

METHODS OF INDUCING IMMUNE TOLERANCE WITH MODIFIED ANTI-CD154
ANTIBODIES

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority from United States Provisional Application No.
5 63/134,413, filed January 6, 2021; the contents of which are hereby incorporated by reference
in their entirety.

SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been submitted
electronically in ASCII format and is hereby incorporated by reference in its entirety. Said
10 ASCII copy, created on January 6, 2022, is named 104545-0079-WO1_-_Sequence_Listing.txt
and is 753,073 bytes in size.

FIELD OF THE DISCLOSURE

[0003] The present disclosure relates to methods of inducing immune tolerance during
transplantation by administering to a transplant recipient anti-CD154 antibodies with modified
15 (e.g., selectively reduced) effector functions.

BACKGROUND OF THE DISCLOSURE

[0004] CD154 (also known as CD40 ligand, CD40L, gp39, TNF-related activation protein
(TRAP), 5c8 antigen, T-BAM) is a protein primarily expressed on activated CD4⁺ T cells and
is recognized as the molecular basis for T cell helper function (Lederman, S., *et al. J. Exp. Med.*
20 175:1091-1101 (1992). CD154 is a member of the TNF superfamily of molecules and is
functionally expressed as a homotrimer. Some of the CD154 units, however, have shortened
peptide chains, such that CD154 trimers can be considered heterotrimers of elements all
encoded by the CD154 gene (Karpusas M, *et al. Structure.* 3(10):1031-9 (1995); Hsu YM, *et*
al. J Biol Chem. 272(2):911-5 (1997)). CD154 binds to CD40 on antigen-presenting cells
25 (APC), which leads to many effects depending on the target cell type. The primary binding
partner for CD154 is CD40, although other binding partners α M β 2 (Mac-1), α 5 β 1 integrin and
 α IIB β 3 have been described (El Fakhry Y, *et al. J Biol Chem.* 287:18055 (2012); Wolf D, *et al.*

Circ Res. 109:1269 (2011); Michel NA, *et al Front Cardiovasc Med.* 4:40 (2017)). CD154 acts as a costimulatory molecule for B cells and affects the function of CD4⁺ T follicular helper cells (TFH cells). On TFH cells, CD154 promotes B cell maturation and function by engaging CD40 on the B cell surface and thereby facilitating cell-cell communication in a humoral immune response. CD40 triggering by CD154 stimulates adaptive immune system processes in B cells including immunoglobulin class switch recombination and somatic hypermutation (Lederman S, *et al. Curr Opin Hematol.* 3(1):77-86 (1996)). Absence of CD154, for example, in the X-linked Hyper IgM syndrome, leads to deficiencies in the formation of germinal centers, class switch recombination and antibody affinity maturation. (Webster EA, *et al. Arthritis Rheum.* 42(6):1291-6 (1999)). The CD40-CD154 interaction is involved in normal T-B cell interactions, including increased co-stimulation, T-cell priming, cytokine production, antibody-class switching and affinity maturation, and antibody production (Lederman, S., *et al. J. Exp. Med.* 175:1091-1101 (1992); Lederman, S., *et al., Journal of Immunol.* 149:3817-3826 (1992); Lederman, S., *et al., Journal of Immunol.* 152:2163 (1994); Cleary, A.M., *et al., Journal of Immunol.*, 155:3329-3337 (1995); Muramatsu, MK *et al. Cell* 102: 553 (2000); Xu Y and Song G, *J. Biomed Sci.* 11(4):426-38 (2004); Quezada SA *et al., Annu Rev Immunol.* 22:307-28 (2004); and U.S. Patent Nos. 5,474,771; 5,933,816; 6,331,615; 6,340,459; 6,403,091; 6,451,310; 6,455,044; 6,592,868; 6,610,294; 6,793,924; 7,070,777; and 9,765,150).

[0005] CD154 also interacts with CD40 on activated endothelial cells (Yellin MJ *et al., J. Exp. Med* 182:1857–1864 (1995)), activated fibroblasts (Yellin, MJ *et al. J Leukoc Biol.* 58:209–216 (1995)), in other cell types and in many cancers (Paulie, S, *et al. Cancer Immunol Immunother*, 20, 23-8 (1985)). Supernatants of severe acute respiratory syndrome-associated coronavirus (SARS-CoV) infected human lung epithelial Calu-3 cells and induce CD40 on dendritic cells (Yoshikawa T, *et al. J. Virol.* 83(7): 3039–3048 (2009)). In the retina, during inflammation, CD40 is expressed on endothelial cells, Müller glia (macroglia in the retina), microglia, ganglion cells, and retinal pigment epithelial cells (Subauste, CS, *Front Immunol* 10:2958 (2019); Portillo J-AC, *et al. J Immunol.* 181:8719–26 (2008); Portillo J-AC, *et al. Diabetologia.* 57:2222–31(2014); Portillo J-AC, *et al., Mol Vis.* 15:1383–9 (2009)). The roles of CD154 in an immune response are normally tightly regulated in tissues over time.

Dysfunctional immune responses can occur with abnormal CD154 expression and function in certain tissues and at certain times, contributing to syndromes such as acute respiratory distress syndrome (ARDS), autoimmune diseases, vasculopathies and the promotion of cancers.

[0006] The soluble form of CD154 (sCD154), which results from the shedding of membrane-bound CD154, plays a role in the production of proinflammatory cytokines and has been linked to various autoimmune and vascular disorders (Yellin, MJ, *et al.*, *J. Immunol.* 152:598 (1994); Yacoub D *et al.*, *J Biol Chem.* 288(50):36083-93 (2013)). Activated platelets produce CD154 and platelet derived CD154, particularly soluble CD154, has been linked to pathology. (Henn V, *et al. Nature* 391:591–594 (1998); Xu H, *et al. Transplantation.* 72(11):1858-61. (2001); Danese S, *et al. Gut.* 52(10):1435-41. (2003); and Charafeddine AH, *et al. Am J Transplant.* 12(11):3143-51 (2012)).

[0007] The monoclonal antibody 5c8 is a murine anti-human CD154 that potently blocks CD154 function. (Lederman, S., *et al. J. Exp. Med.* 175:1091-1101 (1992); Lederman, S., *et al.*, *Journal of Immunol.* 149:3817-3826 (1992); Lederman, S., *et al.*, *Journal of Immunol.* 152:2163 (1994); and Cleary, A.M., *et al.*, *Journal of Immunol.*, 155:3329-3337 (1995)). A humanized anti-human CD154 IgG1 antibody (hu5c8, ruplizumab or ANTOVA®) was generated and tested in non-human primates and humans. A crystal structure of hu5c8 showed the unique binding of hu5c8 to the CD154 trimer and antibody contacts with CD154 monomer (Karpusas M, *et al. Structure.* 9(4):321-9. (2001)). CD154 blockade has demonstrated efficacy in models of autoimmunity, humoral immunity and allotransplantation (Pierson RN 3rd, *et al. Transplantation.* 68(11):1800-5 (1999); Chang AC, *et al. Transplant Proc.* 31(1-2):95 (1999); Kenyon NS, *et al. Proc Natl Acad Sci U S A.* 96(14):8132-7 (1999); Kenyon NS, *et al. Diabetes.* 48(7):1473-81. (1999); Elster EA, *et al. Transplantation.* 72(9):1473-8. (2001); Elster EA, *et al. Transplant Proc.* 33(1-2):675-6 (2001); Cho CS, *et al. Transplantation.* 72(4):587-97 (2001); Pierson RN 3rd, *et al. Immunol Res.* 23(2-3):253-62 (2001); Pfeiffer S, *et al. J Heart Lung Transplant.* 20(2):250 (2001); Xu H, *et al. Transplant Proc.* 33(1-2):223-4 (2001); Xu H, *Transplantation.* 74(7):940-3 (2002); Crowe JE Jr, *et al. Am J Transplant.* 3(6):680-8 (2003); Ferrant JL, *et al.*, *International Immunol* October 5;11:1583 (2004); Kawai T, *et al.*, *Am J Transplant.* 4(9):1391-8 (2004); Preston EH, *et al. Am J Transplant.* 5(5):1032-41 (2005); Xu H, *et al. J Immunol.* 170(5):2776-82 (2003); Wu G, *et al. Xenotransplantation.* 12(3):197-208 (2005); Smith RN, *Am J Transplant.* 6(8):1790-8 (2006); Zhang T, *et al. Transplantation.* 102(3):e90-e100 (2018)). However, clinical trials of hu5c8, in systemic lupus erythematosus (SLE) (Huang W, *et al. Arthritis Rheum.* 46(6):1554–62 (2002); Boumpas DT, *et al.*, *Arthritis Rheum.* 48:719–27. (2003); Grammer AC, *et al. J Clin Invest.* 112:1506–20. (2003)) and transplantation (Kawai T, *et al. Nat Med.* 2000;6:114. (2000); Koyama I, *et al.*,

Transplantation. 77(3):460-2. (2004)) were halted due to an increased incidence of platelet activation and thromboembolic events (Law and Grewal *Adv Exp Med Biol*. 647:8-36 (2009)). One mechanism for platelet activation may relate to CD40 on platelets and activation by soluble CD154 (Inwald DP, et al, *Circ Res*. 92(9):1041-8 (2003)). Several observations suggest that a mechanism for thrombosis in anti-CD154 treated patients is mediated by Fc gamma RIIa receptor (FcγRIIA, FCGR2A, CD32A)-dependent platelet activation by immune complexes, particularly higher ordered complexes, comprised of anti-CD154 antibodies and soluble CD154 (Robles-Carrillo L, et al., *J Immunol*. 185(3):1577-83. (2010)). Eliminating Fc binding to Fc receptors by mutating the Fc region to make aglycosyl hu5c8 (IgG1 N297Q) has been shown to strongly decrease or eliminate such thromboembolism (Shock, A, et al., *Arthritis Res Ther*. 17:234 (2015) and Xie et al., *Journal of Immunol*. 192(9):4083 (2014)), but also reduced the antibody's efficacy in inhibiting or preventing transplant rejection in rhesus renal and islet allotransplantation models (Ferrant JL et al., *International Immunol* (11):1583 (2004)). Entirely eliminating the Fc region, such as in an anti-CD154 pegylated Fab' antibody fragment (Dapirolizumab pegol (DZP), CDP7657, Biogen and UCB) also reduced the risk of thrombotic events but failed to treat systemic lupus erythematosus (SLE) in a Phase IIb clinical trial (Waters J, *Biocentury*; October 26, (2018)). Kim et al. generated an Fc silent anti-human CD154 single domain antibody (dAb; BMS-986004; Letolizumab, BMS2h-572-633-CT-L2) by fusing the variable domain of an anti-human CD154 dAb with the Fc from CTLA4-Ig (abatacept, ORENCIA®) and a linker termed "CT Long Fc" with amino acid sequence EPKSSDK (SEQ ID NO: 325) (Kim SC et al., *Am J Transplant* 17(5):1182-1192 (2017); and U.S. Patent No. 9,765,150). BMS-986004 effectively prevented kidney rejection in nonhuman primates and was also devoid of platelet activation, thrombosis or thromboembolism (Kim SC et al., *Am J Transplant* 17(5):1182-1192 (2017)).

[0008] U.S. Patent No. 9,765,150 also described BMS-986003 (BMS-2h572-633-CT), which shares the same amino acid sequence as BMS-986004, except for a non-native glycine residue at its amino-terminus. BMS-986003, however, induced anti-drug antibodies (ADA) in treated monkeys. The ADA were directed to the dAb (non-Fc) portion of the molecule and these antibodies were shown to block the binding of BMS-986003 to CD154 suggesting the ADA may be neutralizing. In addition, these ADA resulted in increased clearance of BMS- 986003 in several monkeys. In contrast, a chimeric murine 5c8 human IgG1 chimeric antibody had expected long plasma half-life. (U.S. Patent No. 9,765,150).

[0009] While BMS-986004 demonstrated efficacy in an immune thrombocytopenic purpura (ITP) clinical trial, the pharmacokinetic profile may be suboptimal (NCT02273960; “Study to Evaluate Safety and Efficacy in Adult Subjects With ITP (ITP)”); results accessed July 1, 2019).

[0010] Antibodies have a variety of effector functions mediated by the Fc including FcγR binding and complement C1q binding (the first component of complement activation), which relate to effector functions and complement dependent cytotoxicity. Engineering antibodies may result in increasing or decreasing one or more effector functions. At the extreme, the Fc can be removed, for example in a F(ab) construct, but for therapeutic effects, such constructs typically require other changes to increase half-life, such as modification with polyethylene glycol or PEGylation. Entirely eliminating the Fc region can affect an anti-CD154 antibody’s efficacy—an anti-CD154 pegylated Fab’ antibody fragment (Dapirolizumab pegol (DZP), CDP7657, Biogen and UCB) failed to treat SLE in a Phase IIb clinical trial (Waters J, *Biocentury*; October 26, (2018)). A “silent” N297Q IgG1 variant (asialo- or algyco-) of hu5c8 lacked FcγR binding, but was effective in inhibiting the humoral immune response, but not organ rejection in non-human primates. (Tao, M.H. and Morrison, S.L. *J. Immunol.* 143:2595–2601. (1989), Ferrant J.L. *et al.*, *International Immunol* (11):1583 (2004)). Therefore, a solution to balancing efficacy and safety of anti-CD154 antibodies is to engineer an anti-CD154 antibody with a modified Fc with selectively decreased effector function. Prior efforts on modifying effector function have focused on substitutions in the IgG hinge/CH2 region, which can affect FcγR and C1q binding. A consideration in designing antibodies is to maintain the CH2/CH3 region of the Fc domain that is required for interactions with FcRn, the neonatal Fc receptor, which confers extended serum half-life.

[0011] Antibody engineering is a complex and costly technology with unpredictable results *in vivo* (Saeed AF *et al.*, *Frontiers in Microbiology*; Article 495; March (2017)). An antibody engineering strategy including structural changes or other modifications that are optimized for one antibody may compromise another antibody *in vivo* (Yan B, *et al.*, *The Journal of Biol. Chem.* 287(8):5891-97 (2012)). The effect of a mutation on a particular residue (*e.g.*, N297Q) in a particular antibody (*e.g.*, IgG1) can have a very different clinical effect from another kind of mutation at the same antibody (*e.g.*, N297A in IgG1). Moreover, the clinical effects of intramolecular changes within one subtype of antibody (*e.g.*, an L235 mutation in IgG1) may be entirely unpredictable when the same intramolecular changes occur within another subtype

of antibody (*e.g.*, an L235 mutation within IgG4). Intramolecular changes also may result in different clinical effects, depending on how various mutations may pair up within an antibody. Species-specific differences add to the unpredictability of the effect of an Fc receptor mutation on the efficacy vs toxicity of anti-CD154 antibodies. In the past, anti-CD154 antibodies
5 developed for use in transplantation studies did not cause thrombosis in pre-clinical rodent and certain non-human primates, but a number of human patients experienced thromboembolic complications in clinical trials with the same antibodies (*i.e.*, ruplizumab, toralizumab, and ABI793) (Pinelli DF and Ford M.L. *Immunotherapy* 7(4): 399–410 (2015)).

[0012] To reduce graft rejection, immune tolerance to the donor graft is required. Immune
10 tolerance is achieved when the immune system is unresponsive to the donor graft or organ. Immune tolerance is classified into central tolerance wherein the tolerance occurs in the thymus or bone marrow or peripheral tolerance wherein the tolerance occurs in the peripheral tissue and lymph nodes. Furthermore, different organs require different tolerance induction protocols to induce organ-specific tolerance (Madariaga, M, Kreisel, D, & Madsen, J, 20(4),392–399
15 (2015)). Tolerance may be established by achieving mixed chimerism through conditioning the body for the transplant and transplanting donor hematopoietic stem cells. Organ-specific protocols may be required to achieve mixed chimerism. For example, mixed chimerism protocols that achieve tolerance of kidney transplants in monkeys failed to induce tolerance in heart transplant recipients (Kawai T, Cosimi AB, Wee SL, Houser S, Andrews D, Sogawa H,
20 Phelan J, Boskovic S, Nadazdin O, Abrahamian G, Colvin RB, Sach DH, Madsen JC. *Transplantation* 73(11):1757-64 (2002).

[0013] The mechanism of anti-CD154 treatment of transplantation rejection or autoimmunity is not completely understood. Anti-CD154 therapy appears more effective than anti-CD40 therapy, suggesting that blockade of their interaction is not symmetrical. The monoclonal
25 antibody (mAb) hu5c8 appears more effective than a different humanized anti-CD154 mAb, IDEC-131 (O'Neill NA, *et al.* *Transplantation*. 101(9):2038-2047 (2017)). Further, an increase in regulatory T cells, specifically Foxp3+ T cells, associated with anti-CD154 therapy may relate to efficacy (Ferrer IR, *et al.*, *Proc Natl Acad Sci U S A*. 108(51):20701-6 (2011)). Another observation supporting a role for regulatory T cells was that dimeric soluble CD40,
30 but not monovalent CD40 induced T regulatory cells (CD4+CD25+ T cells) and treated transplant rejection (Masunaga T, *et al.* *Transplantation*. 80:1614–1622 (2005)). Those

experiments also showed that valency in CD154 ligation or blockade may be relevant to efficacy (Masunaga T, *et al. Transplantation*. 80:1614–1622 (2005)). Anti-CD154 treatment was shown to be particularly effective in facilitating allotransplant with mixed chimerism (Kawai T, *et al., Am J Transplant*. 4(9):1391-8 (2004) and in xenotransplantation (Längin M, *et al., Nature*. 564(7736):430-433 (2018)).

[0014] To date, there has not been a fully human or humanized anti-CD154 antibody that satisfies the need for a product that can effectively prevent in humans transplant rejections (including graft versus host disease), inflammatory conditions and diseases, autoimmune conditions and diseases, dysfunctional immune responses associated with viral infections and diseases, allergic conditions, atherosclerotic conditions, or neurodegenerative conditions and diseases, with an acceptable level of side effects, such as thromboembolic side effects. This highlights the need for antibodies and variations thereof, that bind to CD154 with high affinity, and inhibit the downstream effects of CD154:CD40 binding, in the absence of toxic side effects such as thrombosis.

SUMMARY OF THE DISCLOSURE

[0015] The present disclosure relates to the induction of immune tolerance in a transplant recipient. The present disclosure also relates to inducing peripheral, central, or organ-specific tolerance through anti-CD154 administration and the transplantation of donor hematopoietic stem cells. The present disclosure also relates to conditioning methods used to prepare the transplant recipient for hematopoietic stem cell transplantation to and reduce graft reject. The present disclosure additionally relates to the structures of anti-CD154 used for the induction of immune tolerance.

[0016] A first aspect of the present disclosure provides a method of inducing immune tolerance in a transplant recipient. In some embodiments, the method comprises administering to the recipient one or more doses of an isolated anti-CD154 antibody, transplanting into the recipient hematopoietic stem cells, and transplanting a donor organ, a donor tissue or donor cell into the recipient, wherein the hematopoietic stem cells produce immune cells that are tolerant of the donor organ, donor tissue or donor cell, thereby inducing immune tolerance in the recipient.

[0017] In some embodiments, the immune tolerance is central tolerance. Optionally, the method further comprises depleting T cells in the thymus. In some embodiments, the method further comprises depleting T cells in the bone marrow. Optionally, the method further comprises depleting T cells in both the thymus and bone marrow.

