACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCC
 GTCAAGGCGGGAGTGGAGACCACACACCTCCAAACAAGCAACAACA
 AGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCC
 CACAGAAGCTACAGCTGCCAGGTACGCATGAAGGGAGCACCGTGGAGA
 AGACAGTGGCCCCCTACAGAAATGTTTCATAG (SEQ ID NO:353)

[0623] 5136_H01 (PGT-131) lambda light chain variable region nucleotide sequence:

CAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCTTGGACAGTCA
 CTCACCATCTCCTGCAGTGGAACCGGCAGTGACATTGGCAGTTGGAATTT
 TGTCTCCTGGTATCAACAATTCCCAGGCAGAGCCCCAACCTCATTATTTT
 TGAGGTCAATAGGCGGCGATCAGGGGTCCCTGATCGCTTCTCTGGTTCCA
 AGTCGGGCAATACGGCCTCCCTGACCGTCTCTGGGCTCCGGTCTGAGGAT
 GAGGCTGAATATTTTTGCAGTTCCCTTTCAGGCAGGTGGGACATTGTTTTT
 GCGGAGGGACCAAGGTGACCGTCCTA (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**.

*MAWALLLLTLITQGTGSWAQSALTQPPSASGSLGQSLTISC***SGTGS***SDIGSWNF*
VSWYQQFPGRAPNLIIFEVNR**RRSGVPDR****FSGSKSGNTASLTVSGLRSEDE**
AEYFCSSLSGRWDIVF**GGG****TKVTVLGQPKAAPSVTLFPPSSEELQANKATL**
VCLISDFYPGAVTVAWKADSSPVKAGVET**TPSKQSN****KYAASSYLSLTPEQ**
WKSHRSYSQVTHEGSTVEKTVAPTECS (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***SGTGS******SDIGSWNF******VSWYQQFPGRAPNLIIFEVN***
RRRSGVPDR***FSGSKSGNTASLTVSGLRSEDEAEYFC******SSLSGRWDIVF******GGG******TKV***
 TVL (SEQ ID NO: 356)

[0626] 5136_H01 (PGT-131) lambda light chain Kabat CDRs:

CDR 1: SGTGS**SDIGSWNF**V (SEQ ID NO: 357)

CDR 2: EVN**RRRS** (SEQ ID NO: 358)

CDR 3: **SSLSGRWDIV** (SEQ ID NO: 359)

[0627] 5136_H01 (PGT-131) lambda light chain Chothia CDRs:

CDR 1: SGTGS**SDIGSWNF**V (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
CTGTCTGAGGTGCATCTGGAGGAGTCGGGCCCAGGACTGGTGAGGCC
CTCGGAGACCTTGTCCCTGACTTGACGGCCTCTGGTGGCTCCATAA
GGGGGGGCGAGTGGGGCGATAGTGACTACCACTGGGGCTGGGTCCG
CCTCTCCCGAAAAGGGACTGGAATGGATTGGAAGTATTCATTGGC
GGGGGACCACCCACTACAACGCGCCCTTCCGGGGGCGAGGCAGATT
GTCGATAGACCTCTCCCGGAATCAATTCTCCCTGCGCCTGACGTCTG
TGACCGCCGAAGACACTGCCGTCTATTATTGTGTGAAGCACAAATAT
CATGACATTGTCATGGTGGTCCCCATTGCGGGCTGGTTTCGACCCCTG
GGGCCAGGGACTCCAGGTCACCGTCTCGAGCGCCTCCACCAAGGGCCC
ATCGGTCTTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGGCACAG
CGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTG
TCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCGGCTGT
CCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTC
CAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCA
GCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAAC
TCACACATGCCCACCGTGCCAGCACCTGAACTCTGGGGGGACCGTCAG
TCTTCCTCTTCCCCCCTAAAACCCAAGGACACCCTCATGATCTCCCGGACCC
CTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC
AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAA
AGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCT
CACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAG
GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAGC
CAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
GAGGAGATGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGCT
TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA
GAACAACCTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCT
TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA
CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC
AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:360)

[0629] 5345_I01 (PGT-137) gamma heavy chain variable region nucleotide sequence:

GAGGTGCATCTGGAGGAGTCGGGCCCAGGACTGGTGAGGCCCTCGGAGA
CCTTGTCCCTGACTTGACGGCCTCTGGTGGCTCCATAAGGGGGGGCGAG
TGGGGCGATAGTGACTACCACTGGGGCTGGGTCCGCCACTCTCCCGAAA
GGGACTGGAATGGATTGGAAGTATTCATTGGCGGGGGACCACTACA
ACGCGCCCTTCCGGGGGCGAGGCAGATTGTGATAGACCTCTCCCGGAAT
CAATTCTCCCTGCGCCTGACGTCTGTGACCGCCGAAGACACTGCCGTCTAT
TATTGTGTGAAGCACAAATATCATGACATTGTCATGGTGGTCCCCATTGCG

GGCTGGTTCGACCCCTGGGGCCAGGGACTCCAGGTCACCGTCTCGAGC(SE
Q 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.

MKHLWFFLLLVAAPRCVLSEVHLEESGPGGLVRPSETLSLTCTASGGSIRGGE
WGDSYHWGWVRHSPEKGLEWIGSIHWRGTTHYNAPFRGRGRLSIDLS
RNQFSLRLTSVTAEDTAVYYCVKHKYHDIVMVVPIAGWFDPWGQGLQV
TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS
CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS
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)

EVHLEESGPGGLVRPSETLSLTCTASGGSIRGGEWGDSYHWGWVRHSPEKGL
*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)

ATGGAAACCCAGCTCAGCTTCTCTTCCTCCTGCTACTCTGGCTCCCAGAT
ACTACTGGAGAAATAATGATGACGCAGTCTCCAGCCATCCTGTCTGTG
TCTCCAGGAGACAGAGCCACACTCTCCTGCAGGGCCAGTCAGAGTGT
GAAGAATAATTTAGCCTGGTACCAGAAGAGACCTGGCCAGGCTCCCA
GACTCCTCATCTTTGATACATCCAGCAGGGCCTCTGGTATCCCTGCCA
GGTTCAGTGGCGGTGGTTCTGGGACAGAGTTCACCTCTACCCGTCAAC
AGCATGCAGTCTGAAGACTTTGCGACTTATTACTGTCAGCAATATGAA
GAGTGGCCTCGGACGTTCCGGCCAGGGGACCAAGGTGGAAATCAAAC

GTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGT
TGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCA
GAGAGGCCAAAGTACAGTGGGAAGGTGGATAACGCCCTCCAATCGGGTAA
CTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGC
CTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAG
TCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAG
AGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO: 394)

[0635] 5345_I01 (PGT-137) kappa light chain variable region nucleotide sequence:

GAAATAATGATGACGCAGTCTCCAGCCATCCTGTCTGTGTCTCCAGGAGA
CAGAGCCACACTCTCCTGCAGGGCCAGTCAGAGTGTGAAGAATAATTTAG
CCTGGTACCAGAAGAGACCTGGCCAGGCTCCAGACTCCTCATCTTTGAT
ACATCCAGCAGGGCCTCTGGTATCCCTGCCAGGTTCAAGTGGCGGTGGTTC
TGGGACAGAGTTCACCTCTACCGTCAACAGCATGCAGTCTGAAGACTTTG
CGACTTATTACTGTCAGCAATATGAAGAGTGGCCTCGGACGTTCCGCCAG
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**.

*METPAQLLFLLLWLPDIT*GEIMMTQSPAILSVPGDRA**TL**SCRASQSVKNN
LAWYQKRPGQAPRLLIFDTSSRASGIPARFSGGGSGTEFTLTVNSMQSED
FATYYCQQYEEWPRTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVV
CLNNFYPPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYLSSTLTL**SKAD**
YEKHKVYACEVTHQGLSSPVTKSFNRGEC (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**)

EIMMTQSPAILSVPGDRA***TL***SCRASQSVKNN***LAWYQKRPGQAPRLLIFDTSS***
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
CACAAAAGTTTCAGGGCAGAGTCACCATCACGAGGGACAGTGGCGCA
AGTACAGTCTACATGGAGTTGCGCGGCCTGACAGCTGACGACACGGC
CATTATTATTGTTTGACCGGCTCAAAACATCGCCTGCGAGATTATTT
TCTGTACAATGAATATGGCCCCAATTATGAAGAGTGGGGTGACTACC
TTGCGACTTTGGACGTCTGGGGCCATGGGACCGCGGTACCGTCTCG
AGCGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCAA
GAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACT
TCCCCGAACCGGTGACGGTGTCTGTGGAAGTCAAGGCGCCCTGACCAGCGGC
GTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG
CAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAG
CCCAAATCTTGTGACAAACTCACACATGCCCACCGTGCCACAGCACCTGA
ACTCCTGGGGGGACCGTCAGTCTTCTCTTCCCCCCTTCCCCAACCAAGGACA
CCCTCATGATCTCCCGGACCCCTGAGGTCAAGTCAACTGGTACGTGGACGGCGTGG
AGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAC
GTACCGTGTGGTCAGCGTCTCACCCTCTGCACCAGGACTGGCTGAATG
GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATC
GAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACACAGGTGT
ACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCT
GACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGG
AGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCT
GGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGA
GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT
CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATG
A (SEQ ID NO: 398)

[0641] 4995_P16 (PGT-145) gamma heavy chain variable region nucleotide sequence:

CAGGTGCAGTTGGTGCAGTCTGGGGCTGAAGTGAAGAAGCCTGGGTCTCT
AGTGAAGGTCTCCTGCAAGGCCTCTGGAAACAGTTTCAGTAATCATGATG
TCCACTGGGTACGACAGGCCACTGGACAGGGGCTTGAATGGATGGGATG
GATGAGTCATGAGGGTGATAAGACAGGCTTGGCACAAAAGTTTCAGGGC
AGAGTCACCATCACGAGGGACAGTGGCGCAAGTACAGTCTACATGGAGTT
GCGCGGCCTGACAGCTGACGACACGGCCATTTATTAATTGTTTGACCGGCT
CAAAACATCGCCTGCGAGATTATTTTCTGTACAATGAATATGGCCCCAATT
ATGAAGAGTGGGGTGACTACCTTGGCACTTTGGACGTCTGGGGCCATGGG
ACCGCGGTACACCGTCTCGAGC (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
*VY***MELRGLTADDTAIYYCLTGSKHRLRDYFLYNEYGP****NYEEWGDYLAT**
LDVWGHGTA*VT***VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT**
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS**SSLGTQTYICNVNHKPSN**
TKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC
VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQV
SLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR
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)

*QVQLVQSGAEVKKPGSSVKVSC***KASGNSFSN*****H******HDVHWVRQATGQGLEWMG***
WMSHEGDKTGLAQKFQGRVTITRDSGASTVY***MELRGLTADDTAIYYCLTG***
SKHRLRDYFLYNEYGP***NYEEWGDYLATLDV******WGHGTA******VT******VSS*** (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: **GSKHRLRDYFLYNEYGP****NYEEWGDYLATLDV** (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: **GSKHRLRDYFLYNEYGP****NYEEWGDYLATLDV** (SEQ ID NO: 380)

[0646] 4995_P16 (PGT-145) kappa light chain nucleotide sequence: coding sequence (variable region in bold)

ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGGTCTCTGGA
TCCGGTGCGGAGGTTGTCATAACTCAGTCTCCACTCTTCCTGCCCCGTC
ACCCCTGGAGAGGCGGCCTCCTTGTCTTGCAAGTGCAGCCACAGCCT
CCAACATTCAACTGGAGCCAACTATTTGGCTTGGTACCTGCAGAGAC
CAGGGCAAACCTCCACGCCTGTTGATCCATTTGGCCACTCATCGGGCC
TCCGGGGTCCCTGACAGATTCAGTGGCAGTGGATCAGGCACAGATTT
TACACTTAAAATCAGTCGAGTGGAGTCTGACGATGTTGGAACCTATTA
TTGCATGCAGGGTCTGCACAGTCCCTGGACGTTCCGGCCAAGGGACCA
AGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCCG
CCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTG

AATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACG
 CCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAA
 GGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGAC
 TACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGA
 GCTCGCCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID
 NO:383)

[0647] 4995_P16 (PGT-145) kappa light chain variable region nucleotide sequence:

GAGGTTGTCATAACTCAGTCTCCACTCTTCCTGCCCGTCACCCCTGGAGAG
 GCGGCCTCCTTGTCTTGCAAGTGCAGCCACAGCCTCCAACATTCAACTGG
 AGCCAACATTTGGCTTGGTACCTGCAGAGACCAGGGCAAACCTCCACGCC
 TGTTGATCCATTTGGCCACTCATCGGGCCTCCGGGGTCCCTGACAGATTCA
 GTGGCAGTGGATCAGGCACAGATTTTACACTTAAATCAGTCGAGTGGAG
 TCTGACGATGTTGGAACCTATTATTGCATGCAGGGTCTGCACAGTCCCTGG
 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*PRLLIHLATHRASGVPDRFSGSGSGTDFTLKISR*
VESDDVGTY*YCMQGLHSPWTF***GQGTKVEIKRTVAAPSVFIFPPSDEQLKS**
GTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST
LTLISKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (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***PGEAASLSCKCSHSLQHS*****TGANYLAWYLQRPQT****PRLLI*
HLATHRASGVPDRFSGSGSGTDFTLKISR*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), HIIHYNTAVLHNPALKS (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), HIIHYNTAVL (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), SIHWRTTHYNAPFRG (SEQ ID NO: 365), and HKYHDIVMVVPIAGWFDP (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), SIHWRTTH (SEQ ID NO: 237), and HKYHDIVMVVPIAGWFDP (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), WMSHEGDKTGLAQKFQG (SEQ ID NO: 379), and GSKHRLRDYFLYNEYGPNYEEWGDYLATLDV (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 GSKHRLRDYFLYNEYGPNYEEWGDYLATLDV (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)

ATGAAACACCTGTGGITCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTCTT
ATCCCAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAGACCTT
CGGAGACCCTGTCCGTACCTGCATCGTCTCTGGGGGCTCCATCAGC
AATTACTACTGGACTTGGATCCGACAGTCCCCAGGAAAGGGACTGGA
GTGGATAGGCTATATTTCTGACAGAGAAACAACGACTTACAATCCCT
CCCTCAACAGTCGAGCCGTCATATCACGAGACACGTCGAAAAACCAA

TTGTCCCTACAATTACGTTCCGTCACCACTGCGGACACGGCCATCTAT
 TTCTGTGCGACAGCGCGCCGAGGACAGAGGATTTATGGAGTGGTTTC
 ATTTGGAGAGTTCTTCTACTACTACTACATGGACGTCTGGGGCAAAG
 GGA CTGCGGTCAACGCTCTCCTCAGCGTCGACCAAGGGCCCATCGGTCTT
 CCTCTGGCACCATCATCCAAGTCGACCTCTGGGGGCACAGCGGCCCTGG
 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAAC
 TCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGTGTCTTACAGTC
 CTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCT
 TGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
 AAGGTGGACAAGAGAGTTGAGCCCCAAATCTTGTGACAAAACCTCACACAT
 GCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTC
 TTCCCCCCTAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGT
 CACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA
 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCG
 GGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTTACCGTCC
 TGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAA
 CAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGG
 CAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGAT
 GACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGCTTCTATCCCA
 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAATA
 CAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAG
 CAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA
 TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCT
 CTCCTGTCTCCGGGTAAATGA (SEQ ID NO: 402)

[0670] 4835_F12 (PGT-124) gamma heavy chain variable region nucleotide sequence:

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAGACCTTCGG
 AGACCCTGTCCGTACCTGCATCGTCTCTGGGGGCTCCATCAGCAAT
 TACTACTGGACTTGGATCCGACAGTCCCCAGGAAAGGGACTGGAGTG
 GATAGGCTATATTTCTGACAGAGAAACAACGACTTACAATCCCTCCCT
 CAACAGTCGAGCCGTCATATCACGAGACACGTCGAAAAACCAATTGT
 CCCTACAATTACGTTCCGTCAACCACTGCGGACACGGCCATCTATTTCT
 GTGCGACAGCGCGCCGAGGACAGAGGATTTATGGAGTGGTTTCATTT
 GGAGAGTTCTTCTACTACTACTACATGGACGTCTGGGGCAAAGGGAC
 TCGGGTCACCGTCTCCTCA (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.

MKHLWFFLLVAAPRWVLSQVQLQESGPGLVRPSETLSVTCIVSGGSISNYY
WTWIRQSPGKGLEWIGYISDRETTTYPNSLNSRAVISRDTSKNQLSLQLR
SVTTADTAIFYCATARRGQRIYGVVSFGEFFYYYYMDVWGKGTA VTVSS
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKT
HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN

KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTTPVLDSGDSFLYSKLTVDKSRWQQGNVFCSCVMH
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)

QVQLQESGPGLVRPSETLSVTCIVSGGSISNYYWTWIRQSPGKGLEWIG***YISD***
RETTTYNPSLNSRAVISRDTSKNQLSLQLRSVTTADTAIYFCAT***ARRGQRIYG***
VVSFGEFFYYYYMDVWGKGTAVTVS (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: ARRGQRIYGVVSFGEFFYYYYMDV (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: ARRGQRIYGVVSFGEFFYYYYMDV (SEQ ID NO: 408)

[0675] 4835_F12 (PGT-124) light chain nucleotide sequence: coding sequence (variable
region in bold)

ATGGCCTGGATCCCTCTCCTCCTCGGCCTCCTCTCTCACTGCACAGGGTCTGT
GACGTCCCTATGTGAGCCCACTGTCAGTGGCCCTGGGGGAGACGGCCA
GGATTTCTCTGTGGACGACAGGCCCTTGAAGTAGAGCTGTGCAGTGG
TATCAACATAAGCCAGGCCAGGCCCTATTTTGCTCATCTATAATAAT
CAAGACCGGCCCTCAGGGATCCCTGAGCGGTTCTCTGGCACCCCTGA
TATTAATTTTGGGACCACGGCCACCCTGACTATCAGCGGGGTCTGAAG
TCGGGGATGAAGCCGACTATTACTGTTCACATGTGGGACTCTAGAAGT
GGTTTCAGTTGGTCTTTTCGGCGGGGCGACCAAGGCTGACCGTCCTAGG
TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGA
GCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACC
CGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGC
GGGAGTGGAGACCACACCCCTCCAAACAAGCAACAACAAGTACGCG
GCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAAAA
GCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGT
GGCCCCCTACAGAATGTTTCATAG (SEQ ID NO: 411)

[0676] 4835_F12 (PGT-124) light chain variable region nucleotide sequence:

TCCTATGTGAGCCCACTGTCAGTGGCCCTGGGGGAGACGGCCAGGAT
TTCCTGTGGACGACAGGCCCTTGAAGTAGAGCTGTGCAGTGGTATC
AACATAAGCCAGGCCAGGCCCTATTTTGCTCATCTATAATAATCAAG

ACCGGCCCTCAGGGATCCCTGAGCGGTTCTCTGGCACCCCTGATATT
 AATTTTGGGACCACGGCCACCCTGACTATCAGCGGGGTCGAAGTCGG
 GGATGAAGCCGACTATTACTGTACATGTGGGACTCTAGAAGTGGT
 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
LVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPE
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**GROALGSRAVQ**WYQHKGPGQAPILLIY**NNQDRPSGI**
 PERFSGTPDINFGTTATLTISGVEVGDEADYY**CHMWDSRSGFSWS**FGGATRL
 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)

ATGAAACACCTGTGGTTCCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCTG
 GTCCCAGGTGCATCTGCAAGAGTCGGGGCCAGGACTGGTGACGCCTT
 CGGAAACCCTGTCCCTCACTTGCACTGTGTGCAATGGCTCCGTCAGT
 GGTCGCTTCTGGAGCTGGATCCGGCAGTCCCAGGGAGAGGACTGG
 AATGGATCGGTTATTTTCTGACACTGACAGGTCTGAATATAATCCTT
 CTCTCAGGAGTCGACTCACCTTATCAGTAGATAGATCTAAGAACCAG
 TTGTCCCTGAGATTGAAGTCCGTGACCGCTGCGGATTCGGCCACTTA
 TTAAGTGTGCGAGAGCACAGCAGGGGAAGAGGATCTATGGAATAGTGT
 CTTTCGGAGAGTTCTTCTATTATTATTACATGGACGCCTGGGGCAAAG
 GGACTCCGGTCACCGTCTCCTCAGCGTCGACCAAGGGCCCATCGGTCTT

CCCTCTGGCACCATCATCCAAGTCGACCTCTGGGGGCACAGCGGCCCTGG
GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAAC
TCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTC
CTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCT
TGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
AAGGTGGACAAGAGAGTTGAGCCCCAAATCTTGTGACAAAACCTCACACAT
GCCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGGACCGTCAGTCTTCCTC
TTCCCCCCTAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGT
CACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA
ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAAGCCGCG
GGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCACCCTCC
TGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAA
CAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGG
CAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGAT
GACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA
GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAATA
CAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAG
CAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA
TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCT
CTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 417)

[0682] 4869_K15 (PGT-133) gamma heavy chain variable region nucleotide sequence:

CAGGTGCATCTGCAAGAGTCGGGGCCAGGACTGGTGACGCCTTCGG
AAACCCTGTCCCTCACTTGCACTGTGTGCAATGGCTCCGTCACTGGT
CGCTTCTGGAGCTGGATCCGGCAGTCCCCAGGGAGAGGACTGGAAT
GGATCGGTTATTTTTCTGACACTGACAGGTCTGAATATAATCCTTCTC
TCAGGAGTCGACTCACCTTATCAGTAGATAGATCTAAGAACCAGTTG
TCCCTGAGATTGAAGTCCGTGACCGCTGCGGATTCGGCCACTTATTA
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.

*MKHLWFFLLLVAAPRWVVSQVHLQESG***PLVTPSETLSLTCTVSNGSVSGRF**
WSWIRQSPGRGLEWIGYFSDTDRSEYNPSLRSLT*SVDRSKNQLSLRLK*
SVTAADSATYYCARAQQ*GKRIYGIVSFG***EFFYYYYMDAWGKGTPVTVSS**
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKT
HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN
KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
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)

QVHLQESGPGLVTPSETLSLTCTVSN***GSVSGRFWSWIRQSPGRGLEWIGYFSD***
TDRSEYNPSLRSRLTLSVDRSKNQLSLRLKSVTAADSATYYCARA***AQOGKRIY***
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: AQOGKRIYGIVSFGEFFYYYYMDA (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: AQOGKRIYGIVSFGEFFYYYYMDA (SEQ ID NO: 423)

[0687] 4869_K15 (PGT-133) light chain nucleotide sequence: coding sequence (variable region in bold)

ATGGCCTGGATCCCTCTCCTCCTCGGCCTCCTCTCTCACTGCACAGGTTCTGA
CACTTCGTTAAACCCACTGTCTCGCTGGCCCCAGGAGCGACGGCCAAAA
TTCCCTGCGGAGAAAGGAGCCGTGGAAGTAGGGCTGTCCAGTGGTAT
CAGCAGAAGCCAGGCCAGGCCCCACATTGATCATTTATAATAATCA
AGACCGGCCCGCAGGGGTCTCTGAACGATTTTCTGGCAATCCTGACG
TCGCTATTGGGGTGACGGCCACCCTGACCATCAGTCGGGTCTGAAGTC
GGGGATGAGGCCGACTATTATTGTCACTATTGGGACAGTAGAAGTCC
CATCAGCTGGATTTTCGGCGGAGGGACCCAGCTGACCGTCTCTGGGTC
AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGC
TTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCG
GGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGG
GAGTGGAGACCACCACACCCTCCAAACAAGCAACAACAAGTACGCGGC
CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAAAAGCT
ACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGC
CCCTACAGAATGTTTCATAG(SEQ ID NO: 426)

[0688] 4869_K15 (PGT-133) light chain variable region nucleotide sequence:

TCGTTAAACCCACTGTCTCGCTGGCCCCAGGAGCGACGGCCAAAATTCC
CTGCGGAGAAAGGAGCCGTGGAAGTAGGGCTGTCCAGTGGTATCAG
CAGAAGCCAGGCCAGGCCCCACATTGATCATTTATAATAATCAAGA
CCGGCCCCGCAGGGGTCTCTGAACGATTTTCTGGCAATCCTGACGTCG
CTATTGGGGTGACGGCCACCCTGACCATCAGTCGGGTCTGAAGTCGGG
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.

*MAWIPLLLGLLSHCTGSDTSLNPLSLAPGATAKIPCGERSRGSRAVQWYQQ
KPGQAPTLIIYNNQDRPAGVSERFSGNPDVAIGVTATLTISRVEVGDEADY
YCHYWDSRSPISWIFGGGTQLTVLGQPKAAPSVTLFPPSSEELQANKATLV
CLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNKYAASSYLSLTPEQW
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
ERFSGNPDVAIGVTATLTISRVEVGDEADY**YCHYWDSRSPISWIFGGGTQLTV*
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)

*ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTCTG
GTCCCAGGTGCATCTGCAAGAGTCGGGGCCAGGACTGGTGACGCCTT
CGGAAACCCTGTCCCTCACTTGCAGTGTGTCGAATGGCTCCGTCAGT
GGTCGCTTCTGGAGCTGGATCCGGCAGTCCCCAGGGAGAGGACTGG
AATGGATCGGTTATTTTCTGACACTGACAGGTCTGAATATAATCCTT
CTCTCAGGAGTCGACTCACCTTATCAGTCGATAGATCCAAGAACCAG
TTGTCCCTAAAATTGAAGTCCGTGACCGCTGCGGATTTCGGCCACTTA
TACTGTGCGAGAGCACAAACAGGGGAAGAGGATCTATGGAATAGTGT
CTTTCGGAGAGTTGTTCTATTATTATTACATGGACGCCTGGGGCAAA
GGGACTCCGGTCAACCGTCTCCTCAGCGTCGACCAAGGGCCCATCGGTC
TTCCCTCTGGCACCATCATCCAAGTCGACCTCTGGGGGCACAGCGGCCCT
GGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGA
ACTCAGGCGCCCTGACCAGCGGCGTGACACACCTTCCCGGCTGTCTACAG*

TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAG
 CTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACA
 CCAAGGTGGACAAGAGAGTTGAGCCCCAAATCTTGTGACAAAACCTCACAC
 ATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCC
 TCTTCCCCCCTAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTT
 CAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG
 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGT
 CCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCC
 AACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAG
 GGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA
 GATGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGCTTCTATC
 CCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAA
 CTACAAGACCACGCCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTA
 TAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC
 TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAG
 CCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 432)

[0694] 4876_M06 (PGT-134) gamma heavy chain variable region nucleotide sequence:

CAGGTGCATCTGCAAGAGTCGGGGCCAGGACTGGTGACGCCTTCGG
 AAACCCTGTCCCTCACTTGCAGTGTGTCGAATGGCTCCGTCACTGGT
 CGCTTCTGGAGCTGGATCCGGCAGTCCCAGGGAGAGGACTGGAAT
 GGATCGGTTATTTTTCTGACACTGACAGGTCTGAATATAATCCTTCTC
 TCAGGAGTCGACTCACCTTATCAGTCGATAGATCCAAGAACCAGTTG
 TCCCTAAAATTGAAGTCCGTGACCGCTGCGGATTCGGCCACTTATTA
 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.

*MKHLWFFLLLVAA*PRWVVSQVHLQESGPGILVTPSETLSLTCTVSNGSVSGRF
 WSWIRQSPGRGLEWIGYFSDTDRSEYNPSLRSLTSLVDRSKNQLSLKLK
 SVTAADSATYYCARAQQKRIYGIVSFGELFYYYMDAWGKGTPVTVSS
 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
 PAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKT
 HTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
 WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN
 KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
 VEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMH
 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
TDRSEYNPSLRSRLTSLVDRSKNQLSLKLKSVTAADSATYYCARAQQGKRIY
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: AQQGKRIYGIVSFGELFYYYMDA (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: AQQGKRIYGIVSFGELFYYYMDA (SEQ ID NO: 436)

[0699] 4876_M06 (PGT-134) light chain nucleotide sequence: coding sequence (variable region in bold)

ATGGCCTGGATCCCTCTCCTCCTCGGCCTCCTCTCTCACTGCACAGGTTCTGA
CACTTCGTTAAACCCACTGTCTGCTGGCCCCGGGAGCGACGGCCAAAA
TTCCCTGCGGAGAAAGGAGCCGTGGAAGTAGGGCTGTCCAGTGGTAT
CAGCAGAAAGCCAGGCCAGGCCCCACATTGATCATTATAATAATCA
AGACCGGCCCGCAGGGGTCTCTGAACGATTTTCTGGCAATCCTGACG
TCGCTATTGGGGTGACGGCCACCCTGACCATCAGTCGGGTCTGAAGTC
GGGGATGAGGGCGACTATTATTGTCACTATTGGGACAGTAGAAGTCC
CATCAGCTGGATTTTCGCCGGAGGGACCCAGTTGACCGTCCTGGGTC
AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGC
TTCAAGCCAACAAGGCCCACTGGTGTGTCTCATAAGTGACTTCTACCCG
GGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGG
GAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGC
CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAAAAGCT
ACAGCTGCCAGGTACGCATGAAGGGAGCACCGTGGAAGAAGACAGTGGC
CCCTACAGAATGTTTCATAG (SEQ ID NO: 437)

[0700] 4876_M06 (PGT-134) light chain variable region nucleotide sequence:

TCGTTAAACCCACTGTCTGCTGGCCCCGGGAGCGACGGCCAAAATTCC
CTGCGGAGAAAGGAGCCGTGGAAGTAGGGCTGTCCAGTGGTATCAG
CAGAAGCCAGGCCAGGCCCCACATTGATCATTATAATAATCAAGA
CCGGCCCCGAGGGGTCTCTGAACGATTTTCTGGCAATCCTGACGTCG
CTATTGGGGTGACGGCCACCCTGACCATCAGTCGGGTCTGAAGTCGGG
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)

*SLNPLSLAPGATAKIPCGERSRGSRAVQWYQQKPGQAPTLIIYNNQDRPAGVS
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)

*ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTCCT
TTCCCAGGTGCAACTACAGGAGTCGGGCCAGGACTGGTGAAGCCTT
CGGAGACCCTTTCCTCACCTGCACTGTCTCTGGTGACTCCATCAACA
CTGGTCATCACTACTGGGGCTGGGTCCGTCAGGTCCCAGGGAAGGGA
CCGGAATGGATTGCTCACATCCACTATAATACGGCTGTCTTGCACAAT
CCGGCCCTCAAGAGTCGAGTCACCATTTTCGATTTTCACCCTGAAGAA
TCTGATTACCCTGAGGCTCAGTAATATGACCGCCGCGGACACGGCCG
TCTATTTCTGCGTTCGATCCGGCGGCGACATTTTATACTATAATGAGT
GGCAAAAACCCCACTGGTTCTATCCCTGGGGCCCGGGAATTTTGGTC
ACCGTCTCGAGCGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACC
CTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCA
AGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTG
ACCAGCGGCGTGACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTA
CTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGA
CCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAA
GAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCC*

CAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCAAAA
 CCCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGT
 GGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGG
 ACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTA
 CAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACT
 GGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCC
 AGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAA
 CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACC
 AGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGC
 CTCCCGTGTCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCG
 TGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATG
 CATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCC
 GGGTAAATGA (SEQ ID NO: 441)

[0706] 5131_A17 (PGT-132) gamma heavy chain variable region nucleotide sequence:

CAGGTGCAACTACAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGG
 AGACCCTTTCCCTCACCTGCACTGTCTCTGGTGACTCCATCAACACTG
 GTCATCACTACTGGGGCTGGGTCCGTCAGGTCCCAGGGAAGGGACC
 GGAATGGATTGCTCACATCCACTATAATACGGCTGTCTTGCACAATCC
 GGCCCTCAAGAGTCGAGTCACCATTTCGATTTTCACCCTGAAGAATCT
 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.

MKHLWFFLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCTVSGDSINTGHHYWG
WVRQVPGKGPEWIAHIHYNTAVLHNPALKSRVTISIFTLKNLITL
RLSNMTAADTAVYFCVRS**GGDILYYNEWQKPHWFYPWGP****GILVT****VSSAS**
 TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
 VLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDRVEPKSCDKTHT
 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL
 PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
 ESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMHLEAL
 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)

QVQLQESGPGLVKPSETLSLTCTVSGDSINTGHHYWG
WVRQVPGKGPEWIAHIHYNTAVLHNPALKSRVTISIFTLKNLITLRLSNMTAADTAVYFCVRS
GGDILYYNEWQKPHWFYPWGP***GILVT******VSS*** (SEQ ID NO: 444)

- [0709] 5131_A17 (PGT-132) gamma heavy chain Kabat CDRs:
 CDR 1: TGHHYWG (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)

*ATGGCCTGGGCTCTGCTCCTCCTCACCTCCTCACTCAGGGCACAGGGTCCTG
 GGCCAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCTTG
 GACAGTCACTACCATCTCCTGCAGTGGAACCGCCAGTGACATTGGC
 AGTTGGAATTTTGTCTCCTGGTATCAACAATTCCCAGGCAGAGCCCC
 CAACCTCATTATTTTGGAGGTCAATAGGCGGCGATCAGGGGTCCCTG
 ATCGCTTCTCTGGTTCCAAGTCGGGCAATACGGCCTCCCTGACCGTC
 TCTGGGCTCCGGTCTGAGGATGAGGCTGAATATTTTGCAGTTCCTT
 TTCAGGCAGGTGGGACATTGTTTTTGGCGGAGGGACCAAGGTGACCG
 TCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCT
 CTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGAC
 TTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGT
 CAAGGCGGGAGTGGAGACCACCACACCTCCAAACAAAGCAACAACAAG
 TACGCGGCCAGCAGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCA
 CAAAAGCTACAGCTGCCAGGTACGCATGAAGGGAGCACCGTGGAGAAG
 ACAGTGGCCCCTACAGAATGTTTCATAG*(SEQ ID NO: 446)

- [0712] 5131_A17 (PGT-132) light chain variable region nucleotide sequence:
- CAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCTTGGACA
 GTCACTACCATCTCCTGCAGTGGAACCGCCAGTGACATTGGCAGTT
 GGAATTTTGTCTCCTGGTATCAACAATTCCCAGGCAGAGCCCCCAAC
 CTCATTATTTTGGAGGTCAATAGGCGGCGATCAGGGGTCCCTGATCG
 CTTCTCTGGTTCCAAGTCGGGCAATACGGCCTCCCTGACCGTCTCTG
 GGCTCCGGTCTGAGGATGAGGCTGAATATTTTGCAGTTCCTTTCA
 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*

AEYFCSSLSGRWDIVFGGGTKVTVLGGPKAAPSVTLFPPSSEELQANKATL
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***SGTASDIGSWNFV***SWYQQFPGRAPNLIIF***EVN***
RRRSGVDPDRFSGSKSGNTASLTVSGLRSEDEAEYFC***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: SSLSGRWDIV (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: SSLSGRWDIV (SEQ ID NO: 359)

[0717] 5138_G07 (PGT-138) gamma heavy chain nucleotide sequence: coding sequence (variable region in bold)

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTCCT
GTCCCAGCCGAGCTGCAGGAGTCGGGGCCAGGACTGGTGGAGGCTT
CGGAGACCCTGTCCCTCACCTGCACTGTGTCCGGCGACTCCACTGCT
GCTTGTGACTATTTCTGGGGCTGGGTCGGGCAGCCCCCAGGGAAGGG
GCTGGAGTGGATTGGAAGTTTGTACATTGTGCAGGTTACTACAATA
GTGGCTGGACCTACCACAACCCGTCTCTCAAGAGTCGACTCACGATT
TCACTCGACACGCCCAAGAATCAGGTCTTCCTGAAGTTAAATTCTGTG
ACCGCCGCGGACACGGCCATTTACTACTGTGCGCGATTTCGGTGGCGA
CGTTTTGGTGTACCACGATTGGCCAAAGCCGGCCTGGGTCCGACCTCT
GGGGCCGGGAGTTTTGGTCACCGTCTCGAGCGCCTCCACCAAGGGC
CCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCAC
AGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG
TGTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCGGCT
GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC
CTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC
CCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAA
AACTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGT
CAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA
CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAG
GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGAC
AAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC

CTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA
GGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
CCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
GAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCT
TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA
GAACAACCTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCT
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
TTTTGGTGTACCACGATTGGCCAAAGCCGGCCTGGGTTCGACCTCTGG
GGCCGGGGAGTTTTGGTCAACCGTCTCGAGC (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.

MKHLWFFLLLVAAAPRWVLSQPQLQESGPGLVEASETLSLTCTVSGDSTAAC
DYFWGWVRQPPGKGLEWIGSLSHCAGYYNSGWTYHNPSLKSRLTISLD
TPKNQVFLKLNSVTAADTAIYYCARFGGDVLVYHDWPKPAWVDLWGR
GVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG
ALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKR
VEPKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV
FSCSVMHEALHNHYTQKSLSLSPGK (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)

*QPQLQESGPGLVEASETLSLTCTVSGDSTAAC**CDYFWGWVRQPPGKGLEWIGS*
LSHCAGYYNSGWTYHNPSLKSRLTISLDTPKNQVFLKLNSVTAADTAIYYCAR
*FGGDVLVYHDWPKPAWVDL*WGRGVLTVSS (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)

ATGGCCTGGGCTCTGCTCCTCCTCACCTCCTCACTCAGGGCACAGGGGCCT
GGGCCAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCCT
GGACAGTCAATCACCATCTCCTGCACTGGAAATATCAATAACTTTGTC
TCCTGGTACCAACAACACCCTGGCAAGGCCCCCAAACTCGTCATTTA
TGGGGTCAATAAGCGCCCCTCAGGTGTCCCTGATCGTTTTTCTGGCT
CCAAGTCTGGCAACGCGGCCTCCCTGACCGTCTCTGGACTCCAGACT
GACGATGAGGCTGTCTATTACTGCGGCTCACTTGCAAGGCAACTGGGA
TGTGGTTTTTCGGCGGAGGGACCAAGTTGACTGTCCTGGGTACGCCAT
GGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGC
CAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCG
TGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGA
GACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGC
TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAAAAGCTACAGCTG
CCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCCTACA
GAATGTTTCATAG(SEQ ID NO: 581)

[0724] 5138_G07 (PGT-138) light chain variable region nucleotide sequence:

CAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCCTGGACA
GTCAATCACCATCTCCTGCACTGGAAATATCAATAACTTTGTCTCCTG
GTACCAACAACACCCTGGCAAGGCCCCCAAACTCGTCATTTATGGGG
TCAATAAGCGCCCCTCAGGTGTCCCTGATCGTTTTTCTGGCTCCAAGT
CTGGCAACGCGGCCTCCCTGACCGTCTCTGGACTCCAGACTGACGAT
GAGGCTGTCTATTACTGCGGCTCACTTGCAAGGCAACTGGGATGTGGT
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.

MAWALLLLTLLTQGTGAWAQSAITQPPSASGSPGQSITISCTGNINNFVSWY
QQHPGKAPKLVIYGVNKRPSGVPDRFSGSKSGNAASLTVSGLQTDDEAV
YYCGSLAGNWDVVFGGGTKLTVLGQPMAPSVTLPSPSEELQANKATLV
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)

QSALTQPPSASGSPGQSITISCTGNINNFVSWYQQHPGKAPKLVIYGVNKRPS
GVPDRFSGSKSGNAASLTVSGLQTDDEAVYYCGSLAGNWDVVFGGGTKLTV
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)

ATGAAACACCTGTGGTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTCCT
GTCCCAGCCGCGAGCTGCAGGAGTCGGGGCCAGGACTGGTGGAGGCTT
CGGAGACCCTGTCCCTCACCTGCACTGTGTCCGGCGACTCCACTGCT
GGTTGTGACTATTTCTGGGGCTGGGTCCGGCAGCCCCAGGGAAGG
GGCTGGAGTGGATTGGGGGTTTGTACATTGTGCAGGTTACTACAAT
ACTGGCTGGACCTACCACAACCCGTCTCTCAAGAGTCGACTCACGAT
TTCACTCGACACGCCCAAGAATCAGGTCTTCCTGAAGTTAAATTCTGT
GACCGCCGCGGACACGGCCATTTACTACTGTGCGCGATTTCGACGGCG
AAGTTTGGTGTACAACGATTGGCCAAAGCCGGCCTGGGTTCGACCTC
TGGGGCCGGGGAACCTTGGTCAACCGTCTCGAGCGCCTCCACCAAGGG
CCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCA
CAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACG
GTGTCGTGGAATCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGC
TGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC
CTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC
CCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAA
AACTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGT
CAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA
CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAG
GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGAC
AAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
CTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA
GGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAG
CCAAAGGGCAGCCCCGAGAACACAGGTGTACACCCTGCCCCATCCCGG
GAGGAGATGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGCT

TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA
 GAACAACACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCT
 TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA
 CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC
 AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 460)

[0730] 5120_N10 (PGT-139) gamma heavy chain variable region nucleotide sequence:

CAGCCGCAGCTGCAGGAGTCGGGGCCAGGACTGGTGGAGGCTTCGG
 AGACCCTGTCCCTCACCTGCACTGTGTCCGGCGACTCCACTGCTGGT
 TGTGACTATTTCTGGGGCTGGGTCCGGCAGCCCCCAGGGAAGGGGCT
 GGAGTGGATTGGGGGTTTGTACATTGTGCAGGTACTACAATACTG
 GCTGGACCTACCACAACCCGTCTCTCAAGAGTCGACTCACGATTTCA
 CTCGACACGCCCAAGAATCAGGTCTTCTGAAGTTAAATTCTGTGAC
 CGCCGCGGACACGGCCATTTACTACTGTGCGCGATTTCGACGGCGAAG
 TTTTGGTGTACAACGATTGGCCAAAGCCGGCCTGGGTGACCTCTGG
 GGCCGGGGAACTTTGGTCAACCGTCTCGAGC (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.

MKHLWFFLLLVAAPRWVLSQPQLQESGPGLVEASETLSLTCTVSGDSTAGC
DYFWGWVRQPPGKGLEWIGGLSHCAGYYNTGWTYHNPSLKSRLTISLD
TPKNQVFLKLNSVTAADTAIYYCARFDGEVLVYNDWPKPAWVDLWGRG
TLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGAL
TSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRV
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)

QPQLQESGPGLVEASETLSLTCTVSGDSTAGCDYFWGWVRQPPGKGLEWIG
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)

ATGGCCTGGGCTCTGCTCCTCCTCACCCTCCTCACTCAGGGCACAGGGGCCT
GGGCCCAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCCT
GGACAGTCAATCACCATCTCCTGCACTGGAACCAGCAATAACTTTGT
CTCCTGGTACCAGCAACACCCAGCCAAGGCCCCCAAACCTCGTCATTT
ATGGGGTCAATAAGCGCCCCCTCAGGTGTCCCTGATCGTTTTTCTGGC
TCCAAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGACTCCAGAC
TGACGATGAGGCTGTCTATTACTGCGGCTCACTTGTAGGCAACTGGG
ATGTGATTTTCGGCGGAGGGACCAAGTTGACCGTCCTGGGTCAGCCC
ATGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAA
GCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGC
CGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTG
GAGACCACACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCA
GCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAAAAGCTACAGC
TGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTA
CAGAATGTTTCATAG(SEQ ID NO: 467)

[0736] 5120_N10 (PGT-139) light chain variable region nucleotide sequence:

CAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCCTGGACA
GTCAATCACCATCTCCTGCACTGGAACCAGCAATAACTTTGTCTCCTG
GTACCAGCAACACCCAGCCAAGGCCCCCAAACCTCGTCATTTATGGGG
TCAATAAGCGCCCCCTCAGGTGTCCCTGATCGTTTTTCTGGCTCCAAGT
CTGGCAACACGGCCTCCCTGACCGTCTCTGGACTCCAGACTGACGAT
GAGGCTGTCTATTACTGCGGCTCACTTGTAGGCAACTGGGATGTGAT
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.

*MAWALLLLTLTQGTGAWAQ*SALTQPPSASGSPGQSITISCTGTSNNFVSWY
QQHPAKAPKLVIYGVNKRPSGVPDRFSGSKSGNTASLTVSGLQTDDEAV
YYCGSLVGNWDVIFGGGTKLTVLGQPMAPSVTLPSPSEELQANKATLV
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***TGTSNNFVS***WYQQHPAKAPKLVIY***GVNKRPS***
GVPDRFSGSKSGNTASLTVSGLQTDDEAVYYC***GSLVGNWDVI***FGGGTKLTVL
(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), YISDRETTTYPNPSLNS (SEQ ID NO: 407), and ARRQRIYGVVSFGGEFFYYYYMDV (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 ARRQRIYGVVSFGGEFFYYYYMDV (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 AQQGKRIYGIVSFGGEFFYYYYMDA (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 AQQGKRIYGIVSFGIEFFYYYYMDA (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 AQQGKRIYGIVSFGELFYYYYYMDA (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 AQQGKRIYGIVSFGELFYYYYYMDA (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), HIHYNTAVLHNPALKS

(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
GTGTCGGGTGCAGTTGGTGGAGTCGGGGGAGGCGTGGTCCAGCCTG
GGAAGTCCGTGAGACTTTCCTGTGTAGTCTCCGATTTCCCCTTCAGCA
AGTATCCTATGTATTGGGTTCCGCCAGGCTCCAGGCAAGGGGCTGGAG
TGGGTGGCAGCCATCTCCGGTGATGCCTGGCATGTGGTCTACTCAA
TTCCGTGCAGGGCCGATTTCTCGTCTCCAGGGACAATGTCAAGAACA
CTCTATATTTAGAAATGAACAGCCTGAAAATTGAGGATACGGCCGTA
TATCGCTGCGCGAGAATGTTCCAGGAGTCTGGTCCACCACGTTTGGA
TCGTTGGAGCGGTGCAAATTACTATTATTCTGGTATGGACGTCTG
GGGCCAAGGGACCACGGTCACCGTCTCGAGCGCCTCCACCAAGGGCC
CATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGT
GTCGTGGAATCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCCGGCTG
TCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCT
CCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCC

AGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAA
 CTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGGACCGTCA
 GTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACC
 CCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
 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
 ATCCTATGTATTGGGTTCGCCAGGCTCCAGGCAAGGGGCTGGAGTGG
 GTGGCAGCCATCTCCGGTGTATGCCTGGCATGTGGTCTACTCAAATTC
 CGTGCAGGGCCGATTTCTCGTCTCCAGGGACAATGTCAAGAACACTC
 TATATTTAGAAATGAACAGCCTGAAATTTGAGGATACGGCCGTATAT
 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.

MELGLSWVFLVGLLRGVQCRVQLVESGGGVVQPGKSVRLSCVVSDFPFISKY
PMYWVRQAPGKGLEWVAAISGDAWHVVYSNSVQGRFLVSRDNVKNL
YLEMNSLKIEDTAVYRCARMFQESGPPRLDRWSGRNYYYYSGMDVWG
QGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS
GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK
RVEPKSCDKTHHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNV
FSCSVMIHEALHNHYTQKSLSLSPGK (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)

RVQLVESGGGVVQPGKSVRLSCVVSDFPFSKYPMYWVRQAPGKGLEWVAA
ISGDAWHVVYSNSVQGRFLVSRDNVKNTLYLEMNSLKIEDTAVYRCARMFQ
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
GCATGCAAAGTAAAGACTTCCCACTTACATTTGGCGGCGGGACCAAG
GTGGATCTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCC
ATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAA
TAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCC
TCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGA
CAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTAC
GAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTC
GCCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:480)

[0767] 6831_A21 (PGT-151) light chain variable region nucleotide sequence:

GACATTGTGATGACCCAGACTCCTCTCTCTTTGTCCGTCACCCCTGGA
CAGCCGGCCTCCATCTCCTGCAAGTCCAGTGAGAGCCTCCGACAAAG
TAATGGAAAGACCTCTTTGTATTGGTATCGGCAGAAGCCAGGCCAGT
CTCCACAACCTCCTAGTGTTTGAAGTTTCTAATCGATTCTCTGGCGTGT
CGGATAGGTTTGTGGCAGCGGGTCAGGGACAGACTTCACTGAGA
ATCAGCCGGGTAGAGGCTGAGGATGTTGGATTTTATTACTGCATGCA
AAGTAAAGACTTCCCACTTACATTTGGCGGCGGGACCAAGGTGGATC
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.

MRLPAQLLGLLMLWIPEFTADIVMTQTPLSLSVTPGQPASISCKSSESRLQSN
*GKTSLYWYRQKPGQSPQLLVFEVSNRFSGVSDRFVGS****SGTDFTLRISRV***
EAEDVGFFYYCMQSKDFPLTFGGG***TKVDLKRTVAAPSVFIFPPSDEQLKSGT***
ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLT
SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (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****KSSESRLQSNGKTSLYWYRQKPGQSPQLLVF***
EVSNRFS***GVSDRFVGS******SGTDFTLRISRV******EAEDVGFFYYCMQSKDFPLTFGGG***
TKVDLK (SEQ ID NO: 483)

[0770] 6831_A21 (PGT-151) light chain Kabat CDRs:

CDR 1: KSSESRLQSN***GKTSLY*** (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: KSSESRLQSN***GKTSLY*** (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
CTGTCCGGGTGCAGTTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTG
GGAAGTCCGTGAGACTTTCCTGTGTAGTCTCTGATTTCCCCTTTCAGCA
AGTATCCTATGTATTGGGTTCGCCAGGCTCCAGGCAAGGGGCTGGAG
TGGGTGGCAGCCATCTCCGCTGATGCCTGGCATGTGGTCTACTCAGG
CTCCGTGCAGGGCCGATTTCTCGTCTCCAGGGACAACCTCCAAGAACA
TTCTGTATTTGGAATGAACACCCTGAAAATTGAGGACACGGCCGTA
TATCGCTGCGCGAGAATGTTCCAGGAGTCTGGTCCACCACGTTTCGA
TTCTTGAGCGGTTCGAAATTACTACTATTACTCTGGTATGGACGTCTG
GGGCCAAGGGACCAACGGTCAACGTCTCGAGCGCCTCCACCAAGGGCC
CATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGT
GTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCGGCTG
TCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCT
CCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCC
AGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAA

CTCACACATGCCCCACCGTGCCCCAGCACCTGAACTCCTGGGGGGACCGTCA
 GTCITCTCTTCCCCCAAAACCCAAGGACACCCCTCATGATCTCCCGGACC
 CCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
 CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA
 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC
 TCACCGTCTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA
 GGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
 CCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
 GAGGAGATGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGCT
 TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA
 GAACAATAACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCT
 TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA
 CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC
 AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:487)

[0773] 6889_I17 (PGT-152) gamma heavy chain variable region nucleotide sequence:

CGGGTGCAGTTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGA
 AGTCCGTGAGACTTTCCTGTGTAGTCTCTGATTTCCCTTCAGCAAGT
 ATCCTATGTATTGGGTTCGCCAGGCTCCAGGCAAGGGGCTGGAGTGG
 GTGGCAGCCATCTCCGCTGATGCCTGGCATGTGGTCTACTCAGGCTC
 CGTGCAGGGCCGATTTCTCGTCTCCAGGGACAACCTCCAAGAACATTC
 TGTATTTGGAAATGAACACCCTGAAAATTGAGGACACGGCCGTATAT
 CGCTGCGCGAGAATGTTCCAGGAGTCTGGTCCACCACGTTTCGATTC
 TTGGAGCGGTGCAAATTACTACTATTACTCTGGTATGGACGTCTGGG
 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
PMYWVRQAPGKGLEWVAAISADAWHVVSQSVQGRFLVSRDNSKNILY
*LEMNTLKI*EDTAVYRCARMFQESGPPRFDSWSGRNYYYYSGMDVWGQ
 GTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG
 ALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKR
 VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
 EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
 GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNV
 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
*ISADAWHVVSQSVQGRFLVSRDNSKNILYLEMNTLKI*EDTAVYRCAR***MFQ***
*ESGPPRFDSWSGRNYYYYSGMDVWGQ*TTVTVSS (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
 GCGTGTCGGATAGGTTTGTGGCAGCGGGTCAGGGACAGACTTCACA
 CTGAGAATCAGCCGGGTAGAGGCTGAGGATGTTGGATTTTATTACTG
 CATGCAAAGTAAAGACTTCCCACTCACCTTTGGCGGCGGGACCAAGG
 TGGATCTCAACCGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCA
 TCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAAT
 AACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCT
 CCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGAC
 AGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACG
 AGAAACACAAAGTCTACGCTGCGAAGTCACCCATCAGGGCCTGAGCTCG
 CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:494)*

- [0779] 6889_I17 (PGT-152) light chain variable region nucleotide sequence:
- GACATTGTGATGACCCAGACTCCTCTCTCTTTGTCCGTCGACCCCTGGA
 CAGCCGGCCTCCATCTCCTGCAAGTCCAGTCAGAGCCTCCGACAAAG
 TAATGGAAAGACCTCTTTGTATTGGTATCAGCAGAAGCCAGGCCAGT
 CTCCACAACCTCCTAATATTTGAAGTTTCTAATCGATTCTCTGGCGTGT
 CGGATAGGTTTGTGGCAGCGGGTCAGGGACAGACTTCACACTGAGA
 ATCAGCCGGGTAGAGGCTGAGGATGTTGGATTTTATTACTGCATGCA
 AAGTAAAGACTTCCCACTCACCTTTGGCGGCGGGACCAAGGTGGATC
 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
 GKTSLYWYQQKPGQSPQLLIFEVSNRFGVSDRFVGSFGTDFTLRISRV*

EAEDVGFYYCMQSKDFPLTFGGGTKVDLNRTVAAPSVFIFPPSDEQLKSGT
ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSLSTLT
SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 496)

[0781] 6889_I17 (PGT-152) light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

DIVMTQTPLSLSDPGQPASISCKSSOSLRQSNGKTSLYWYQQKPGQSPQLLIF
EVSNRFSGVSDRFVGSSTGDTFTLRISRVEAEDVGFYYCMQSKDFPLTFGGG
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
GTGTCAAGGTGCAGTTGGTGGAGTCGGGGCGGAGGCGTGGTCCAGCCTG
GGAAGTCCCTGAGACTCTCCTGTGTAGTCTCTAATTTTCTCTTCAATA
AACGTACATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGACTAGAG
TGGATAGCAGTCATTTCTCTGATGCCATTACGTAGACTACGCAAGT
TCCGTGCGGGGCCGATCCCTCATCTCCAGAGACAATTCCAAAAATAG
TTTATATCTAGACATGAATAACCTGAAAATTGAGGACACGGCCACATA
TTATTGTGCAAGAGATAGAGACGGATATGGTCCACCACAGATCCAGA
CTTGAGACGGTCGATACCTCCACCTTATTCTGGAATAGACGCCTGG
GGCCTAGGGACCACGGTCAACCGTCTCGAGCGCCTCCACCAAGGGCCCA
TCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGT
CGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACACCTTCCCGGCTGTC
CTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC
AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCAG
CAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGAGACAAAAT
CACACATGCCCACCGTGCCAGACCTGAACTCCTGGGGGGACCGTCAGT
CTTCTCTTCCCCCAAACCAAGGACACCTCATGATCTCCCGGACCCC
TGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCA
AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAA
GCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC

ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGG
TCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG
AGGAGATGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTC
TATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGA
ACAACTACAAGACCACGCCTCCCGTGGTGGACTCCGACGGCTCCTTCTTC
CTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACG
TCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
AAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 499)

[0785] 6891_F06 (PGT-153) gamma heavy chain variable region nucleotide sequence:

CAGGTGCAGTTGGTGGAGTCGGGCGGAGGCGTGGTCCAGCCTGGGA
AGTCCCTGAGACTCTCCTGTGTAGTCTCTAATTTTCTCTTCAATAAAC
GTCACATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGACTAGAGTG
GATAGCAGTCATTTCTCTGATGCCATTACGCTAGACTACGCAAGTTC
CGTGCGGGGCCGATCCCTCATCTCCAGAGACAATTCAAAAATAGTT
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
GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPK
SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
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******HMHWVRQAPGKGLEWIAV***
ISSDAIHVDYASSVRGRSLISRDNSKNSLYLD***MNNLKIEDTATYYCARD******DRDGY***
GPPQIQTWSGRYLHLYSGIDA***WGLGTTVTVSS*** (SEQ ID NO: 502)

[0788] 6891_F06 (PGT-153) gamma heavy chain Kabat CDRs:

CDR 1: KRHMH (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
GGCCAGTCTCCACAACCCCTGATCCAGGAAGTTTCCATTTCGTTCTCT
GGAGTGCCAGGTAGATTTCGCTGGCAGCGGATCAGGGACAGACTTCAC
ACTGAAAATCAGCCGGGTGGAGGCTGAAGATGTTGGAGTTTATTTCT
GCATTGCAAAGTAAAGACTTTCCACTCACTTTTGGCGGAGGGACCAAG
GTGGACCTCAATCGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCC
ATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAA
TAACCTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCC
TCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGA
CAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTAC
GAGAAACACAAAGTCTACGCTGCGAAGTCACCCATCAGGGCCTGAGCTC
GCCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:508)*

[0791] 6891_F06 (PGT-153) light chain variable region nucleotide sequence:

*GACATTGTGCTGACCCAGAGCCCCCTCTTTCTGTCCGTCAGTCCTGG
ACAGCCGGCCTCCATCTCCTGTAAGTCTAGTCAGAGCCTCCGACAAA
GTAATGGAAAGACATATTTGTATTGGTACGTACAAAAGTCCGGCCAG
TCTCCACAACCCCTGATCCAGGAAGTTTCCATTTCGCTTCTCTGGAGTG
CCAGGTAGATTTCGCTGGCAGCGGATCAGGGACAGACTTCACACTGAA
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 VYFCMQSKDFPLTFGGGTKVDLNRTVAAPSVFIFPPSDEQLKSGT
ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLT
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)

DIVLTQSPLFLSVSPGQPASIS**CSSQSLROSNGKTYLY**WYVQKSGQSPQPLIQ
EVSIRFSGVPGRFAGSGSGTDFTLKISRVEAEDVGVYFC**MSKDFPLT**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: MSKDFPLT (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: MSKDFPLT (SEQ ID NO: 486)

[0796] 6843_G20 (PGT-154) gamma heavy chain nucleotide sequence: coding sequence (variable region in bold)

ATGGAATTGGGGCTGAGCTGGGTTTTCTCGTTGCTCTCTTAAGAGGTGTCCA
GTGTCAGGTGCAGCTGGTGGAATCGGGAGGAGGCGTGGTCCAGCCTG
GAAAGTCCCTCAGACTCTCATGTGTCGTCTCTAATTTTCATCTTTAATA
AATATCCTATGTATTGGGTCCGCCAGGCTCCAGGCAAGGGGGCTGGAG
TGGGTGGCAGCCATCTCCGCTGATGCCTGGCATGTAGACTACGCAGC
CTCCGTGAAGGACCGATTTCTCATCTCCAGAGACAATTTCCAAGAATG
CTCTATATTTGGAAATGAACACCCCTGAGAGTTGAAGACACGGGTATC
TACTACTGTGCGAGAAATATAGAGGAGTTTAGTGTTCCACAGTTCGA
TTCTTGAGCGGTTCGAAGCTACTACCACTATTTTGGGATGGACGTCT
GGGGCCAAGGGACCAACGGTCACCGTCTCGAGCGCCTCCACCAAGGGC
CCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGGCAC
AGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG
TGTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCGGCT
GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC
CTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC
CCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAA
AACTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGT
CAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCCTCATGATCTCCCGGA
CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAG
GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGAC
AAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
CTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA
GGTCTCCAACAAAGCCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAG
CCAAAGGGCAGCCCCGAGAACACAGGTGTACACCCCTGCCCCCATCCCGG
GAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCT

TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA
 GAACAACCTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCT
 TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA
 CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC
 AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 514)

[0797] 6843_G20 (PGT-154) gamma heavy chain variable region nucleotide sequence:

CAGGTGCAGCTGGTGGAAATCGGGAGGAGGCGTGGTCCAGCCTGGAA
 AGTCCCTCAGACTCTCATGTGTCGTCTCTAATTTTCATCTTTAATAAAT
 ATCCTATGTATTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGG
 GTGGCAGCCATCTCCGTGATGCCTGGCATGTAGACTACGCAGCCTC
 CGTGAAGGACCGATTTCTCATCTCCAGAGACAATTCCAAGAATGCTC
 TATATTTGGAAATGAACACCCTGAGAGTTGAAGACACGGGTATCTAC
 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****NFIFNK******YPMY****WVRQAPGKGLEWVAA*
ISADAWHVDYAASVKDRFLISRDNSKNALYLEMNTLRVEDTGIYYCARNIEE
FSVPQFDSWSGRSYYHYFGMDV***WGQ****TTVTVSS*
 TSGVHTFPAVLQSSGLYSLSSVTVPSSTLTQTYICNVNHKPSNTKVDKRV
 PKSCDKTHTCPPCPAPELGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
 EDPVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
 KCKVSNKALPAPIEKTISKAKGQPREPVYTLPPSREEMTKNQVSLTCLVKGF
 YPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
 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***NFIFNK******YPMY***WVRQAPGKGLEWVAA
ISADAWHVDYAASVKDRFLISRDNSKNALYLEMNTLRVEDTGIYYCARNIEE
FSVPQFDSWSGRSYYHYFGMDV***WGQ***TTVTVSS (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
GGAGTGTCCGACAGGTTTCGCTGGCAGCGGGTCACGTACACAATTCAC
ATTGAAAATTAGTCGGGTGGAGGCTGAAGATGTTGGCGTTTATTACT
GCA TGCAAAGTAGAGACTTCCCAATCACTTTTGGCGGAGGGACCAGG
GTGGATCTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCC
ATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAA
TAAC TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCC
TCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGA
CAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTAC
GAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTC
CCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:522)

[0803] 6843_G20 (PGT-154) light chain variable region nucleotide sequence:

GACATTGTGATGACTCAGACTCCTGTCTCTCTGTCCGTCAGTCTTGGA
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
VEAEDVG VYYCMQSRDFPITFGGGTRVDLKR TVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLT
LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 524)

[0805] 6843_G20 (PGT-154) light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

DIVMTQTPVSLSVSLGQAASISCSSESLSGRGDGRITYLHWYRQKPGQTPQLL
 MYEVSTRFSGVSDRFAGSGSRTQFTLKISRVEAEDVGVYYCMQSRDFPITFG
 GGTRVDLK (SEQ ID NO: 525)

[0806] 6843_G20 (PGT-154) light chain Kabat CDRs:

CDR 1: SSESLSGRGDGRITYLH (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: SSESLSGRGDGRITYLH (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)

ATGGAATTGGGGCTGAGCTGGGTTTTCTCGTCGTTCTCCTAAGAGGTGTCCA
CTGTCAGGTGCATCTGGTGGAGTCGGGGGGAGGCGTGGTCCAACCTG
GGAAGTCCCTAAGACTCTCCTGTGAAACCTCTGGCTTCATCTTCAACG
AATATCCCATGTATTGGATCCGCCAGGCTCCAGGCAAGGGACCGGAG
TGGGTGGCCGCCATCTCCGCTGACGCCTGGCATGTGGACTACGCAGG
CTCCGTGCGGGGCCGATTTACCGTCTCCAGAGACAATTCTAAGAATT
CTCTATATTTAGACATGAAGAGTCTGAAAGTTGAAGACACGGCTATAT
ATTTCTGTGCGAAAGATGGGGAGGAACACAAGGTACCACAATTGCAT
TCCTGGAGCGGACGAACTTATATCACTACACTGGTTTTGACGTCTG
GGGCCCAAGGACCAACGGTCACCGTCTCGAGCGCCTCCACCAAGGGCC
CATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGT
GTCGTGGAACCTCAGGCGCCCTGACCAGCGCGGTGCACACCTTCCCGGCTG
TCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCT
CCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCC
AGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAA
CTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGGACCGTCA
GTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACC
CCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA
AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC
TCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA
GGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAG
CCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCGG
GAGGAGATGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCT
TCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA
GAACAACCTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCT
TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA

CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC
AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:529)

[0809] 6892_D19 (PGT-155) gamma heavy chain variable region nucleotide sequence:

CAGGTGCATCTGGTGGAGTCGGGGGGAGGCGTGGTCCAACCTGGGA
AGTCCCTAAGACTCTCCTGTGAAACCTCTGGCTTCATCTTCAACGAAT
ATCCCATGTATTGGATCCGCCAGGCTCCAGGCAAGGGACCGGAGTGG
GTGGCCGCCATCTCCGCTGACGCCTGGCATGTGGACTACGCAGGCTC
CGTGCGGGGCCGATTACCGTCTCCAGAGACAATTCTAAGAATTCTC
TATATTTAGACATGAAGAGTCTGAAAGTTGAAGACACGGCTATATAT
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.

MELGLSWVFLVVLLRGVHCQVHLVESGGGVVQPGKSLRLSCETSGFIFNEY
PMYWIRQAPGKGPEWVA*AI***SADAWHVDYAGSVRGRFTVSRDNSKNSLY**
LDMKSLKVEDTAIYFCAKDGE**EHKVPQLHSW****SGRNLYHYTGFDVWGPG**
TTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL
TSGVHTFPAVLQSSGLYSLSSVTVPS**SSLGTQTYICNVNHKPSNTKVDKRV**
E**PKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE**
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
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)

QVHLVESGGGVVQPGKSLRLSCETSGFIFNEYPMYWIRQAPGKGPEWVAAI
ADAWHVDYAGSVRGRFTVSRDNSKNSLYLDMKSLKVEDTAIYFCAKDGE
EHKVPQLHSWSGRNLYHYTGFDVWGPGTTVTVSS (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: DGEHVKVPQLHSWSGRNLYHYTGFDV (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: DGEHVKVPQLHSWSGRNLYHYTGFDV (SEQ ID NO: 535)

[0814] 6892_D19 (PGT-155) light chain nucleotide sequence: coding sequence (variable region in bold)

ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGATACCTGAACT
TGCTGCAGACATTGTGATGACCCAGTCTCCTGTCTCTCTGTCCGTCAC
CCTCGGACAGCCGGCCTCCATGTCCTGCAAGTCCAGTCAGAGTGTCC
GACAGAGTGATGGCAAGACTTTCTTATATTGGTATCGACAGAAGCCA
GGCCAGTCTCCACAACCTGTTAATATATGAGGGTTCGAGTCGATTCTCT
GGAGTGTGAGATAGGATCTCTGGCAGCGGGTCAGGGACAGACTTCAC
ACTGAGGATCAGTCGAGTGGAGGCTGAGGATGCTGGCGTTTACTTCT
GCTTGCAAACATAAGACTTCCCCCTCACTTTTGGCGGAGGGACCAGG
GTGGATCTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCC
ATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAA
TAAGTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCC
TCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGA
CAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTAC
GAGAAACACAAAGTCTACGCTGCGAAGTCACCCATCAGGGCCTGAGCTC
GCCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:537)

[0815] 6892_D19 (PGT-155) light chain variable region nucleotide sequence:

GACATTGTGATGACCCAGTCTCCTGTCTCTCTGTCCGTCACCCTCGGA
CAGCCGGCCTCCATGTCCTGCAAGTCCAGTCAGAGTGTCCGACAGAG
TGATGGCAAGACTTTCTTATATTGGTATCGACAGAAGCCAGGCCAGT
CTCCACAACCTGTTAATATATGAGGGTTCGAGTCGATTCTCTGGAGTGT
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.

MRLPAQLLGLMLWIPELAADIVMTQSPVLSVTLGQPASMSCKSSQSVRQS
DGKTFLYWYRQKPGQSPQLLIYEGSSRFSGVSDRISGSGSGTDFTLRISRV
EAEDAGVYFCLQTKDFPLTFGGGTRVDLKRVAAPSVFIFPPSDEQLKSGT
ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLT
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)

*DIVMTQSPVLSVTLGQPASMSCK**KSSQSVRQSDGKTFLYWYRQKPGQSPQLLI*
*YEGSSRFSGVSDRISGSGSGTDFTLRISRVEAEDAGVYFCL**QTKDFPLTFGGG*
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
TCCTGGAGCGGACGAACTTATATCACTACACTGGTTTTGACGTCTG
GGGCCCAGGGACCACGGTCAACCGTCTCGAGCGCCTCCACCAAGGGCC
CATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGT
GTCGTGGAATCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCGGCTG
TCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCT
CCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCC
AGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAA
CTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGGACCGTCA
GCTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACC
CCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA
AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC
TCACCGTCTTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA
GGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAG
CCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
GAGGAGATGACCAAGAACCAGGTACGCCTGACCTGCCTGGTCAAAGGCT
TCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA
GAACAACACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCT
TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA
CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC
AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO: 544)

[0821] 6808_B09 (PGT-156) gamma heavy chain variable region nucleotide sequence:

CAGGTGCATCTGGTGGAGTCGGGGGGAGGCGTTGTCCAACCTGGAA
 AGTCCCTAAGACTCTCCTGTGAAACCTCTGGCTTCATCTTCAATCAAT
 ATCCCATGTATTGGGTCCGCCAGGCTCCAGGCAAGGGACCGGAGTGG
 GTGGCCGCCATCTCCGCTGATGCCTGGCATGTGGACTACCCAGGCTC
 CGTGCGGGGCCGATTTACCGTCTCCAGAGACAATTCCAAGAGTTCTC
 TATATTTAGACATGAAGAGTCTGAAAGTTGAAGACACGGCTATATATT
 TCTGTGCGAAAGATGGGGAGGAAACAAAGGTACCACAATTGCATTCC
 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
LDMKSLKVEDTAIYFCAKDGE**HKVPQLHSW****SGRNLYHYTGFDVWGPG**
TTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL
TSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRV
E
PKSCDKHTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
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
SADAWHVDYPGSVRGRFTVSRDNSKSSLYLDMKSLKVEDTAIYFCAKDGE
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**)

ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGATACCTGAACT
 TGCTGCAGACATTGTGATGACCCAGTCTCCTGTCTCTCTGTCCGTCAC
 CCTCGGACAGCCGGCCTCCATGTCCTGCAAGTCCAGTCAGACTGTCC
 GACAGAGTGATGGCAAGACTTTCTTATATTGGTATCGACAGAAGGCA
 GGCCAGTCTCCACAACCTGTTAATATATGAGGGTTCGAATCGATTCTCT
 GGAGTGTCAGATAGGATCTCTGGCAGCGGGTCCGGGGACAGATTTCAC
 ACTGAGAATCAGTCGAGTGGAGGCTGAGGATGTTGGCGTTTATTTCT
 GCCTGCAAACTAAAGACTTCCCCCTCACTTTTGGCGGAGGGACCAGG
 GTGGATATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCC
 ATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGTGCCTGCTGAA
 TAACTTCTATCCCAGAGAGGGCCAAAGTACAGTGGAAGGTGGATAACGCCC
 TCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGA
 CAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTAC
 GAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTC
 GCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:551)

[0827] 6808_B09 (PGT-156) light chain variable region nucleotide sequence:

GACATTGTGATGACCCAGTCTCCTGTCTCTCTGTCCGTCACCCCTCGGA
 CAGCCGGCCTCCATGTCCTGCAAGTCCAGTCAGACTGTCCGACAGAG
 TGATGGCAAGACTTTCTTATATTGGTATCGACAGAAGGCAGGCCAGT
 CTCCACAACCTGTTAATATATGAGGGTTCGAATCGATTCTCTGGAGTGT
 CAGATAGGATCTCTGGCAGCGGGTCCGGGGACAGATTTCACTGAGA
 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**.

MRLPAQLLGLMLWIPELAADIVMTQSPVLSVTLGQPASMSCKSSQTVRQS
DGKTFLYWYRQKAGQSPQLLIYEGSNRFSGVSDRISGSGSGTDFTLRISR
 VEAEDVG **VYFCLQTKDFPLTFGGG**TRVDIKRTVAAPSVFIFPPSDEQLKSG
 TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLT
 LSKADYEEKHKVYACEVTHQGLSSPVTKSFNRGEC (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**KSSQTVROS*****SDGKTFLYWYRQKAGQSPQLL***
IYEGSNRFSGVSDRISGSGSGTDFTLRISRVEAEDVG ***VYFCLQTKDFPLTFGG***
 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
GGGCCAGGGACACGGTCACCGTCTCGAGCGCCTCCACCAAGGGCC
CATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGT
GTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCGGCTG
TCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCT
CCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCC
AGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAA
CTCACACATGCCACCGTGCCAGCACCTGAACCTCTGGGGGGACCGTCA
GTCTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACC
CCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
CAAGTTCAACTGGTACGTGGACGGCGTGAGGTGCATAATGCCAAGACA
AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC
TCACCGTCTGCAACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA
GGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAG
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
PMYWIRQAPGKGLEWVA AISADAWHVDYAGSVRGRFTVSRDNSKNSLY
LDMNSLTVEDTAIYFCAKDGE EHEVPQLHSWSGRNLYHYTGVDIWGPC
TTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL
TSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVE
PKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFS
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)

*EVHLVESGGGVVQPGKSLRLSCVTSGFIFKQYPMYWIRQAPGKGLEWVA AI
SADAWHVDYAGSVRGRFTVSRDNSKNSLYLDMNSLTVEDTAIYFCAKDGE
EHEVPQLHSWSGRNLYHYTGVDIWGP GTTVTVSS (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: DGE EHEVPQLHSWSGRNLYHYTGVDI (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: DGE EHEVPQLHSWSGRNLYHYTGVDI (SEQ ID NO: 561)

[0838] 6892_C23 (PGT-157) light chain nucleotide sequence: coding sequence (variable region in bold)

*ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGATACCTGAACT
TACTGCAGACATTGTGATGACCCAGACTCCTGTCTCTCTGTCCGTCAC
CCTCGGACAGCCGGCCTCCATGTCCTGTAAGTCCAGTCAGAGCCTCC
GACAAAGTGATGGCAAGACTTTCTTGATTGGTATCGACAGAAGGCA
GGCCAGTCTCCACAACTCCTAATATCTGAGGCTTCGAATCGATTCTCT*

GGAGTGTGATAGGTTCTCTGGCAGCGGTTGAGGGACAGACTTCAC
 ACTGAAAATCAGTCGGGTGGAGGCTGAGGATGTTGGCATTATTTCT
 GCATGCAAATAAGACTTCCCCCTCACTTTTGGCGGAGGGACCAAG
 GTGGATCTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCC
 ATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCGTCTGAA
 TAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCC
 TCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGA
 CAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTAC
 GAGAAACACAAAGTCTACGCTGCGAAGTCACCCATCAGGGCCTGAGCTC
 GCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:563)

[0839] 6892_C23 (PGT-157) light chain variable region nucleotide sequence:

GACATTGTGATGACCCAGACTCCTGTCTCTCTGTCCGTCACCCCTCGG
 ACAGCCGGCCTCCATGTCCTGTAAGTCCAGTCAGAGCCTCCGACAAA
 GTGATGGCAAGACTTTCTTGTATTGGTATCGACAGAAGGCAGGCCAG
 TCTCCACAACCTCCTAATATCTGAGGCTTCGAATCGATTCTCTGGAGTG
 TCAGATAGGTTCTCTGGCAGCGGTTGAGGGACAGACTTCACACTGAA
 AATCAGTCGGGTGGAGGCTGAGGATGTTGGCATTATTTCTGCATGC
 AAATAAGACTTCCCCCTCACTTTTGGCGGAGGGACCAAGGTGGAT
 CTCAA (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.

MRLPAQLLGLMLWIPELTADIVMTQTPVSLSVTLGQPASMSCKSSQSLRQS
DGKTFLYWYRQKAGQSPQLLISEASNRFSGVSDRFSGSGSGTDFTLKISR
 VEAEDVGIYFCMQTKDFPLTFGGG**TKVD**LKRTVAAPSVFIFPPSDEQLKSG
 TASVVCLLNFPYREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLT
 LSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 565)

[0841] 6892_C23 (PGT-157) light chain variable region amino acid sequence: (Kabat CDRs underlined, Chothia CDRs in bold italics)

DIVMTQTPVSLSVTLGQPASMSCKSSQSLRQSDGKTFLYWYRQKAGQSPQLL
 ISEASNRFSGVSDRFSGSGSGTDFTLKISRVEAEDVGIYFCMOTKDFPLTFGG
 GTKVDLK (SEQ ID NO: 566)

[0842] 6892_C23 (PGT-157) light chain Kabat CDRs:

CDR 1: KSSQSLRQSDGKTFLY (SEQ ID NO: 567)

CDR 2: EASNRFS (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)

ATGGAATTGGGGCTGAGCTGGGTTTTCCTCGTCGCTCTCCTAAGAGGTGTCCA
CTGTGAGGTGCGTCTGATGGAGTCGGGGGGAGGCGTGGTCCAGCCTG
GGAAGTCCCTCAGACTCTCCTGTGTAACCTCTGGCTTCATCTTCAAAA
AATATCCTATGTAAGTCCGCGGCTCCAGGCAAGGGGCTGGAG
TGGGTGGCCGCGCATCTCCGCTGATGCCTGGCATGTGGACTACCCAGG
CTCCGTGCGGGGCGGATTTACCGTCTCAAGAGACAACCTCCAAGAATT
CTCTATATTTAGACATGAATAGTCTGACAGTAGAAGACACGGCTATAT
ATTTTGTGCGAAAGATGGGGAGGAACACGAAGTCCCACAACCTGCAC
TCCTGGAGCGGACGAAATTTATATCACTACACTGGTGTAGACGTCTG
GGGCCCAGGGACACGGTCACCGTCTCGAGCGCTCCACCAAGGGCC
CATCGGTCTTCCCCCTGGCACCTCTCCTCAAGAGCACCTCTGGGGGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGT
GTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCGGCTG
TCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCT
CCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCC
AGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAA
CTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTCA
GTCTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACC
CCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA
AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC
TCACCGTCTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA
GGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAG
CCAAAGGGCAGCCCCGAGAACACAGGTGTACACCCTGCCCCCATCCCGG
GAGGAGATGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGCT
TCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA
GAACAACACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCT
TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA
CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC
AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:570)

[0845] 6881_N05 (PGT-158) gamma heavy chain variable region nucleotide sequence:

GAGGTGCGTCTGATGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGA
AGTCCCTCAGACTCTCCTGTGTAACCTCTGGCTTCATCTTCAAAAAAT
ATCCTATGTAAGTCCGCGGCTCCAGGCAAGGGGCTGGAGTGG
GTGGCCGCGCATCTCCGCTGATGCCTGGCATGTGGACTACCCAGGCTC
CGTGCGGGGCGGATTTACCGTCTCAAGAGACAACCTCCAAGAATTCTC
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
*PMYWIRQAPGKGLEWVA****AI****SADAWHVDYPGSVRGRFTVSRDNSKNSLY*
*LDMNSLTVEDTAIYFCAKD*GEEHEVPQLHSW****SGRNLYHYTGVDVWGPG***
TTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL
TSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVE
PKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
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)

*EVRLMESGGGVVQPGKSLRLSCVTSG****FIFKKYPMYWIRQAPGKGLEWVA******AI***
SADAWHVDYPGSVRGRFTVSRDNSKNSLYLDMNSLTVEDTAIYFCAKD***GEE***
HEVPQLHSW***SGRNLYHYTGVDVWGPGTTVTVSS*** (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: DGEEHEVPQLHSWSGRNLYHYTGVDV (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: DGEEHEVPQLHSWSGRNLYHYTGVDV (SEQ ID NO: 574)

[0850] 6881_N05 (PGT-158) light chain nucleotide sequence: coding sequence (variable
region in bold)

ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGATACCTGAAGT
GACTGCAGACATTGTGATGACCCAGACTCCTGTCTCTGTGTCCGTAC
CCTCGGACAGCCGGCCTCCATGTCTGCAAGTCCAGTCAGAGCGTCC
GACAAAGTGATGGCAAGACTTTTTTATATTGGTATCGACAGAAGGCA
GGCCAGTCTCCACAACCTCTTAATATATGAGGCTTCGAAGCGATTCTCT
GGAGTGTCTCAGATAGGTTCTCTGGCAGCGGGTCAGGGACAGACTTCAC
ACTGAAAATCAGTCGGGTGGGGGCTGAGGATGTTGGCGTTTATTTCT
GCATGCAAACTAAAGACTTCCCCCTTACTTTTGGCGGAGGGACCAAG

GTGGATCTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCC
 ATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAA
 TAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCC
 TCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGA
 CAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTAC
 GAGAAACACAAAGTCTACGCTGCGAAGTCACCCATCAGGGCCTGAGCTC
 GCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:576)

[0851] 6881_N05 (PGT-158) light chain variable region nucleotide sequence:

GACATTGTGATGACCCAGACTCCTGTCTCTGTGTCCGTCACCCCTCGG
 ACAGCCGGCCTCCATGTCCTGCAAGTCCAGTCAGAGCGTCCGACAAA
 GTGATGGCAAGACTTTTTTATATTGGTATCGACAGAAGGCAGGCCAG
 TCTCCACAACCTCTTAATATATGAGGCTTCGAAGCGATTCTCTGGAGTG
 TCAGATAGGTTCTCTGGCAGCGGGTCAGGGACAGACTTCACACTGAA
 AATCAGTCGGGTGGGGGCTGAGGATGTTGGCGTTTATTTCTGCATGC
 AAATAAGACTTCCCCCTTACTTTTGGCGGAGGGACCAAGGTGGAT
 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
DGKTFLYWYRQKAGQSPQLLIYEASKRFSGVSDRFSGSGSGTDFTLKISR
 VGAEDVG**VYFCMQTKDFPLTFGGG**TKVDLKRTVAAPSVFIFPPSDEQLKS
 GTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSST
 LTLSKADYEEKHKVYACEVTHQGLSPVTKSFNRGEC (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**KSSQSVROS****DGKTFLY**WYRQKAGQSPQLL
 IY**EASKRFS**GVSDRFSGSGSGTDFTLKISR**VGAEDVG****VYFCMQTKDFPLT**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), AISADAWHVYSGSVQG (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), AISADAWHV (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:

KSSQSLRQSNGKTSLY (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: KRHMH (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: KSSQSLRQSNGKTYLY (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: KSSQSLRQSNGKTYLY (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), MVTPIFGKAKYSQRFEG (SEQ ID NO: 105), DRRVPIATDNWLDP (SEQ ID NO: 9), SYAFS (SEQ ID NO: 110), MITPVFGETKYAPRFQG (SEQ ID NO: 111), DRRVVPMTDNWLDP (SEQ ID NO: 8), DYLLH (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), TKHGRRIGVVAFKWFTYFYMDV (SEQ ID NO: 262), DAYWS (SEQ ID NO: 169), YVHHSGDTNYPNPSLKR (SEQ ID NO: 170), ALHGKRIYGIVALGELFTYFYMDV (SEQ ID NO: 171), ACTYFWG (SEQ ID NO: 185), SLSHCQSFWSGWTFHNPSLKS (SEQ ID NO: 186), FDGEVLVYNHWPKEAWVDL (SEQ ID NO: 187), ACDYFWG (SEQ ID NO: 201), GLSHCAGYYNTGWTYHNPSLKS (SEQ ID NO: 202), FDGEVLVYHDWPKPAWVDL (SEQ ID NO: 203), TGHYYWG (SEQ ID NO: 217), HIHYTTAVLHNPSLKS (SEQ ID NO:

218), SGGDILYYYEWQKPHWFSP (SEQ ID NO: 219), GGEWGDKDYHWG (SEQ ID NO: 233), SIHWGRGTTHYKESLRR (SEQ ID NO: 234), HRHHDVFMVLVPIAGWFDV (SEQ ID NO: 235), GTDWGENDFHYG (SEQ ID NO: 250), SIHWGRGTTHYKTSFRS (SEQ ID NO: 251), HKYHDIFRVVPVAGWFDP (SEQ ID NO: 252), KYDVH (SEQ ID NO: 277), WMSHEGDKTESAQRFG (SEQ ID NO: 278), GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV (SEQ ID NO: 279), WISHERDKTESAQRFG (SEQ ID NO: 293), GSKHRLRDYVLYDDYGLINQQEWNDYLEFLDV (SEQ ID NO: 308), RCNYFWG (SEQ ID NO: 320), SLSHCRSYNTDWTYHNPSLKS (SEQ ID NO: 321), FGGEVLVYRDWPKPAWVDL (SEQ ID NO: 322), ACNSFWG (SEQ ID NO: 326), SLSHCASYWNRGWYHNPSLKS (SEQ ID NO: 335), FGGEVLRYTDWPKPAWVDL (SEQ ID NO: 336), TGHYHWG (SEQ ID NO: 348), HIHYNTAVLHNPALKS (SEQ ID NO: 349), SGGDILYIEWQKPHWFYP (SEQ ID NO: 350), GGEWGDSYHWG (SEQ ID NO: 364), SIHWGRGTTHYNAPFRG (SEQ ID NO: 365), HKYHDIVMVVPIAGWFDP (SEQ ID NO: 366), NHDVH (SEQ ID NO: 378), WMSHEGDKTGLAQKFQG (SEQ ID NO: 379), GSKHRLRDYFLYNEYGPNEYEWGDYLATLDV (SEQ ID NO: 380), NYWT (SEQ ID NO: 406), YISDRETTTYNPSLNS (SEQ ID NO: 407), ARRGQRIYGVVSFGEFFYYMDV (SEQ ID NO: 408), GRFWS (SEQ ID NO: 421), YFSDTDRSEYNPSLRS (SEQ ID NO: 422), AQQGKRIYGIVSFGEFFYYMDA (SEQ ID NO: 423), AQQGKRIYGIVSFGELFYMDA (SEQ ID NO: 436), SGGDILYYNEWQKPHWFYP (SEQ ID NO: 445), SLSHCAGYYNSGWYHNPSLKS (SEQ ID NO: 455), FGGEVLVYHDWPKPAWVDL (SEQ ID NO: 456), GCDYFWG (SEQ ID NO: 464), FDGEVLVYNDWPKPAWVDL (SEQ ID NO: 465), KYPMY (SEQ ID NO: 475), AISGDAWHVVYSNSVQG (SEQ ID NO: 476), MFQESGPPRLDRWSGRNYYYSGMDV (SEQ ID NO: 477), AISADAWHVYSGSVQG (SEQ ID NO: 491), MFQESGPPRFDSWSGRNYYYSGMDV (SEQ ID NO: 492), KRHMH (SEQ ID NO: 503), VISSDAIHVDYASSVRG (SEQ ID NO: 504), DRDGYGPPQIQTWSGRYLHLYSGIDA (SEQ ID NO: 505), AISADAWHVDYAASVKD (SEQ ID NO: 518), NIEFSVPQFDSWSGRSYHYFGMDV (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), MVTPIFGAEK (SEQ ID NO: 269), DRRVPIATDNWLDP (SEQ ID NO: 9), GGAFSS (SEQ ID NO: 270), MITPVFGETK (SEQ ID NO: 271), DRRVVPMATDNWLDP (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), YVHHS GDTN (SEQ ID NO: 173), ALHGKRIYGI VALGELFTYFYMDV (SEQ ID NO: 171), GESTGACT (SEQ ID NO: 188), SLSHCQSFWSGSGWTF (SEQ ID NO: 189), FDGEVLVYNHWP KPAWVDL (SEQ ID NO: 187), GDSTAACD (SEQ ID NO: 204), GLSHCAGYYNTGW TY (SEQ ID NO: 205), FDGEVLVYHDWPKPAWVDL (SEQ ID NO: 203), GESINTGH (SEQ ID NO: 220), HIHYTTAVL (SEQ ID NO: 221), SGGDILYYYEWQKPHWFSP (SEQ ID NO: 219), GDSIRGGEWGD KD (SEQ ID NO: 236), SIHWRTGTH (SEQ ID NO: 237), HRHHDVFM LVPIAGWFDV (SEQ ID NO: 235), GGSMTGTDWGEND (SEQ ID NO: 253), SIHWRTGTH (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), 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), SLSHCASYWNRGW TY (SEQ ID NO: 338), FGGEVLRYTDWPKPAWVDL (SEQ ID NO: 336), GDSINTGH (SEQ ID NO: 351), HIHYNTAVL (SEQ ID NO: 352), SGGDILYYIEWQKPHWFYP (SEQ ID NO: 350), GGSIRGGEWGDSD (SEQ ID NO: 367), SIHWRTGTH (SEQ ID NO: 237), HKYHDIVMVVPIAGWFDP (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), ARRGQRIYGVVSFGGEFFYYYYMDV (SEQ ID NO: 408), NGSVSG (SEQ ID NO: 424), YFSDTDRSE (SEQ ID NO: 425), AQQGKRIYGIVSFGGEFFYYYYMDA (SEQ ID NO: 423), AQQGKRIYGIVSFGELFYFFYYMDA (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), QQSFTPT (SEQ ID NO: 42), RASQTIHTYLN (SEQ ID NO: 113), GASTLQS (SEQ ID NO: 114), QQSYSTPT (SEQ ID NO: 43), SGSKLGDKYVS (SEQ ID NO: 120), ENDRRPS (SEQ ID NO: 121), QAWETTTTTFVF (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),

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), KSSES LRQSNGKTS LY (SEQ ID NO: 484), EVSNRFS (SEQ ID NO:
 485), MQSKDFPLT (SEQ ID NO: 486), KSSQSLRQSNGKTS LY (SEQ ID NO: 498),
 KSSQSLRQSNGKTYLY (SEQ ID NO: 512), EVSIRFS (SEQ ID NO: 513),
 SSSES LRGRDGR TYLH (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), 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), QAWETTTTTFVF (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.