- 5 [0018] In some embodiments, the immune tolerance is peripheral tolerance. Optionally, the method further comprises depleting T cells in the lymph nodes. In some embodiments, the method further comprises depleting T cells in peripheral tissue. Optionally, the method further comprises depleting T cells in both lymph nodes and peripheral tissue.

- [0019] In some embodiments, the method of inducing immune tolerance is organ-specific
10 tolerance. In some embodiments, the method further comprises depleting T cells from the heart, a kidney, both kidneys, the liver, a partial liver, a lung, both lungs, the pancreas, the intestines, islet cells, the face, one hand, both hands, one arm, both arm, one foot, both feet, one leg, both legs, or the skin or a combination thereof.

- [0020] In some embodiments, the T cells are depleted by a method selected from a group
15 consisting of total body irradiation, administration of abatacept, administration of one or more BCL-2 inhibitors, administration of busulfan, administration of fludarabine phosphate, administration of cyclophosphamide, administration of one or more immunosuppressive T cell-depleting antibodies, administration of one or more anti- $\alpha\beta$ T cell receptor antibodies, and administration of one or more CD122 antagonists or a combination thereof.

- 20 [0021] In some embodiments, the one or more T cell-depleting antibodies are selected from the group consisting of anti-CD4, anti-CD8, anti-CD45, anti-CTLA4, anti-CD20, and anti-CD33 antibodies or a combination thereof.

[0022] In some embodiments, the method of inducing immune tolerance results in mixed chimerism.

- 25 [0023] In some embodiments, the anti-CD154 antibody is administered prior to transplantation of the hematopoietic stem cells. Optionally, the anti-CD154 antibody is administered subsequently to transplantation of the hematopoietic stem cells. In some embodiments, the anti-CD154 antibody is administered simultaneously with the transplantation of the hematopoietic stem cells. In some embodiments, the hematopoietic stem cells are
30 transplanted by a bone marrow transplant.

[0024] In some embodiments, the anti-CD154 antibody is administered at a dose of 5-50 mg/kg. Optionally, the anti-CD154 antibody is administered at a dose of 10-40 mg/kg. In some embodiments, the anti-CD154 antibody is administered at a dose of 20-30 mg/kg. Optionally, the anti-CD154 antibody is administered subcutaneously, intravenously, intravitreally, orally, via inhalation, transdermally, or rectally.

[0025] In some embodiments the anti-CD154 antibody comprises a human or humanized variable domain, wherein the variable domain comprises a heavy chain variable region (VH) and a light chain variable region (VL), and wherein the VH is operably linked to a human Fc domain with modified effector function. In some embodiments, the anti-CD154 antibody has one or more effector functions reduced. Optionally, one or more effector functions are eliminated. In some embodiments, the VH is operably linked to a human Fc region, wherein the human Fc region comprises a human hinge sequence and the human Fc domain, wherein the human hinge sequence is between the VH and the human Fc domain. In some embodiments, the hinge comprises the amino acid sequence of any one of SEQ ID NOs: 76-90.

[0026] In some embodiments, the Fc domain is derived from an IgG4 Fc (or crystallizable fragment) region and comprises one or more amino acid modifications that modifies effector functions. In some embodiments, the antibody comprises an amino acid modification at any one of the positions selected from the group consisting of S228, L235, G237, E318, and N297 or a combination thereof, wherein the numbering of amino acid residues is according to the EU index as set forth in Edelman. In some embodiments, the antibody comprises an amino acid modification selected from the group consisting of S228P, F234A, L235A, L235E, G237A, E318A, and N297Q or a combination thereof.

[0027] In some embodiments, the Fc domain is derived from an IgG1 Fc (or crystallizable fragment) region and comprises one or more amino acid modifications that modifies effector functions. In some embodiments, the antibody comprises an amino acid modification at any one of the positions selected from the group consisting of E216, R217, K218, C219, C220, C226, C229, P230, E233, L234, L235, G236, G237, P238, S239, V240, F241, K246, L251, T260, D265, V266, H268, W277, N297, E318, K322, P329, A330, P331, Q347, N348, T350, L351, K360, T366, N390, K392, T394, D399, S400, F405, Y407, K409, T411, or a combination thereof, wherein the numbering of amino acid residues is according to the EU index as set forth in Edelman. Optionally, the antibody comprises an amino acid modification selected from the group consisting of C220S, C226S, C229S, P230S, E233P, L234A, L234F,

L234V, L235A, L235E, L235V, G236E, G237A, P238S, D265S, D265A, H268Q, W277T, N297G, N297Q, N297D, N297A, E318A, K322A, P329G, P329A, A330S, P331S, Q347R, Q347E, Q347K, T350V, L351Y, K360D, K360E, T366A, T366I, T366L, T366M, T366V, N390R, N390K, N390D, K392V, K392M, K392R, K392L, K392F, K392E, T394W, D399R, D399W, D399K, S400E, S400D, S400R, S400K, F405A, F405I, F405M, F405T, F405S, F405V, F405W, Y407A, Y407I, Y407L, Y407V, K409F, K409I, K409S, K409W, T411N, T411R, T411Q, T411K, T411D, T411E, T411W, ΔE216-E222, K246R/L251E/T260R, InR234/235, InV235/236, InR236/237, InR237/238, InV238/239, InN238/239, InL238/239, InE238/239, InG238/239, InS239/240, InG240/241, InE240/241, InG240/241, InL238/239/P238Q, InE238/239/N348A, InS239/240/V266A, and InR237/238/G236A or a combination thereof.

[0028] In some embodiments, the Fc domain is derived from an IgG2 Fc (or crystallizable fragment) crystallizable fragment region and comprises one or more amino acid modifications that modifies effector functions. In some embodiments, the antibody comprises an amino acid modification at any one of the positions selected from the group consisting of V234, G237, P238, H268, V309, A330, and P331 or a combination thereof, wherein the numbering of amino acid residues is according to the EU index as set forth in Edelman. In some embodiment, the antibody comprises an amino acid modification selected from the group consisting of V234A, G237A, P238S, H268Q, H268A, V309L, A330S, and P331S, or a combination thereof. In some embodiments, the Fc domain comprises the amino acid sequence selected from the group consisting of SEQ ID NOs: 3-9, 12-18, and 238-241. Optionally, the Fc region comprises the amino acid sequence selected from the group consisting of SEQ ID NOs: 21-37, 40-56, and 243-251.

[0029] In some embodiments, the VH comprises a heavy chain CDR1 having the amino acid sequence of SEQ ID NO: 57, a heavy chain CDR2 having the amino acid sequence of SEQ ID NO: 58, and a heavy chain CDR3 having the amino acid sequence of SEQ ID NO: 59. Optionally, the VH comprises the amino acid sequence selected from the group consisting of SEQ ID NO: 63, 64, 252 and 253. Furthermore, in some embodiments, the VL comprises a light chain CDR1 having the amino acid sequence of SEQ ID NO: 60, a light chain CDR2 having the amino acid sequence of SEQ ID NO: 61, and a light chain CDR3 having the amino acid sequence of SEQ ID NO: 62. Optionally, the VL comprises the amino acid sequence of SEQ ID NO: 65 or 66.

[0030] In some embodiments, the antibody further comprises a CH1 domain, wherein the CH1 domain is operably linked to the C-terminal end of the VH and the N-terminal end of the hinge. In some embodiments, the CH1 domain comprises an amino acid sequence that is at least 80% identical to the amino acid sequence of any one of SEQ ID NOs: 67, 70, and 73. In some embodiments, the antibody comprises a linker between the VH and the Fc domain. In some embodiments, the antibody comprises a linker between the VH and the hinge. In some embodiments, the antibody comprises a linker between the VH and the CH1 domain.

[0031] In some embodiments, the linker comprises the amino acid sequence of any one of SEQ ID NOs: 199-223 and 327-330. In some embodiments, the VH is operably linked to the amino acid sequence of any one of SEQ ID NOs: 3-9, 12-18, 21-37, 40-56, 238-241, and 243-251. In some embodiments, the heavy chain comprises the amino acid sequence of any one of SEQ ID NOs: 121-132, 135-146, 149, 151-160, 163, 165-174, 266-277, and 279-288. In some embodiments, the light chain comprises the amino acid sequence of SEQ ID NO: 195 or 196.

[0032] In some embodiments, the antibody is monoclonal. In some embodiments, the antibody is chimeric. Optionally, the antibody is humanized. In some embodiments, the antibody is human.

[0033] In some embodiments, the binding of the antibody to human CD154 inhibits the interaction between human CD154 and human CD40. In some embodiments, the antibody blocks the activation of one or more of B cells, macrophages, dendritic cells, or endothelial cells by inhibiting binding of CD154 to CD40. In some embodiments, the antibody has one or more of the following effects when administered to a subject: decreased risk of thrombosis or thromboembolic events compared to hu5c8 antibody, decreased activation of platelets expressing CD154, inhibition of CD154 shedding, and alteration of the expression or activity of downstream targets of CD154-CD40 signaling.

[0034] In some embodiments, the antibody has a K_D of less than 50 pM for CD154, such as 5-25 pM or 9.5-23 pM. In some embodiments, the antibody does not comprise the amino acid sequence consisting of any one of SEQ ID NOs: 119, 120, 133, 134, 147, 148, 150, 161, 162, 164, 230, 234 and 278.

[0035] In some embodiments, the transplant recipient is human. Optionally, the transplant recipient is non-human. In some embodiments, the transplant recipient is a non-human primate.

In some embodiments, the transplant recipient is a monkey. In some embodiments, the transplant is an allogeneic transplant, autologous transplant or a xenogeneic transplant.

[0036] In some embodiments, the donor cell is an engineered cell or an ex-vivo expanded cell. In some embodiments, one or more genes in the donor cell is modified using one or more techniques selected from a group consisting of transduction to express a cDNA, a CRISPR/Cas9 system, RNAi technology and retroviral technology. In some embodiments, the donor cell is modified to express a chimeric antigen receptor (CAR) on its surface. In some embodiments, the donor cell is selected from a group consisting of a stem cell, a regulatory T cell, a CAR-T cell, a CAR-B cell, a tumor-infiltrating lymphocyte (TIL).

[0037] In some embodiment, the disclosed method promotes a long-term survival of the donor organ, donor tissue or donor cell for at least 6 months post-transplant, at least 1 year post-transplant, and at least 5 years post-transplant.

[0038] In some embodiments, the anti-CD154 antibody is administered locally. Optionally, the anti-CD154 antibody is administered systemically.

BRIEF DISCRIPTION OF THE DRAWINGS

[0039] Figure 1 provides a T-cell depleting regimen for inducing immune tolerance in a non-human primate (NHP) transplant recipient. The recipient is treated with total body irradiation (TBI; 1.5 Gy $\times$ 2) on days -6, -5. The recipient also undergoes thymic irradiation (TI; 7 Gy) on day -1. Intravenous anti-T-cell antibody (50 mg/kg/day) is administered on days -2, -1 and 0. On day 0, kidney and bone marrow (BM) are transplanted into the recipient. Further, anti-CD154 mAb (20 mg/kg/day) is administered to the recipient on days 0, 3, 7, 14, 21, 28, 42, 56, 70, 84 and then monthly until graft failure or 180 days post-transplant.

DETAILED DESCRIPTION OF THE DISCLOSURE

Definitions and General Techniques

[0040] Unless otherwise defined herein, scientific and technical terms used in this application shall have the meanings that are commonly understood by those of ordinary skill in the art. Generally, nomenclature used in connection with, and techniques of, cell and tissue culture, molecular biology, immunology, microbiology, genetics and protein and nucleic acid

chemistry and hybridization described herein are those well-known and commonly used in the art. In case of conflict, the present specification, including definitions, will control.

[0041] The methods and techniques of the present disclosure will employ, unless otherwise indicated, conventional techniques of molecular biology (including recombinant techniques), microbiology, cell biology, biochemistry and immunology, which are within the skill of the art. Such techniques are explained fully in the literature, such as Green MR & Sambrook J. *Molecular Cloning: A Laboratory Manual*, 4th ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (2012); Ausubel *et al.*, *Short Protocols in Molecular Biology: A Compendium of Methods from Current Protocols in Molecular Biology*, 5th ed., Wiley, John & Sons, Inc. (2002); Harlow and Lane *Using Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1998); and Coligan *et al.*, *Short Protocols in Protein Science*, Wiley, John & Sons, Inc. (2003); Oligonucleotide Synthesis (M.J. Gait, ed., 1984); Methods in Molecular Biology, Humana Press; Cell Biology: A Laboratory Notebook (J.E. Cellis, ed., 1998) Academic Press; Animal Cell Culture (R.I. Freshney, ed., 1987); Introduction to Cell and Tissue Culture (J.P. Mather and P.E. Roberts, 1998) Plenum Press; Cell and Tissue Culture: Laboratory Procedures (A. Doyle, J.B. Griffiths, and D.G. Newell, eds., 1993-1998) J. Wiley and Sons; Methods in Enzymology (Academic Press, Inc.); Gene Transfer Vectors for Mammalian Cells (J.M. Miller and M.P. Calos, eds., 1987); Current Protocols in Molecular Biology (F.M. Ausubel *et al.*, eds., John Wiley & Sons, Inc., 2003); PCR: The Polymerase Chain Reaction, (Mullis *et al.*, eds., 1994), each of which is incorporated herein by reference.

[0042] Enzymatic reactions and purification techniques are performed according to manufacturer's specifications, as commonly accomplished in the art or as described herein. The nomenclature used 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.

[0043] Standard techniques are used for chemical syntheses, and chemical analyses.

[0044] Throughout this specification and embodiments, the word "comprise," or variations such as "comprises" or "comprising," will be understood to imply the inclusion of a stated integer or group of integers but not the exclusion of any other integer or group of integers. "Comprising" may be synonymous with "including" or "containing."

[0045] It is understood that wherever embodiments are described herein with the language “comprising,” otherwise analogous embodiments described in terms of “consisting of” and/or “consisting essentially of” are also provided. As used herein, “consisting of” is a closed term that includes only the specific elements recited, and “consisting essentially of” includes the
5 specific elements recited and may include additional unrecited, nonmaterial elements.

[0046] The term “including” is used to mean “including but not limited to.” “Including” and “including but not limited to” are used interchangeably.

[0047] Any example(s) following the term “e.g.” or “for example” is not meant to be exhaustive or limiting.

10 [0048] Unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular.

[0049] The articles “a”, “an” and “the” are used herein to refer to one or to more than one (i.e., to at least one) of the grammatical object of the article. By way of example, “an element” means one element or more than one element. As used herein, the term “about” modifying the
15 quantity of an ingredient, parameter, calculation, or measurement in the compositions of the disclosure or employed in the methods of the disclosure refers to variation in the numerical quantity that can occur, for example, through typical measuring and liquid handling procedures used for making isolated polypeptides or pharmaceutical compositions in the real world; through inadvertent error in these procedures; through differences in the manufacture, source,
20 or purity of the ingredients employed to make the compositions or carry out the methods; and the like without having a substantial effect on the chemical or physical attributes of the compositions or methods of the disclosure. Such variation can be within an order of magnitude, typically within 10%, more typically still within 5%, of a given value or range. The term “about” also encompasses amounts that differ due to different equilibrium conditions for a
25 composition resulting from a particular initial mixture. Whether or not modified by the term “about”, the paragraphs include equivalents to the quantities. Reference to “about” a value or parameter herein includes (and describes) embodiments that are directed to that value or parameter per se. For example, description referring to “about X” includes description of “X.”
Numeric ranges are inclusive of the numbers defining the range.

30 [0050] Notwithstanding that the numerical ranges and parameters setting forth the broad scope of the disclosure are approximations, the numerical values set forth in the specific examples are reported as precisely as possible. Any numerical value, however, inherently

contains certain errors necessarily resulting from the standard deviation found in their respective testing measurements. Moreover, all ranges disclosed herein are to be understood to encompass any and all subranges subsumed therein. For example, a stated range of “1 to 10” should be considered to include any and all subranges between (and inclusive of) the minimum value of 1 and the maximum value of 10; that is, all subranges beginning with a minimum value of 1 or more, *e.g.*, 1 to 6.1, and ending with a maximum value of 10 or less, *e.g.*, 5.5 to 10.

[0051] Exemplary methods and materials are described herein, although methods and materials similar or equivalent to those described herein can also be used in the practice or testing of the present application. The materials, methods, and examples are illustrative only and not intended to be limiting.

Definitions

[0052] The following terms, unless otherwise indicated, shall be understood to have the following meanings:

[0053] As used herein, the term “antibody” or “Ab” refers to an immunoglobulin molecule (*e.g.*, complete antibodies, antibody fragment or modified antibodies) capable of recognizing and binding to a specific target or antigen, such as a carbohydrate, polynucleotide, lipid, polypeptide, etc., through at least one antigen recognition site, located in the variable region of the immunoglobulin molecule. As used herein, the term “antibody” can encompass any type of antibody, including but not limited to monoclonal antibodies, polyclonal antibodies, human antibodies, engineered antibodies (including humanized antibodies, fully human antibodies, chimeric antibodies, single-chain antibodies, artificially selected antibodies, CDR-granted antibodies, etc.) that specifically bind to a given antigen (*e.g.*, CD154). Further, “antibody” and/or “immunoglobulin” (Ig) refers to a polypeptide comprising at least two heavy (H) chains (about 50-70 kDa) and two light (L) chains (about 25 kDa), optionally inter-connected by disulfide bonds. There are two types of light chain: λ and κ . In humans, λ and κ light chains are similar, but only one type is present in each antibody. Heavy chains are classified as mu, delta, gamma, alpha, or epsilon, and define the antibody’s isotype as IgM, IgD, IgG, IgA, and IgE, respectively. See generally, Fundamental Immunology Ch. 7 (Paul, W., ed., 2nd ed. Raven Press, N.Y. (1989)) (incorporated by reference in its entirety). The antibodies disclosed herein may be “functionally divalent” or “functionally monovalent”. In other words, the antibodies disclosed herein may have one antigen-binding site (monovalent) or two antigen-

binding sites that are typically linked by disulfide bonds (divalent). In some embodiments, the anti-CD154 antibody is an IgG1 antibody. The anti-CD154 antibody may be an IgG2 antibody. Optionally, the anti-CD154 antibody is an IgG4 antibody. In some embodiments, the anti-CD154 antibody does not contain the final lysine residue at its C-terminal end in order to improve antibody stability. See *e.g.*, Jiang G *et al.*, *J Pharm Sci.* Jul;105(7):2066-72 (2016); and Hintersteiner B. *MAbs.* 2016 Nov/Dec;8(8):1548-1560 (2016). It is known in the art that each heavy chain and light chain is expressed comprising a leader sequence (also known as a signal sequence) at its N terminus, which is used to transport the newly synthesized chains into the endoplasmic reticulum. During post-translational processing, the leader sequences are removed and, therefore, are not present in the final chain or the mature antibody.

[0054] As used herein, the term “monoclonal antibody” or “mAb” refers to an antibody that is produced by an identical set of immune cells that are each clones of a unique parent cell. Monoclonal antibodies have monovalent affinity (i.e., they bind to the same epitope).

[0055] As used herein, the term “chimeric” antibody refers to an antibody or antigen-binding fragment thereof comprising portions from two or more different species (*e.g.*, mouse and human). Chimeric antibodies can be produced with mouse variable regions of desired specificity spliced onto human constant domain gene segments (for example, U.S. patent No. 4,816,567). In this manner, non-human antibodies can be modified to make them more suitable for human clinical application. The term “chimeric” may refer to a non-native sequence that has been manipulated to have one or more changes relative a native sequence. A chimeric antibody as used herein means an antibody that comprises regions from two or more different antibodies.

[0056] As used herein, the term “humanized” antibodies refers to chimeric antibodies from a non-human species, whose amino acid sequences have been modified to increase their similarity to antibodies produced in humans. In some embodiments, humanized antibodies are chimeric immunoglobulins, immunoglobulin chains, or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen binding subsequences of antibodies) that contain minimal sequence derived from a non-human immunoglobulin. Optionally, humanized antibodies are derived from human immunoglobulins (i.e., recipient antibodies) in which residues from one or more complementary determining regions (CDRs) of the recipient antibody are replaced by residues from one or more CDRs of an antibody from a non-human species (donor antibody) having the desired specificity, affinity, and capacity. In some embodiments, the non-human

species is a mouse, a rat, or a rabbit. Humanized or CDR-grafted mAbs are particularly useful as therapeutic agents for humans because they are not cleared from the circulation as rapidly as mouse antibodies and do not typically provoke an adverse immune reaction. Generally, a humanized antibody has one or more amino acid residues introduced into it from a non-human source.

[0057] In some embodiments, the chimeric antibody is a humanized antibody, *e.g.*, a humanized anti-CD154 antibody. A humanized anti-CD154 antibody may comprise the amino acid sequence of one or more human framework regions and/or the amino acid sequence from at least a portion of a human constant region and further comprises sequences derived from a non-human antibody, for example non-human (*e.g.*, mouse) CDR sequences. In some embodiments, the humanized antibody comprises a human constant region. Optionally, all of the framework regions in the humanized antibody are human framework regions.

[0058] Humanized antibodies can be generated by replacing non-human sequences of the Fv variable region that are not directly involved in antigen binding with equivalent sequences from human Fv variable regions. General methods for generating humanized antibodies are provided by Morrison, S. L., *Science*, 229:1202-1207 (1985), by Oi *et al.*, *BioTechniques*, 4:214 (1986), by Jones *et al.*, *Nature* 321:522-525 (1986), by Riechmann *et al.*, *Nature*, 332:323-327 (1988), by Verhoeven *et al.*, *Science*, 239: 1534-1536 (1988)), by Staelens *et al.* 2006 *Mol Immunol* 43: 1243-1257, and by U.S. Pat. No. 5,225,539; U.S. Pat. No. 5,585,089; U.S. Pat. No. 5,693,761; U.S. Pat. No. 5,693,762; U.S. Pat. No. 5,859,205; and U.S. Pat. No. 6,407,213, each incorporated herein by reference. Those methods include isolating, manipulating, and expressing the nucleic acid sequences that encode all or part of immunoglobulin Fv variable regions from at least one of a heavy or light chain. Sources of such nucleic acid are well known to those skilled in the art and, for example, may be obtained from a hybridoma producing an antibody against a predetermined target, as described above, from germline immunoglobulin genes, or from synthetic constructs. The recombinant DNA encoding the humanized antibody can then be cloned into an appropriate expression vector. Humanized antibodies are typically human antibodies in which some CDR residues and possibly some framework residues are substituted by residues from analogous sites in rodent antibodies. See, for example, U.S. Patent Nos. 5,225,539; 5,585,089; 5,693,761; 5,693,762; 5,859,205, each incorporated herein by reference. See also U.S. Patent No. 6,180,370, and PCT International Publication No. WO 01/27160 (each incorporated herein by reference), where humanized antibodies and techniques

for producing humanized antibodies having improved affinity for a predetermined antigen are disclosed. Furthermore, humanized and chimeric antibodies can be modified to comprise residues that are not found in the recipient antibody or in the donor antibody in order to further improve antibody properties, such as, for example, affinity or effector function.

- 5 [0059] As used herein, the term “human antibodies” refers to antibodies having variable and constant regions derived from human germline immunoglobulin sequences. Human antibodies can include amino acid residues not encoded by human germline immunoglobulin sequences (*e.g.*, mutations introduced by random or site-specific mutagenesis *in vitro* or by somatic mutation *in vivo*). However, the term “human antibody” does not include antibodies in which
- 10 CDR sequences derived from the germline of another mammalian species, such as a mouse, have been grafted onto human framework sequences (*i.e.*, humanized antibodies). The term encompasses antibodies with sequences derived from human genes, but which have been changed, *e.g.*, to decrease possible immunogenicity, increase affinity, eliminate cysteines that might cause undesirable folding, etc. The term also encompasses such antibodies produced
- 15 recombinantly in non-human cells, which might impart glycosylation not typical of human cells. For the generation of human antibodies, see Mendez *et al.* *Nature Genetics* 15:146-156 (1997), Green and Jakobovits *J. Exp. Med.* 188:483-495 (1998), Lonberg, *Nature Biotechnology*, Vol. 23(5): 1117-1125 (2005); Jakobovits, “Therapeutic Antibodies from XenoMouse Transgenic Mice,” Chapter 7, *Recombinant Antibodies for Immunotherapy*,
- 20 Cambridge University Press, New York, 2009, Murphy, “VelocImmune: Immunoglobulin Variable Region Humanized Mice,” Chapter 8, *Recombinant Antibodies for Immunotherapy*, Cambridge University Press, New York, 2009, Murphy *et al.*, *PNAS*, 2014, vol. 111(14): 5153-5158, Brüggemann *et al.*, *Arch. Immunol. Ther. Exp.*, 2015, vol. 63:101-108, the disclosures of which are hereby incorporated by reference in their entirety. Human antibodies and methods
- 25 of making them are further discussed in U.S. patents 5,939,598; 6,673,986; 6,114,598; 6,075,181; 6,162,963; 6,150,584; 6,713,610; 6,657,103; 6,586,251; as well as U.S. patent application publications US 2006-0015957 A1; and International Patent Publication Nos. WO 98/24893; and WO 2007/117410. The disclosures of each of the above-cited patents, applications, and references are hereby incorporated by reference in their entirety.
- 30 [0060] As used herein, the term “amino acid modification” refers to at least one amino acid substitution, insertion, deletion or mutation in an amino acid sequence compared to a wild-type amino acid sequence. Such modifications are within the ordinary skill of an artisan. Certain

modifications, including amino acid deletions, substitutions and additions, of the Fc region have been demonstrated to alter the binding of the Fc region to its ligands and/or receptors resulting in a concomitant change in effector function (see, *e.g.*, (Shields *et al.*, J Biol Chem 276:6591-6604 (2001); Presta *et al.*, Biochem Soc Trans 30:487-490 (2002); Escobar-Cabrera E *et al.* Antibodies. 6: 7 (2017); Duncan AR *et al.* Nature. 1988; 332: 738-740 (1988); Duncan AR *et al.* Nature. 332: 563-564 (1988); Hezareh M *et al.* J Virol. 75: 12161-12168 (2001); Oganessian V *et al.* Acta Crystallogr D Biol Crystallogr; 64: 700-704 (2008); Schlothauer T *et al.* Protein Eng Des Sel. Oct; 29(10):457-466 (2016); Tao MH *et al.* J. Immunol. 143: 2595-2601 (1989); Von Kreudenstein TS *et al.* MAbs. 5(5):646-654 (2013); Wang X *et al.* Protein Cell. 9(1):63-73 (2018); U.S. Patent Publications 20040132101; 20070111260; 20110287032; 20180194860; U.S. Patent No. US 8409568; International Publication No. WO2017/177337, incorporated by reference in their entirety. An amino acid deletion is indicated as “Δ”, and an insertion is indicated as “In”. For instance, a deletion of the amino acid sequence from E216 to E222 is indicated as ΔE216-E222. An insertion of an arginine (R) between amino acid residues 234 and 235, *e.g.*, would be indicated as InR234/235.

[0061] As used herein, the term “Fc domain” refers to the crystallizable fragment of an antibody following papain digestion. The Fc domain comprises two identical protein fragments derived from the hinge region and the second and third constant domains of IgA, IgD, and IgG antibody isotypes or the hinge region and the second, third, and fourth constant domains of IgM and IgE antibody isotypes. The Fc domain is the portion of an antibody that binds to cell surface Fc receptors and certain proteins of the complement system. The term “Fc region” refers to the Fc domain in combination with a hinge region. The hinge region is typically between the C-terminus of a variable domain and the N-terminus of the Fc domain. Although the boundaries of the Fc region may vary, the human IgG heavy chain Fc region as defined herein comprises residue E216 to its carboxyl-terminus of the CH3 domain (or the CH4 domain for IgM and IgE antibodies), wherein the numbering is in the EU format as in Edelman GM *et al.*, (1969) *Proc. Natl. Acad. USA*, 63, 78-85. The “EU format as set forth in Edelman” refers to the residue numbering of the human IgG1 EU antibody as described in Edelman GM *et al. supra*. The human IgG2 and human IgG4 residue numbering is also in the EU format (See Dillon TM, *et al.*, J Biol Chem. Jun 6;283(23):16206-15 (2008); Aalberse RC and Schuurman J *et al.*, Immunology 105:9-19 (2002); and Scholthauer T *et al.*, Protein Engineering, Design and Selection, 29(10): 457-466, (2016). The terms “Fc domain” and “Fc region” may refer to

these sequences in isolation, or these sequences in the context of an antibody, antibody fragment, or Fc fusion protein. An Fc variant protein may be an antibody, Fc fusion, or any protein or protein domain that comprises an F domain or an Fc region. The amino acid sequence of a non-naturally occurring Fc domain or Fc region (also referred to herein as a
5 “variant Fc domain” or a “variant Fc region,” respectively) may comprise an amino acid modification. Any new amino acid residue appearing in the sequence of a variant Fc domain or a variant Fc region as a result of an insertion or substitution may be referred to as a non-naturally occurring amino acid residue. Polymorphisms have been observed at a number of Fc domain positions, including but not limited to positions 270, 272, 312, 315, 356, and 358, and
10 thus slight differences between the presented sequence and sequences in the prior art may exist. [0062] As used herein, the term “linker” refers to a polypeptide sequence that joins two or more antibody domains. The characteristics of linkers and their suitability for particular purposes are known in the art. See, *e.g.*, Chen *et al.* Adv Drug Deliv Rev. October 15; 65(10): 1357–1369 (2013) (disclosing various types of linkers, their properties, and associated linker
15 designing tools and databases), which is incorporated herein by reference. The linker may be flexible, rigid, or *in vivo* cleavable. Preferably, the linker is flexible. Flexible linkers typically comprise small non-polar (*e.g.* Gly) or polar (*e.g.*, Ser or Thr) amino acids. The most commonly used flexible linkers have sequences consisting primarily of stretches of Gly and Ser residues (“GS” linker). Optionally, flexible linkers comprise repeats of 5 Gly and Ser
20 residues. Non-limiting examples of flexible linker include (Gly-Gly-Gly-Gly-Ser)_n (SEQ ID NO: 327), (Ser-Ser-Ser-Ser-Gly)_n (SEQ ID NO: 328), (Gly-Ser-Ser-Gly-Gly)_n (SEQ ID NO: 329), and (Gly-Gly-Ser-Gly-Gly)_n (SEQ ID NO: 330), where n may be any integer between 1 and 5. The linker is optionally between 5 and 25 amino acid residues long. Other suitable linkers may be selected from the group consisting of AS (SEQ ID NO: 214), AST (SEQ ID
25 NO: 215), TVAAPS (SEQ ID NO: 216), TVA (SEQ ID NO: 217), ASTSGPS (SEQ ID NO: 218), KESGSVSSEQLAQFRSLD (SEQ ID NO: 219), EGKSSGSGSESKST (SEQ ID NO: 220), (Gly)₆ (SEQ ID NO: 221), (Gly)₈ (SEQ ID NO: 222), and GSAGSAAGSGEF (SEQ ID NO: 223). In general, a flexible linker should provide good flexibility and solubility and may serve as a passive linker to keep a distance between functional domains. The length of the
30 flexible linkers can be adjusted to allow for proper folding or to achieve optimal biological activity of the fusion proteins.

[0063] As used herein, the twenty conventional amino acids and their abbreviations follow conventional usage. See *Immunology--A Synthesis* (2nd Edition, E. S. Golub and D. R. Gren, Eds., Sinauer Associates, Sunderland, Mass. (1991)), which is incorporated herein by reference.

- 5 [0064] A “conservative amino acid substitution” is one in which an amino acid residue is replaced with a different amino acid residue with similar biochemical properties (*e.g.*, charge, hydrophobicity, or size). Typically, conservative amino acid substitutions do not substantially change a protein’s functional properties. When comparing proteins with conservative substitutions, the percent sequence identity or degree of similarity may be adjusted to account
10 for the conservative nature of the substitution. Such adjustments are well-known to those of skill in the art. See, *e.g.*, Pearson, *Methods Mol. Biol.* 243:307-31 (1994).

- [0065] Groups of amino acids with similar biochemical properties that may be used in conservative substitutions include 1) amino acid residues with aliphatic side chains: glycine, alanine, valine, leucine, and isoleucine; 2) amino acid residues with aliphatic-hydroxyl side
15 chains: serine and threonine; 3) amino acid residues with amide-containing side chains: asparagine and glutamine; 4) amino acid residues with aromatic side chains: phenylalanine, tyrosine, and tryptophan; 5) amino acid residues with basic side chains: lysine, arginine, and histidine; 6) amino acid residues with acidic side chains: aspartic acid and glutamic acid; and 7) amino acid residues with sulfur-containing side chains: cysteine and methionine. Preferred
20 conservative amino acids substitution groups include: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, glutamate-aspartate, and asparagine-glutamine.

- [0066] Each heavy chain is comprised of a heavy chain variable domain (VH) and multiple heavy chain constant domains (CH). For IgA, IgD, and IgG antibodies, the heavy chain
25 typically comprises three domains: CH1, CH2 and CH3. For IgM and IgE antibodies, the heavy chain typically comprises four domains: CH1, CH2, CH3, and CH4. In some embodiments, the antibody comprises two domains: CH2 and CH3. Each light chain comprises a light chain variable domain (VL) and a light chain constant domain. The light chain typically comprises one domain: CL. Light chain variable domains are encoded by two gene segments:
30 a variable (V) gene segment, which encodes the first 95-101 amino acids of the light chain, and a joining (J) gene segment, which encodes about 12 or more amino acids. Heavy chain variable domains are encoded by three gene segments and include a diversity (D) gene segment, which

encodes about 3 or more amino acids, between the V and J gene segments. The VH and VL domains can be further subdivided into regions of hypervariability, called “complementarity determining regions” (CDR) that are separated by more conserved “framework regions” (FR). Each VH and VL is composed of three CDRs and four FRs, arranged from amino-terminus to carboxyl-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4.

[0067] The pairing of the variable domains of the heavy chain and light chain (VH and VL) forms the antibody binding site that interacts with an antigen. Thus, each antibody typically has two binding sites. With the exception of multifunctional / multispecific (*e.g.*, bifunctional or bispecific) antibodies, the two binding sites are the same. The Fc regions of the constant regions of the antibodies typically mediate the binding of antibodies to host tissues and factors, including various cells of the immune system (*e.g.*, effector cells) and the first component (C1q) of the classical complement system.

[0068] Residues in a variable domain are numbered according to Edelman, also known as the EU numbering system, which is a numbering system used for heavy chain variable domains or light chain variable domains of the compilation of antibodies. See, Edelman *Proc Natl Acad Sci U S A.* May;63(1):78-85 (1969) and Kabat, E. A., Wu, T. T., Perry, H., Gottesman, K., and Foeller, C. (1991) *Sequences of Proteins of Immunological Interest*, 5th ed., NIH Publication No. 91-3242, Bethesda, MD. The Eu numbering of residues may be determined for a given antibody by alignment at regions of homology of the sequence of the antibody with a “standard” EU numbered sequence. Variable region CDRs (CDR L1, CDR L2, CDR L3, CDR H1, CDR H2, CDR H3) are identified according to contact based on crystal structures as defined in Karpusas *et al. Structure.* Apr 4;9(4):321-9 (2001) and numbered in accordance with Edelman.

[0069] As used herein, the term “operably linked” refers to a first structure that has been placed in a functional relationship with a second structure. In the context of an antibody, a targeting structure may be operably linked to a structure that confers effector function. For example, the antigen-binding sequence of an antibody (*e.g.*, variable region or VH or VL domain) may be operatively linked to a Fc region. In the context of a polynucleotide, a coding sequence may be operatively linked to a non-coding regulatory sequence, such as a promoter, an enhance, a signal sequence, a ribosome binding sequence, a splice acceptor sequence, a splice donor sequence, a termination sequence, etc. Two operably linked structures may be directly connected. Alternatively, two operably linked structures may be connected via one or

more intermediary structures. For example, the antigen-binding portion of an antibody may be operably linked to the Fc region via a CH1 domain, a hinge region and/or a linker sequence. Similarly, operably linked non-coding regulatory sequences include both sequences that are contiguous with the coding sequence and sequences that act in *trans* or at a distance to control the coding sequence.

[0070] As used herein, the term “effector function” refers to the responses triggered by the interaction of antibodies and antibody-antigen complexes with cells of the immune system. These effector functions typically involve one of three major mechanisms: antibody-dependent cell-mediated cytotoxicity (ADCC), complement-dependent cytotoxicity (CDC), and opsonization and phagocytosis. In ADCC, Fc receptors on cytotoxic T cells, natural killer (NK) cells, or macrophages bind to the Fc regions of antibodies bound to a target cell, resulting in the secretion of substances, such as lytic enzymes, perforin, granzymes and tumor necrosis factor, which mediate the destruction of the target cell. In CDC, cell death is induced via activation of the complement cascade. See Daeron, *Annu. Rev. Immunol.*, 15:203-234 (1997); Ward and Ghetie, *Therapeutic Immunol.*, 2:77-94 (1995); and Ravetch and Kinet, *Annu. Rev. Immunol.* 9:457-492 (1991)). In opsonization and phagocytosis, the Fc region of a pathogen-bound antibody binds to a Fc receptor on the surface of a phagocyte, inducing phagocytosis. Such effector functions generally require the Fc region to be combined with a binding domain (e.g. an antibody variable domain) and can be assessed using standard assays that are known in the art (see, e.g., WO 05/018572, WO 05/003175, and U.S. Pat. No. 6,242,195). The Fc domain of the antibody mediates immune effector mechanisms. IgG antibodies activate effector pathways of the immune system by binding to members of the family of cell surface Fcγ receptors and to C1q of the complement system. Ligation of effector proteins by clustered antibodies triggers a variety of responses, including release of inflammatory cytokines, regulation of antigen production, endocytosis, and cell killing. These responses can provoke unwanted side effects such as inflammation and thrombosis. Accordingly, the present disclosure further relates to anti-CD154 antibodies, with modified effector functions, including antibodies in which one or more effector functions is reduced or eliminated. Without being bound by theory, it is believed that the anti-CD154 antibodies disclosed herein do not cause platelet activation or aggregation, because the antibodies comprising the mutated Fc regions do not bind FcγRIIa (also known as CD32a) on the platelet surface.