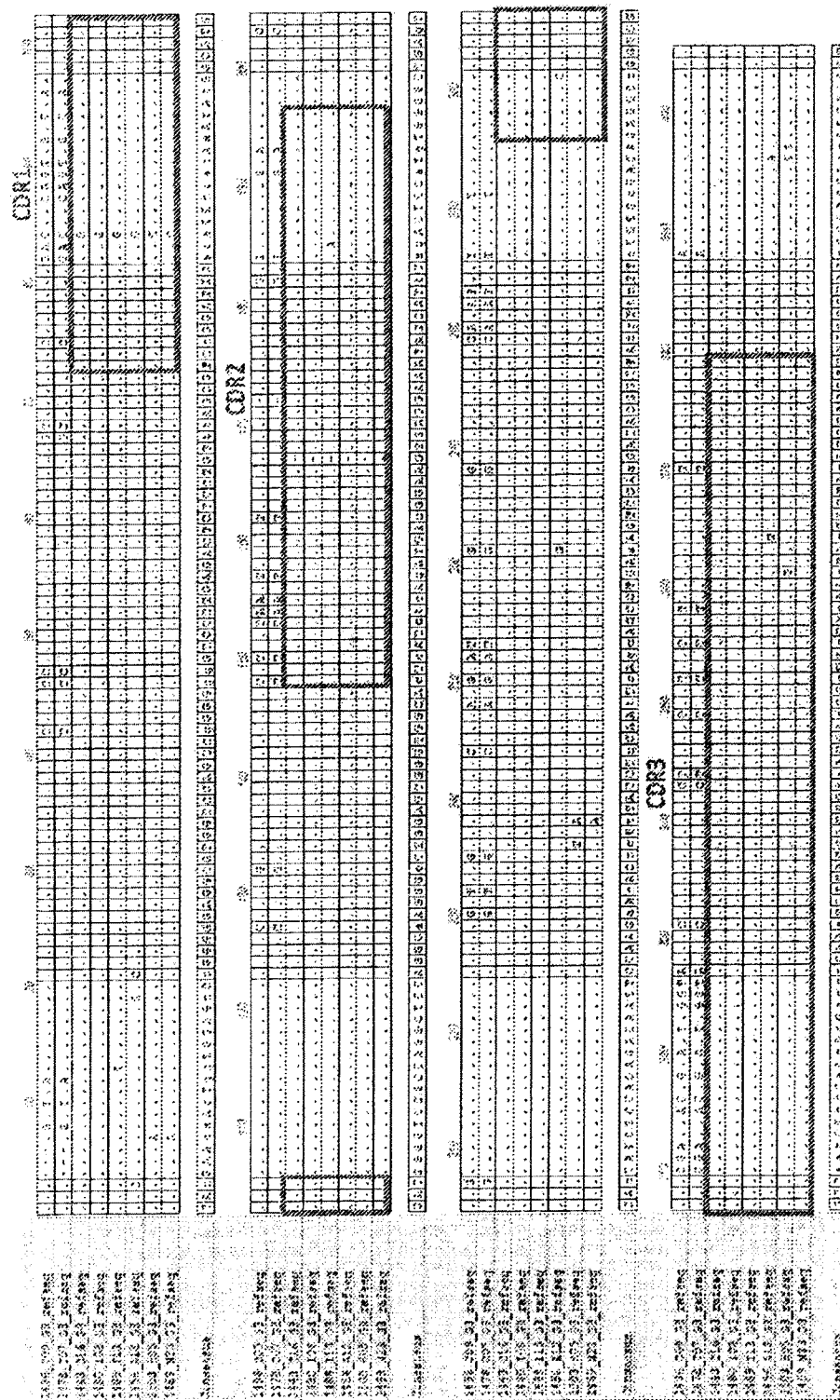
[0887] Exemplary alleles of the IGLV2-8 germline gene include, but are not limited to, IGLV2-8*01 and IGLV2-8*02. Antibodies of the invention are derived from the IGLV3-21 germline gene, or an allele thereof. Exemplary alleles of the IGLV3-21 germline gene include, but are not limited to, IGLV3-21*01, 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, L12088, 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.

Table 7. Alignment of heavy chain coding sequences of 1443 C16 sister clones to 1443 C16 and 1496 C09.

Kabat CDR sequences for the PG16 sister clones are highlighted in boxes.



Kabat CDR sequences for the PG16 sister clones are highlighted in boxes.

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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 AATGGAACCAGAAAGTGACGTTGGTGGATTTGACTCTGTCTCC (SEQ
ID NO: 82)

1456 A12 AATGGAACCAGCCGTGACGTTGGTGGATTTGACTCTGTCTCC (SEQ
ID NO: 83)

1503 H05 AATGGAACCAGAAAGTGACGTTGGTGGATTTGACTCTGTCTCC (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); Riechmann *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

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 244

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 244

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 IS CLAIMED ARE DEFINED AS FOLLOWS:

1. An antibody, comprising a heavy chain with a CDR 1 comprising the amino acid sequence SYAFS (SEQ ID NO: 110), a CDR 2 comprising the amino acid sequence MITPVFGETKYAPRFQG (SEQ ID NO: 111), and a CDR 3 comprising the amino acid sequence DRRVVPMATDNWLDP (SEQ ID NO: 8), and a light chain with a CDR 1 comprising the amino acid sequences of RASQTIHTYLN (SEQ ID NO: 113), a CDR 2 comprising the amino acid sequence GASTLQS (SEQ ID NO: 114), and a CDR 3 comprising the amino acid sequence QQSYSTPRT (SEQ ID NO: 43), wherein the CDRs are per Kabat definition.

2. The antibody of claim 1, wherein heavy chain variable sequence comprises the amino acid sequence of SEQ ID NO: 35 and light chain variable sequence comprises the amino acid sequence of SEQ ID NO: 36.

3. A fragment of the antibody of claim 1 or 2, wherein the fragment has the same binding specificity as the antibody of claim 1 or 2.

4. The fragment of claim 3, which is selected from the group consisting of the Fab, Fab', F(ab')₂, Fv, single chain Fv, diabody, and domain antibody (dAb) fragments.

5. An isolated nucleic acid molecule encoding the antibody of claim 1 or 2, or the fragment thereof of claim 3 or 4.

6. The nucleic acid molecule of claim 5, wherein the nucleic acid molecule comprises the nucleotide sequence of SEQ ID NO: 109 encoding a heavy chain variable sequence and the nucleotide sequence of SEQ ID NO: 112 encoding a light chain variable sequence.

7. The nucleic acid molecule according to claim 5 or 6, which is selected from the group consisting of cDNA, hnRNA, and mRNA.

8. A vector comprising the nucleic acid molecule of any one of claims 5 to 7.
9. A cell comprising the nucleic acid molecule of any one of claims 5 to 7.
10. An immortalized B cell clone expressing the antibody of claim 1 or 2.
11. A pharmaceutical composition comprising a pharmaceutically acceptable carrier and the antibody of claim 1 or 2, or the fragment of claim 3 or 4 or the nucleic acid molecule as recited in any one of claims 5 to 7.

FIG. 1A Heavy Chain Tree

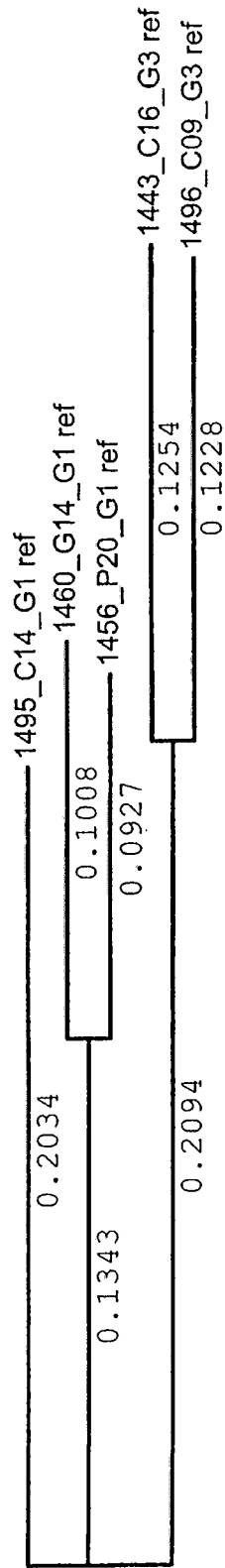


FIG. 1B Light Chain Tree

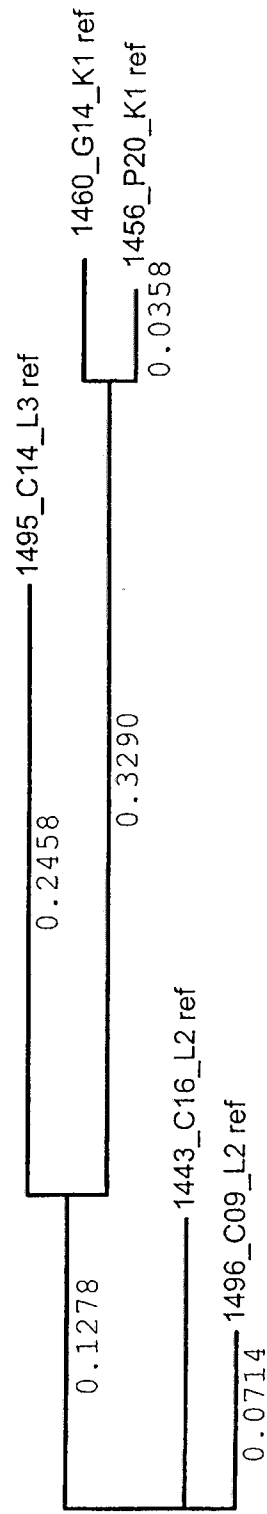


FIG. 2

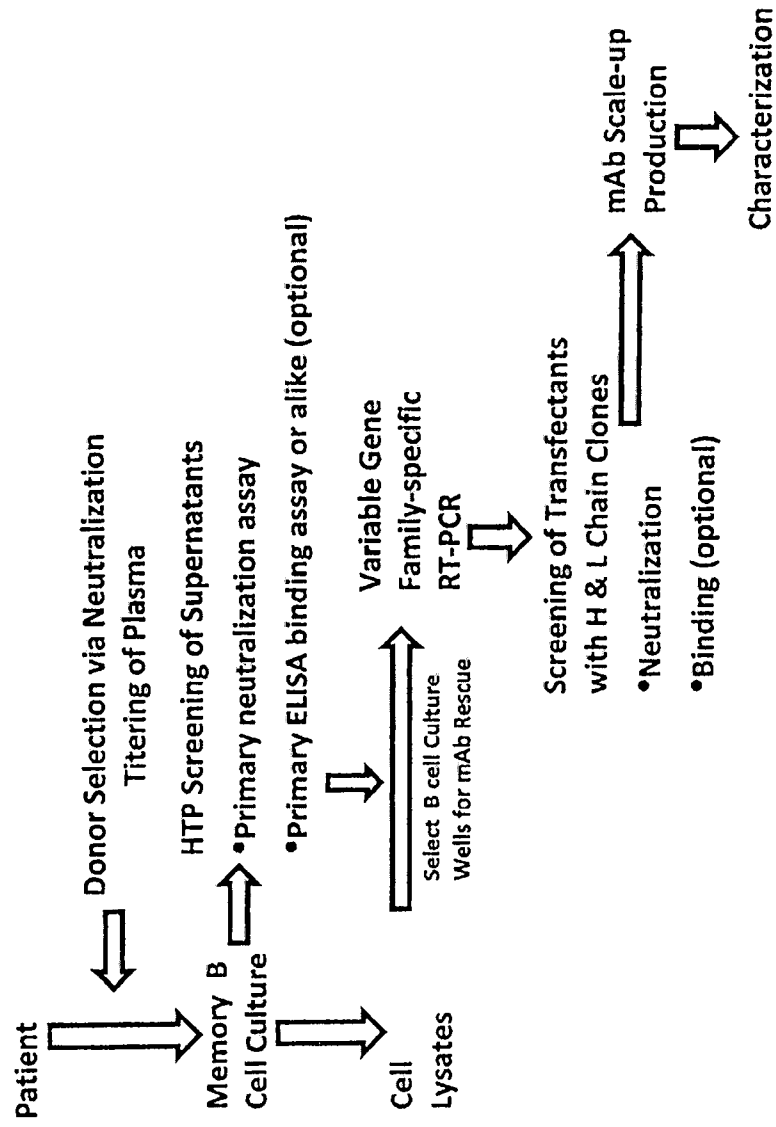
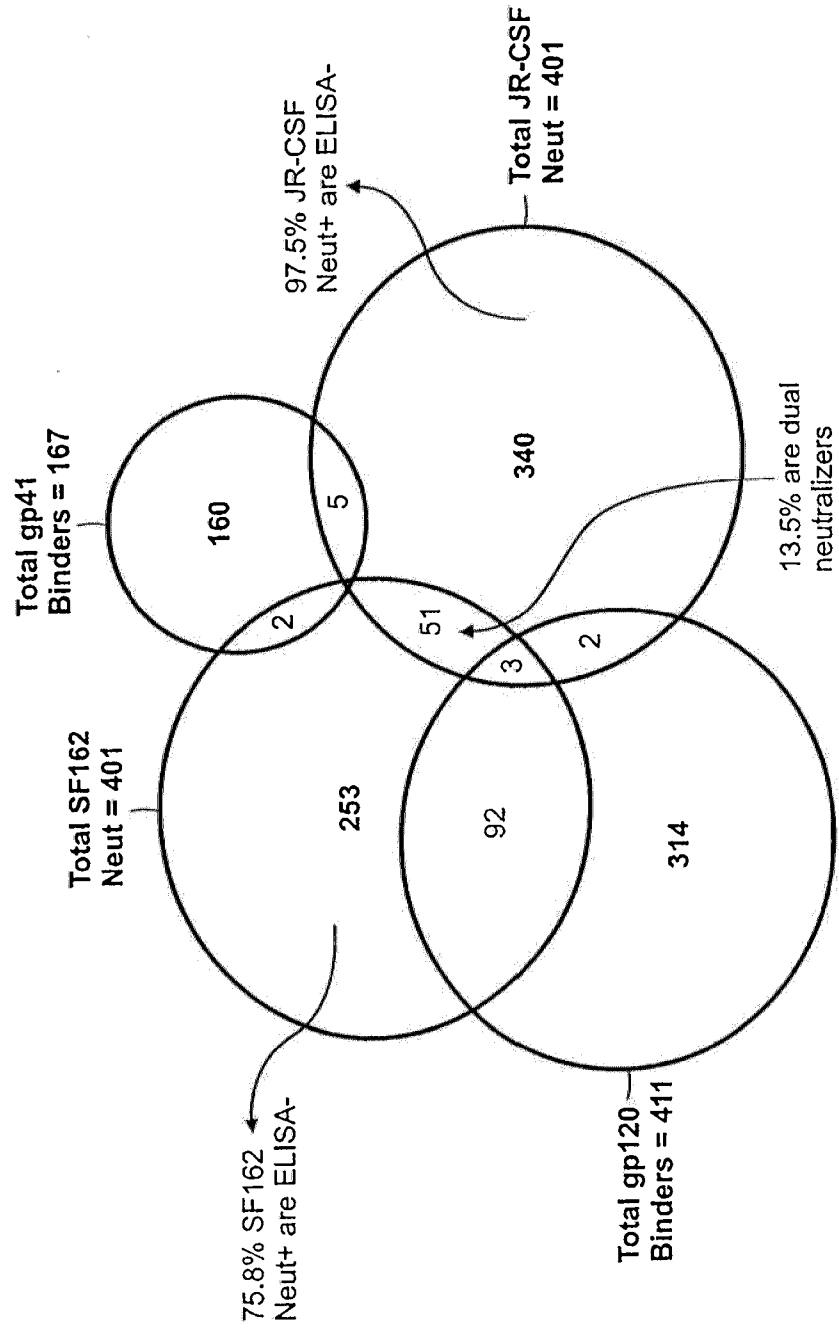


FIG. 3A



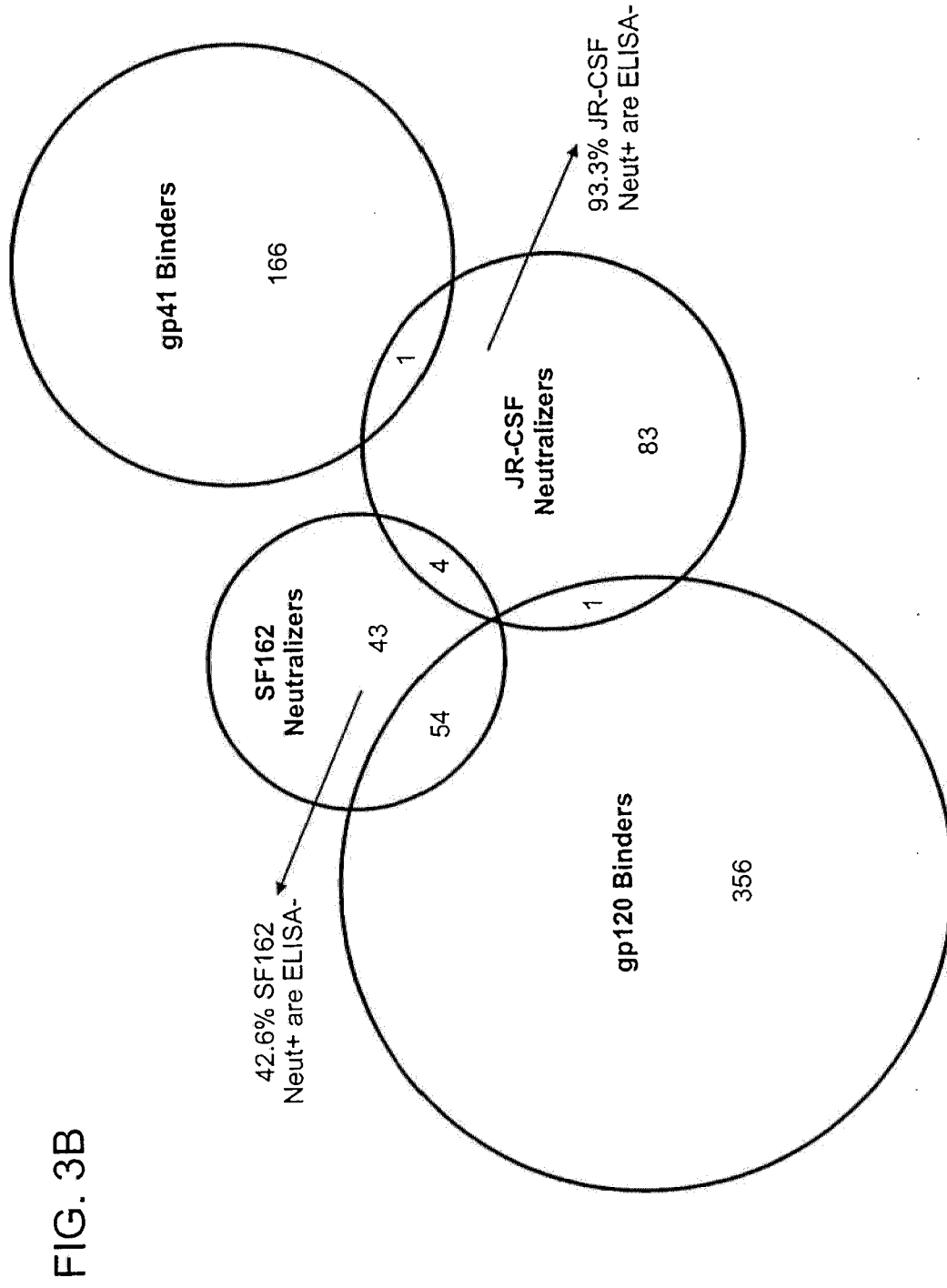


FIG. 4 PG9 and PG16 Neutralization Assays

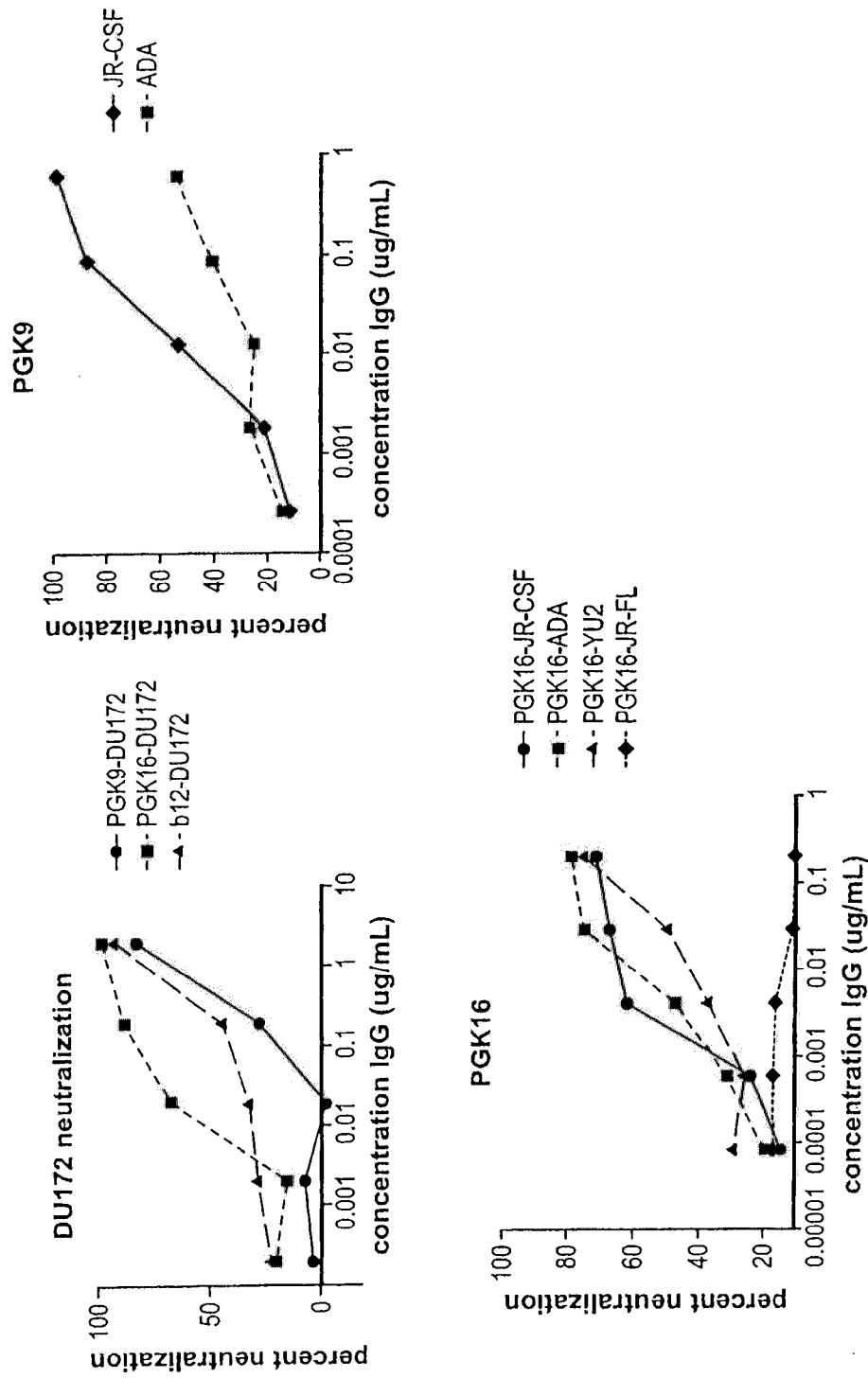




FIG. 5

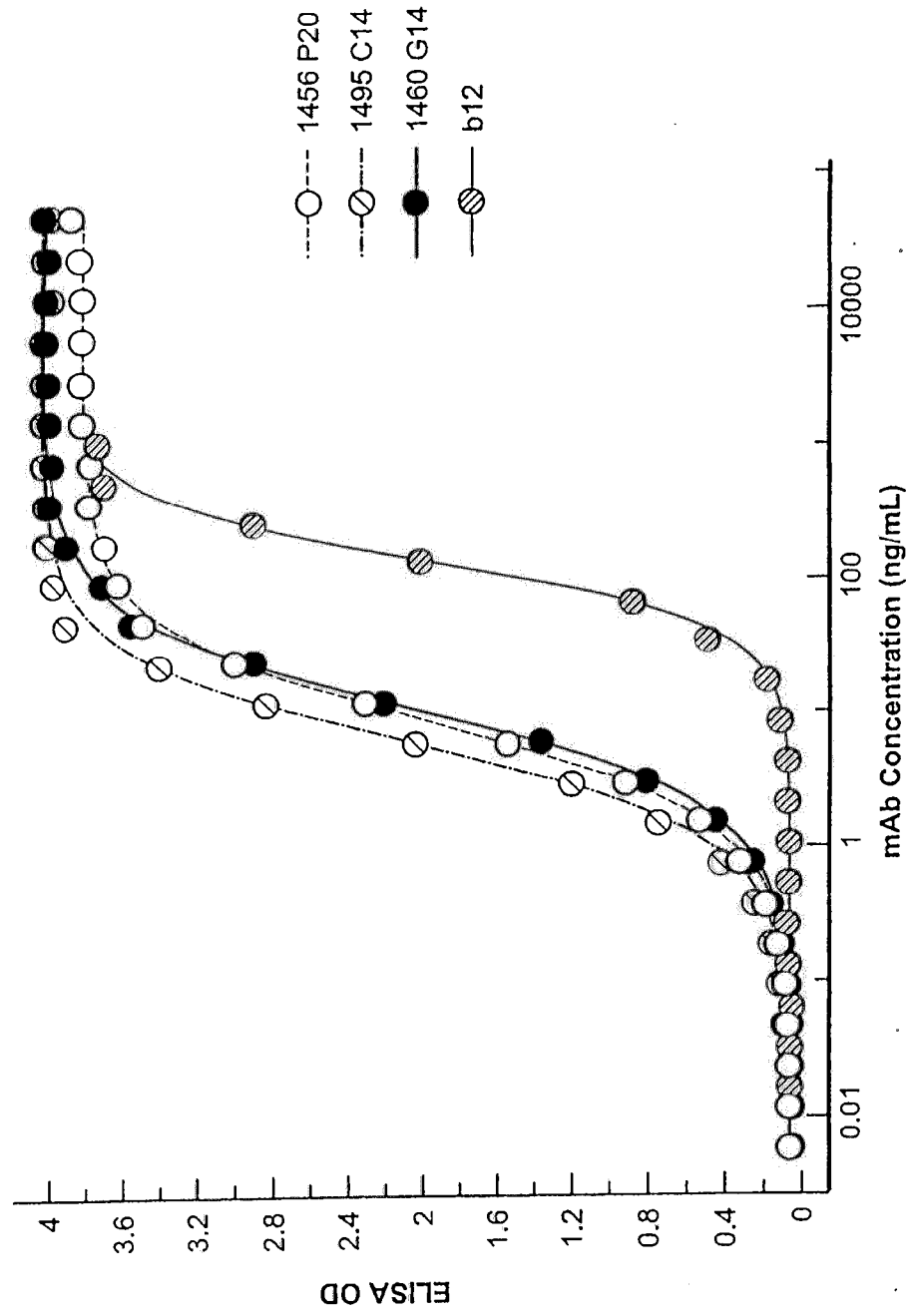


FIG. 6

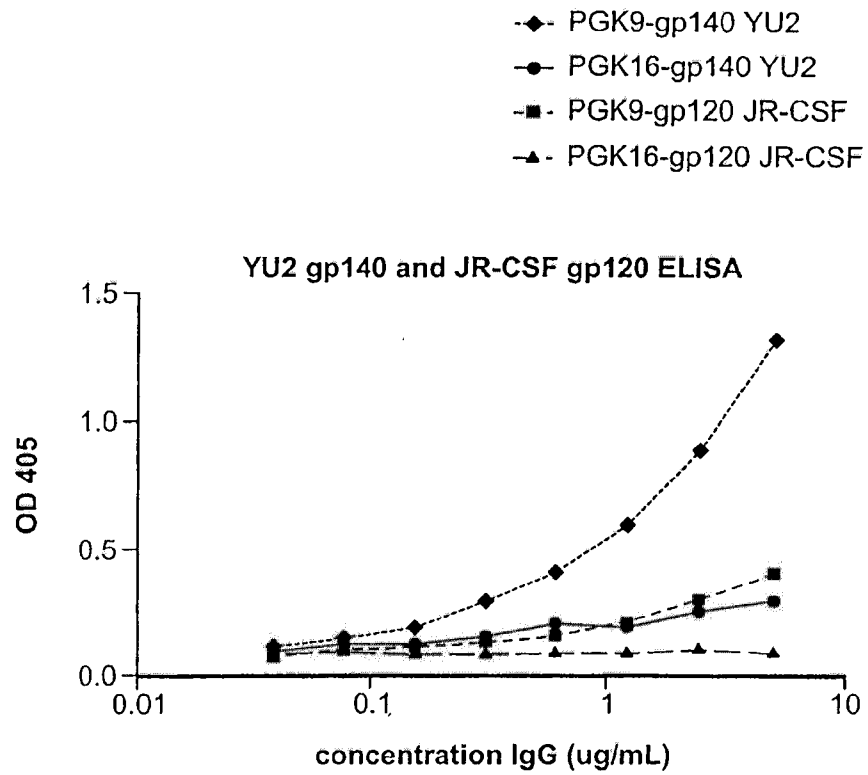


FIG. 6 (continued)