[0071] As used herein, the term “modified effector functions” refers to a Fc domain or an Fc region whose effector functions differ from a wild-type immunoglobulin Fc domain or Fc region. In some embodiments, one or more effector functions are reduced. Optionally, one or more effector functions are eliminated. The modified or reduced effector functions may be the result of lower binding affinity of the Fc region of the antibodies disclosed herein to effector molecules (*e.g.*, FcγRs and/or C1q). For example, the anti-CD154 antibodies disclosed herein have reduced Fc receptor binding and complement activation compared with that of wild-type anti-CD154 antibodies. In some embodiments, a variant Fc region has a reduced antibody dependent cell-mediated cytotoxicity (ADCC). Effector function of an anti-CD154 antibody may be determined using one of many known assays, including the CDC assay, the ADCC assay, and the phagocytosis assay (see Xu-Rong Jiang *et al.*, *Nature Reviews Drug Discovery* 10: 101–111 (2011) and Liu *et al.*, *The Journal of Biological Chemistry* 292:1876-1883 (2017)). The anti-CD154 one or more of the antibody's effector functions may be reduced by at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 95% relative to the effector function of a wild-type anti-CD154 antibody.

[0072] As used herein, the terms “CD154,” “CD40 ligand” and “CD40L” may be used interchangeably and refer to a mammalian protein that is primarily expressed on the surfaces of activated T cells, a soluble form of CD154 that is cleaved and released by activated T cells, is a member of the TNF superfamily, and binds the CD40 protein on antigen presenting cells. The term CD154 is intended to include recombinant CD154 and recombinant chimeric forms of CD154, which can be prepared by standard recombinant expression methods. In some embodiments, CD154 refers to human CD154.

[0073] As used herein, the term “inhibits” refers to the property of an antibody, or other molecule, that prevents the interaction of CD154 with CD40 or one that inhibits the binding of CD154 to CD40, or one that inhibits CD154 cleavage or shedding. In some embodiments, the antibody inhibits the binding of CD154 to CD40 by at least about 20%, preferably 40%, more preferably 60%, even more preferably 80%, or even more preferably 85%. Optionally, the antibody inhibits CD154 cleavage or shedding by at least about 20%, preferably 40%, more preferably 60%, even more preferably 80%, or even more preferably 85%. The inhibitory potential of anti-CD154 antibodies may be determined, for example, by their ability to inhibit up-regulation of a specific downstream target gene of CD40. For example, an anti-CD154 antibody may alter the expression, activity, or activation of kinases and genes that respond to

CD154-CD40 signaling. An anti-CD154 antibody may inhibit the upregulation of CD23 expression, inhibit the upregulation of CD69 expression, inhibit the upregulation and activity of activation-induced cytidine deaminase (AID), inhibit rescue from apoptosis, inhibit upregulation of NF- κ B activity, inhibit immunoglobulin isotype class switching, inhibit immunoglobulin CDR somatic hypermutation, alter the expression or activity of molecules within the TNF-receptor associated factor (TRAF) family such as TRAF-2, TRAF3 (also known as CRAF1), TRAF-5 and TRAF-6, kinase activation or inhibit the expression of other genes that respond to CD154-CD40 signaling. See, for example, Lederman, S., *et al. J. Exp. Med.* 175:1091-1101. (1992); Lederman, S., *et al., Journal of Immunol.* 149:3817-3826. (1992); Lederman, S., *et al., Journal of Immunol.* 152:2163. (1994); Cleary, A.M., *et al., Journal of Immunol.*, 155:3329-3337 (1995); Cheng *et al., Science.* 267(5203):1494-8 (1995), Bankert KC *et al., Journal of Immunol.* 194:4319-4327 (2015), Ishida TK *et al Proc Natl Acad Sci U S A.* 93(18):9437-42 (1996). Muramatsu, MK *et al.* 2000. *Cell* 102: 553 (2000); Buchta CM and Bishop GA., *Journal of Immunol.* 192(1):145-50. (2014), Arcipowski KM, *et al. International Immunology.* 26(3):149-58 (2014); Mambetsariev N, *et al., Proc Natl Acad Sci U S A.* 113(4):1032-7 (2016), Arcipowski KM, Bishop GA., *PLoS One.* 7(7) (2012); Bishop GA. *Journal of Immunol.* 91(7):3483-5. (2013); Peters AL and Bishop GA. *Journal of Immunol.* 185(11):6555-62. (2010); Rowland SL, *et al., Journal of Immunol.* 179(7):4645-53. (2007), Benson RJ, *et al., European Journal of Immunol.* 6(9):2535-43. (2006).

[0074] As used herein, the term “immune response” refers to reaction of body’s immune system to the presence of a substance which is not recognized as a constituent of the body itself. An immune response may be a humoral immune response, a cell-mediated immune response, or a mixed humoral and cell-mediated immune response. A humoral response may be an antibody-mediated response. A cell-mediated response may be one or more of a cytotoxic T-cell mediated immune response, a macrophage mediated response, a natural killer (NK) cell mediated immune response or a cytokine mediated response. A mixed humoral and cell-mediated response may be one or more of an antibody-mediated response, a cytotoxic T-cell mediated immune response, a macrophage mediated response, a natural killer (NK) cell mediated immune response or a cytokine mediated response. The immune response can refer to an adaptive and/or an innate immune response. For the various types of immune responses, see David Chaplin *J Allergy Clin Immunol* February; 125(2 Suppl 2): S3–23 (2010).

- [0075] As used herein, the term “affinity” of an antibody refers to the strength of interaction between the antibody’s antigen-binding site and an epitope. An antibody’s affinity for an antigen is typically expressed as the binding affinity equilibrium dissociation constant (K_D) of a particular antibody-antigen interaction. An antibody is said to specifically bind an antigen when the K_D is ≤ 1 mM, preferably ≤ 100 nM. High affinity antibodies are generally considered to have a K_D in the low nanomolar (10^{-9}) range, and very high affinity antibodies are generally considered to have a K_D in picomolar (10^{-12}) range. A K_D binding affinity constant can be measured by surface plasmon resonance, for example using the BIACORE[®] system (Pharmacia Biosensor AB, Uppsala, Sweden and Piscataway, N.J.) as discussed in Example 3. See also, Jonsson *et al.*, *Ann. Biol. Clin.* 51:19-26 (1993); Jonsson *et al.*, *Biotechniques* 11:620-627 (1991); Jonsson *et al.*, *J. Mol. Recognit.* 8:125-131 (1995); Johnsson *et al.*, *Anal. Biochem.* 198:268-277 (1991); Hearty S *et al.*, *Methods Mol Biol.* 907:411-42 (2012), each incorporated herein by reference. The K_D may also be measured using a KINEXA[®] system (Sapidyne Instruments, Hanover, Germany and Boise, ID).
- [0076] As used herein, the terms “ k_a ” or “affinity constant” and “ k_d ” or “dissociation constant” refer to the amount of antibody-antigen complex that exists at the point when equilibrium concentration between antibody and antigen is reached. K_D is the ratio of k_d to k_a .
- [0077] As used herein, the term “avidity” refers to the overall strength of an antibody-antigen complex. Avidity relates to three major parameters: the affinity of the antibody for the epitope; the valency of both the antibody and antigen; and the structural arrangement of the parts that interact. As used herein, “avidity” describes the increased affinity that occurs as result of multiple antigen binding sites on an immunoglobulin.
- [0078] As used herein, the term “transplantation” refers to process of surgically removing a cell or tissue or organ from a first organism (the donor) and placing it into a second organism (the recipient). The donor may be a human or a non-human organism. In some embodiments, the donor is a primate. The donor may be a non-human primate. Optionally, the donor is a human. In some embodiments, the donor is a pig or mini-swine. The recipient may be a human or a non-human organism. Preferably, the recipient is a human. Optionally, the recipient is a non-human primate. The cell, tissue or organ being transferred is referred to as the “transplant” or “graft.” A “xenotransplant” refers to the transfer of a cell or tissue or organ from a donor of a certain species (such as a monkey or pig) into a recipient of a different species (such as a human).

- [0079] As used herein, the term “engineered cell” refers to a cell that is modified from its natural state. An engineered cell may be modified using one or more techniques such as transduction to express a cDNA, a CRISPR/Cas9 system, RNAi technology and retroviral technology. For example, the cell may be modified to express a chimeric antigen receptor (CAR) on its surface. Examples of cells that may be transplanted include, but are not limited to a stem cell, a regulatory T (Treg) cell, a CAR-T cell (see Zhang, C *et al. Biomarker Research* (5)22. (2017), a CAR-B cell (Voss JE *et al., Elife.* Jan 17;8. (2019), and a tumor-infiltrating lymphocyte (TIL) (Zhang L *et al., Clin Cancer Res.* May 15;21(10):2278-88. doi: 10.1158/1078-0432.CCR-14-2085 (2015).
- [0080] As used herein, the term “ex-vivo expanded cell” refers to a cell that is produced in an ex-vivo method to enhance the yield of that cell (such as a hematopoietic stem cell (HSC)) to be used in clinical applications, such as transplantation. See, *e.g.*, Xie J, and Zhang C *Sci China Life Sci.* Sep;58(9):839-53 (2015) which reviews the methods to expand the numbers of HSCs, including culture systems such as stroma/HSC co-culture, continuous perfusion and fed-batch cultures, and those supplemented with extrinsic ligands, membrane transportable transcription factors, complement components, protein modification enzymes, metabolites, or small molecule chemicals. The desired cell to be transplanted may also be expanded ex-vivo by applying endogenous Notch-signaling activators (see, *e.g.*, Ex vivo expansion of human hematopoietic stem and progenitor cells Dahlberg A, *et al., Blood* 117:6083-6090 (2011).
- [0081] As used herein, the term “transplant rejection” refers to the phenomenon that occurs when a transplanted cell, tissue, or organ from a donor is rejected by the recipient’s immune system. The recipient’s immune system may mount an adaptive immune response (cellular immunity) mediated by killer T cells inducing apoptosis of the donor cells, a humoral immunity mediated by activated B cells secreting antibodies, and/or an innate immune response mediated by phagocytes and soluble immune proteins (see Ochanda J *et al., Cell Mol Immunol.* Apr;16(4):350-356 (2019); Koo J, and Wang HL. *Surg Pathol Clin.* Jun;11(2):431-452 (2018); Wang H, and Yang YG, *Curr Opin Organ Transplant.* Apr;17(2):162-7 (2012); and da Silva MB, *World J Transplant.* Feb 24;7(1):1-25 (2017)).
- [0082] As used herein, the term “hematopoietic chimerism”, “mixed chimerism”, or “mixed allogeneic chimerism” refers to the coexistence of both host and donor hematopoietic cells that arises due to the engraftment of donor pluripotent hematopoietic stem cells into the host. The host and donor cells may be tolerant of each other. Mechanisms of hematopoietic chimerism

are known in the art. See Pasquet L, *et al. Front Immunol.* 2:80 (2011) and Nikolic B, and Sykes M, *Immunol Res.* 16(3):217-28. (1997) incorporated herein by reference. In some embodiments, such hematopoietic chimerism results in “central tolerance.” The mechanisms of “central tolerance” in such chimeras may involve central, intrathymic clonal deletion, selection of regulatory T cells and/or other related immune mechanisms. See, e.g., Nikolic B, and Sykes M, *Immunol Res.* 16(3):217-28. (1997) and Hogquist KA *et al., Nature Reviews Immunology* 5:772–782 (2005), incorporated herein by reference. In some embodiments, such hematopoietic chimerism results in “peripheral tolerance.” The mechanisms of “peripheral tolerance” in such chimeras may involve peripheral clonal deletion, conversion to regulatory T cells and/or other related immune mechanisms. See, e.g., Nikolic B, and Sykes M, *Immunol Res.* 16(3):217-28. (1997) and Mueller D, *Nature Immunology.* 11(1): 21–27 (2010). In some embodiments, such hematopoietic chimerism results in “organ-specific tolerance.” The mechanisms of “organ-specific tolerance” in such chimeras varies from organ to organ and may require mixed chimerism procedures. See, e.g. Madariaga, M, Kreisel, D, & Madsen, J, 20(4),392–399 (2015). In some embodiments, the hematopoietic stem cells are isolated or purified. Optionally, the hematopoietic stem cells are passenger cells that are transplanted with an organ, e.g. a kidney or liver transplant. Stem cells may be derived from bone marrow or fat cells/adipose tissue of the donor.

[0083] As used herein, the term “conditioning” or “conditioned” refers to the preparation of a recipient for stem cell transplantation, such as a hematopoietic cell transplantation. Gyurkocza B and Sandmaier *BM Blood* 124:344-353 (2014) provides a review of high-dose, reduced-intensity, and nonmyeloablative conditioning regimens and the most commonly used agents, such as total body irradiation, fludarabine phosphate, cyclophosphamide, T cell-depleting antibodies. Monoclonal antibodies, such as anti-CD20 Ab, anti-CD33 Ab, and anti-CD45 Ab, may also be used alone or in combination with conventional therapies as part of a conditioning regimen to prevent transplant rejection. See, e.g., Topcuoglu P *et al.; Progress in Stem Cell Transplantation*; December (2015). Other agents that may be used in conditioning regimens include, but are not limited to, BCL-2 inhibitors (Perini GF *et al., Journal of Hematology & Oncology* 11:65 (2018) and anti-CTLA4 Abs (Pree I *et al., Transplantation.* Mar 15; 83(5): 663–667 (2007). Conditioning regimens may include chemotherapeutic agents including, but not limited to, Alemtuzumab (CAMPATH™), Busulfan, Carboplatin,

Carmustine, Cyclophosphamide, Cytarabine (Ara-C), Daunorubicin, Etoposide (VP-16), Fludarabine, Melphalan, Rituximab, and Vincristine.

[0084] The term “isolated antibody” refers to an antibody that is at least partially free of the other biological molecules present in the cells used to produce them. The other biological molecules from which an isolated antibody is free include nucleic acid molecules, proteins, lipids, carbohydrates, cellular debris and culture medium. The term “isolated antibody” does not require, but does encompass, a complete absence of such other biological molecules. The term “isolated antibody” also does not refer to a complete absence of other molecules, such as water, buffers, salts or the components of pharmaceutical formulations. Thus, a molecule that is chemically synthesized or synthesized in a cell-free system will be “isolated” from its naturally associated components. A molecule may also be “isolated” using purification techniques well known in the art.

[0085] Molecule purity or homogeneity may be assayed by a number of means well known in the art. For example, the purity of an antibody sample may be assayed using polyacrylamide gel electrophoresis and staining of the gel to visualize the antibody using techniques well known in the art. For certain purposes, higher resolution may be provided by using HPLC or other means well known in the art for purification. The purity of a nucleic acid sample may be assayed using the spectrophotometric absorbance of the sample 260nm to that of 280nm using techniques well known in the art. For certain purposes, higher resolution may be provided by using means well known in the art for purification.

[0086] Examples of isolated antibodies include, but are not limited to, an anti-CD154 antibody that has been affinity purified using CD154, and an anti-CD154 antibody that has been synthesized by a cell line *in vitro*.

[0087] The term “percent sequence identity” in the context of polypeptide sequences is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the reference polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Such conservative substitutions are considered (in addition to identical residues) in calculating the “percent sequence similarity” of two sequences. Residue positions that are not identical but are similar differ by conservative amino acid substitutions.

[0088] Alignment for purposes of determining percent amino acid sequence identity, sequence similarity or sequence homology, such as between a wild type protein and a mutein thereof, can be achieved in various ways that are within the skill in the art, for instance, using publicly available sequence analysis computer software, such as BLAST, BLAST-2, ALIGN, 5 Megalign (DNASTAR), Gap, BESTFIT[®], and other programs in programs in Wisconsin Package Version 10.0 or Genetics Computer Group (GCG), Madison, Wisconsin. Those skilled in the art can determine appropriate parameters for aligning sequences, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. Polypeptide sequences also can be compared using FASTA using default or 10 recommended parameters. In the context of polypeptide sequences, FASTA takes the query amino acid sequence and searches a sequence database using local sequence alignment to identify similar sequences within the database (Pearson, *Methods Enzymol.* 183:63-98 (1990); Pearson, *Methods Mol. Biol.* 132:185-219 (2000); Pearson *Curr Protoc Bioinformatics*. Mar 24;53:3.9.1-25 (2016); each herein incorporated by reference). BLAST, especially blastp or 15 tblastn, using default parameters may be used to compare a query sequence to a database containing sequences from different organisms. See, e.g., Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990); Altschul *et al.*, *Nucleic Acids Res.* 25:3389-402 (1997); Eser *et al.*, *PLoS One*. 22;9(12): e115445 (2014), each herein incorporated by reference.

[0089] The terms “transplant recipient” “patient,” “subject,” and “individual” are used 20 interchangeably herein and refer to either a human or a non-human animal in need to treatment. These terms include mammals, such as humans, and non-human primates (e.g., monkey). Optionally, the transplant recipient is a human. The transplant recipient may be a non-human primate, e.g., a monkey. In some embodiments, the subject is in need of inhibition or reduction of an immune response.

25 [0090] The term “primate” refers to a mammal of the order primates, which includes the anthropoids and prosimians, characterized by refined development of the hands and feet, a shortened snout, and a large brain. The mammalian order Primates includes humans, apes, monkeys, and prosimians, or lower primates.

[0091] As used herein, the term “therapeutically effective amount” refers to that amount of 30 the therapeutic agent being administered which will relieve to some extent one or more of the symptoms of the condition being treated. With respect to the treatment of transplant rejection, a therapeutically effective amount refers to that amount which has at least one of the following

effects: reduces, inhibits or prevents acute or chronic rejection of the transplanted cell, tissue or organ and one or more symptoms associated with the rejection, prolongs graft survival, reduces thrombosis, reduces the risk of life-threatening infections, cancers and other complications, such as cardiovascular diseases, and kidney failure. *See, for example, Romano et al. Front Immunol.* 10:43 (2019) and Ingulli E. *Pediatr Nephrol.* 25(1):61–74 (2010) for mechanisms of cellular rejection in transplantation. With respect to the treatment of autoimmune disease and antibody-mediated inflammatory disease, a therapeutically effective amount refers to that amount which has at least one of the following effects: reduces one or more symptoms associated with the autoimmune disease such as fatigue, muscle aches, low fever, inflammation, skin rashes, etc.

[0092] The pharmaceutical compositions may include a therapeutically effective amount, or a prophylactically effective amount, of an antibody disclosed herein. A therapeutically effective amount of the antibody may vary according to factors such as the disease state, age, sex, and weight of the individual, and the ability of the antibody or antibody portion to elicit a desired response in the individual. A therapeutically effective amount is also one in which any toxic or detrimental effects of the antibody are outweighed by the therapeutically beneficial effects. It is routine in the art for the skilled artisan to determine a therapeutically effective amount of an antibody disclosed herein based on these factors. A “prophylactically effective amount” refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired prophylactic result. Typically, since a prophylactic dose is used in subjects prior to transplantation or at an earlier stage of transplant rejection, the prophylactically effective amount may be less than the therapeutically effective amount.