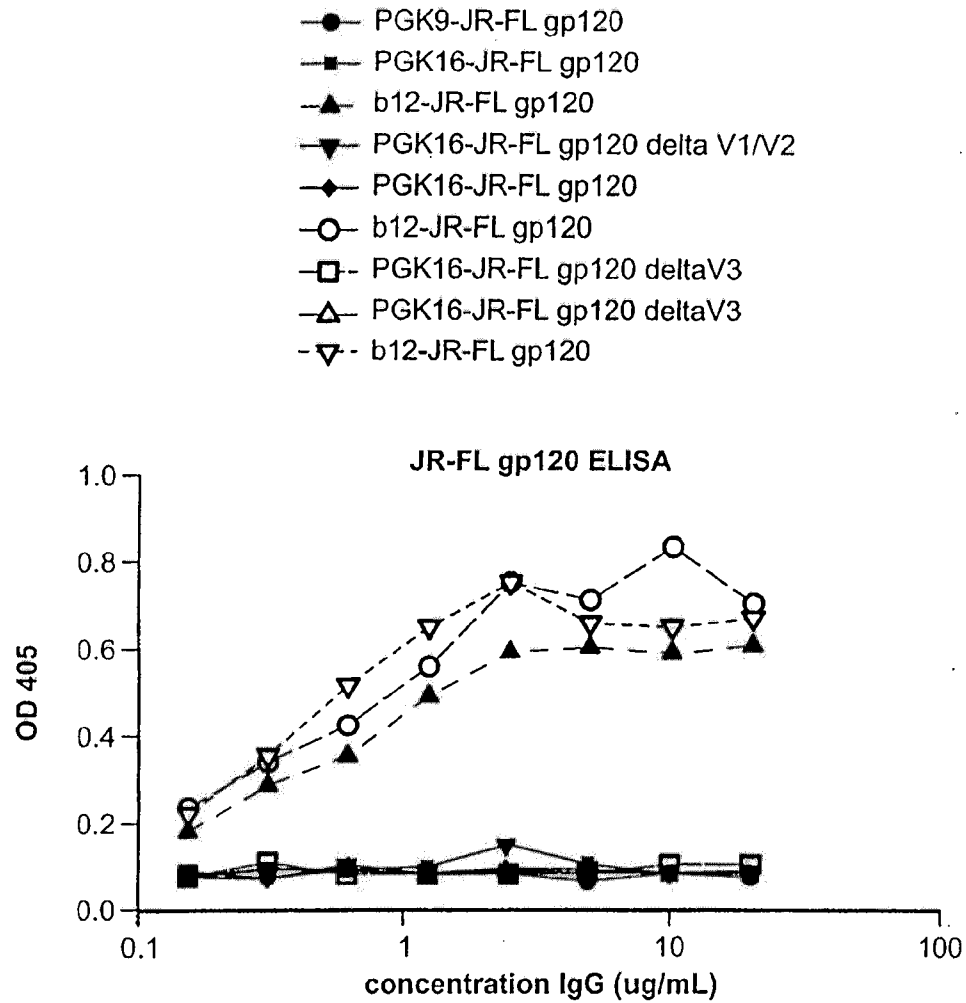


FIG. 6 (continued)

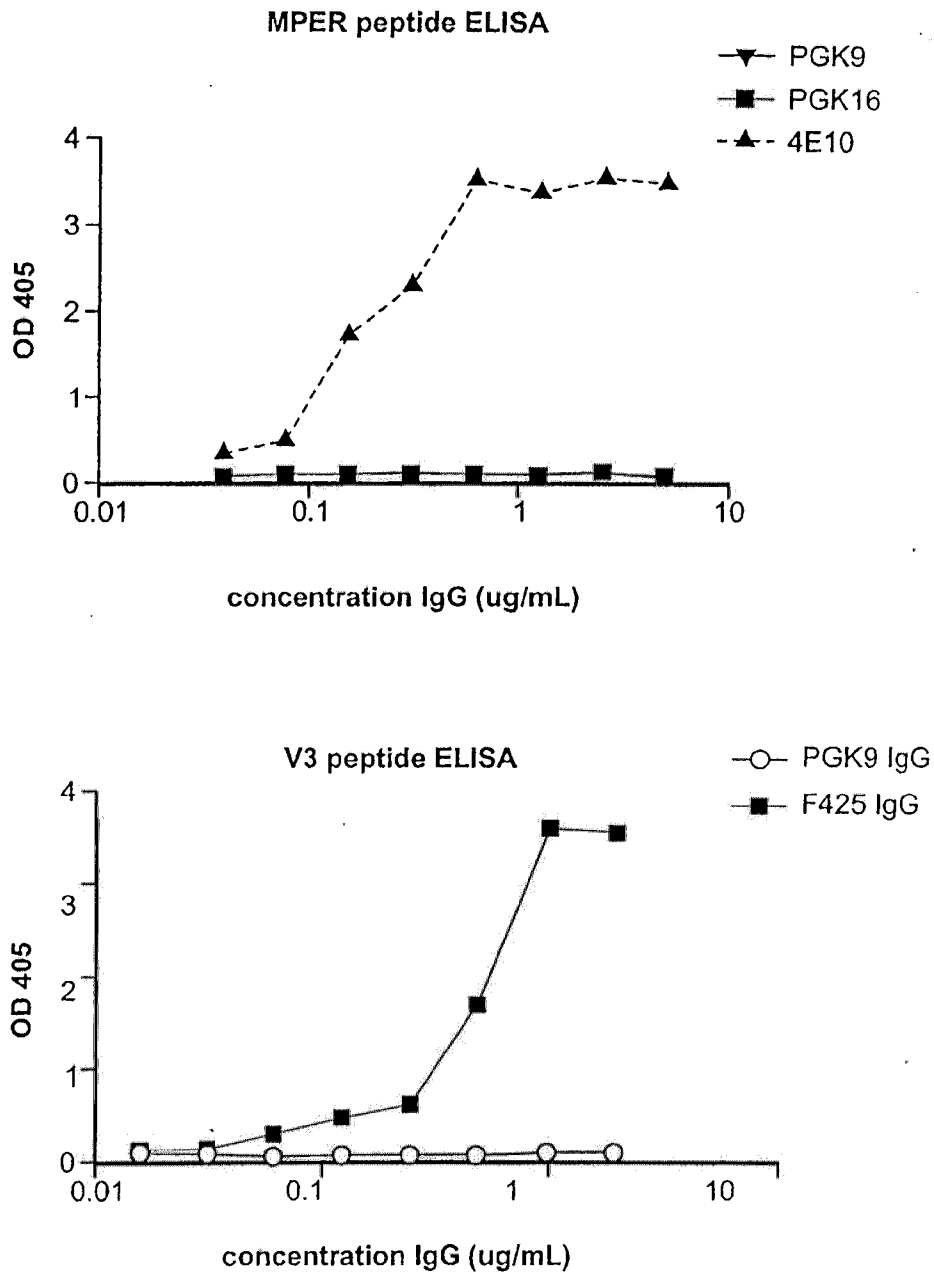


FIG. 7

Binding of PG16 and PG9 to HIV-1YU2 gp160 expressed on Cell Surface in the presence and absence of sCD4

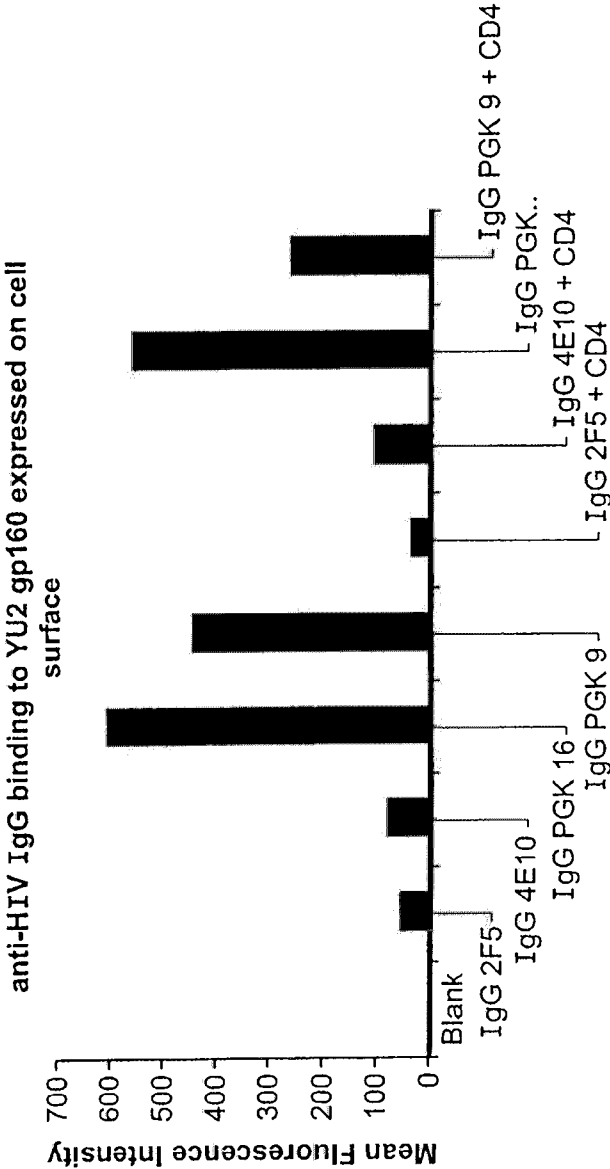


FIG. 8

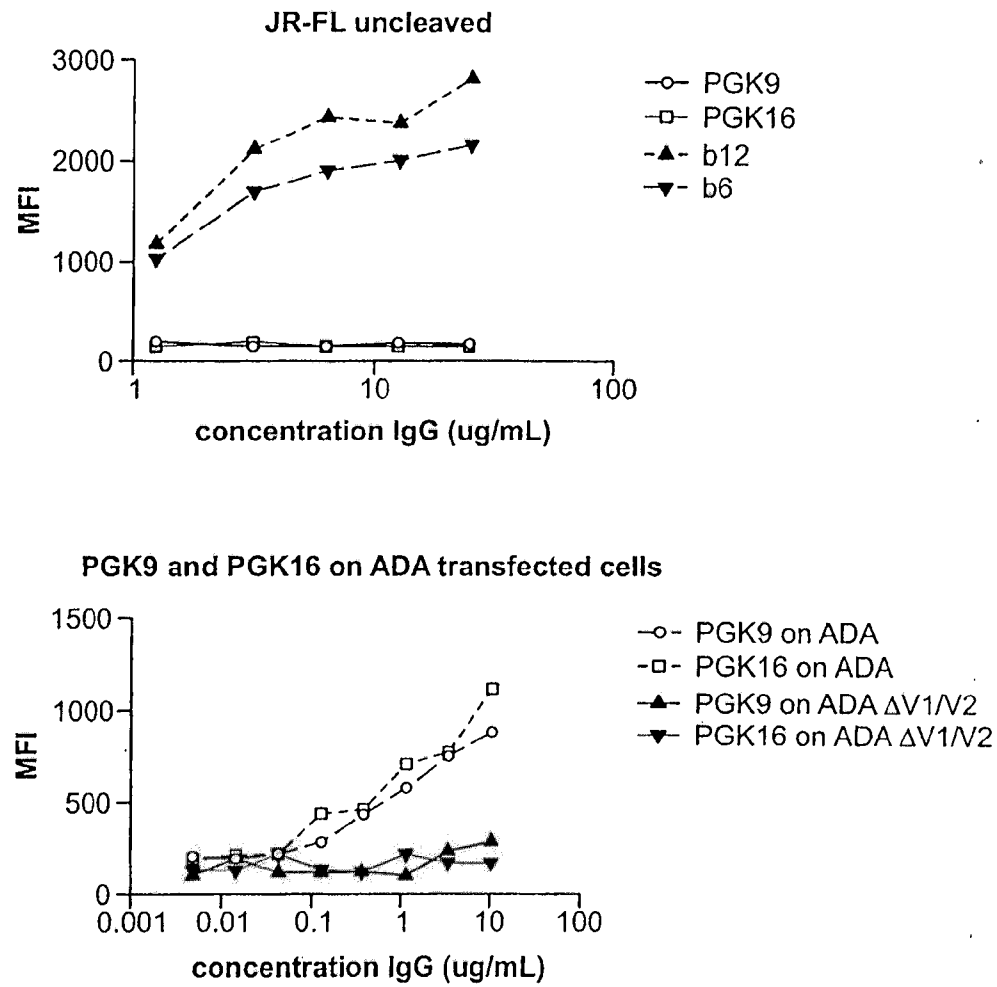
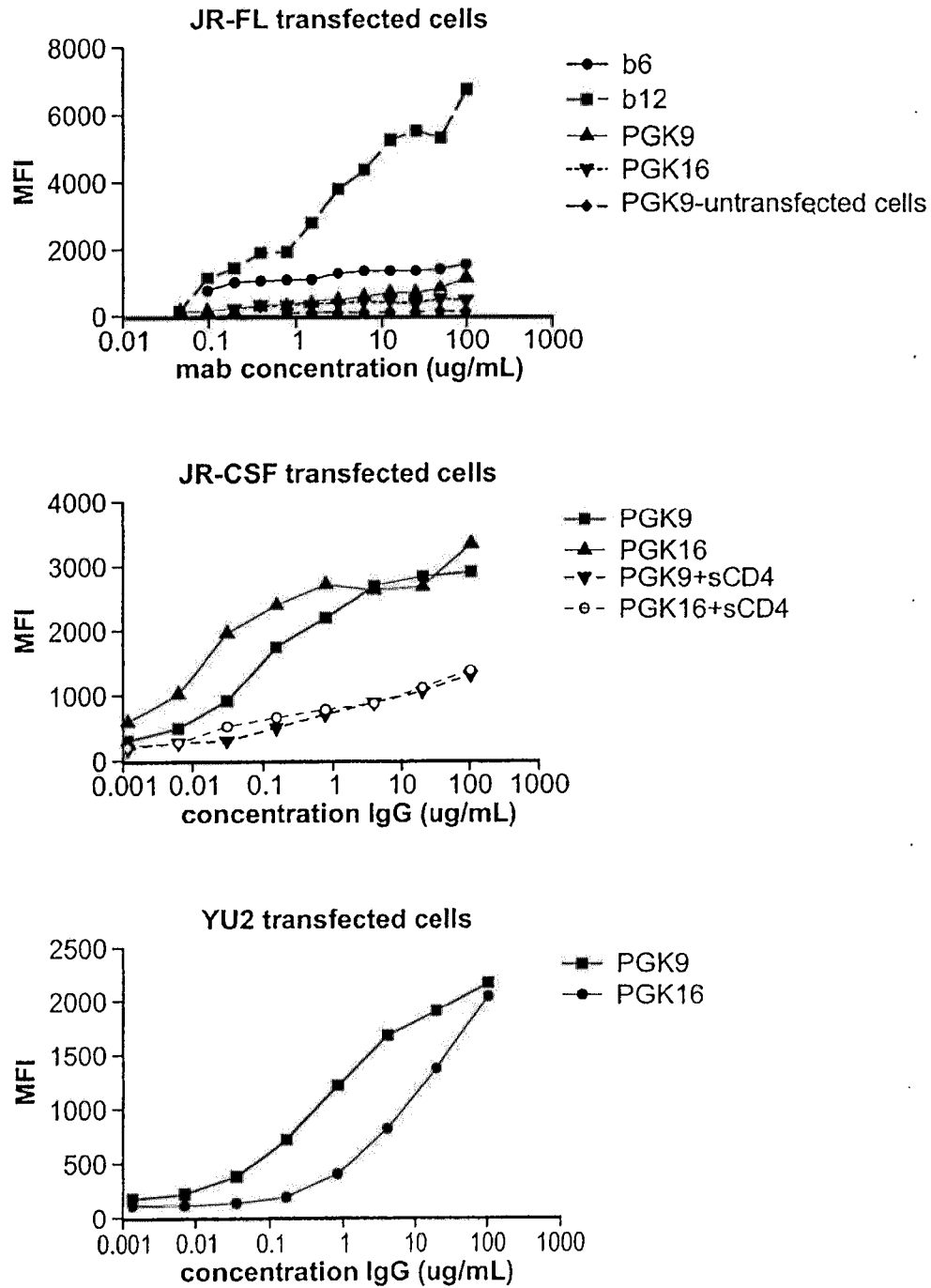


FIG. 8 (continued)



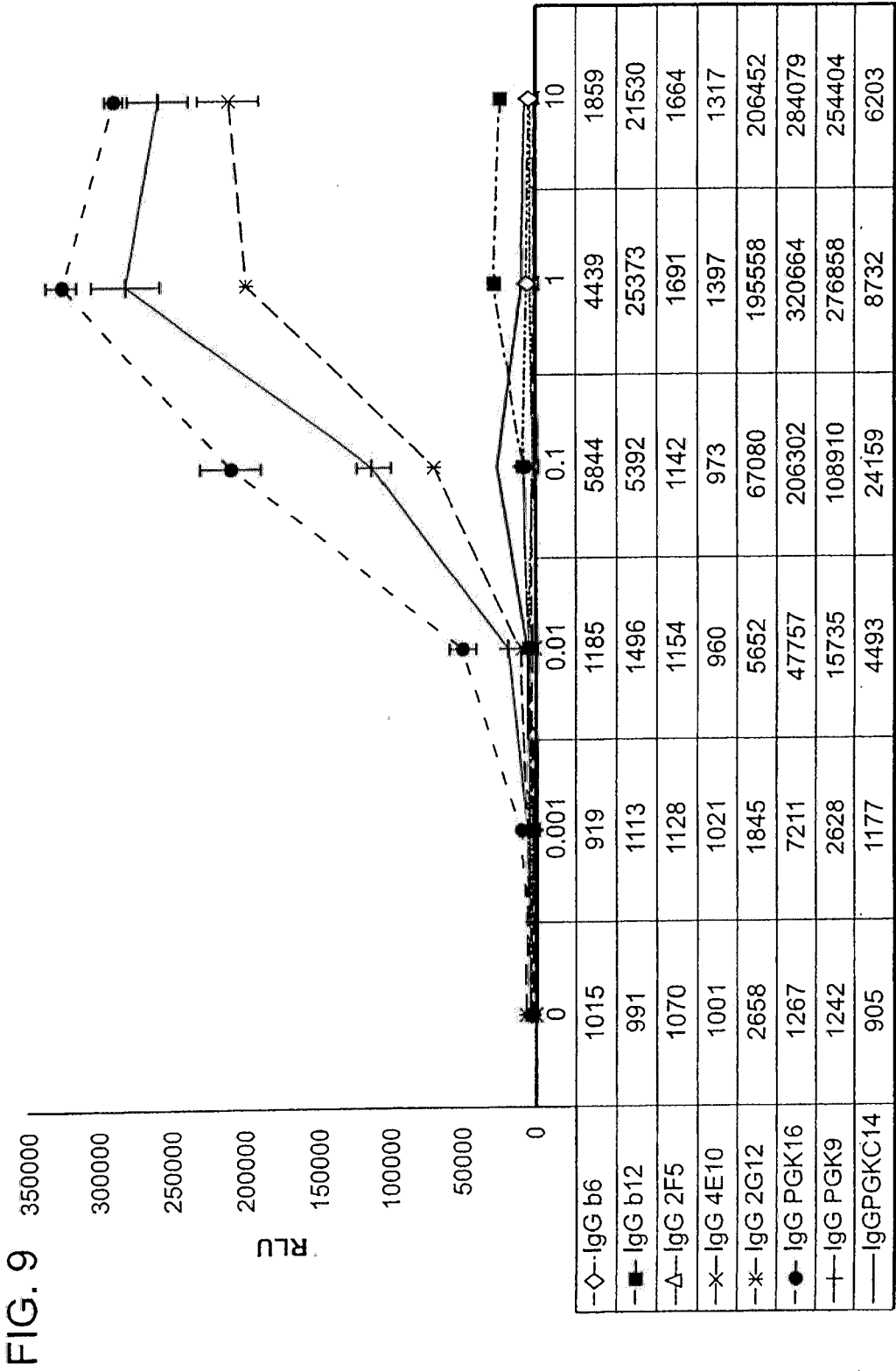
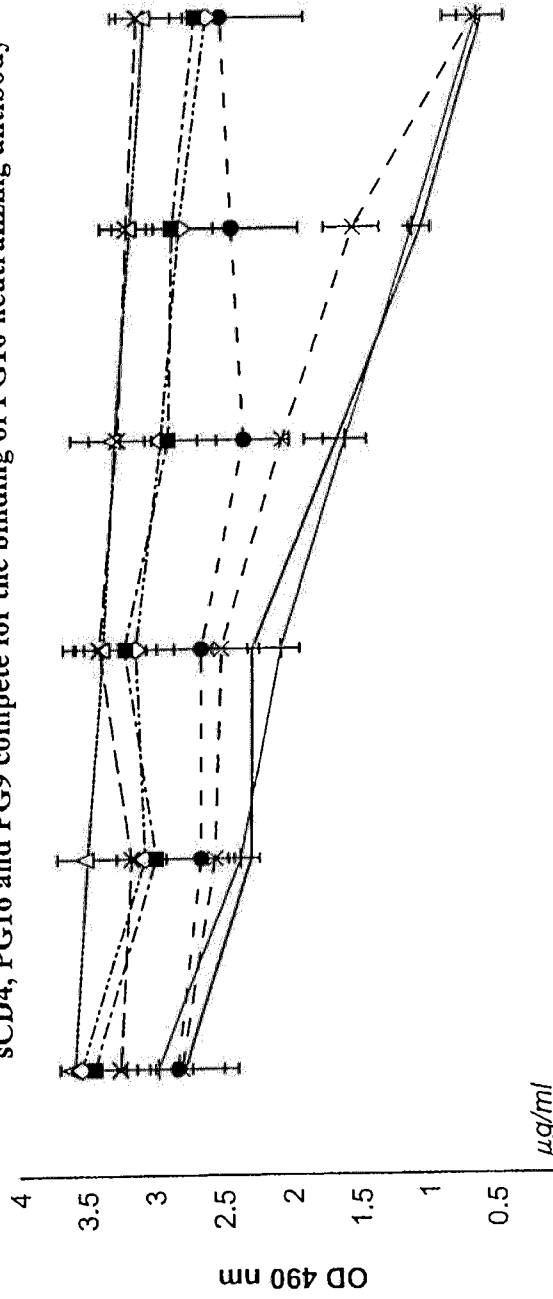


FIG. 10A

sCD4, PG16 and PG9 compete for the binding of PG16 neutralizing antibody



Competitor	0	0.16	0.8	4	20	100
—◇— IgG b12	3.531	3.078	3.109	2.94	2.7785	2.5845
—■— IgG 2F5	3.445	3.006	3.1795	2.894	2.8445	2.6715
—△— IgG 4E10	3.6335	3.4945	3.38	3.2915	3.14	3.0615
—×— sCD4	3.2585	3.1515	3.378	3.2465	3.17	3.0995
—*— Fab b12	2.822	2.562	2.5045	2.069	1.552	0.6635
—●— IgG PGK16	2.821	2.647	2.6485	2.344	2.4195	2.478
—+— IgG PGK9	2.9655	2.3705	2.0925	1.6105	1.12	0.671
—*— IgG PGK9	2.7735	2.311	2.283	1.67	1.0425	0.5965