[0093] As used herein, the terms “treat”, “treating” and “treatment” refer the administration of a therapeutic agent, such as a composition containing any of the antibodies disclosed herein, internally or externally to a subject or patient having one or more disease symptoms, or being suspected of having a disease, for which the agent has therapeutic activity. “Treat”, “treating” and “treatment” refer to therapeutic treatments and/or prophylactic treatments. Therapeutic treatment includes, *e.g.*, a method of alleviating or reducing the severity of a condition or abolishing a condition and includes alleviating or reducing the severity of one or more symptoms of the condition. If the treatment is administered prior to clinical manifestation of a condition, the treatment is considered prophylactic. The alleviation or reduction of a disease symptom can be assessed by any clinical measurement typically used by physicians or other

skilled artisans to assess the severity or progression of that symptom. The terms further refer to a postponement of development of one or more disease symptoms and/or a reduction in the severity of one or more disease symptoms. The terms further include ameliorating existing uncontrolled or unwanted disease symptoms, preventing additional disease symptoms, and
5 ameliorating or preventing the underlying causes of such disease symptoms. Thus, the terms denote that a beneficial result has been conferred on the subject.

[0094] With respect to the treatment of transplant rejection, treatment may refer to the alleviation, reduction, or delay of rejection of the transplanted cell, tissue or organ or one or more symptoms associated with the rejection. Treatment may also result in prolonging graft
10 survival, reducing thrombosis, and/or reducing the risk of life-threatening infections, cancers and other complications, such as cardiovascular diseases, and kidney failure. With respect to the treatment of autoimmune disease, treatment may refer to dampening of the body's immune responses and controlling the autoimmune reaction. With respect to the treatment of antibody-mediated inflammatory disease, treatment may refer to reducing one or more symptoms
15 associated with the autoimmune disease such as fatigue, muscle aches, low fever, inflammation, skin rashes, etc. With regard to treatment with the antibodies disclosed herein, these terms may simply mean that the life expectancy and quality of life of an individual receiving a transplant or an individual affected with an autoimmune or inflammatory disease will be increased or that one or more of the symptoms associated with transplant rejection or
20 the autoimmune or inflammatory disease will be reduced.

[0095] As used herein, the terms "prevent", "preventing" and "prevention" refer to the prevention or delay of the recurrence or onset of, or a reduction in one or more symptoms of a condition in a subject as a result of the administration of an anti-CD154 antibody of the disclosure. For example, in the context of the administration of a therapy to a subject,
25 "prevent", "preventing" and "prevention" refer to the inhibition, reduction, or delay in the development or onset of the rejection of that transplant or associated thrombosis or the prevention or delay of the recurrence, onset, or development of one or more symptoms associated with the transplantation in a subject (*e.g.*, a solid organ transplant) or the administration of a combination of therapies (*e.g.*, a combination of a solid organ transplant
30 and an immunosuppressant).

[0096] As used herein, the terms "administering" or "administration of" the antibodies or compositions of this disclosure to a subject refers to contacting the antibodies or

compositions to the subject or to a cell, tissue, organ, or biological fluid of the subject. Such administration can be carried out using one of a variety of methods known to those skilled in the art. For example, an antibody or a composition of this disclosure can be administered systemically or locally. In some embodiments, the composition can be administered
5 subcutaneously, intravenously, intravitreally, orally, via inhalation, transdermally, or rectally. Administering can also be performed, for example, once, a plurality of times, and/or over one or more extended periods. In some embodiments, the administration includes both direct administration (including self-administration) and indirect administration, including the act of prescribing a drug.

10 Anti-CD154 Antibodies

[0097] The methods of the present disclosure utilize anti-CD154 antibodies with modified effector functions that bind to mammalian CD154, more preferably human CD154. In some embodiments, one or more effector functions are reduced. Optionally, one or more effector functions are eliminated. In some embodiments, the antibodies with one or more reduced
15 effector functions demonstrate reduced binding to Fc receptors relative to an antibody having wild-type IgG1 heavy chain. Optionally, the reduced binding to the Fc receptor is 10- to 3200-fold weaker than the binding demonstrated by a wild-type IgG heavy chain. In some embodiments, the K_D for Fc γ R1A binding the Fc domain of the antibody with reduced effector function is between 0.1-100 nM, such as 0.3-92 nM. Optionally, the K_D for CD16aF binding
20 the Fc domain of the antibody with one or more reduced effector functions is greater than 2 μ M. In some embodiments, the K_D for CD16aV binding the Fc domain of the antibody with one or more reduced effector functions is greater than 0.4 μ M. Optionally, the K_D for CD32aH binding the Fc domain of the antibody with one or more reduced effector functions is greater than 0.5 μ M. In some embodiments, the K_D for CD32bF binding the Fc domain of the antibody
25 with one or more reduced effector functions is greater than 1 μ M.

[0098] In some embodiments, the isolated antibodies are fully human monoclonal antibodies. In some embodiments, the isolated antibodies are chimeric antibodies. In some embodiments, the isolated antibodies are humanized antibodies. In some embodiments, human anti-CD154 antibodies are produced by immunizing a non-human transgenic animal, *e.g.*, a rodent, whose
30 genome comprises human immunoglobulin genes so that the transgenic animal produces human antibodies.

- [0099] In some embodiments, the anti-CD154 antibody comprises a human or humanized variable region, wherein the variable region comprises a heavy chain variable domain (VH) and a light chain variable domain (VL), and wherein the VH is operably linked to a human Fc domain with modified effector functions. In some embodiments, one or more effector functions of the human Fc domain are reduced. Optionally, one or more effector functions of the human Fc domain are eliminated. Optionally, the VH is operably linked to a human Fc region, wherein the human Fc region comprises a human hinge sequence and the human Fc domain, wherein the human hinge sequence is between the VH and the human Fc domain. In some embodiments, one or more effector functions of the human Fc region are reduced. Optionally, one or more effector functions of the human Fc region are eliminated. The hinge may comprise the amino acid sequence of any one of SEQ ID NOs: 76-90. In some embodiments, the hinge comprises the amino acid sequence of SEQ ID NO: 76. Optionally, the hinge comprises the amino acid sequence of SEQ ID NO: 77. The hinge may comprise the amino acid sequence of SEQ ID NO: 78. In some embodiments, the hinge comprises the amino acid sequence of SEQ ID NO: 79. Optionally, the hinge comprises the amino acid sequence of SEQ ID NO: 80. The hinge may comprise the amino acid sequence of SEQ ID NO: 81. In some embodiments, the hinge comprises the amino acid sequence of SEQ ID NO: 82. Optionally, the hinge comprises the amino acid sequence of SEQ ID NO: 83. The hinge may comprise the amino acid sequence of SEQ ID NO: 84. In some embodiments, the hinge comprises the amino acid sequence of SEQ ID NO: 85. Optionally, the hinge comprises the amino acid sequence of SEQ ID NO: 86. The hinge may comprise the amino acid sequence of SEQ ID NO: 87. In some embodiments, the hinge comprises the amino acid sequence of SEQ ID NO: 88. Optionally, the hinge comprises the amino acid sequence of SEQ ID NO: 89. The hinge may comprise the amino acid sequence of SEQ ID NO: 90.
- [0100] In some embodiments, the human Fc domain is derived from an IgG1 Fc (or crystallizable fragment) region. Optionally, the human Fc domain is derived from an IgG1 constant region. The human Fc domain may be derived from an IgG2 Fc (or crystallizable fragment) region. In some embodiments, the Fc domain is derived from an IgG2 constant region. The human Fc domain may be derived from an IgG4 Fc (or crystallizable fragment) region. In some embodiments, the Fc domain is derived from an IgG4 constant region. In some embodiments, the human Fc region is derived from an IgG1 Fc (or crystallizable fragment) region. Optionally, the human Fc region is derived from an IgG1 constant region.

In some embodiments, the human Fc region is derived from an IgG2 Fc (or crystallizable fragment) region. In some embodiments, the Fc region is derived from an IgG2 constant region. Optionally, the human Fc region is derived from an IgG4 Fc (or crystallizable fragment) region. The human Fc region may be derived from an IgG4 constant region.

- 5 [0101] In some embodiments, the Fc domain of the antibody disclosed herein comprises one or more amino acid modifications that modify effector functions, including reducing or eliminating one or more effector functions. In some embodiments, the Fc domain comprises an amino acid sequence that is at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% or 99% identical to the amino acid sequence of any one of SEQ ID NOs: 3-9, 12-18, and 238-241.
- 10 Optionally, the Fc domain comprises an amino acid sequence that is at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% or 99% similar to the amino acid sequence of any one of SEQ ID NOs: 3-9, 12-18, and 238-241. The Fc domain may comprise an amino acid sequence selected from the group consisting of SEQ ID NOs: 3-9, 12-18, and 238-241. In some embodiments, the Fc domain comprises an amino acid sequence that is at least 70%, 75%, 80%, 85%, 90%,
- 15 95%, 97%, 98% or 99% identical to the amino acid sequence of any one of SEQ ID NOs: 3-9, 12-18, and 236-241. Optionally, the Fc domain comprises an amino acid sequence that is at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% or 99% similar to the amino acid sequence of any one of SEQ ID NOs: 3-9, 12-18, and 236-241. In some embodiments, the Fc domain comprises the amino acid sequence of SEQ ID NO: 3. Optionally, the Fc domain comprises
- 20 the amino acid sequence of SEQ ID NO: 4. In some embodiments, the Fc domain comprises the amino acid sequence of SEQ ID NO: 5. Optionally, the Fc domain comprises the amino acid sequence of SEQ ID NO: 6. In some embodiments, the Fc domain comprises the amino acid sequence of SEQ ID NO: 7. Optionally, the Fc domain comprises the amino acid sequence of SEQ ID NO: 8. In some embodiments, the Fc domain comprises the amino acid sequence
- 25 of SEQ ID NO: 9. Optionally, the Fc domain comprises the amino acid sequence of SEQ ID NO: 12. In some embodiments, the Fc domain comprises the amino acid sequence of SEQ ID NO: 13. Optionally, the Fc domain comprises the amino acid sequence of SEQ ID NO: 14. In some embodiments, the Fc domain comprises the amino acid sequence of SEQ ID NO: 15. Optionally, the Fc domain comprises the amino acid sequence of SEQ ID NO: 16. In some
- 30 embodiments, the Fc domain comprises the amino acid sequence of SEQ ID NO: 17. Optionally, the Fc domain comprises the amino acid sequence of SEQ ID NO: 18. In some embodiments, the Fc domain comprises the amino acid sequence of SEQ ID NO: 236.

- Optionally, the Fc domain comprises the amino acid sequence of SEQ ID NO: 237. In some embodiments, the Fc domain comprises the amino acid sequence of SEQ ID NO: 238. Optionally, the Fc domain comprises the amino acid sequence of SEQ ID NO: 239. In some embodiments, the Fc domain comprises the amino acid sequence of SEQ ID NO: 240.
- 5 Optionally, the Fc domain comprises the amino acid sequence of SEQ ID NO: 241. In some embodiments, the Fc domain does not comprise the amino acid sequence of SEQ ID NO: 236. Optionally, the Fc domain does not comprise the amino acid sequence of SEQ ID NO: 237. In some embodiments, the Fc domain does not comprise the amino acid sequence of SEQ ID NOs: 236 and 237.
- 10 [0102] In some embodiments, the Fc region of the antibody of an antibody disclosed herein comprises one or more amino acid modifications that modify effector functions, including reducing or eliminating one or more effector functions. In some embodiments, the Fc region comprises an amino acid sequence that is at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% or 99% identical to the amino acid sequence of any one of SEQ ID NOs: 21-37, 40-56 and 243-
- 15 251. Optionally, the Fc region comprises an amino acid sequence that is at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% or 99% similar to the amino acid sequence of any one of SEQ ID NOs: 21-37, 40-56 and 243-251. The Fc region may comprise an amino acid sequence selected from the group consisting of SEQ ID NOs: 21-37, 40-56 and 243-251. In some embodiments, the Fc region comprises an amino acid sequence that is at least 70%, 75%, 80%,
- 20 85%, 90%, 95%, 97%, 98% or 99% identical to the amino acid sequence of any one of SEQ ID NOs: 21-37, 40-56 and 242-251. Optionally, the Fc region comprises an amino acid sequence that is at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% or 99% similar to the amino acid sequence of any one of SEQ ID NOs: 21-37, 40-56 and 242-251. The Fc region may comprise an amino acid sequence selected from the group consisting of SEQ ID NOs: 21-
- 25 37, 40-56 and 242-251. In some embodiments, the Fc region comprises the amino acid sequence of SEQ ID NO: 21. Optionally, the Fc region comprises the amino acid sequence of SEQ ID NO: 22. In some embodiments, the Fc region comprises the amino acid sequence of SEQ ID NO: 23. Optionally, the Fc region comprises the amino acid sequence of SEQ ID NO: 24. In some embodiments, the Fc region comprises the amino acid sequence of SEQ ID NO:
- 30 25. Optionally, the Fc region comprises the amino acid sequence of SEQ ID NO: 26. In some embodiments, the Fc region comprises the amino acid sequence of SEQ ID NO: 27. Optionally, the Fc region comprises the amino acid sequence of SEQ ID NO: 28. In some

embodiments, the Fc region comprises the amino acid sequence of SEQ ID NO: 29. Optionally, the Fc region comprises the amino acid sequence of SEQ ID NO: 30. In some embodiments, the Fc region comprises the amino acid sequence of SEQ ID NO: 31. Optionally, the Fc region comprises the amino acid sequence of SEQ ID NO: 32. In some
5 embodiments, the Fc region comprises the amino acid sequence of SEQ ID NO: 33. Optionally, the Fc region comprises the amino acid sequence of SEQ ID NO: 34. In some embodiments, the Fc region comprises the amino acid sequence of SEQ ID NO: 35. Optionally, the Fc region comprises the amino acid sequence of SEQ ID NO: 36. In some embodiments, the Fc region comprises the amino acid sequence of SEQ ID NO: 37. In some
10 embodiments, the Fc region comprises the amino acid sequence of SEQ ID NO: 40. Optionally, the Fc region comprises the amino acid sequence of SEQ ID NO: 41. In some embodiments, the Fc region comprises the amino acid sequence of SEQ ID NO: 42. Optionally, the Fc region comprises the amino acid sequence of SEQ ID NO: 43. In some embodiments, the Fc region comprises the amino acid sequence of SEQ ID NO: 44. Optionally, the Fc region
15 comprises the amino acid sequence of SEQ ID NO: 45. In some embodiments, the Fc region comprises the amino acid sequence of SEQ ID NO: 46. Optionally, the Fc region comprises the amino acid sequence of SEQ ID NO: 47. In some embodiments, the Fc region comprises the amino acid sequence of SEQ ID NO: 48. Optionally, the Fc region comprises the amino acid sequence of SEQ ID NO: 49. In some embodiments, the Fc region comprises the amino
20 acid sequence of SEQ ID NO: 50. Optionally, the Fc region comprises the amino acid sequence of SEQ ID NO: 51. In some embodiments, the Fc region comprises the amino acid sequence of SEQ ID NO: 52. Optionally, the Fc region comprises the amino acid sequence of SEQ ID NO: 53. In some embodiments, the Fc region comprises the amino acid sequence of SEQ ID NO: 54. Optionally, the Fc region comprises the amino acid sequence of SEQ ID NO: 55. In
25 some embodiments, the Fc region comprises the amino acid sequence of SEQ ID NO: 56. In some embodiments, the Fc region comprises the amino acid sequence of SEQ ID NO: 242. Optionally, the Fc region comprises the amino acid sequence of SEQ ID NO: 243. In some embodiments, the Fc region comprises the amino acid sequence of SEQ ID NO: 244. Optionally, the Fc region comprises the amino acid sequence of SEQ ID NO: 245. In some
30 embodiments, the Fc region comprises the amino acid sequence of SEQ ID NO: 246. Optionally, the Fc region comprises the amino acid sequence of SEQ ID NO: 247. In some embodiments, the Fc region comprises the amino acid sequence of SEQ ID NO: 248.

Optionally, the Fc region comprises the amino acid sequence of SEQ ID NO: 249. In some embodiments, the Fc region comprises the amino acid sequence of SEQ ID NO: 250. Optionally, the Fc region comprises the amino acid sequence of SEQ ID NO: 251. In some embodiments, the Fc domain does not comprise the amino acid sequence of SEQ ID NO: 236.

- 5 Optionally, the Fc domain does not comprise the amino acid sequence of SEQ ID NO: 237. In some embodiments, the Fc domain does not comprise the amino acid sequence of SEQ ID NO: 242. Optionally, the Fc domain does not comprise the amino acid sequence of SEQ ID NOs: 236, 237 and 242.

[0103] In some embodiments, the antibody comprising the IgG4-derived Fc domain or Fc region comprises an amino acid modification at any one of the positions selected from the group consisting of S228, L235, L236, G237, E318, and N297 or a combination thereof, wherein the numbering of amino acid residues is according to the EU index as set forth in Edelman GM *et al.*, *Proc. Natl. Acad. USA*, 63, 78-85 (1969). In preferred embodiments, the antibody comprising the IgG4-derived Fc domain or Fc region comprises an amino acid
10 modification selected from the group consisting of S228P, L235A, L235E, L236E, G237A, E318A, and N297Q or a combination thereof.

[0104] In some embodiments, the antibody comprising the IgG1-derived Fc domain or Fc region comprises an amino acid modification at any one of the positions selected from the group consisting E216, R217, K218, C219, C220, C226, C229, P230, E233, L234, L235, G236,
20 G237, P238, S239, V240, F241, K246, L251, T260, D265, V266, H268, W277, N297, E318, K322, P329, A330, P331, Q347, N348, T350, L351, K360, T366, N390, K392, T394, D399, S400, F405, Y407, K409, T411 or a combination such amino acid modifications, wherein the numbering of amino acid residues is according to the EU index as set forth in Edelman GM *et al.*, *Proc. Natl. Acad. USA*, 63, 78-85 (1969). In preferred embodiments, the antibody
25 comprising the IgG1-derived Fc domain or Fc region comprises an amino acid modification selected from the group consisting of C220S, C226S, C229S, P230S, E233P, L234A, L234F, L234V, L235A, L235E, L235V, G236E, G237A, P238S, D265S, D265A, H268Q, W277T, N297G, N297Q, N297D, N297A, E318A, K322A, P329G, P329A, A330S, P331S, Q347R, Q347E, Q347K, T350V, L351Y, K360D, K360E, T366A, T366I, T366L, T366M, T366V,
30 N390R, N390K, N390D, K392V, K392M, K392R, K392L, K392F, K392E, T394W, D399R, D399W, D399K, S400E, S400D, S400R, S400K, F405A, F405I, F405M, F405T, F405S, F405V, F405W, Y407A, Y407I, Y407L, Y407V, K409F, K409I, K409S, K409W, T411N,

T411R, T411Q, T411K, T411D, T411E, T411W, Δ E216-E222, K246R/L251E/T260R, InR234/235, InV235/236, InR236/237, InR237/238, InV238/239, InN238/239, InL238/239, InE238/239, InG238/239, InS239/240, InG240/241, InE240/241, InG240/241, InL238/239/P238Q, InE238/239/N348A, InS239/240/V266A, and InR237/238/G236A or a combination thereof.

[0105] In some embodiments, the antibody comprising the IgG2-derived Fc domain or Fc region comprises an amino acid modification at any one of the positions selected from the group consisting of V234, G237, P238, H268, V309, A330, and P331 or a combination thereof, wherein the numbering of amino acid residues is according to the EU numbering as set forth in Edelman. In preferred embodiments, the antibody comprising the IgG2-derived Fc domain or Fc region comprises an amino acid modification selected from the group consisting of V234A, G237A, P238S, H268Q, H268A, V309L, A330S, P331S, or a combination thereof.