FIG. 10B

sCD4, PG16 and PG9 compete for the binding of PG9 neutralizing antibody

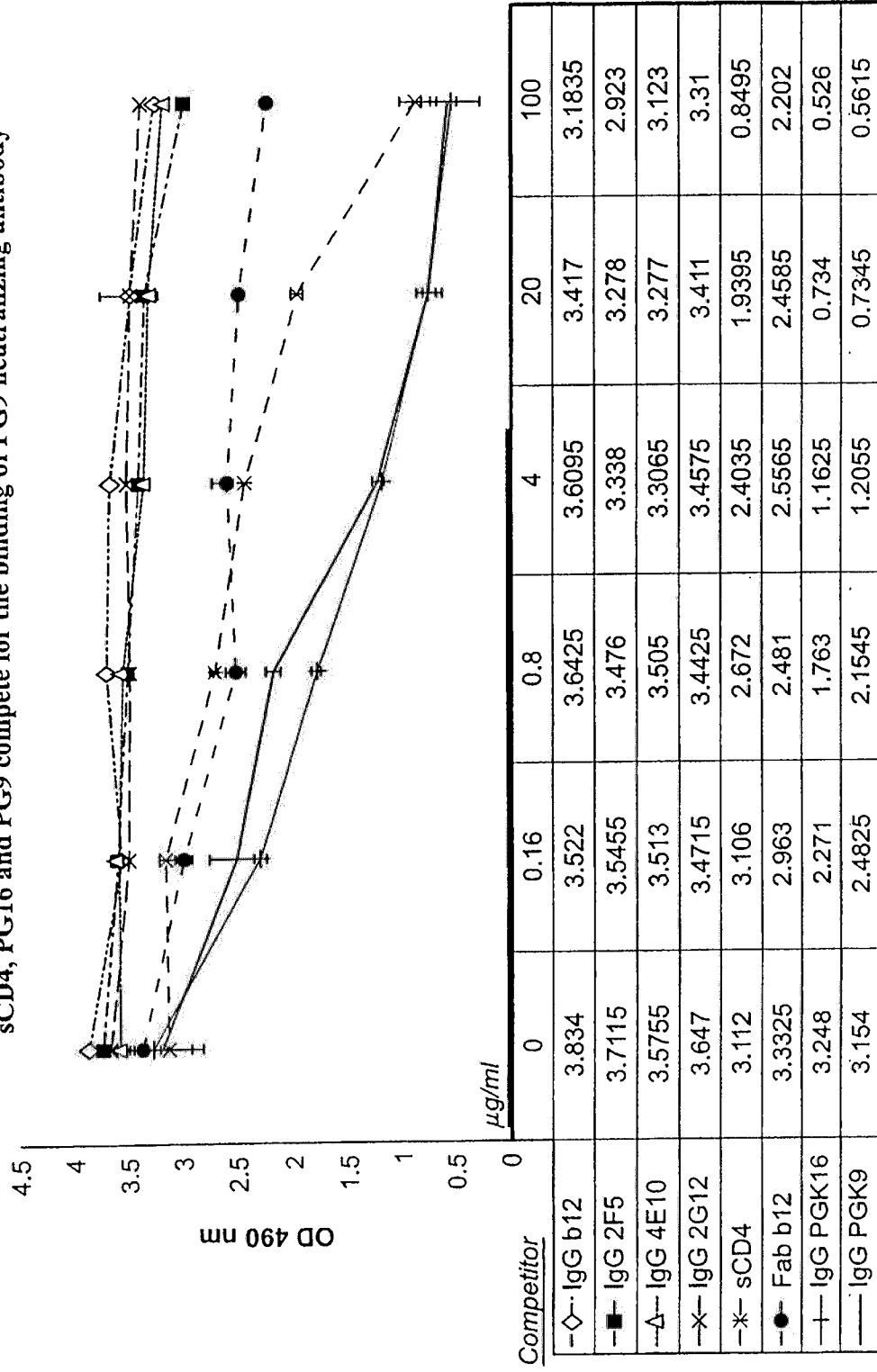


FIG. 11A

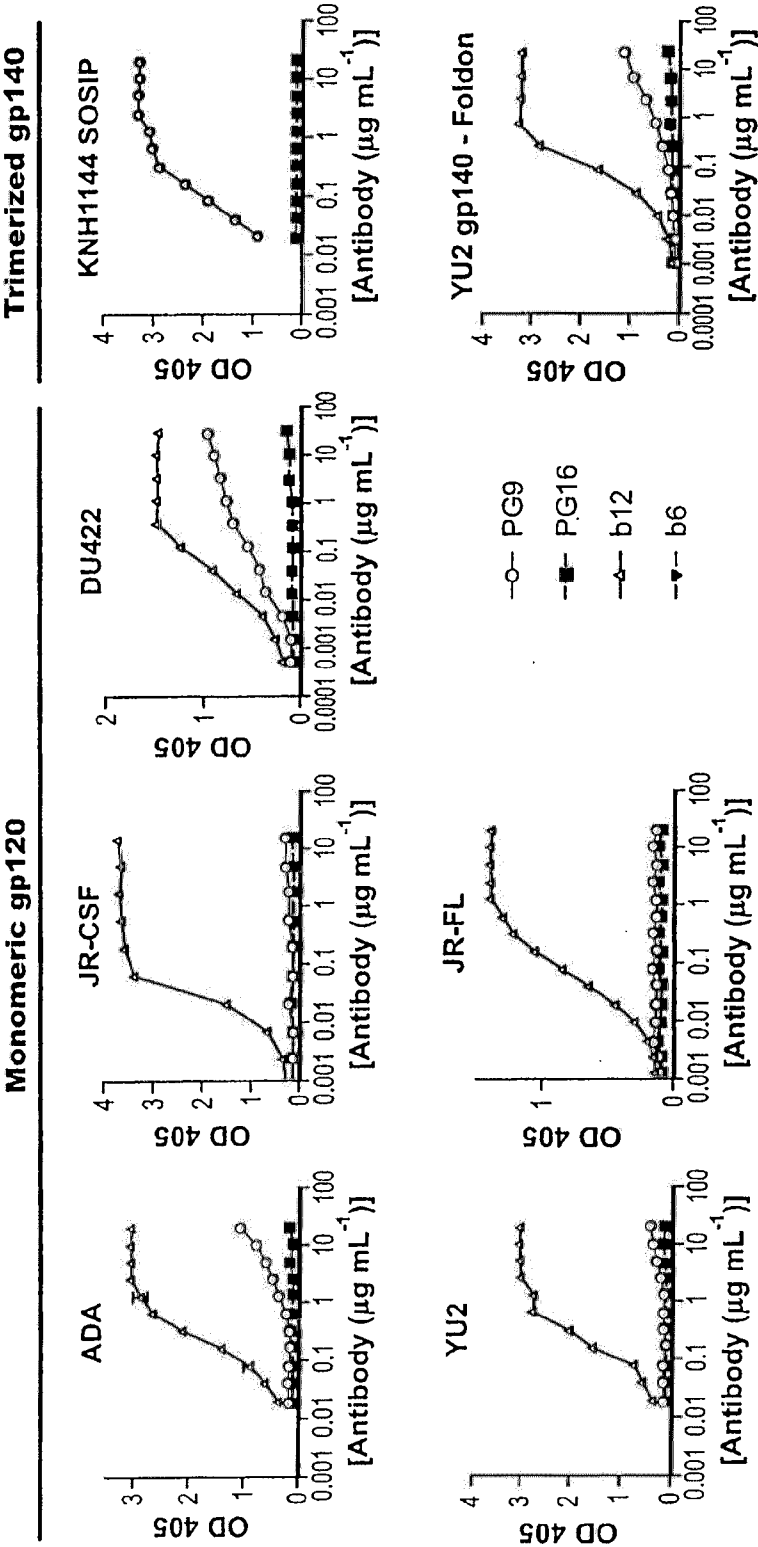


FIG. 11B

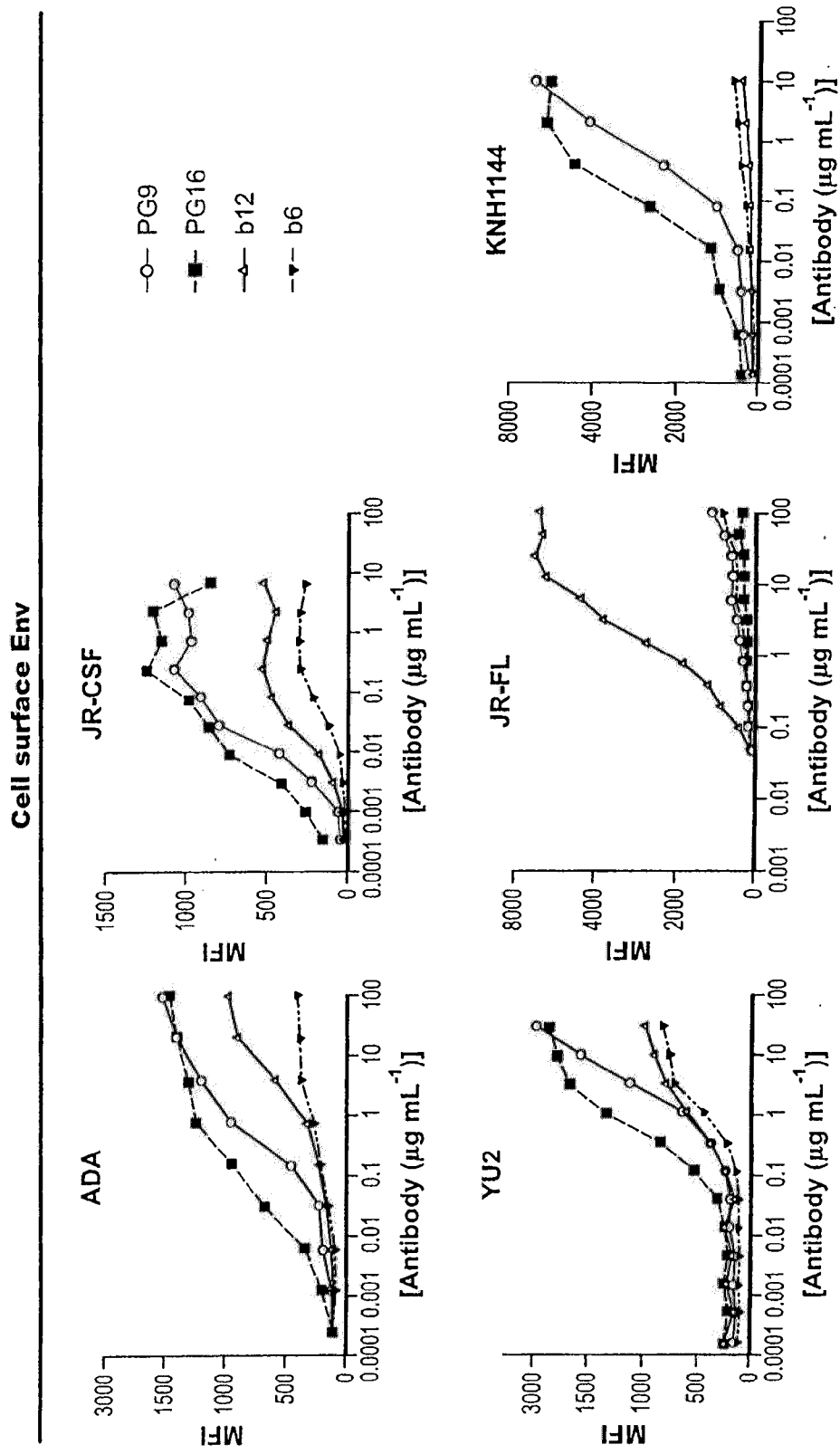


FIG. 12

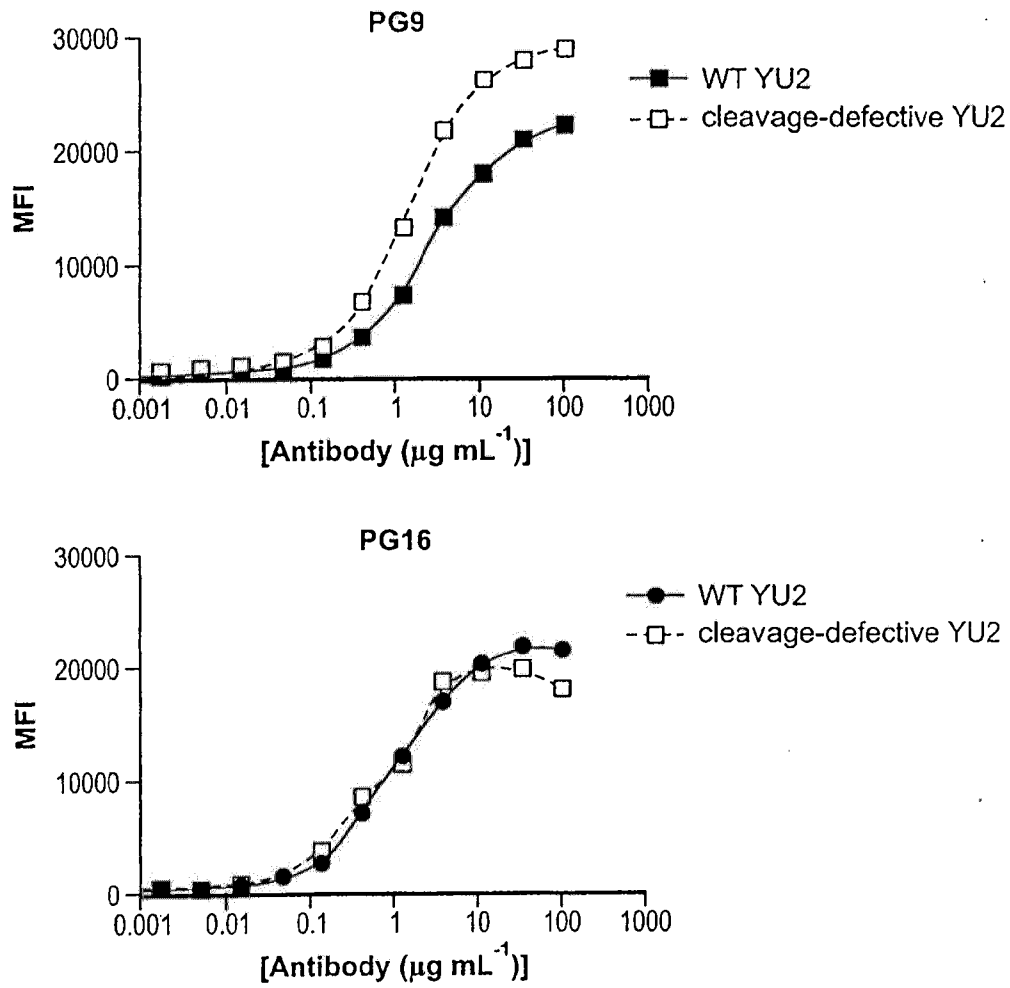


FIG. 13A

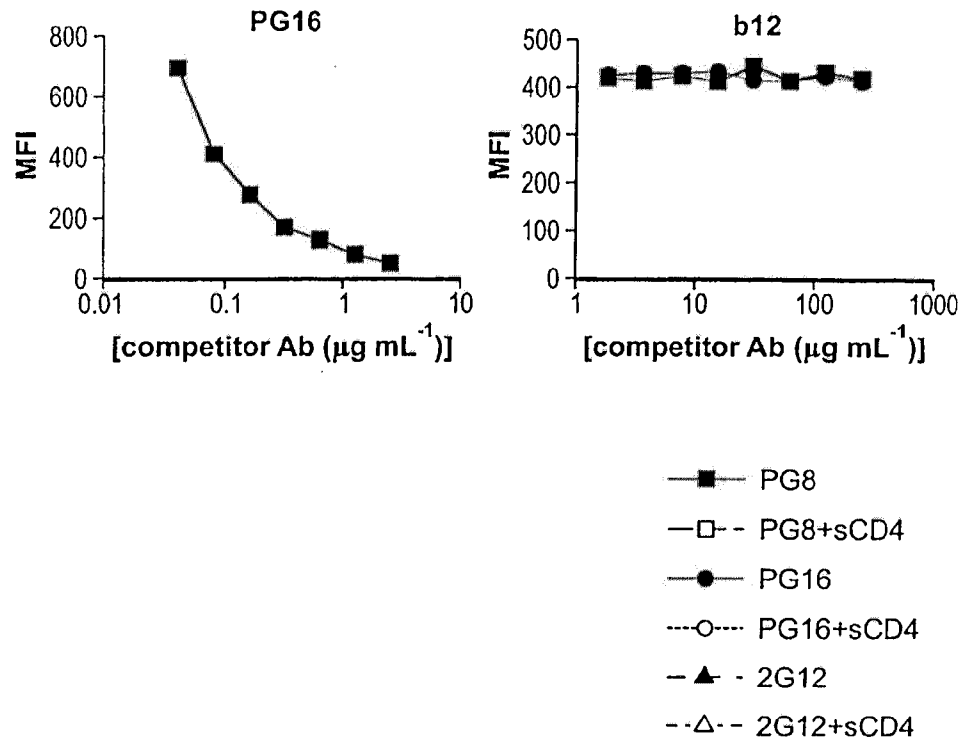


FIG. 13B

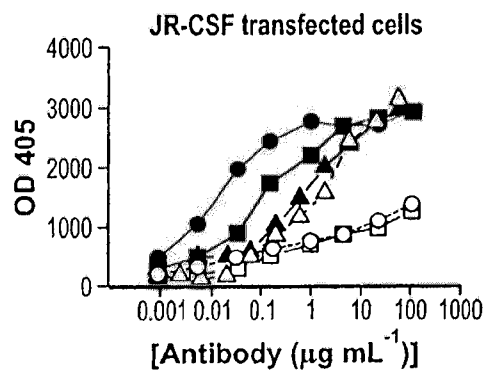
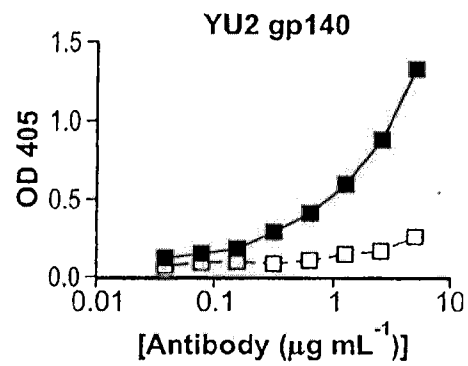


FIG. 13C



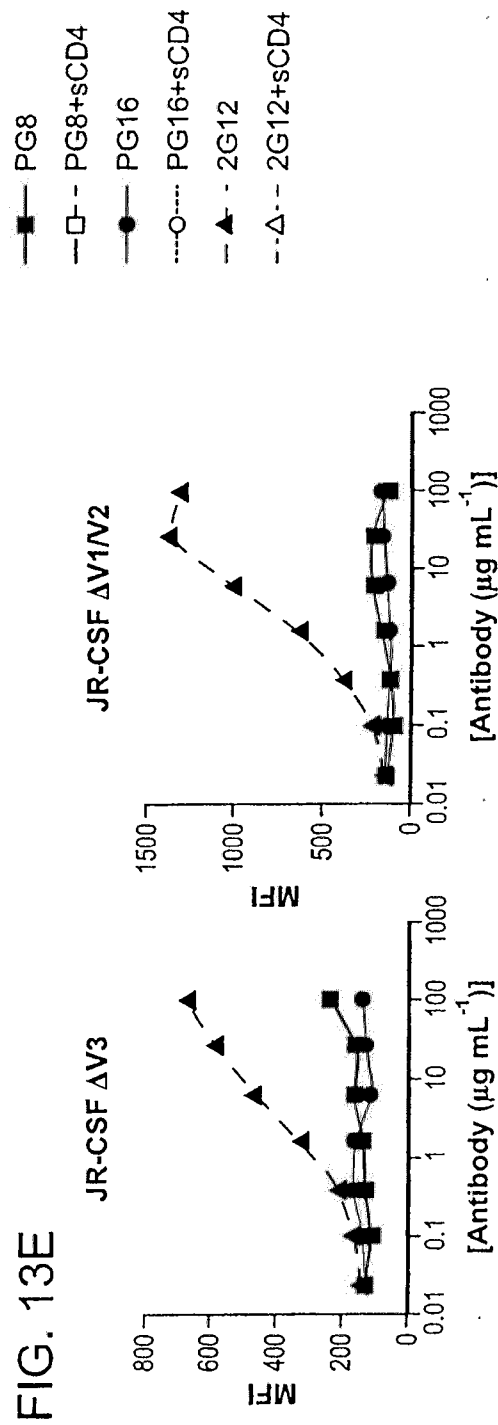
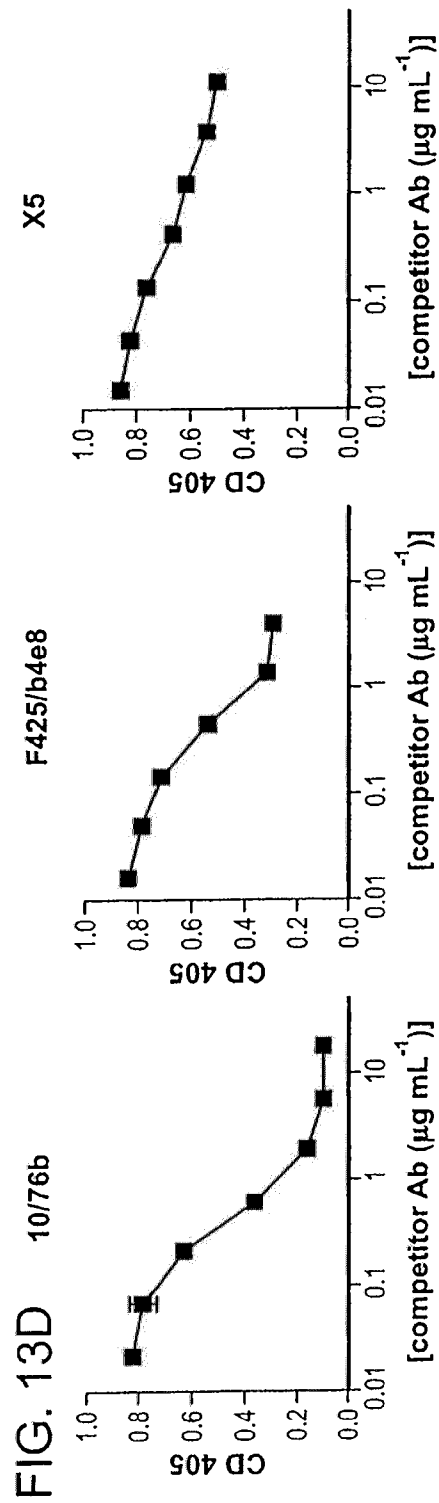


FIG. 14

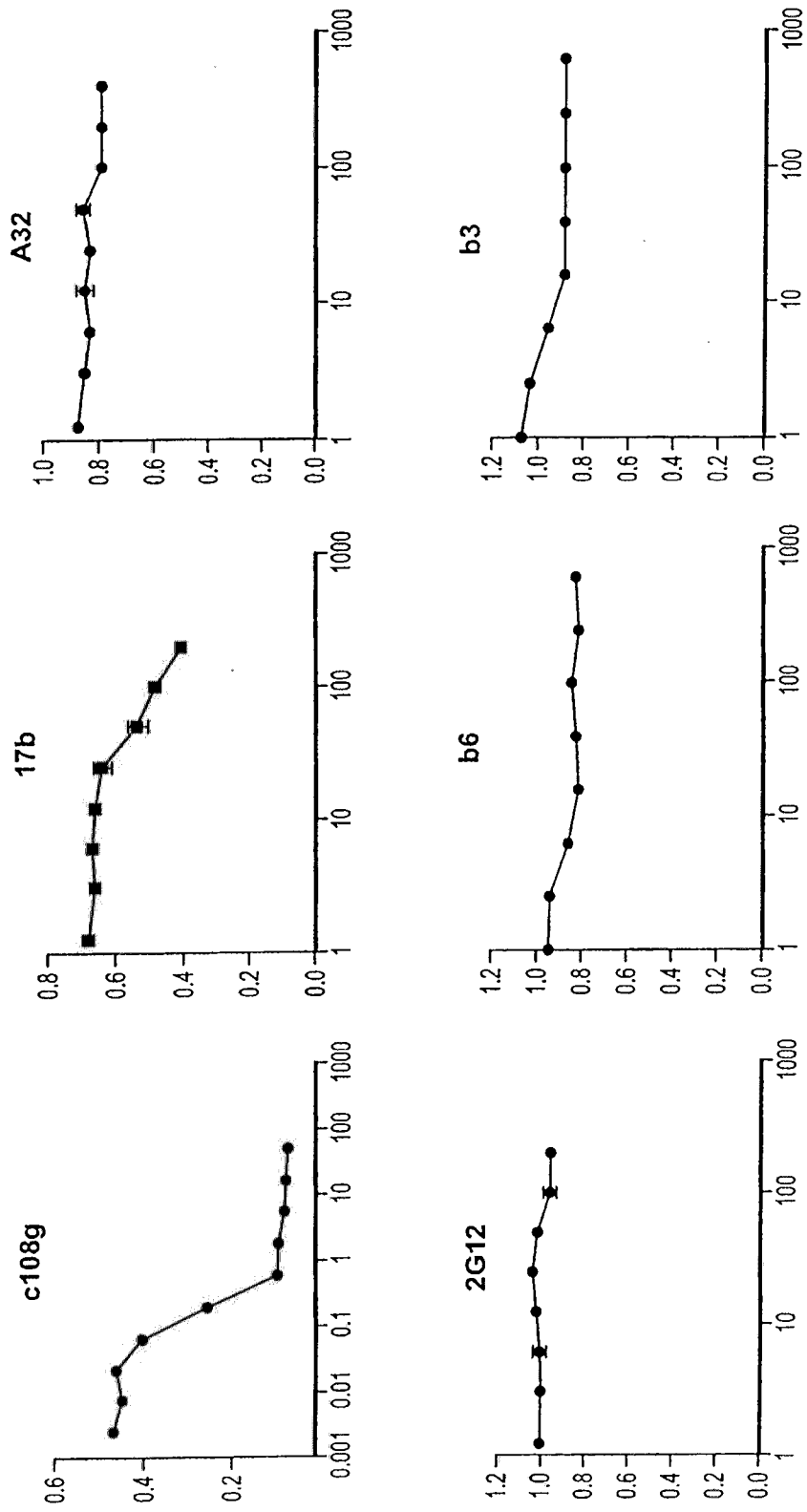


FIG. 15

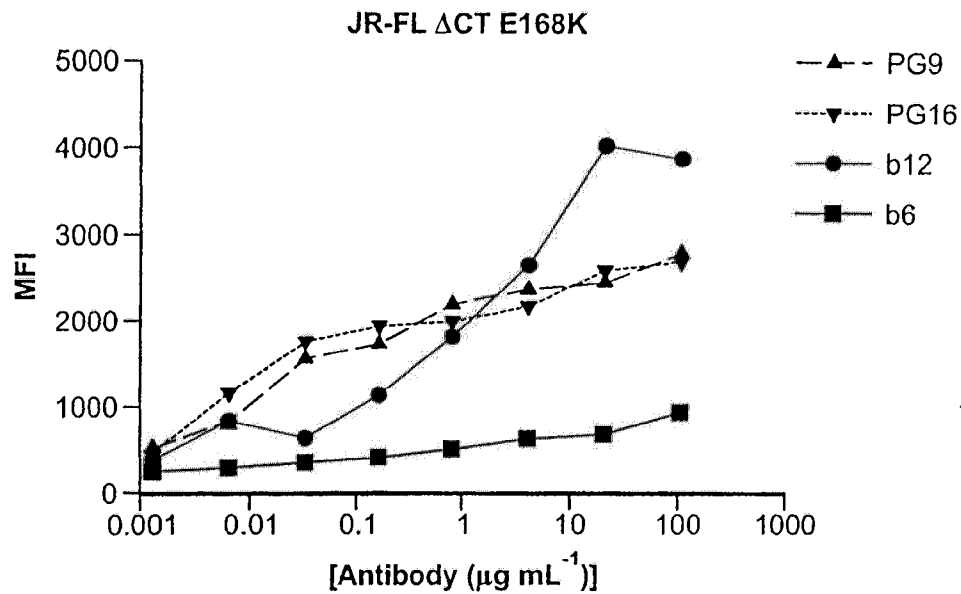


FIG. 16

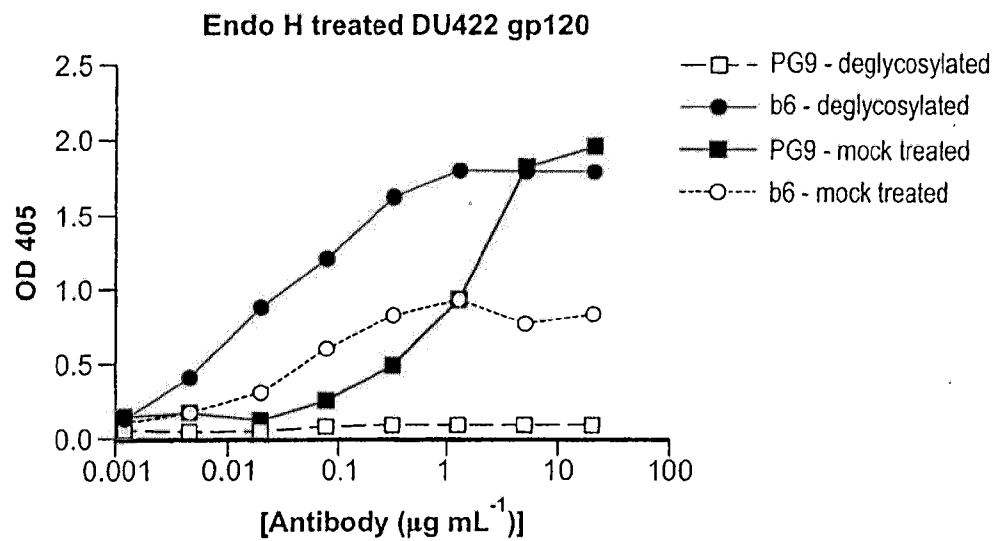


FIG. 17

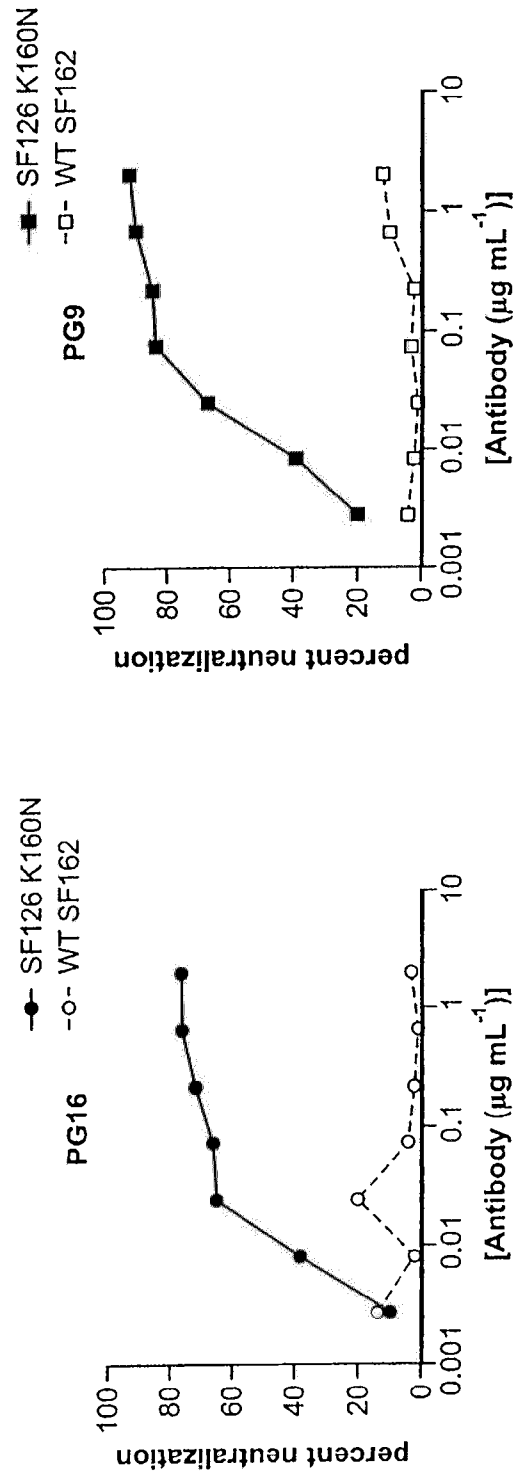


FIG. 18

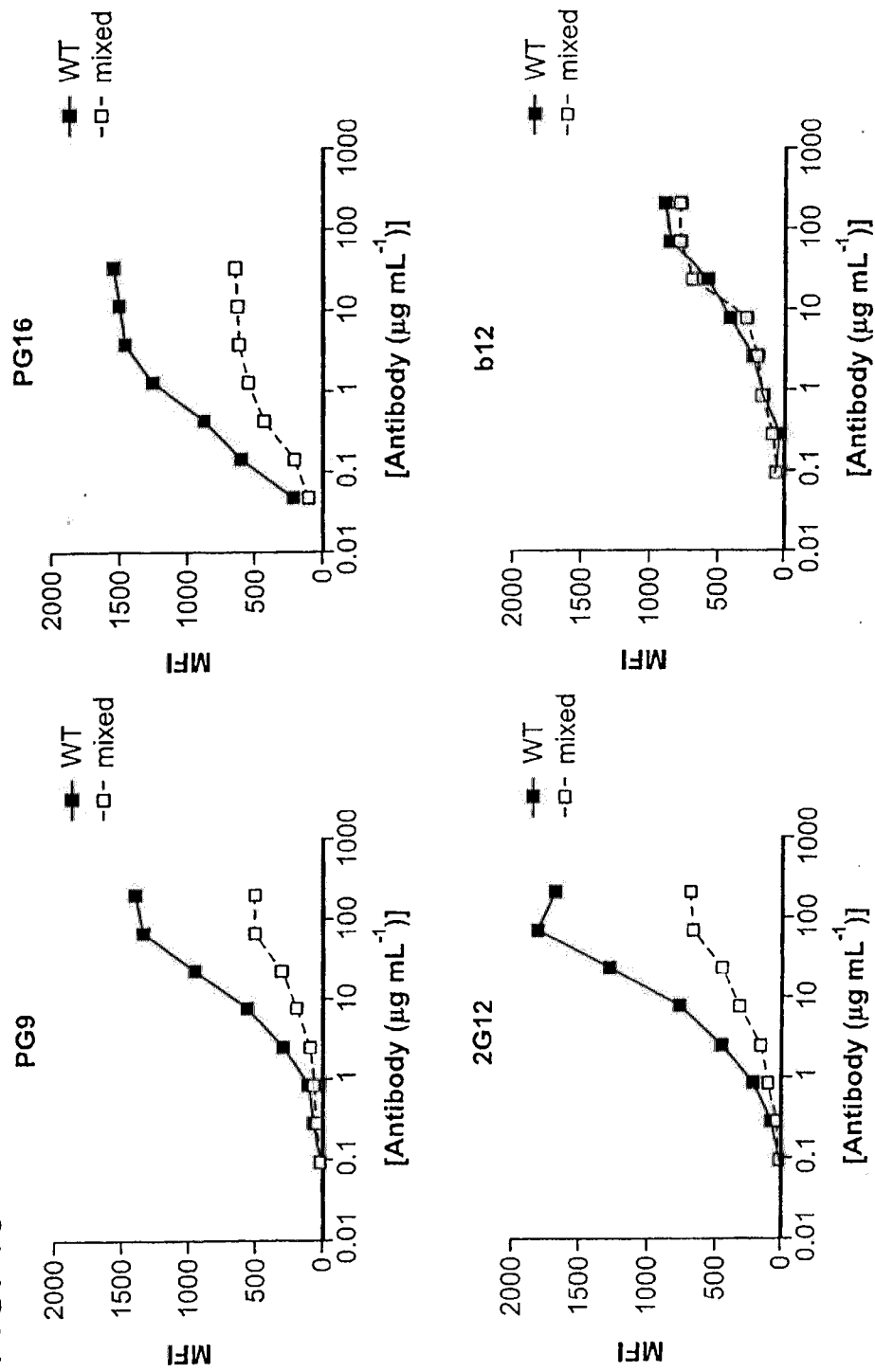


FIG. 19

VH

	1443 C16	1456 A12	1408 I08	1503 H05	1489 I13	1469 M23
1443 C16	0	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

VL

VL

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

Nucleotide

Protein

FIG. 20A

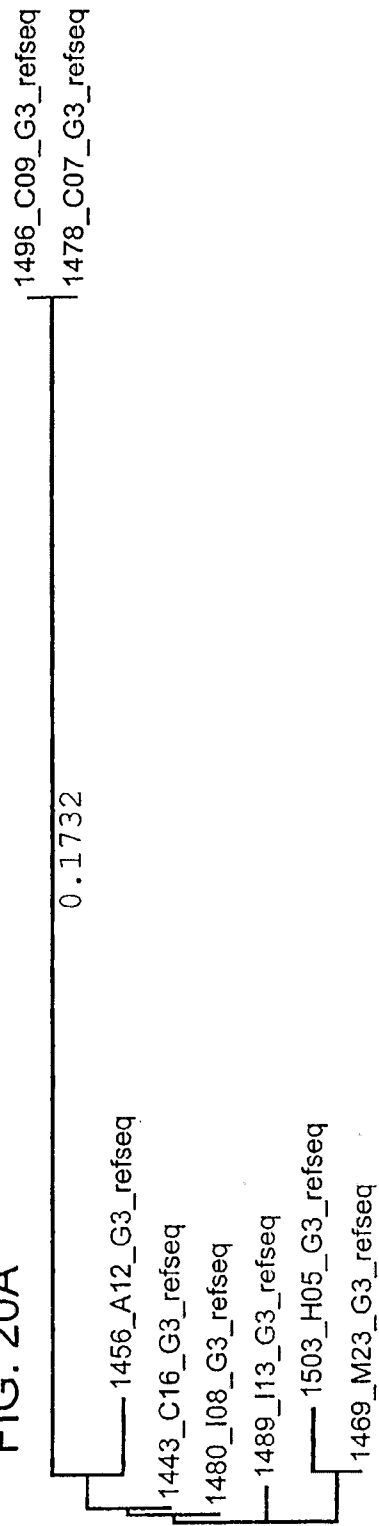


FIG. 20B

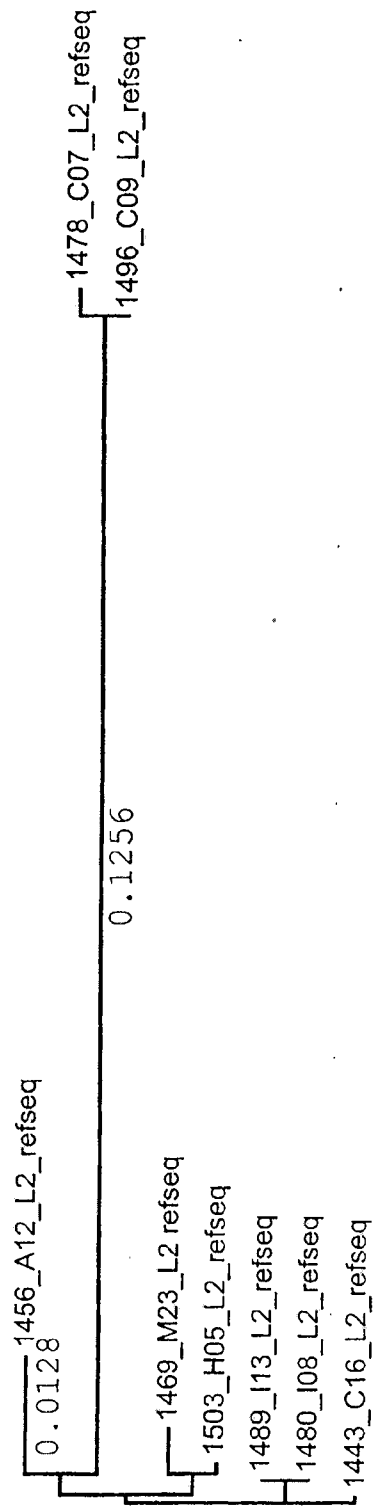


FIG. 21A

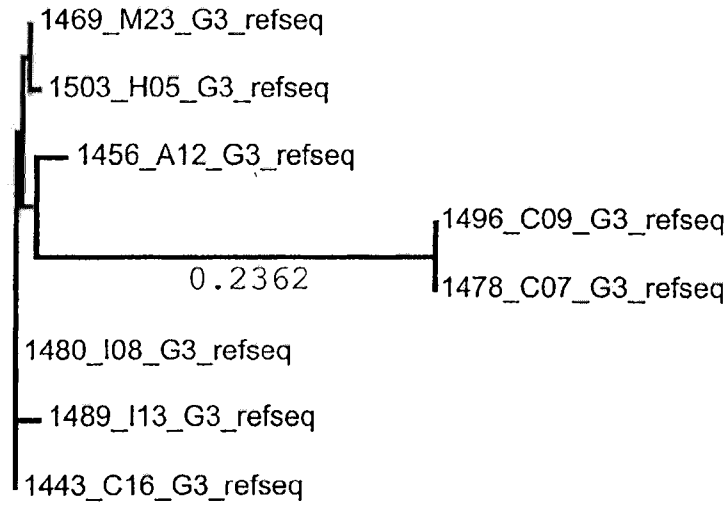


FIG. 21B

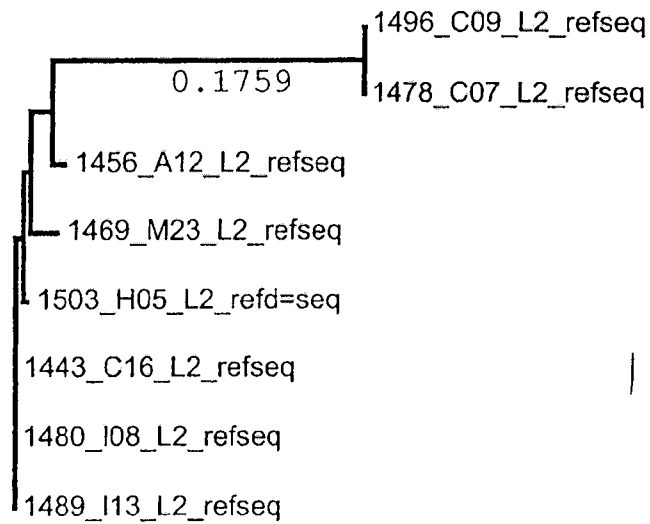


FIGURE 22

Number of HIV-Neutralizing Hits Detected in Primary Screening

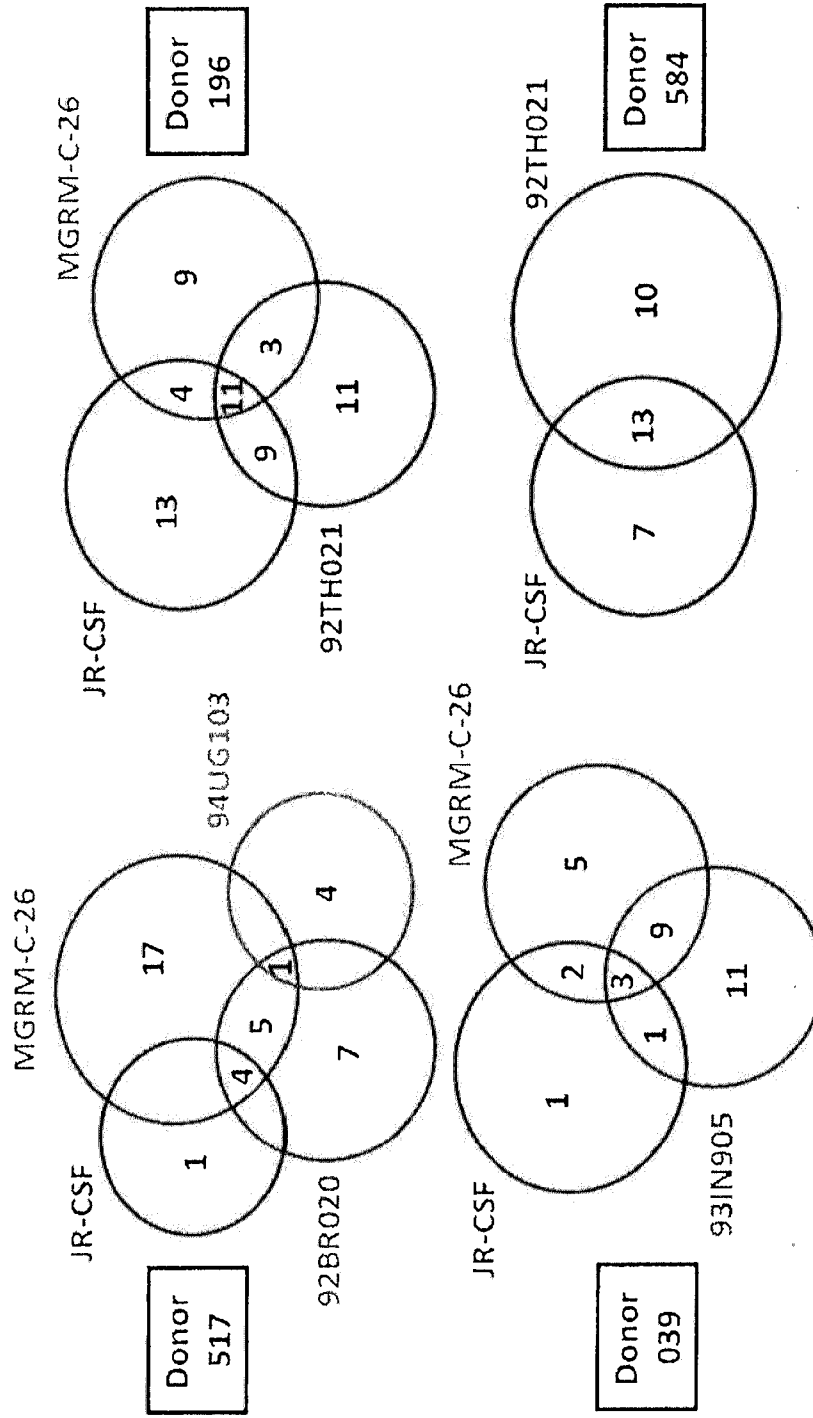
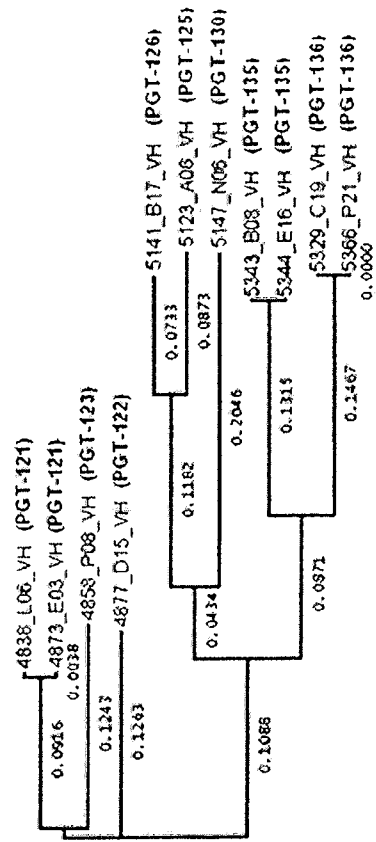


FIGURE 23

Heavy Chain Variable Gene Relationship Tree



0.03

FIGURE 24

Light Chain Variable Gene Relationship Tree

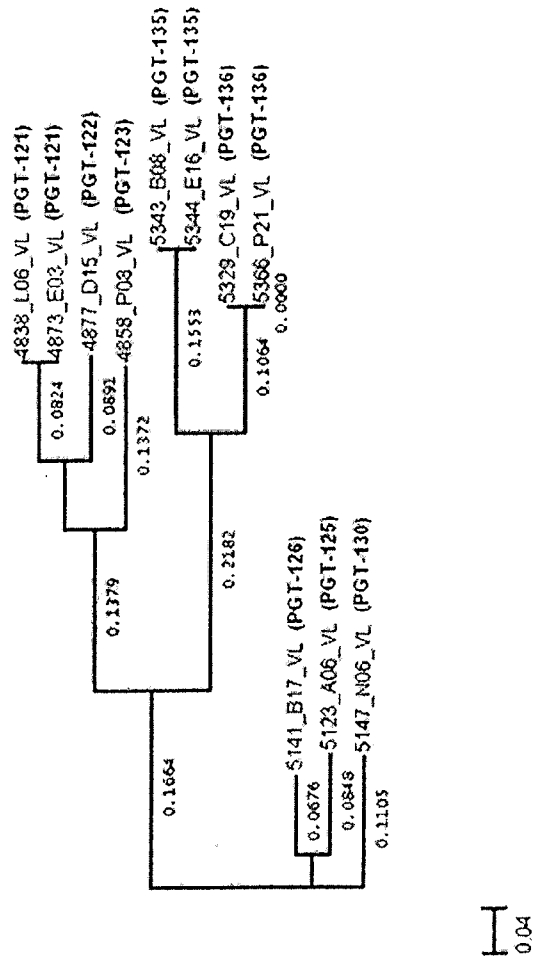


FIGURE 25

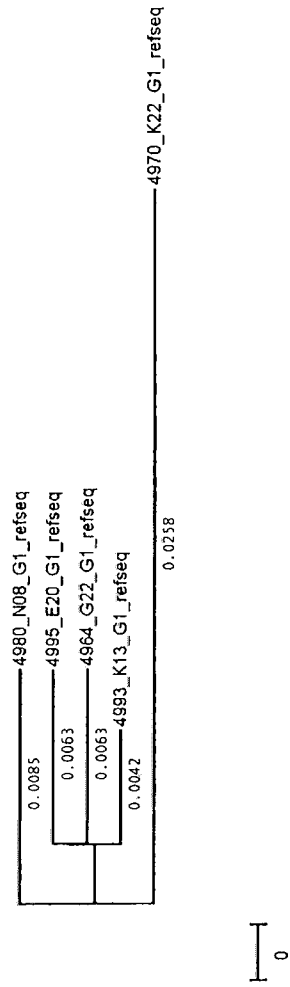


FIGURE 26

4980_N08_K2_refseq	0.0076
4984_G22_K2_refseq	
4993_K13_K2_refseq	
4995_E20_K2_refseq	0.0077
4970_K22_K2_refseq	0.0077

0

FIGURE 27

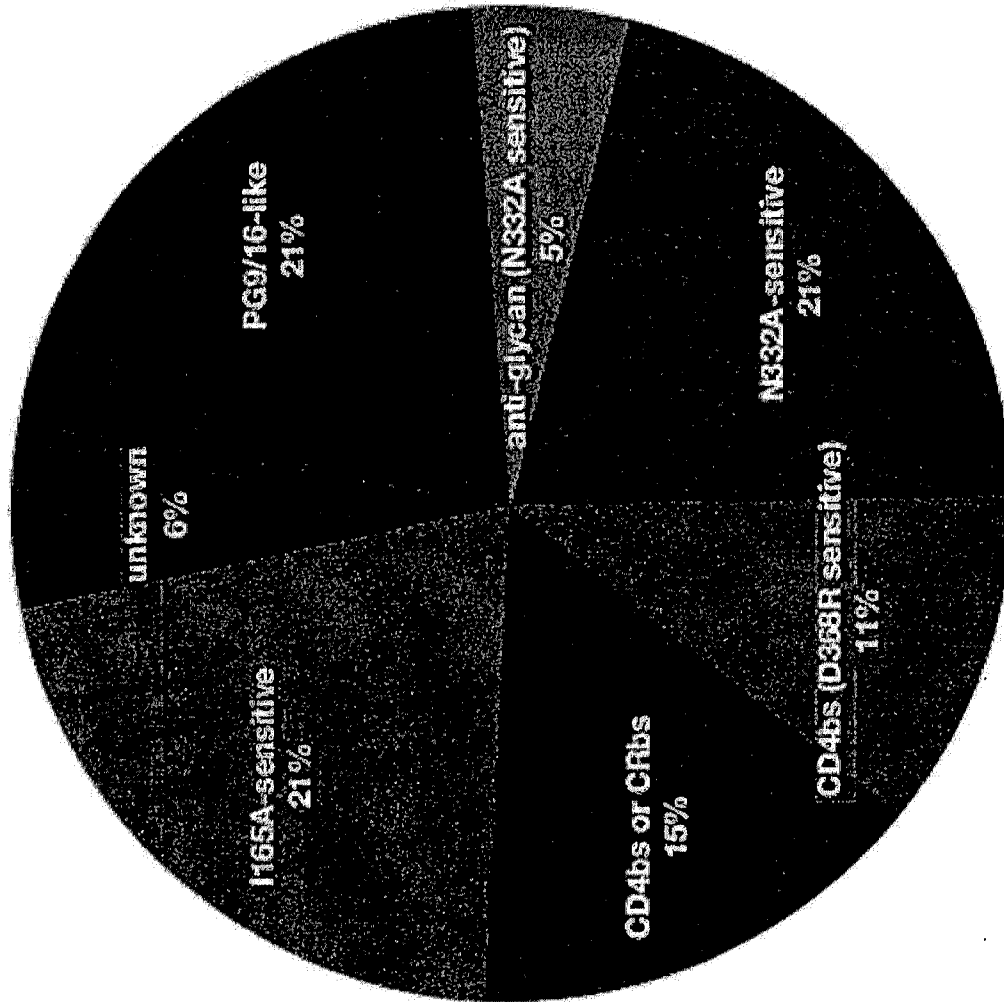


FIGURE 28

I-STAR™ Human bNAb Discovery Platform

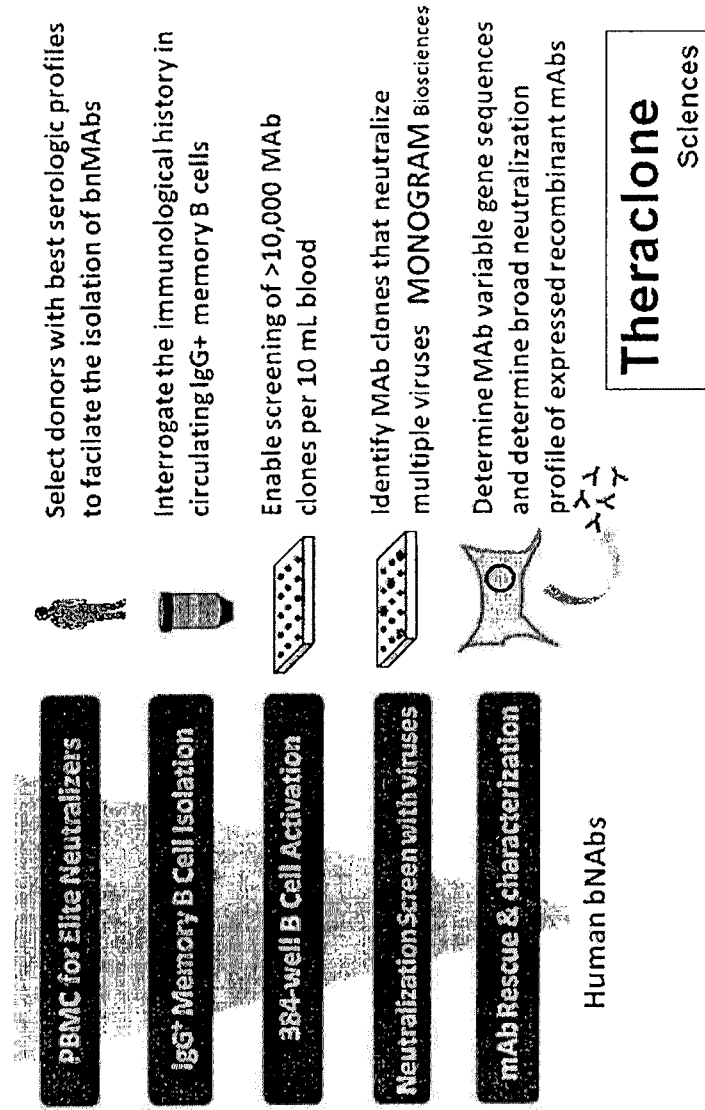


FIGURE 29

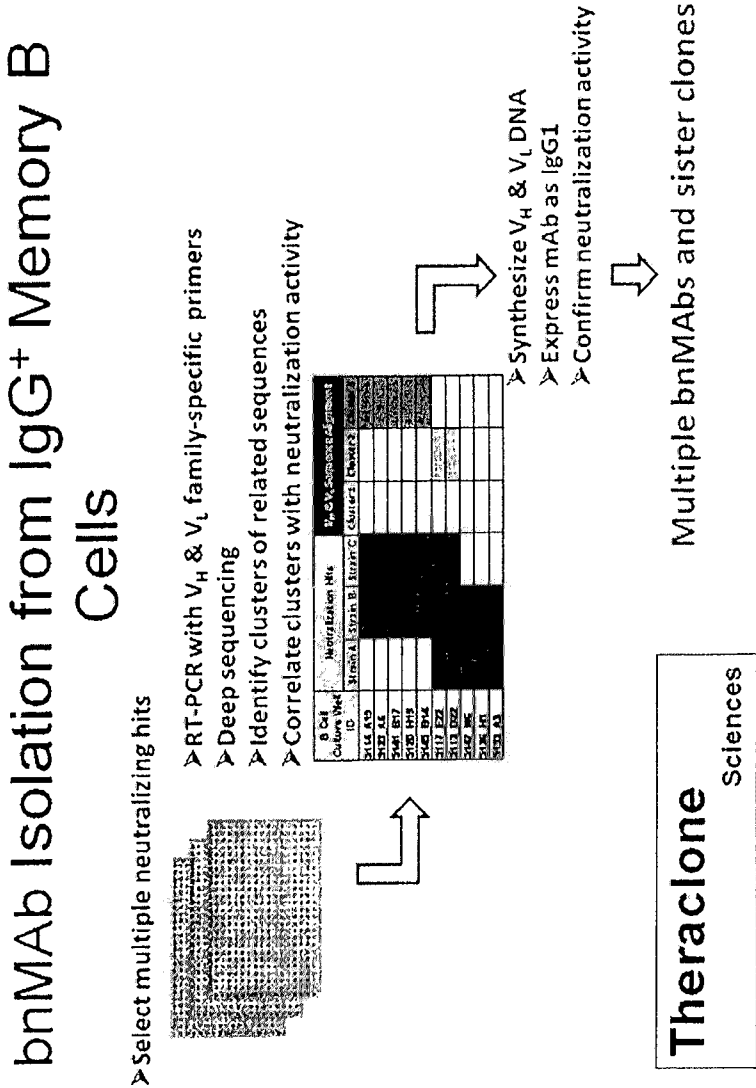
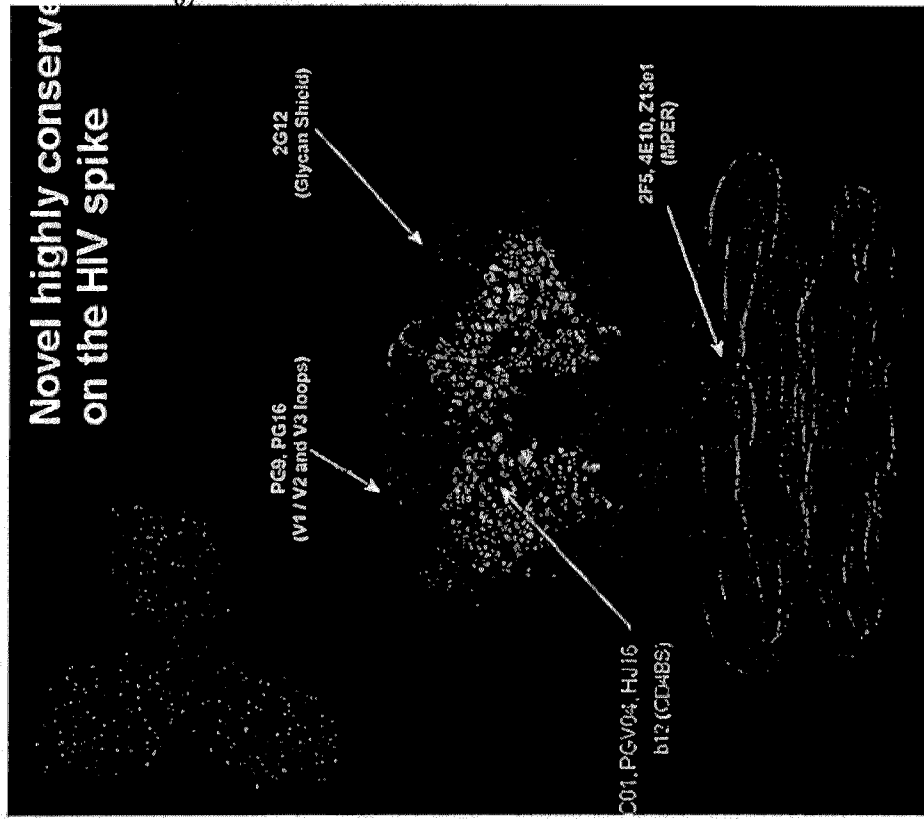


FIGURE 30



FIGURE 31



s 17, 36 and 39

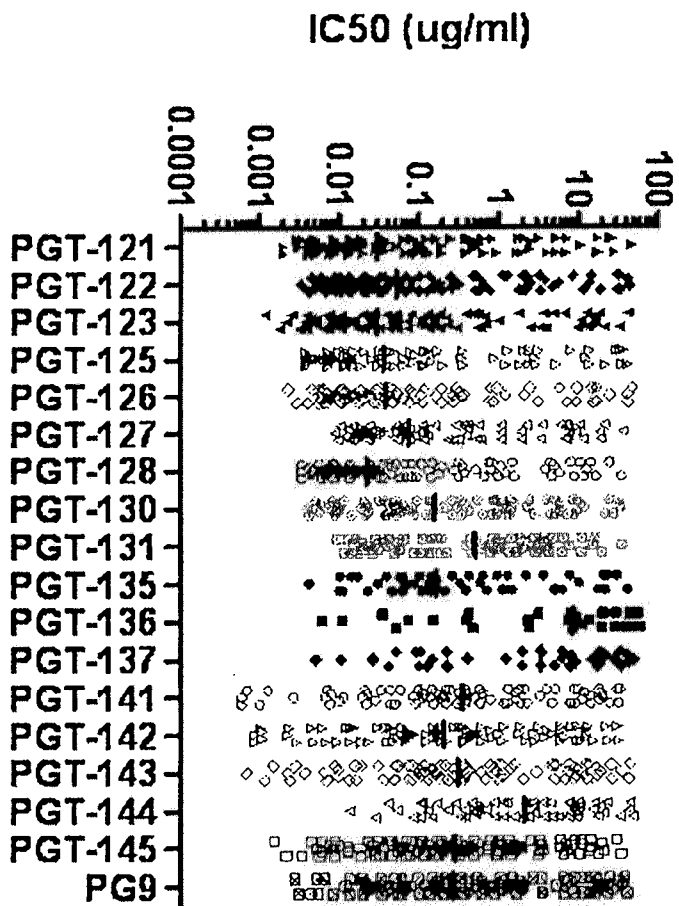
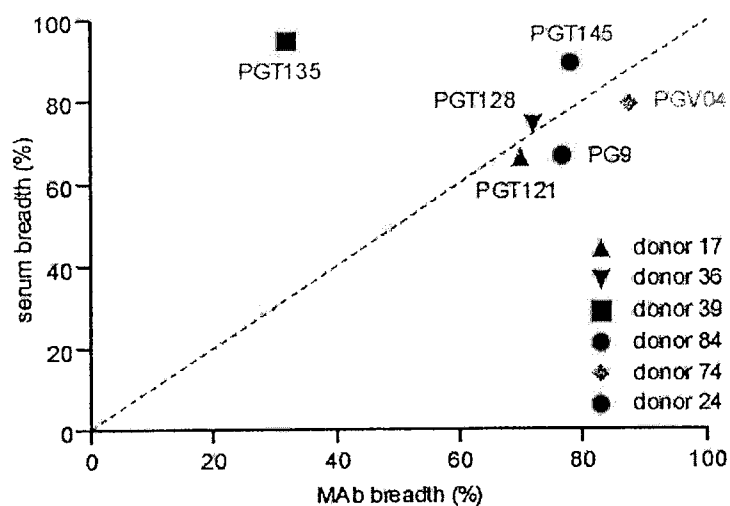


FIGURE 32

FIGURE 33

A



B

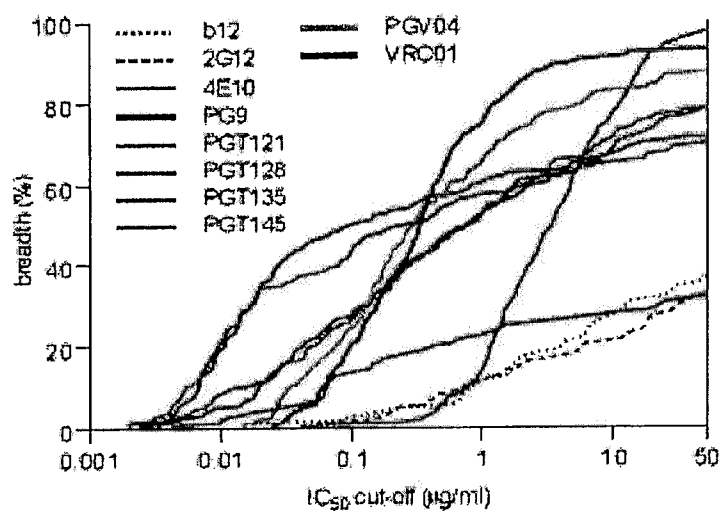
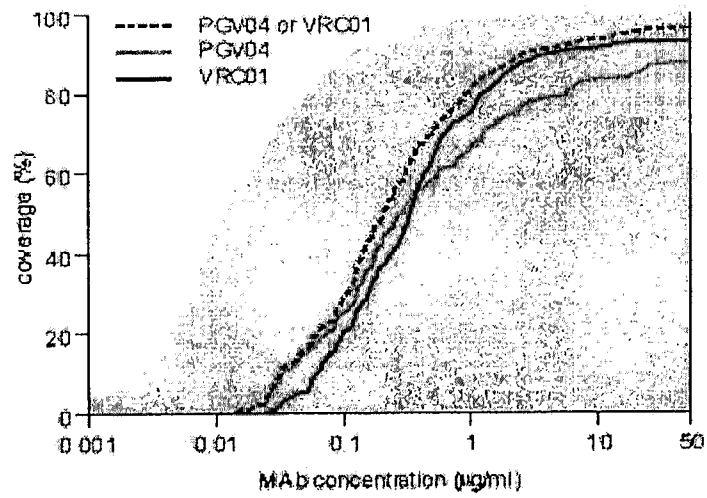