[0106] In some embodiments, the VH comprises (a) a heavy chain CDR1 having the amino acid sequence of SEQ ID NO: 57, (b) a heavy chain CDR2 having the amino acid sequence of SEQ ID NO: 58, and (c) a heavy chain CDR3 having the amino acid sequence of SEQ ID NO: 59; and the VL comprises (a) a light chain CDR1 having the amino acid sequence of SEQ ID NO: 60, (b) a light chain CDR2 having the amino acid sequence of SEQ ID NO: 61, and (c) a light chain CDR3 having the amino acid sequence of SEQ ID NO: 62.

[0107] In some embodiments, the VH comprises an amino acid sequence that is at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% or 99% identical to the amino acid sequence of SEQ ID NO: 63, 64, 252 or 253. Optionally, the VH comprise an amino acid sequence that is at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% or 99% similar to the amino acid sequence of SEQ ID NO: 63, 64, 252 or 253. The VH may comprise the amino acid sequence of SEQ ID NO: 63, 64, 252 or 253. In some embodiments, the VH comprises the amino acid sequence of SEQ ID NO: 63. Optionally, the VH comprises the amino acid sequence of SEQ ID NO: 64. In some embodiments, the VH comprises the amino acid sequence of SEQ ID NO: 252. Optionally, the VH comprises the amino acid sequence of SEQ ID NO: 253. In some embodiments, the VH does not comprise the amino acid sequence of SEQ ID NO: 233.

[0108] In some embodiments, the VL comprises an amino acid sequence that is at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% or 99% identical to the amino acid sequence of SEQ ID NO: 65 or 66. Optionally, the VL comprise an amino acid sequence that is at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% or 99% similar to the amino acid sequence of SEQ ID

NO: 65 or 66. The VL may comprise the amino acid sequence of SEQ ID NO: 65 or 66. In some embodiments, the VL comprises the amino acid sequence of SEQ ID NO: 65. Optionally, the VL comprises the amino acid sequence of SEQ ID NO: 66.

[0109] In some embodiments, the antibody further comprises a CH1 domain, wherein the CH1 domain is operably linked to (a) the C-terminal end of the VH, and (b) the N-terminal end of the hinge. Optionally, the CH1 domain comprises an amino acid sequence that is at least 80% 85%, 90%, 95%, 97%, 98% or 99% identical to the amino acid sequence of any one of SEQ ID NOs: 67, 70, and 73. The CH1 domain may comprise an amino acid sequence that is at least 80% 85%, 90%, 95%, 97%, 98% or 99% similar to the amino acid sequence of any one of SEQ ID NOs: 67, 70, and 73. In some embodiments, the CH1 domain comprises the amino acid sequence of any one of SEQ ID NO: 67, 70, and 73. The CH1 domain may comprise the amino acid sequence of SEQ ID NO: 67. Optionally, the CH1 domain comprises the amino acid sequence of SEQ ID NO: 70. In some embodiments, the CH1 domain comprises the amino acid sequence of SEQ ID NO: 73.

[0110] In some embodiments, the antibody comprises a linker between the VH and the Fc domain. Optionally, the linker comprises the amino acid sequence of any one of SEQ ID NOs: 199-223 and 327-330. In some embodiments, the linker comprises the amino acid sequence of any one of SEQ ID NOs: 199-223. The linker may comprise the amino acid sequence of any one of SEQ ID NOs: 327-330. In some embodiments, the linker comprises the amino acid sequence of SEQ ID NO: 199. Optionally, the linker comprises the amino acid sequence of SEQ ID NO: 200. In some embodiments, the linker comprises the amino acid sequence of SEQ ID NO: 201. Optionally, the linker comprises the amino acid sequence of SEQ ID NO: 202. In some embodiments, the linker comprises the amino acid sequence of SEQ ID NO: 203. Optionally, the linker comprises the amino acid sequence of SEQ ID NO: 204. In some embodiments, the linker comprises the amino acid sequence of SEQ ID NO: 205. Optionally, the linker comprises the amino acid sequence of SEQ ID NO: 206. In some embodiments, the linker comprises the amino acid sequence of SEQ ID NO: 207. Optionally, the linker comprises the amino acid sequence of SEQ ID NO: 208. In some embodiments, the linker comprises the amino acid sequence of SEQ ID NO: 209. Optionally, the linker comprises the amino acid sequence of SEQ ID NO: 210. In some embodiments, the linker comprises the amino acid sequence of SEQ ID NO: 211. Optionally, the linker comprises the amino acid sequence of SEQ ID NO: 212. In some embodiments, the linker comprises the amino acid sequence of

SEQ ID NO: 213. Optionally, the linker comprises the amino acid sequence of SEQ ID NO: 214. In some embodiments, the linker comprises the amino acid sequence of SEQ ID NO: 215. Optionally, the linker comprises the amino acid sequence of SEQ ID NO: 216. In some embodiments, the linker comprises the amino acid sequence of SEQ ID NO: 217. Optionally, the linker comprises the amino acid sequence of SEQ ID NO: 218. In some embodiments, the linker comprises the amino acid sequence of SEQ ID NO: 219. Optionally, the linker comprises the amino acid sequence of SEQ ID NO: 220. In some embodiments, the linker comprises the amino acid sequence of SEQ ID NO: 221. Optionally, the linker comprises the amino acid sequence of SEQ ID NO: 222. In some embodiments, the linker comprises the amino acid sequence of SEQ ID NO: 223. Optionally, the linker comprises the amino acid sequence of SEQ ID NO: 327. In some embodiments, the linker comprises the amino acid sequence of SEQ ID NO: 328. Optionally, the linker comprises the amino acid sequence of SEQ ID NO: 329. In some embodiments, the linker comprises the amino acid sequence of SEQ ID NO: 330. The linker may be between the VH and the hinge. In some embodiments, the linker is between the VH and the CH1 domain.

[0111] In some embodiments, the VH is operably linked to an amino acid sequence that is at least 80% 85%, 90%, 95%, 97%, 98% or 99% identical to the amino acid sequence of any one of SEQ ID NOs: 3-9, 12-18, 21-37, 40-56, 238-241, and 243-251. Optionally, the VH is operably linked to an amino acid sequence that is at least 80% 85%, 90%, 95%, 97%, 98% or 99% similar to the amino acid sequence of any one of SEQ ID NOs: 3-9, 12-18, 21-37, 40-56, 238-241, and 243-251. The VH may be operably linked to the amino acid sequence of any one of SEQ ID NOs: 3-9, 12-18, 21-37, 40-56, 238-241, and 243-251. In some embodiments, the VH is operably linked to the amino acid sequence of SEQ ID NO: 3. Optionally, the VH is operably linked to the amino acid sequence of SEQ ID NO: 4. The VH may be operably linked to the amino acid sequence of SEQ ID NO: 5. In some embodiments, the VH is operably linked to the amino acid sequence of SEQ ID NO: 6. Optionally, the VH is operably linked to the amino acid sequence of SEQ ID NO: 7. The VH may be operably linked to the amino acid sequence of SEQ ID NO: 8. In some embodiments, the VH is operably linked to the amino acid sequence of SEQ ID NO: 9. Optionally, the VH is operably linked to the amino acid sequence of SEQ ID NO: 12. The VH may be operably linked to the amino acid sequence of SEQ ID NO: 13. In some embodiments, the VH is operably linked to the amino acid sequence of SEQ ID NO: 14. Optionally, the VH is operably linked to the amino acid sequence of SEQ

ID NO: 15. The VH may be operably linked to the amino acid sequence of SEQ ID NO: 16. In some embodiments, the VH is operably linked to the amino acid sequence of SEQ ID NO: 17. Optionally, the VH is operably linked to the amino acid sequence of SEQ ID NO: 18. The VH may be operably linked to the amino acid sequence of SEQ ID NO: 21. In some
5 embodiments, the VH is operably linked to the amino acid sequence of SEQ ID NO: 22. Optionally, the VH is operably linked to the amino acid sequence of SEQ ID NO: 23. The VH may be operably linked to the amino acid sequence of SEQ ID NO: 24. In some embodiments, the VH is operably linked to the amino acid sequence of SEQ ID NO: 25. Optionally, the VH is operably linked to the amino acid sequence of SEQ ID NO: 26. The VH may be operably
10 linked to the amino acid sequence of SEQ ID NO: 27. In some embodiments, the VH is operably linked to the amino acid sequence of SEQ ID NO: 28. Optionally, the VH is operably linked to the amino acid sequence of SEQ ID NO: 29. The VH may be operably linked to the amino acid sequence of SEQ ID NO: 30. In some embodiments, the VH is operably linked to the amino acid sequence of SEQ ID NO: 31. Optionally, the VH is operably linked to the
15 amino acid sequence of SEQ ID NO: 32. The VH may be operably linked to the amino acid sequence of SEQ ID NO: 33. In some embodiments, the VH is operably linked to the amino acid sequence of SEQ ID NO: 34. Optionally, the VH is operably linked to the amino acid sequence of SEQ ID NO: 35. The VH may be operably linked to the amino acid sequence of SEQ ID NO: 36. In some embodiments, the VH is operably linked to the amino acid sequence
20 of SEQ ID NO: 37. Optionally, the VH is operably linked to the amino acid sequence of SEQ ID NO: 40. The VH may be operably linked to the amino acid sequence of SEQ ID NO: 41. In some embodiments, the VH is operably linked to the amino acid sequence of SEQ ID NO: 42. Optionally, the VH is operably linked to the amino acid sequence of SEQ ID NO: 43. The VH may be operably linked to the amino acid sequence of SEQ ID NO: 44. In some
25 embodiments, the VH is operably linked to the amino acid sequence of SEQ ID NO: 45. Optionally, the VH is operably linked to the amino acid sequence of SEQ ID NO: 46. The VH may be operably linked to the amino acid sequence of SEQ ID NO: 47. In some embodiments, the VH is operably linked to the amino acid sequence of SEQ ID NO: 48. Optionally, the VH is operably linked to the amino acid sequence of SEQ ID NO: 49. The VH may be operably
30 linked to the amino acid sequence of SEQ ID NO: 50. In some embodiments, the VH is operably linked to the amino acid sequence of SEQ ID NO: 51. Optionally, the VH is operably linked to the amino acid sequence of SEQ ID NO: 52. The VH may be operably linked to the

amino acid sequence of SEQ ID NO: 53. In some embodiments, the VH is operably linked to the amino acid sequence of SEQ ID NO: 54. Optionally, the VH is operably linked to the amino acid sequence of SEQ ID NO: 55. The VH may be operably linked to the amino acid sequence of SEQ ID NO: 56. Optionally, the VH is operably linked to the amino acid sequence of SEQ ID NO: 236. The VH may be operably linked to the amino acid sequence of SEQ ID NO: 237. Optionally, the VH is operably linked to the amino acid sequence of SEQ ID NO: 238. The VH may be operably linked to the amino acid sequence of SEQ ID NO: 239. In some embodiments, the VH is operably linked to the amino acid sequence of SEQ ID NO: 240. Optionally, the VH is operably linked to the amino acid sequence of SEQ ID NO: 241. In some embodiments, the VH is operably linked to the amino acid sequence of SEQ ID NO: 242. The VH may be operably linked to the amino acid sequence of SEQ ID NO: 243. Optionally, the VH is operably linked to the amino acid sequence of SEQ ID NO: 244. The VH may be operably linked to the amino acid sequence of SEQ ID NO: 245. Optionally, the VH is operably linked to the amino acid sequence of SEQ ID NO: 246. The VH may be operably linked to the amino acid sequence of SEQ ID NO: 247. Optionally, the VH is operably linked to the amino acid sequence of SEQ ID NO: 248. The VH may be operably linked to the amino acid sequence of SEQ ID NO: 249. Optionally, the VH is operably linked to the amino acid sequence of SEQ ID NO: 250. The VH may be operably linked to the amino acid sequence of SEQ ID NO: 251. Optionally, the VH is not operably linked to the amino acid sequence of SEQ ID NO: 236. In some embodiments, the VH is not be operably linked to the amino acid sequence of SEQ ID NO: 237. Optionally, the VH is not be operably linked to the amino acid sequence of SEQ ID NO: 242. In some embodiments, the VH is not be operably linked to the amino acid sequence of SEQ ID NOs: 236 and 237. Optionally, the VH is not be operably linked to the amino acid sequence of SEQ ID NOs: 236, 237 and 242.

[0112] In some embodiments, the heavy chain comprises an amino acid sequence that is at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% or 99% identical to the amino acid sequence of any one of SEQ ID NOs: 121-132, 135-146, 149-160, 163-174 and 266-288. Optionally, the heavy chain comprises an amino acid sequence that is at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% or 99% similar to the amino acid sequence of any one of SEQ ID NOs: 121-132, 135-146, 149-160, 163-174 and 266-288. The heavy chain may comprise the amino acid sequence of any one of SEQ ID NOs: 121-132, 135-146, 149-160, 163-174 and 266-288. In some embodiments, the heavy chain comprises an amino acid sequence that is at least 70%,

75%, 80%, 85%, 90%, 95%, 97%, 98% or 99% identical to the amino acid sequence of any one of SEQ ID NOs: 121-132, 135-146, 149-160, 163-174, 266-277, and 279-288. Optionally, the heavy chain comprises an amino acid sequence that is at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% or 99% similar to the amino acid sequence of any one of SEQ ID NOs: 121-132, 135-146, 149-160, 163-174, 266-277, and 279-288. The heavy chain may comprise the amino acid sequence of any one of SEQ ID NOs: 121-132, 135-146, 149-160, 163-174, 266-277, and 279-288. In some embodiments, the heavy chain comprises an amino acid sequence that is at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% or 99% identical to the amino acid sequence of any one of SEQ ID NOs: 121-132, 135-146, 149, 151-160, 163, 165-174 and 266-288. Optionally, the heavy chain comprises an amino acid sequence that is at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% or 99% similar to the amino acid sequence of any one of SEQ ID NOs: 121-132, 135-146, 149, 151-160, 163, 165-174 and 266-288. The heavy chain may comprise the amino acid sequence of any one of SEQ ID NOs: 121-132, 135-146, 149, 151-160, 163, 165-174 and 266-288. In some embodiments, the heavy chain comprises an amino acid sequence that is at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% or 99% identical to the amino acid sequence of any one of SEQ ID NOs: 121-132, 135-146, 149, 151-160, 163, 165-174, 266-277, and 279-288. Optionally, the heavy chain comprises an amino acid sequence that is at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% or 99% similar to the amino acid sequence of any one of SEQ ID NOs: 121-132, 135-146, 149, 151-160, 163, 165-174, 266-277, and 279-288. The heavy chain may comprise the amino acid sequence of any one of SEQ ID NOs: 121-132, 135-146, 149, 151-160, 163, 165-174, 266-277, and 279-288. In some embodiments, the heavy chain comprises an amino acid sequence that is at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% or 99% identical to the amino acid sequence of any one of SEQ ID NOs: 121-132, 135-146, 149, 151-160, 163, 165-174, 267-271, 273-277, and 279-288. Optionally, the heavy chain comprises an amino acid sequence that is at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% or 99% similar to the amino acid sequence of any one of SEQ ID NOs: 121-132, 135-146, 149, 151-160, 163, 165-174, 267-271, 273-277, and 279-288. The heavy chain may comprise the amino acid sequence of any one of SEQ ID NOs: 121-132, 135-146, 149, 151-160, 163, 165-174, 267-271, 273-277, and 279-288. In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO: 121. Optionally, the heavy chain comprises the amino acid sequence of SEQ ID NO: 122. The heavy chain may comprise the amino acid sequence of SEQ ID NO: 123. In some

embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO: 124. Optionally, the heavy chain comprises the amino acid sequence of SEQ ID NO: 125. The heavy chain may comprise the amino acid sequence of SEQ ID NO: 126. In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO: 127.

5 Optionally, the heavy chain comprises the amino acid sequence of SEQ ID NO: 128. The heavy chain may comprise the amino acid sequence of SEQ ID NO: 129. In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO: 130. Optionally, the heavy chain comprises the amino acid sequence of SEQ ID NO: 131. The heavy chain may comprise the amino acid sequence of SEQ ID NO: 132. In some

10 embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO: 135. Optionally, the heavy chain comprises the amino acid sequence of SEQ ID NO: 136. The heavy chain may comprise the amino acid sequence of SEQ ID NO: 137. In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO: 138. Optionally, the heavy chain comprises the amino acid sequence of SEQ ID NO: 139. The

15 heavy chain may comprise the amino acid sequence of SEQ ID NO: 140. In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO: 141. Optionally, the heavy chain comprises the amino acid sequence of SEQ ID NO: 142. The heavy chain may comprise the amino acid sequence of SEQ ID NO: 143. In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO: 144.

20 Optionally, the heavy chain comprises the amino acid sequence of SEQ ID NO: 145. The heavy chain may comprise the amino acid sequence of SEQ ID NO: 146. In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO: 149. Optionally, the heavy chain comprises the amino acid sequence of SEQ ID NO: 150. The heavy chain may comprise the amino acid sequence of SEQ ID NO: 151. In some

25 embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO: 152. Optionally, the heavy chain comprises the amino acid sequence of SEQ ID NO: 153. The heavy chain may comprise the amino acid sequence of SEQ ID NO: 154. In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO: 155. Optionally, the heavy chain comprises the amino acid sequence of SEQ ID NO: 156. The

30 heavy chain may comprise the amino acid sequence of SEQ ID NO: 157. In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO: 158. Optionally, the heavy chain comprises the amino acid sequence of SEQ ID NO: 159. The

heavy chain may comprise the amino acid sequence of SEQ ID NO: 160. In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO: 163. Optionally, the heavy chain comprises the amino acid sequence of SEQ ID NO: 164. The heavy chain may comprise the amino acid sequence of SEQ ID NO: 165. In some
5 embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO: 166. Optionally, the heavy chain comprises the amino acid sequence of SEQ ID NO: 167. The heavy chain may comprise the amino acid sequence of SEQ ID NO: 168. In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO: 169. Optionally, the heavy chain comprises the amino acid sequence of SEQ ID NO: 170. The
10 heavy chain may comprise the amino acid sequence of SEQ ID NO: 171. In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO: 172. Optionally, the heavy chain comprises the amino acid sequence of SEQ ID NO: 173. The heavy chain may comprise the amino acid sequence of SEQ ID NO: 174. In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO: 266. Optionally, the heavy chain comprises the amino acid sequence of SEQ ID NO: 267. The
15 heavy chain may comprise the amino acid sequence of SEQ ID NO: 268. In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO: 269. Optionally, the heavy chain comprises the amino acid sequence of SEQ ID NO: 270. The heavy chain may comprise the amino acid sequence of SEQ ID NO: 271. The heavy chain
20 may comprise the amino acid sequence of SEQ ID NO: 272. In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO: 273. Optionally, the heavy chain comprises the amino acid sequence of SEQ ID NO: 274. The heavy chain may comprise the amino acid sequence of SEQ ID NO: 275. Optionally, the heavy chain comprises the amino acid sequence of SEQ ID NO: 276. The heavy chain may comprise the amino acid sequence
25 of SEQ ID NO: 277. In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO: 278. In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO: 279. Optionally, the heavy chain comprises the amino acid sequence of SEQ ID NO: 280. The heavy chain may comprise the amino acid sequence of SEQ ID NO: 281. In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO: 282. Optionally, the heavy chain comprises the amino acid sequence of SEQ ID NO: 283. The
30 heavy chain may comprise the amino acid sequence of SEQ ID NO: 284. In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO: 285.