FIGURE 33

C



D

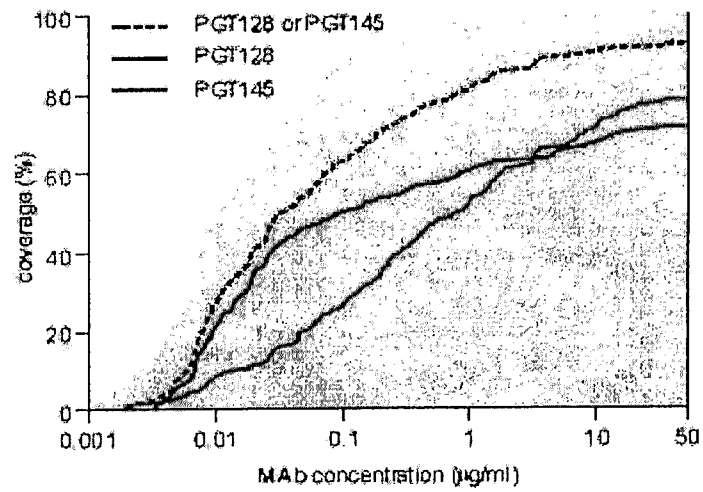


FIGURE 34

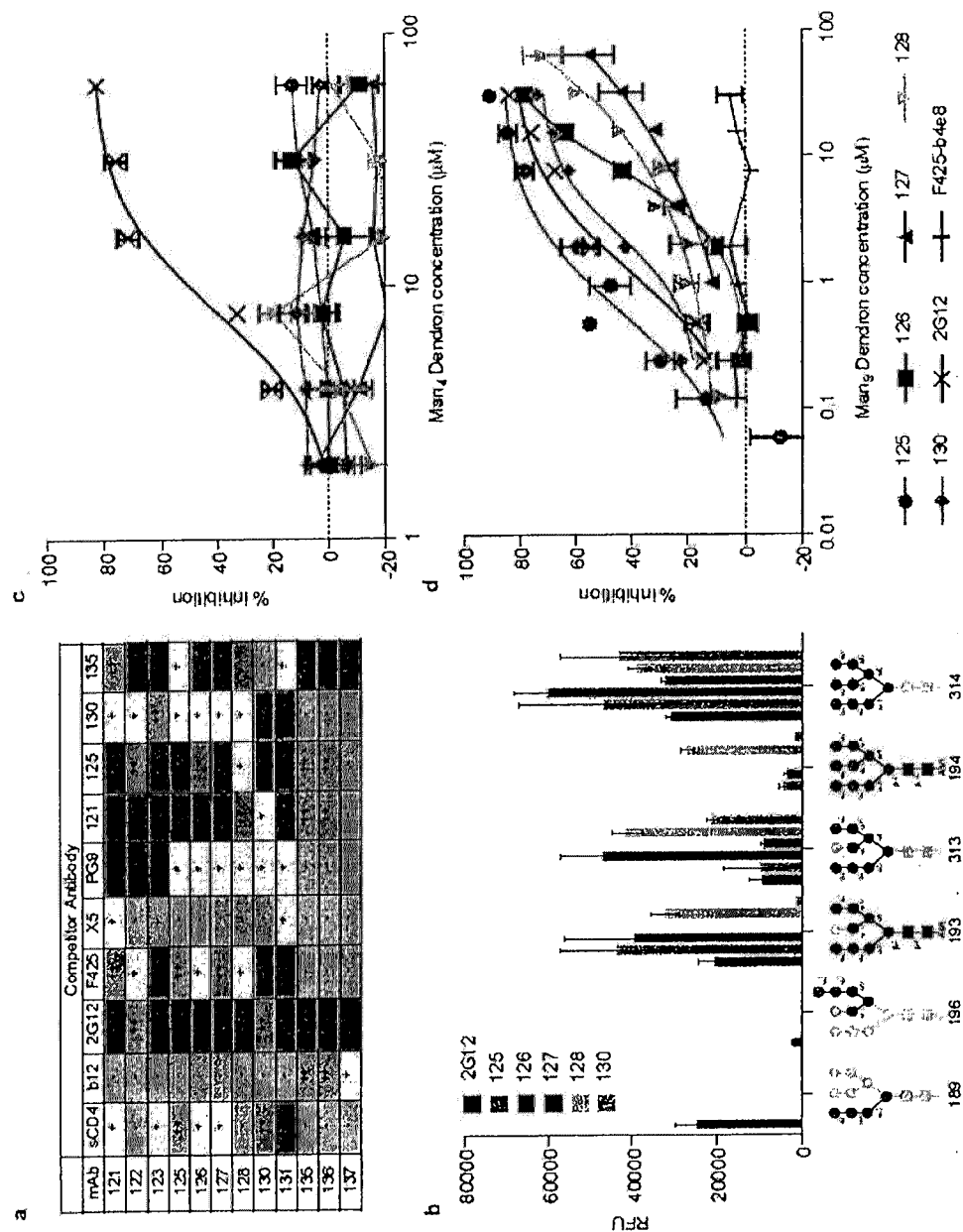


FIGURE 35

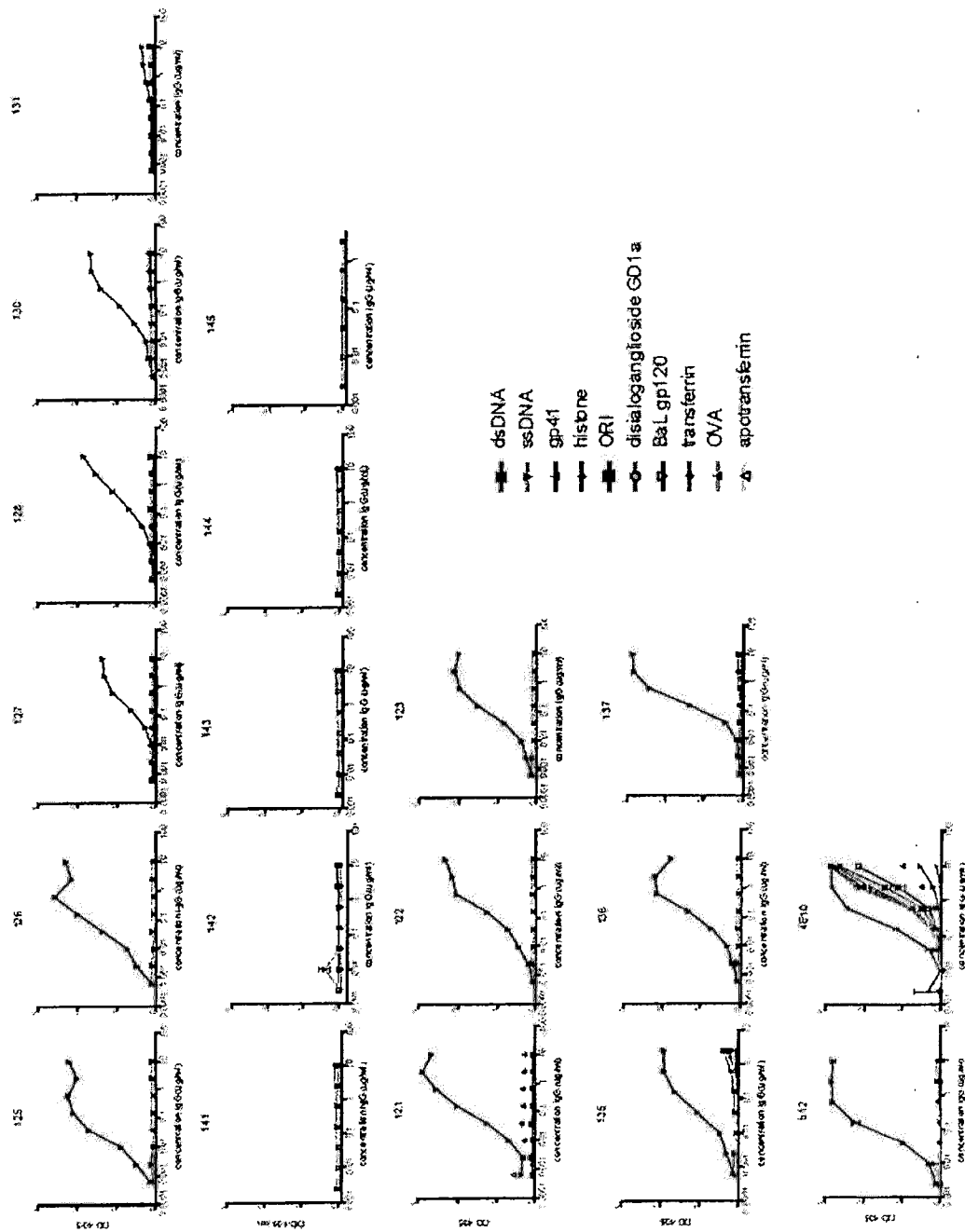


FIGURE 36

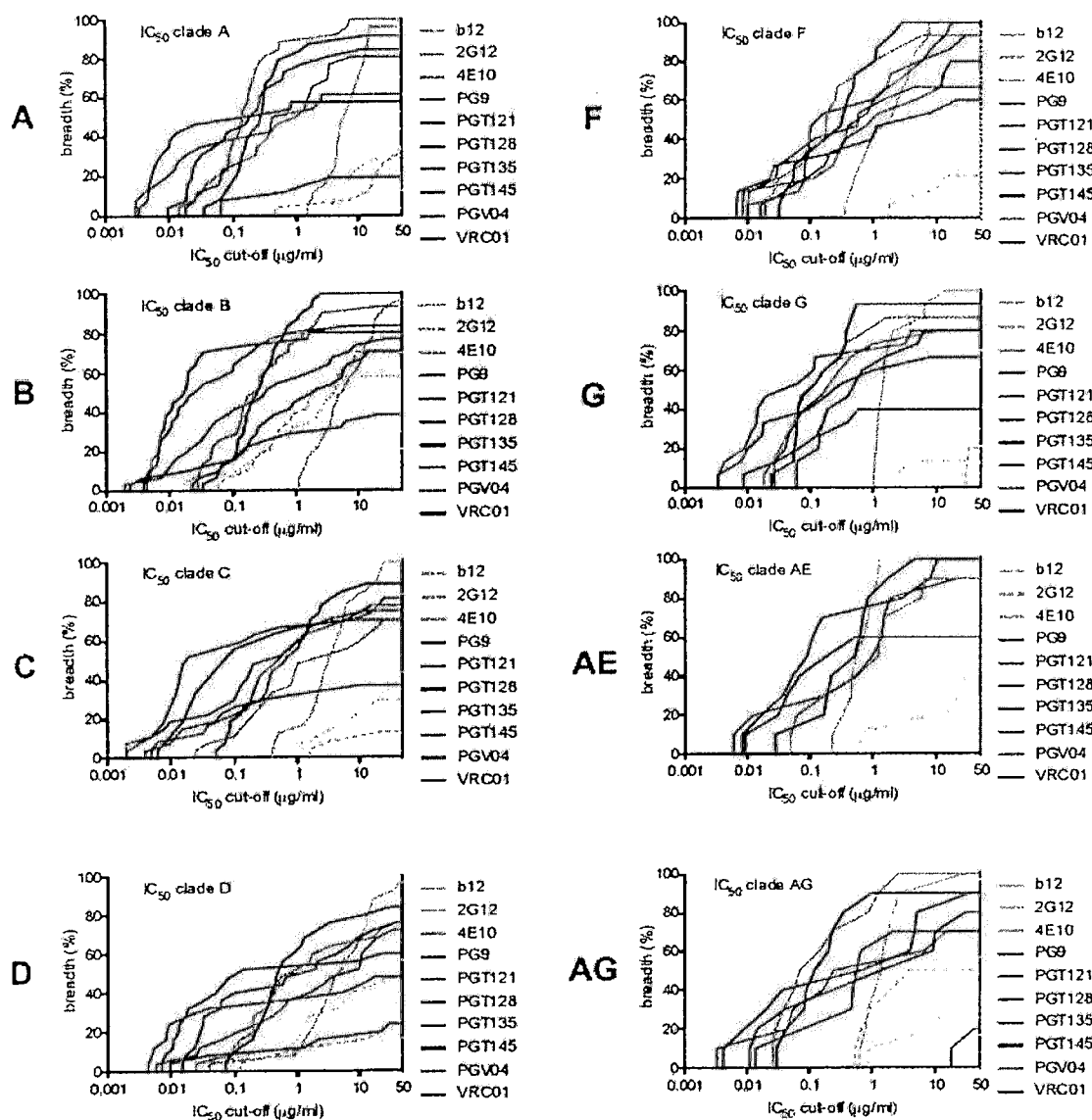
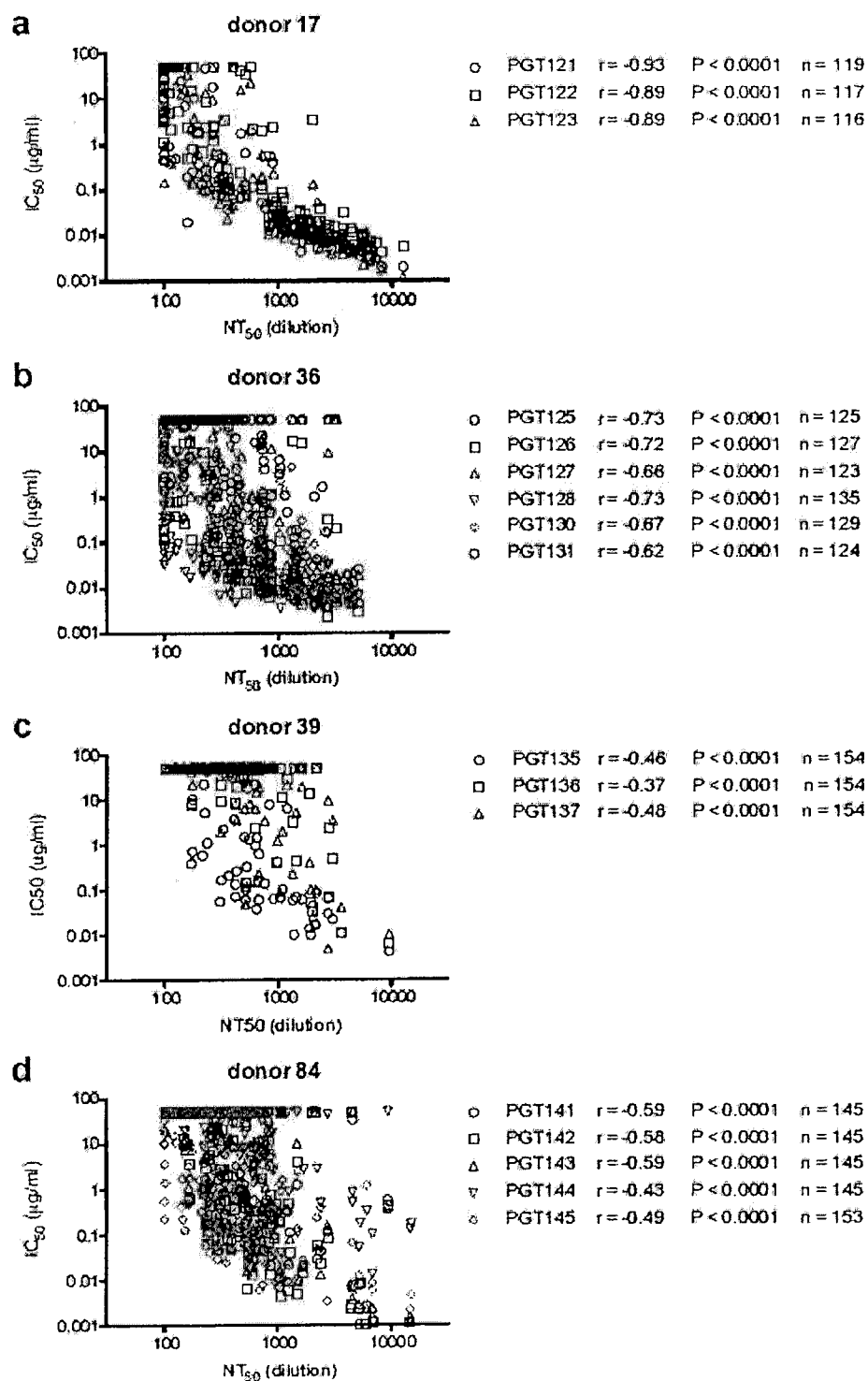


FIGURE 37



A)

Recombinant gp120

OD 405

antibody concentration ($\mu\text{g/ml}$)

141

142

143

144

145

b12

PG9

2G12

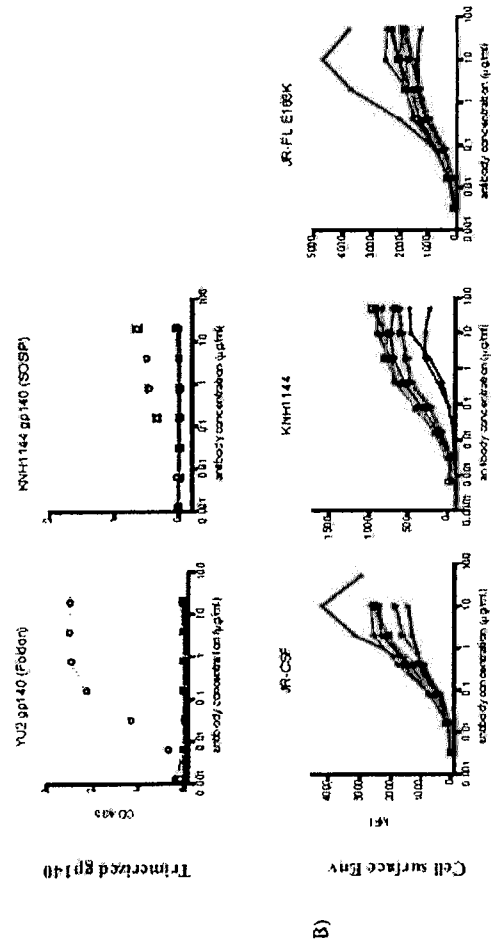


FIGURE 39

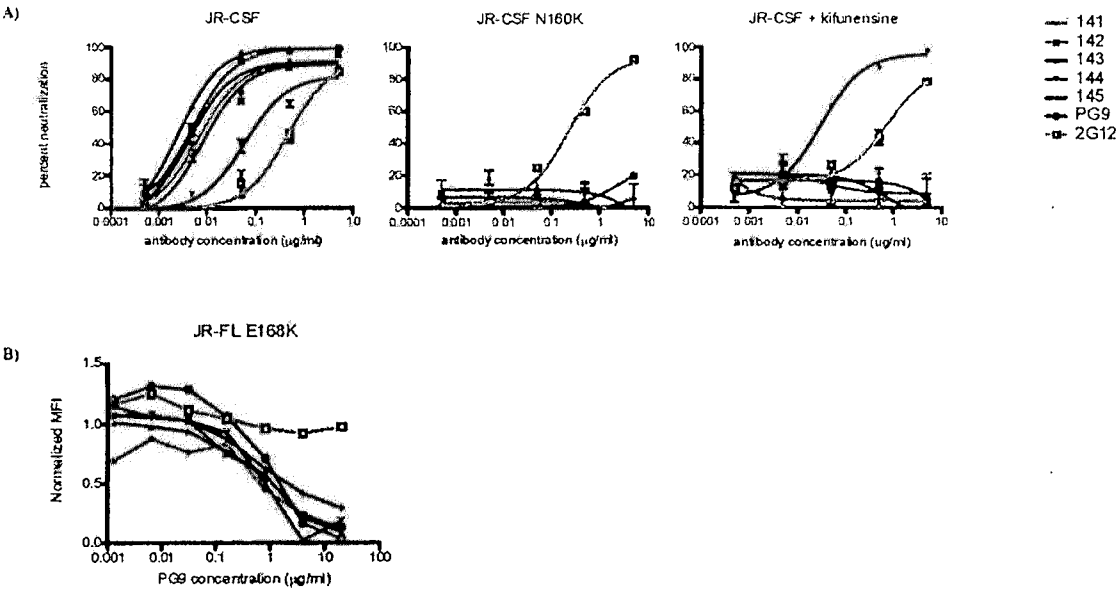


FIGURE 40

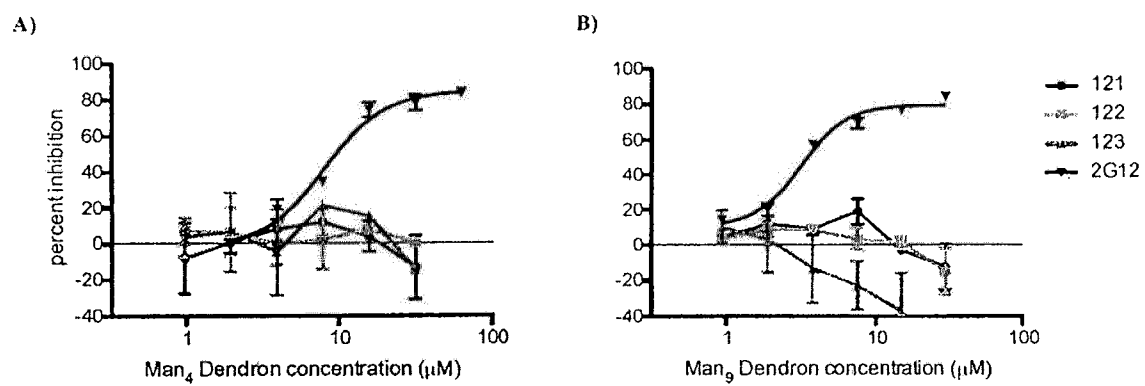


FIGURE 41

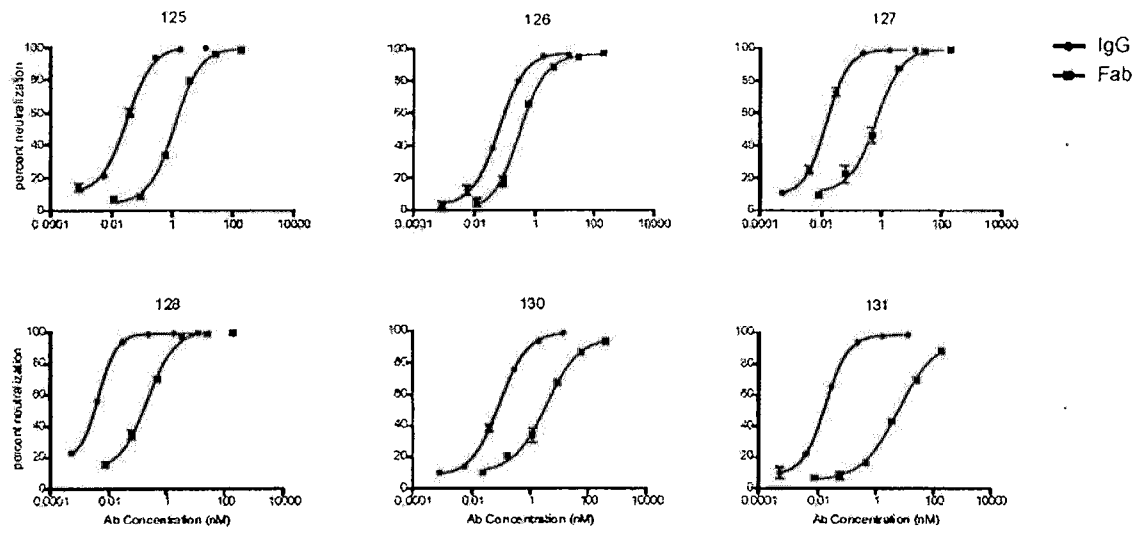


FIGURE 42

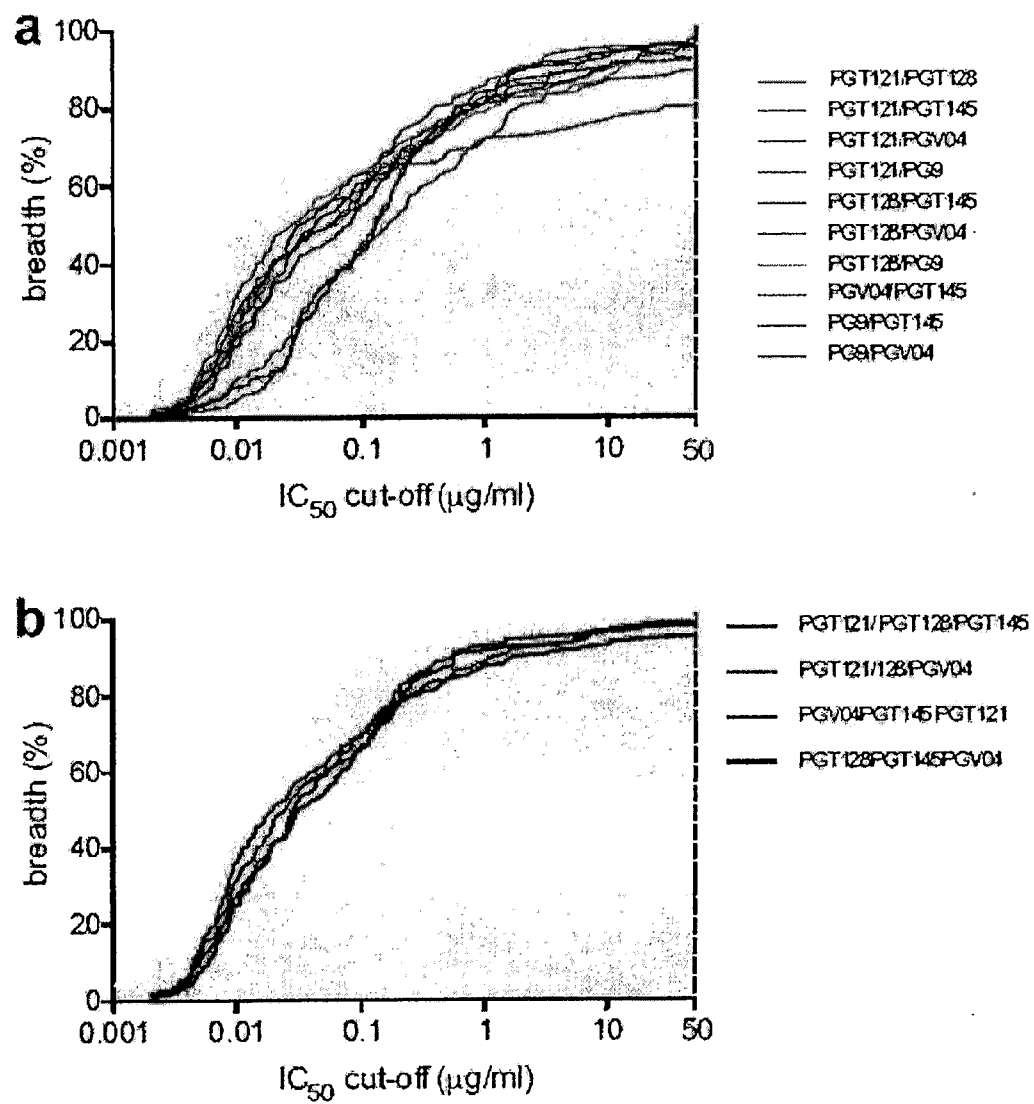


FIGURE 43

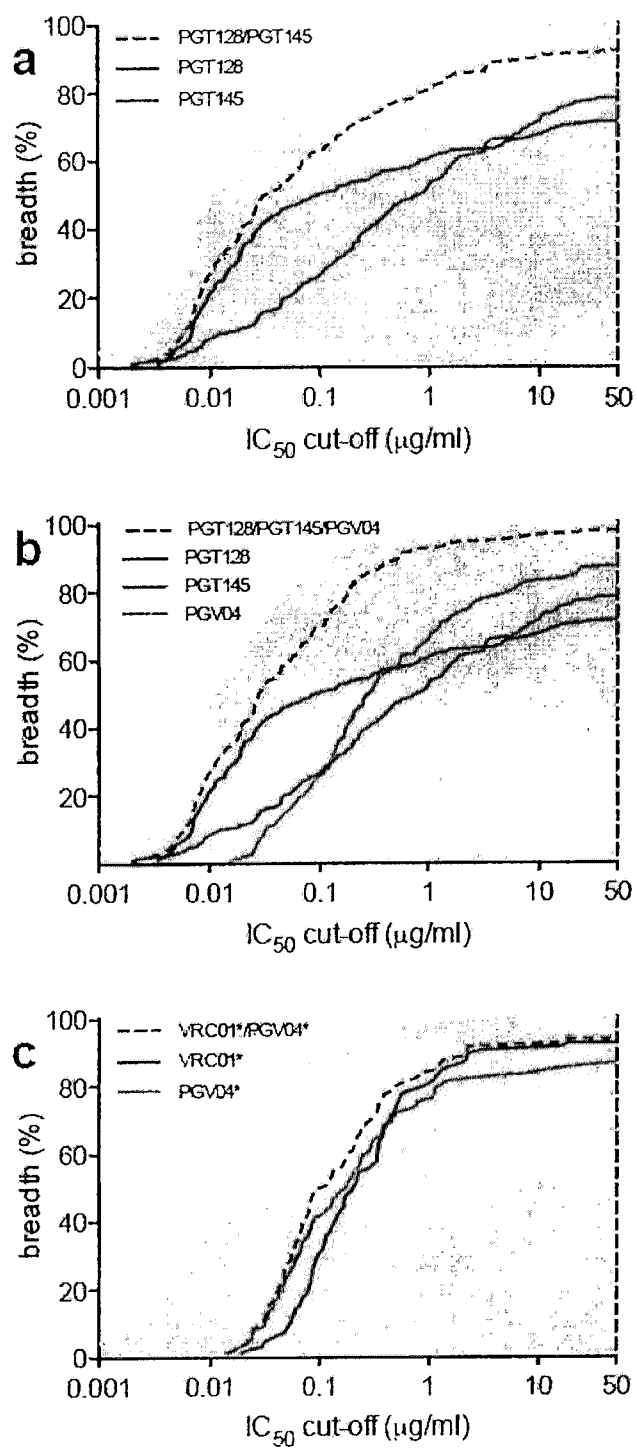


FIGURE 44