Optionally, the heavy chain comprises the amino acid sequence of SEQ ID NO: 286. The heavy chain may comprise the amino acid sequence of SEQ ID NO: 287. In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO: 288. Optionally, the heavy chain does not comprise the amino acid sequence of SEQ ID NO: 150.

5 In some embodiments, the heavy chain does not comprise the amino acid sequence of SEQ ID NO: 164. Optionally, the heavy chain does not comprise the amino acid sequence of SEQ ID NOs: 150 and 164. In some embodiments, the heavy chain does not comprise the amino acid sequence of SEQ ID NO: 234. Optionally, the heavy chain does not comprise the amino acid sequence of SEQ ID NO: 266. In some embodiments, the heavy chain does not comprise the amino acid sequence of SEQ ID NO: 272. In some embodiments, the heavy chain does not

10 comprise the amino acid sequence of SEQ ID NO: 278. Optionally, the heavy chain does not comprise the amino acid sequence of SEQ ID NOs: 234 and 278. In some embodiments, the heavy chain does not comprise the amino acid sequence of SEQ ID NOs: 234, 266, 272 and 278. Optionally, the heavy chain does not comprise the amino acid sequence of SEQ ID NOs:

15 150, 164, 234 and 278. In some embodiments, the heavy chain does not comprise the amino acid sequence of SEQ ID NOs: 150, 164, 234, 266, 272 and 278.

[0113] In some embodiments, the light chain comprises an amino acid sequence that is at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% or 99% identical to the amino acid sequence of any one of SEQ ID NOs: 195 and 196. Optionally, the light chain comprises an amino acid

20 sequence that is at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% or 99% similar to the amino acid sequence of any one of SEQ ID NOs: 195 and 196. The light chain may comprise the amino acid sequence of SEQ ID NO: 195 or 196. In some embodiments, the light chain comprises the amino acid sequence of SEQ ID NO: 195. Optionally, the light chain comprises the amino acid sequence of SEQ ID NO: 196.

25 [0114] In some embodiments, the antibody is monoclonal. Optionally, the antibody is a chimeric antibody. The antibody may be a humanized antibody. In some embodiments, the antibody is a human antibody.

[0115] In some embodiments, the binding of the antibody to human CD154 inhibits the interaction between human CD154 and human CD40. Optionally, the antibody blocks the

30 activation of one or more of B cells, macrophages, dendritic cells, or endothelial cells by inhibiting binding of CD154 to CD40. In some embodiments, a reduced level of thrombosis is observed after administration of the antibody compared to level of thrombosis after

administration of the 5c8 or hu5c8 antibody. Optionally, the antibody does not cause thrombosis when administered to a subject.

[0116] In some embodiments, the antibody has one or more of the following effects when administered to a subject: (a) decreased risk of thrombosis or thromboembolic events compared to hu5c8 antibody; (b) decreased activation of platelets expressing CD154; (c) inhibition of CD154 shedding; and (d) alteration of the expression or activity of downstream targets of CD154-CD40 signaling. Optionally, the administration of the antibody results in a decreased risk for thrombosis or thromboembolic events, compared to a subject where a 5c8 or hu5c8 antibody has been administered. In some embodiments, the administration of the antibody results in a decreased activation of platelets expressing CD154. Optionally, the administration of the antibody results in the inhibition of CD154 shedding. In some embodiments, the administration of the antibody results in the alteration the expression of activity of downstream targets of CD154-CD40 signaling.

[0117] In some embodiments, the human Fc domain with modified effector functions does not comprise the amino acid sequence consisting of any one of SEQ ID NOs: 1, 2, 10, 11, 231, and 236. Optionally, the human Fc domain with modified effector functions does not comprise the amino acid sequence consisting of SEQ ID NO: 1. In some embodiments, the human Fc domain with modified effector functions does not comprise the amino acid sequence consisting of SEQ ID NO: 2. Optionally, the human Fc domain with modified effector functions does not comprise the amino acid sequence consisting of SEQ ID NO: 10. In some embodiments, the human Fc domain with modified effector functions does not comprise the amino acid sequence consisting of SEQ ID NO: 11. Optionally, the human Fc domain with modified effector functions does not comprise the amino acid sequence consisting of SEQ ID NO: 231. In some embodiments, the human Fc domain with modified effector functions does not comprise the amino acid sequence consisting of SEQ ID NO: 236. In some embodiments, the antibody does not comprise the amino acid sequence consisting of any one of SEQ ID NOs: 1, 2, 10, 11, 231, and 236. Optionally, the antibody does not comprise the amino acid sequence consisting of SEQ ID NO: 1. In some embodiments, the antibody does not comprise the amino acid sequence consisting of SEQ ID NO: 2. Optionally, the antibody does not comprise the amino acid sequence consisting of SEQ ID NO: 10. In some embodiments, the antibody does not comprise the amino acid sequence consisting of SEQ ID NO: 11. Optionally, the antibody does not

comprise the amino acid sequence consisting of SEQ ID NO: 231. In some embodiments, the antibody does not comprise the amino acid sequence consisting of SEQ ID NO: 236.

[0118] Optionally, the human Fc region with modified effector functions does not comprise the amino acid sequence consisting of any one of SEQ ID NOs: 19, 20, 38, 39, 232, and 235.

5 In some embodiments, the human Fc region with modified effector functions does not comprise the amino acid sequence consisting of SEQ ID NO: 19. Optionally, the human Fc region with modified effector functions does not comprise the amino acid sequence consisting of SEQ ID NO: 20. In some embodiments, the human Fc region with modified effector functions does not comprise the amino acid sequence consisting of SEQ ID NO: 20. Optionally, the human Fc
10 region with modified effector functions does not comprise the amino acid sequence consisting of SEQ ID NO: 38. In some embodiments, the human Fc region with modified effector functions does not comprise the amino acid sequence consisting of SEQ ID NO: 39. Optionally, the human Fc region with modified effector functions does not comprise the amino acid sequence consisting of SEQ ID NO: 232. In some embodiments, the human Fc region
15 with modified effector functions does not comprise the amino acid sequence consisting of SEQ ID NO: 235. Optionally, the antibody does not comprise the amino acid sequence consisting of any one of SEQ ID NOs: 19, 20, 38, 39, 232, and 235. In some embodiments, the antibody does not comprise the amino acid sequence consisting of SEQ ID NO: 19. Optionally, the antibody does not comprise the amino acid sequence consisting of SEQ ID NO: 20. In some
20 embodiments, the antibody does not comprise the amino acid sequence consisting of SEQ ID NO: 20. Optionally, the antibody does not comprise the amino acid sequence consisting of SEQ ID NO: 38. In some embodiments, antibody does not comprise the amino acid sequence consisting of SEQ ID NO: 39. Optionally, the antibody does not comprise the amino acid sequence consisting of SEQ ID NO: 232. In some embodiments, the antibody does not
25 comprise the amino acid sequence consisting of SEQ ID NO: 235.

[0119] In some embodiments, the heavy chain with modified effector functions does not comprise the amino acid sequence consisting of any one of SEQ ID NOs: 119, 120, 133, 134, 147, 148, 150, 161, 162, 164, 230, 234, and 278. Optionally, the heavy chain with modified effector functions does not comprise the amino acid sequence consisting of SEQ ID NO: 119.

30 In some embodiments, the heavy chain with modified effector functions does not comprise the amino acid sequence consisting of SEQ ID NO: 120. Optionally, the heavy chain with modified effector functions does not comprise the amino acid sequence consisting of SEQ ID

NO: 133. In some embodiments, the heavy chain with modified effector functions does not comprise the amino acid sequence consisting of SEQ ID NO: 134. Optionally, the heavy chain with modified effector functions does not comprise the amino acid sequence consisting of SEQ ID NO: 147. In some embodiments, the heavy chain with modified effector functions does not
5 comprise the amino acid sequence consisting of SEQ ID NO: 148. In some embodiments, the heavy chain with modified effector functions does not comprise the amino acid sequence consisting of SEQ ID NO: 150. Optionally, the heavy chain with modified effector functions does not comprise the amino acid sequence consisting of SEQ ID NO: 161. In some
10 embodiments, the heavy chain with modified effector functions does not comprise the amino acid sequence consisting of SEQ ID NO: 162. In some embodiments, the heavy chain with modified effector functions does not comprise the amino acid sequence consisting of SEQ ID NO: 164. Optionally, the heavy chain with modified effector functions does not comprise the amino acid sequence consisting of SEQ ID NO: 230. In some embodiments, the heavy chain
15 with modified effector functions does not comprise the amino acid sequence consisting of SEQ ID NO: 234. Optionally, the heavy chain with modified effector functions does not comprise the amino acid sequence consisting of SEQ ID NO: 278. In some embodiments, the antibody does not comprise the amino acid sequence consisting of any one of SEQ ID NOs: 119, 120, 133, 134, 147, 148, 150, 161, 162, 164, 230, 234, and 278. Optionally, the antibody does not
20 comprise the amino acid sequence consisting of SEQ ID NO: 119. In some embodiments, the antibody does not comprise the amino acid sequence consisting of SEQ ID NO: 120. Optionally, the antibody does not comprise the amino acid sequence consisting of SEQ ID NO: 133. In some embodiments, the antibody does not comprise the amino acid sequence consisting of SEQ ID NO: 134. Optionally, the antibody does not comprise the amino acid sequence
25 consisting of SEQ ID NO: 147. In some embodiments, the antibody does not comprise the amino acid sequence consisting of SEQ ID NO: 148. Optionally, the antibody does not comprise the amino acid sequence consisting of SEQ ID NO: 161. In some embodiments, the antibody does not comprise the amino acid sequence consisting of SEQ ID NO: 162. In some
30 embodiments, the heavy chain with modified effector functions does not comprise the amino acid sequence consisting of SEQ ID NO: 164. Optionally, the antibody does not comprise the amino acid sequence consisting of SEQ ID NO: 230. In some embodiments, the antibody does not comprise the amino acid sequence consisting of SEQ ID NO: 234. Optionally, the heavy chain with modified effector functions does not comprise the amino acid sequence consisting

of SEQ ID NO: 278. In some embodiments, the antibody does not comprise the amino acid sequence consisting of any one of SEQ ID NOs: 1, 2, 10, 11, 19, 20, 38, 39, 119, 120, 133, 134, 147, 148, 150, 161, 162, 164, 230, 231, 232, 234, 235, 236, and 278.

Properties of the Anti-CD154 Antibodies

5 *Binding Affinity of Anti-CD154 Antibodies to CD154*

[0120] The binding affinity (K_D) and dissociation rate (k_{off}) of an anti-CD154 antibody to CD154 can be determined by methods known in the art. The binding affinity can be measured by ELISA, RIA, flow cytometry, or surface plasmon resonance (SPR), such as with the BIACORE[®] system. The dissociation rate can be measured by SPR. Optionally, the binding
10 affinity and dissociation rate are measured by SPR. In some embodiments, the binding affinity and dissociation rate are measured using BIACORE[®]. The skilled artisan can determine whether an antibody disclosed herein has substantially the same K_D as another anti-CD154 antibody by using methods known in the art. Such methods of determining K_D and k_{off} can be used during the initial screening stage, as well as during subsequent optimization stages. In
15 some embodiments, the antibody has a K_D for CD154 of less than 50 pM. Optionally, the antibody has a K_D for CD154 of less than 25 pM. In some embodiments, the antibody has a K_D for CD154 of 5-25 pM. Optionally, the antibody has a K_D for CD154 of 9.5-23 pM.

Inhibition of CD154 Activity by Anti-CD154 Antibody

[0121] Anti-CD154 antibodies that inhibit CD154 binding to CD40 can be identified using
20 any one of a number of assays, e.g., competitive binding assays, FACS analysis, B cell activation assays, B cell proliferation assays, T cell activation assays, T cell proliferation assays. See, e.g., Barr *et al.*, Immunology, 102(1):39-43 (2001); and Blair *et al.*, J. Exp. Med., 191(4):651-660 (2001). For example, neutralizing anti-CD154 antibodies can be identified by their inhibition of up-regulation of a specific downstream target gene of CD154, such as CD23,
25 CD44H, CD54, TRAF-3 and NF κ B. In some embodiments, the anti-CD154 antibodies have an IC₅₀ of no greater than 500 nM, 300 nM, 200 nM, 150 nM, 100 nM, 50 nM, 20 nM, 10 nM, or 1 nM.

Effector function - Platelet assays

[0122] The effector function of the anti-CD154 can be identified using any one of a number of assays, *e.g.*, *in vitro* platelet activation and/or aggregation assays. See, *e.g.*, U.S. Patent No. 9,765,150; Langer F *et al.*, *Thromb Haemost.* Jun;93(6):1137-46 (2005); McKenzie, S.E. *et al.*,
5 *J Immunol* 162 (7) 4311-4318 (1999); and Scholthauer T *et al.*, *Protein Engineering, Design and Selection*, 29(10): 457-466, (2016). Blood from human donors or mice expressing FcγRIIA (CD32a) on platelets may be used to assay platelet function. Platelet activation may be detected by flow cytometry using antibodies against platelet activation markers P-selectin (CD62P) and PAC-1 (activated GPIIb/IIIa). Platelet aggregation analysis may be analyzed
10 using a minicell impedance device and quantifying the area-under-the-curve as a measure of the platelet aggregation impedance curve.

Pharmaceutical Compositions and Administration

[0123] The methods disclosed herein may also utilize a pharmaceutical composition comprising an anti-CD154 antibody described herein and a pharmaceutically acceptable
15 carrier. In some embodiments, the pharmaceutical composition comprises a therapeutically effective amount of the anti-CD154 antibody described herein.

[0124] The antibodies disclosed herein may be incorporated into pharmaceutical compositions suitable for administration to a subject. Typically, the pharmaceutical composition comprises an antibody disclosed herein and a pharmaceutically acceptable carrier.
20 As used herein, “pharmaceutically acceptable carrier” and “pharmaceutically acceptable excipient” are used interchangeably refer to any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like that are physiologically compatible. Pharmaceutically acceptable carriers are well known in the art. See, *e.g.*, Remington's Pharmaceutical Sciences and U.S. Pharmacopeia: National
25 Formulary, Mack Publishing Company, Easton, PA (1984), incorporated herein by reference. Some examples of pharmaceutically acceptable carriers are water, saline, phosphate buffered saline, dextrose, glycerol, ethanol and the like, as well as combinations thereof. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, or sodium chloride in the composition. Additional examples of
30 pharmaceutically acceptable substances are wetting agents or minor amounts of auxiliary

substances such as wetting or emulsifying agents, preservatives, or buffers, which enhance the shelf life or effectiveness of the antibody. Pharmaceutical compositions may be prepared by mixing an antibody disclosed herein with acceptable carriers, excipients, or stabilizers in the form of, *e.g.*, lyophilized powders, slurries, aqueous solutions or suspensions (see, *e.g.*,
5 Hardman, *et al.* (2001) Goodman and Gilman's The Pharmacological Basis of Therapeutics, McGraw-Hill, New York, NY; Gennaro (2000) Remington: The Science and Practice of Pharmacy, Lippincott, Williams, and Wilkins, New York, NY; Avis, *et al.* (eds.) (1993) Pharmaceutical Dosage Forms: Parenteral Medications, Marcel Dekker, NY; Lieberman, *et al.* (eds.) (1990) Pharmaceutical Dosage Forms: Tablets, Marcel Dekker, NY; Lieberman, *et al.* (eds.) (1990) Pharmaceutical Dosage Forms: Disperse Systems, Marcel Dekker, NY; Weiner
10 and Kotkoskie (2000) Excipient Toxicity and Safety, Marcel Dekker, Inc., New York, NY; each incorporated herein by reference).

[0125] The pharmaceutical compositions may be in a variety of forms, for example, liquid, semi-solid and solid dosage forms, such as liquid solutions (*e.g.*, injectable and infusible
15 solutions), dispersions or suspensions, tablets, pills, powders, liposomes and suppositories. The preferred form depends on the intended mode of administration and therapeutic application. In some embodiments, the pharmaceutical compositions are in the form of injectable or infusible solutions, such as compositions similar to those used for passive immunization of humans. Optionally, mode of administration is parenteral (*e.g.*, intravenous,
20 subcutaneous, intraperitoneal, intramuscular). In some embodiments, the mode of administration is intravitreal injection. The pharmaceutical composition may be administered by intravenous infusion or injection. In some embodiments, the antibody is administered by intramuscular or subcutaneous injection. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampoules, pre-filled syringes, or in multi-dose containers, with or without
25 an added preservative. The pharmaceutical compositions may take such forms as suspensions, solutions, or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Alternatively, the active ingredient may be prepared in powder form for reconstitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

30 [0126] Therapeutic compositions typically must be sterile and stable under the conditions of manufacture and storage. The composition may be formulated as a solution, microemulsion,

dispersion, liposome, or other ordered structure suitable to high drug concentration. Sterile injectable solutions may be prepared by incorporating the anti-CD154 antibody in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Dispersions may be prepared by incorporating the anti-CD154 antibody into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation include vacuum drying and freeze-drying that yield a powder of the anti-CD154 antibody and any additional desired ingredient from a previously sterile-filtered solution thereof. The proper fluidity of a solution can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and/or by the use of surfactants. Prolonged absorption of injectable compositions can be brought about by including in the composition an agent that delays absorption, for example, monostearate salts and gelatin.

[0127] The pharmaceutical compositions may be administered by a variety of methods known in the art. In some embodiments, the preferred route/mode of administration is subcutaneous, intramuscular, or intravenous infusion. In some embodiments, the mode of administration is intravitreal. As will be appreciated by the skilled artisan, the route and/or mode of administration will vary depending upon the desired results.

[0128] In some embodiments, the pharmaceutical compositions may be prepared with a carrier that will protect the antibody against rapid release, such as a controlled release formulation, including implants, transdermal patches, and microencapsulated delivery systems. Biodegradable, biocompatible polymers, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid, may be used. Methods for the preparation of such formulations are generally known to those skilled in the art. See, *e.g.*, Sustained and Controlled Release Drug Delivery Systems J. R. Robinson, ed., Marcel Dekker, Inc., New York, 1978, which is incorporated herein by reference.

[0129] Additional active compounds also can be incorporated into the compositions. In certain embodiments, an anti-CD154 antibody disclosed herein is co-formulated with and/or co-administered with one or more additional therapeutic agents. These agents include, without

limitation, antibodies that bind other targets, anti-thrombotic drugs, anti-platelet drugs, non-steroidal anti-inflammatory drugs (NSAIDs) and anti-allergy drugs. Such combination therapies may require lower dosages of the anti-CD154 antibody as well as the co-administered agents, thus avoiding possible toxicities or complications associated with the various
5 monotherapies.

[0130] Dosage regimens may be adjusted to provide the optimum desired response (*e.g.*, a therapeutic or prophylactic response). For example, a single bolus can be administered, several divided doses can be administered over time or the dose can be proportionally reduced or increased as indicated by the exigencies of the therapeutic situation. It may be advantageous
10 to formulate parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. The term “dosage unit form” as used herein refers to physically discrete units suited as unitary dosages for the mammalian subjects to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage
15 unit forms may be dictated by and directly dependent on (a) the unique characteristics of the anti-CD154 antibody and the particular therapeutic or prophylactic effect to be achieved, and (b) the limitations inherent in the art of compounding such an antibody for the treatment of sensitivity in individuals.

[0131] An exemplary, non-limiting range for a therapeutically or prophylactically effective
20 amount of an antibody disclosed herein is 5 to 50 mg/kg. The therapeutically or prophylactically effective amount of an antibody disclosed herein may be about 5 to about 50 mg/kg. In some embodiments, a therapeutically or prophylactically effective amount of an antibody disclosed herein is 5 to 30 mg/kg. The therapeutically or prophylactically effective amount of an antibody disclosed herein may be about 5 to about 30 mg/kg. Optionally, the
25 therapeutically or prophylactically effective amount of an antibody disclosed herein is 5 mg/kg, 10 mg/kg, 15 mg/kg, 20 mg/kg, 25 mg/kg, 30 mg/kg, 35 mg/kg, 40 mg/kg, 45 mg/kg or 50 mg/kg. In some embodiments, the therapeutically or prophylactically effective amount of an antibody disclosed herein is about 5 mg/kg, about 10 mg/kg, about 15 mg/kg, about 20 mg/kg, about 25 mg/kg, about 30 mg/kg, about 35 mg/kg, about 40 mg/kg, about 45 mg/kg or about
30 50 mg/kg. Dosage values may vary with the type and severity of the condition to be alleviated. For any particular subject, specific dosage regimens may be adjusted over time according to

the individual need and the professional judgment of the person administering or supervising the administration of the compositions, and that dosage ranges set forth herein are exemplary only and are not intended to limit the scope or practice of the paragraphed composition.

Methods of Inducing Tolerance

5 [0132] A first aspect of the present disclosure provides a method of inducing tolerance in a transplant recipient. In some embodiments, the method comprises administering to the recipient an anti-CD154 antibody disclosed herein, transplanting into the recipient hematopoietic stem cells, and transplanting a donor organ, donor tissue, or donor cell into the recipient, wherein the transplanted hematopoietic stem cells produce immune cells that are
10 tolerant of the donor organ, donor tissue or donor cell, thereby inducing tolerance in the recipient. Optionally, a therapeutically effective amount of the anti-CD154 antibody is administered. In some embodiments, the anti-CD154 is administered in a pharmaceutical composition disclosed herein. The anti-CD154 antibody may be administered simultaneously with the transplantation of the hematopoietic stem cells. In some embodiments, the anti-CD154
15 antibody is administered sequentially with the transplantation of the hematopoietic stem cells. Optionally, the anti-CD154 antibody is administered prior to the transplantation of the hematopoietic stem cells. The anti-CD154 antibody may be administered subsequent to the transplantation of the hematopoietic stem cells. In some embodiments, the hematopoietic stem cells are transplanted by a bone marrow transplant. In some embodiments, the anti-CD154 is
20 administered in a single dose. Optionally, the anti-CD154 antibody is administered in multiple doses. In some embodiments, one of the multiple doses is simultaneous with the transplantation of hematopoietic stem cells and the other doses are administered prior and/or subsequent to the transplantation of hematopoietic stem cells. Optionally, one of the multiple doses is simultaneous with the transplantation of hematopoietic stem cells and the other doses
25 are administered prior to the transplantation of hematopoietic stem cells. In some embodiments, one of the multiple doses is simultaneous with the transplantation of hematopoietic stem cells and the other doses are administered subsequent to the transplantation of hematopoietic stem cells. In some embodiments, one of the multiple doses is simultaneous with the transplantation of hematopoietic stem cells and the other doses are administered prior
30 and subsequent to the transplantation of hematopoietic stem cells.

[0133] In some embodiments, the immune tolerance is central tolerance. In some
embodiments, the method further comprises depleting T cells in the thymus. Optionally, the
method of inducing immune tolerance further comprises depleting T cells in the bone marrow.
In some embodiments, the method of inducing immune tolerance further comprises depleting
5 T cells in both the thymus and bone marrow.

[0134] In some embodiments, the immune tolerance is peripheral tolerance. In some
embodiments, the method further comprises depleting T cells in the lymph nodes. Optionally,
the method further comprises depleting T cells in peripheral tissue. In some embodiments, the
method further comprises depleting T cells in both lymph nodes and peripheral tissue.

10 [0135] In some embodiments, the method of inducing immune tolerance is organ-specific
tolerance. In some embodiments, the method further comprises depleting T cells from the
heart, a kidney, both kidneys, the liver, a partial liver, a lung, both lungs, the pancreas, the
intestines, islet cells, the face, one hand, both hands, one arm, both arm, one foot, both feet,
one leg, both legs, or the skin or a combination thereof. In some embodiments, the method
15 further comprises depleting T cells the heart. In some embodiments, the method further
comprises depleting T cells from a kidney. In some embodiments, the method further
comprises depleting T cells from both kidneys. In some embodiments, the method further
comprises depleting T cells from a liver. In some embodiments, the method further comprises
depleting T cells from a partial liver. In some embodiments, the method further comprises
20 depleting T cells from a lung. In some embodiments, the method further comprises depleting
T cells from both lungs. In some embodiments, the method further comprises depleting T cells
from a pancreas. In some embodiments, the method further comprises depleting T cells from
the intestines. In some embodiments, the method further comprises depleting T cells from islet
cells. In some embodiments, the method further comprises depleting T cells from the face. In
25 some embodiments, the method further comprises depleting T cells from one hand. In some
embodiments, the method further comprises depleting T cells from both hands. In some
embodiments, the method further comprises depleting T cells from one arm. In some
embodiments, the method further comprises depleting T cells from both arms. In some
embodiments, the method further comprises depleting T cells from one foot. In some
30 embodiments, the method further comprises depleting T cells from both feet. In some
embodiments, the method further comprises depleting T cells from one leg. In some

embodiments, the method further comprises depleting T cells from both legs. In some embodiments, the method further comprises depleting T cells from the skin.

[0136] In some embodiments, the method further comprises a treatment regimen to condition the recipient for hematopoietic stem cell transplantation. In some embodiments, the method further comprises more than one treatment regimen to condition the recipient for hematopoietic stem cell transplantation. In some embodiments, the method to condition the recipient for hematopoietic stem cell transplantation selected from a group consisting of total body irradiation, administration of abatacept, administration of one or more BCL-2 inhibitors, administration of busulfan, administration of fludarabine phosphate, administration of cyclophosphamide, administration of one or more immunosuppressive T cell-depleting antibodies, administration of one or more anti- $\alpha\beta$ T cell receptor antibodies, and administration of one or more CD122 antagonists or a combination thereof.

[0137] In some embodiments, the T cells are depleted by a method selected from a group consisting of total body irradiation, administration of abatacept, administration of one or more BCL-2 inhibitors, administration of busulfan, administration of fludarabine phosphate, administration of cyclophosphamide, administration of one or more immunosuppressive T cell-depleting antibodies, administration of one or more anti- $\alpha\beta$ T cell receptor antibodies, and administration of one or more CD122 antagonists or a combination thereof. In some embodiments, the T cells are depleted by total body irradiation. In some embodiments, the T cells are depleted by administration of abatacept. In some embodiments, the T cells are depleted by administration of a BCL-2 inhibitor. In some embodiments, the T cells are depleted by administration of more than one BCL-2 inhibitor. In some embodiments, the T cells are depleted by administration of busulfan. In some embodiments, the T cells are depleted by administration of fludarabine phosphate. In some embodiments, the T cells are depleted by administration of cyclophosphamide. In some embodiments, the T cells are depleted by administration of a T cell-depleting antibody. In some embodiments, T cells are depleted by administration of more than one T cell-depleting antibody. In some embodiments, the T cells are depleted by administration of an anti- $\alpha\beta$ T cell receptor antibody. In some embodiments, the T cells are depleted by administration of more than one anti- $\alpha\beta$ T cell receptor antibody. In some embodiments, the T cells are depleted by administration of a CD122 antagonist. In some embodiments, the T cells are depleted by administration of more than one CD122 antagonist.

[0138] In some embodiments, the one or more T cell-depleting antibodies are selected from the group consisting of anti-CD4, anti-CD8, anti-CD45, anti-CTLA4, anti-CD20, and anti-CD33 antibodies or a combination thereof.

[0139] In some embodiments, the method of inducing immune tolerance results in mixed allogeneic chimerism. Optionally, the method of inducing immune tolerance results in mixed chimerism.

[0140] In some embodiments, the anti-CD154 antibody is administered prior to transplantation of the hematopoietic stem cells. Optionally, the anti-CD154 antibody is administered subsequently to transplantation of the hematopoietic stem cells. In some embodiments, the anti-CD154 antibody is administered simultaneously with the transplantation of the hematopoietic stem cells. In some embodiments, the hematopoietic stem cells are transplanted by a bone marrow transplant. In some embodiments, the anti-CD154 is administered in a single dose. Optionally, the anti-CD154 antibody is administered in multiple doses. In some embodiments, one of the multiple doses is simultaneous with the transplantation of hematopoietic stem cells and the other doses are administered prior and/or subsequent to the transplantation of hematopoietic stem cells. Optionally, one of the multiple doses is simultaneous with the transplantation of hematopoietic stem cells and the other doses are administered prior to the transplantation of hematopoietic stem cells. In some embodiments, one of the multiple doses is simultaneous with the transplantation of hematopoietic stem cells and the other doses are administered subsequent to the transplantation of hematopoietic stem cells. In some embodiments, one of the multiple doses is simultaneous with the transplantation of hematopoietic stem cells and the other doses are administered prior and subsequent to the transplantation of hematopoietic stem cells.

[0141] In some embodiments, the anti-CD154 antibody is administered at a dose of 5-50 mg/kg. In some embodiments, the anti-CD154 antibody is administered at a dose of 10-40 mg/kg. In some embodiments, the anti-CD154 antibody is administered at a dose of 20-30 mg/kg.

[0142] In some embodiments, the anti-CD154 antibody is administered subcutaneously, intravenously, intravitreally, orally, via inhalation, transdermally, or rectally. In some embodiments, the anti-CD154 antibody is administered subcutaneously. In some embodiments, the anti-CD154 antibody is administered intravenously. In some embodiments, the anti-CD154

antibody is administered intravitreally. In some embodiments, the anti-CD154 antibody is administered orally. In some embodiments, the anti-CD154 antibody is administered via inhalation. In some embodiments, the anti-CD154 antibody is administered transdermally. In some embodiments, the anti-CD154 antibody is administered rectally.

5 [0143] Any of the antibodies disclosed herein may be used in the methods of inducing tolerance. In some embodiments, the anti-CD154 antibody is a human, chimeric or humanized antibody. In some embodiments, the anti-CD154 antibody is a human antibody. In some embodiments, the anti-CD154 antibody is a chimeric antibody. In some embodiments, the anti-CD154 antibody is a humanized antibody.

10 [0144] Optionally, the transplant recipient is a human. In some embodiments, the transplant recipient is non-human. The transplant recipient may be a non-human primate, such as a monkey. Optionally, the anti-CD154 antibody is human antibody, and the transplant recipient is human. In some embodiments, the anti-CD154 antibody is a humanized antibody, and the transplant recipient is human. Alternatively, the transplant recipient may be a mammal (*e.g.*, a
15 monkey) that expresses CD154 that the anti-CD154 antibody cross-reacts with. The antibody may be administered to a non-human mammal expressing CD154 with which the antibody cross-reacts (*e.g.*, a cynomolgus monkey) for veterinary purposes or as an animal model of human transplantation or disease. Such animal models may be useful for evaluating the therapeutic efficacy of antibodies disclosed herein.

20 [0145] The antibody may be administered once. Optionally, the antibody is administered multiple times. The antibody may be administered from three times daily to once every six months or longer. The administering may be on a schedule such as three times daily, twice daily, once daily, once every two days, once every three days, once weekly, once every two weeks, once every month, once every two months, once every three months, once every six
25 months, twice weekly, three times weekly, four times weekly, twice every two weeks, three times every two weeks and four times every two weeks. The antibody may also be administered continuously via a minipump. The antibody may be administered via a mucosal, buccal, intranasal, inhalable, intravenous, intravitreal, subcutaneous, intramuscular, parenteral, or intratumor route. In some embodiments, the anti-CD154 antibody is administered
30 systemically, such as subcutaneously, intravenously, orally, via inhalation, transdermally, or rectally. Optionally, the anti-CD154 antibody is administered locally. In some embodiments,

the anti-CD154 antibody is administered intravitreally. The antibody may be administered once, at least twice or for at least the period of time until the condition is treated, palliated or cured. The antibody generally will be administered for as long as the condition is present. The antibody will generally be administered as part of a pharmaceutical composition as described
5 *supra*. The dosage of antibody will generally be in the range of 5 to 50 mg/kg. The dosage of antibody may be about 5 to about 50 mg/kg. In some embodiments, dosage of antibody is 5 to 30 mg/kg. The dosage of antibody may be about 5 to about 30 mg/kg. Optionally, the dosage of antibody is 5 mg/kg, 10 mg/kg, 15 mg/kg, 20 mg/kg, 25 mg/kg, 30 mg/kg, 35 mg/kg, 40 mg/kg, 45 mg/kg or 50 mg/kg. In some embodiments, the dosage of antibody is about 5 mg/kg,
10 about 10 mg/kg, about 15 mg/kg, about 20 mg/kg, about 25 mg/kg, about 30 mg/kg, about 35 mg/kg, about 40 mg/kg, about 45 mg/kg or about 50 mg/kg.

[0146] In some embodiments, an anti-CD154 antibody disclosed herein is administered to a subject who expresses inappropriately high levels of CD154. The transplant may be an allogeneic transplant, autologous transplant or a xenogeneic transplant of a donor cell, tissue,
15 or organ. In some embodiments, the transplant is an allogeneic transplant. Optionally, the transplant is an autologous transplant. In some embodiments, the transplant is a xenogeneic transplant.

[0147] The donor cell may be an engineered cell or an ex-vivo expanded cell. For example, the donor cell may be modified using one or more techniques such as transduction to express
20 a cDNA, a CRISPR/Cas9 system, RNAi technology and retroviral technology. Optionally, the donor cell is modified to express a chimeric antigen receptor (CAR) on its surface. Examples of cells that may be transplanted include, but are not limited to, a stem cell, a regulatory T (Treg) cell, a CAR-T cell, a CAR-B cell, and a tumor-infiltrating lymphocyte (TIL). In some embodiments, the donor cell is a stem cell. In some embodiments, the donor cell is a regulatory
25 T (Treg) cell. In some embodiments, the donor cell is a CAR-T cell. In some embodiments, the donor cell is a CAR-B cell. In some embodiments, the donor cell is a tumor-infiltrating lymphocyte (TIL).

[0148] The induction of tolerance by any of the methods disclosed herein may prevent a transplant rejection in the subject. For example, the induction of tolerance may prevent an
30 acute or a chronic humoral rejection of a grafted cell, tissue, or organ. The rejection may be

an acute or chronic graft rejection in a graft recipient of an allogeneic transplant or xenotransplant. The methods disclosed herein may promote a long-term graft survival of the grafted cell, tissue, or organ. Optionally, the long-term graft survival is at least 6 months post-transplant, at least 1-year post-transplant or at least 5 years post-transplant. In some
5 embodiments, the long-term graft survival is at least 6 months post-transplant. In some embodiments, the long-term graft survival is at least 1-year post-transplant. In some embodiments, the long-term graft survival is at least 5 years post-transplant.

[0149] The transplant rejection may be associated with the transplantation of hematopoietic cell or bone marrow, an allogeneic transplant of pancreatic islet cells, graft vs host disease, or
10 a solid organ transplant selected from the group consisting of a heart transplant, a kidney transplant, a liver transplant, a lung transplant, a pancreas transplant, a kidney-pancreas transplant, a heart-lung transplant, kidney-heart transplant, a kidney-heart-pancreas transplant, a heart-liver transplant, a heart-liver-kidney transplant, a heart-lung-kidney transplant, a heart-lung-liver transplant, a lung-kidney transplant, a lung-liver transplant, a liver-intestines-
15 pancreas transplant, an intestines-pancreas transplant, a liver-kidney-intestines-pancreas transplant, and a kidney-intestines transplant.

[0150] In some embodiments, the method comprises administering to said transplant recipient a therapeutically effective amount of an anti-CD154 antibody disclosed herein in combination with one or more additional agents. Optionally, the one or more additional agents is selected
20 from the group consisting of anti-thrombotic drugs, anti-platelet drugs and non-steroidal anti-inflammatory drugs (NSAIDs). The anti-CD154 antibody may be administered simultaneously with the one or more additional agents. In some embodiments, the anti-CD154 antibody is administered sequentially with the one or more additional agents. Optionally, the anti-CD154 antibody is administered prior to the one or more additional agents. The anti-CD154 antibody
25 may be administered subsequent to the one or more additional agents. In some embodiments, the anti-CD154 antibody is administered in the same composition as the one or more additional agents. Optionally, the anti-CD154 antibody and the one or more additional agents are administered in separate compositions.

[0151] Examples of anti-thrombotic drugs include but are not limited to a glycoprotein IIb/IIIa
30 receptor antagonist, a direct or indirect factor Xa inhibitor and an anticoagulant. Examples of

anticoagulants include, but are not limited to, heparin, warfarin, rivaroxaban (XARELTO®), ximelgatran (EXANTA®), dabigatran (PRADAXA®), apixaban (ELIQUIS®), edoxaban (SAVAYSA®), enoxaparin (LOVENOX®), and fondaparinux (ARIXTRA®). Examples of anti-thrombotic drugs include, but are not limited to, those disclosed in US Patent Nos.

5 4,782,069; 5,332,822; 5,492,895; 5,612,363; 5,691,364; 5,693,641; 5,721,214; 5,726,173; 5,753,635; 5,846,970; 5,849,759; 5,889,005; 6,107,280; 6,140,351; 6,150,329; 6,180,627; 6,200,976; 6,242,432; 6,248,770; 6,271,215; 6,280,731; 6,287,794; 6,300,330; 6,300,342; 6,333,338; 6,395,731; 6,417,203; 6,432,955; 6,444,672; 6,451,832; 6,458,793; 6,486,129; 6,500,803; 6,583,173; 6,599,881; 6,723,723; 6,730,672; 6,753,331; 6,774,110; 6,797,710; and

10 6,924,296, incorporated in their entirety for all purposes. Examples of glycoprotein IIb/IIIa receptor antagonists include, but are not limited to, abciximab (REOPRO®), rivaroxaban (XARELTO®), apixaban (ELIQUIS®), edoxaban (SAVAYSA®), idrabiotaparinux, tirofiban (AGGRASTAT®), and eptifibatide (INTEGRILIN®). The direct or indirect factor Xa inhibitors include, but are not limited to, apixaban (ELIQUIS®), idrabiotaparinux,

15 fondaparinux (ARIXTRA®), and rivaroxaban (XARELTO®).

[0152] Examples of anti-platelet drugs include, but are not limited to, TXA2 pathway inhibitors, the adenosine diphosphate (ADP) pathway inhibitors, thrombin inhibitors, Protease activated receptor-1 (PAR-1) inhibitors and phosphodiesterase (PDE) inhibitors. Examples of ADP pathway inhibitors include, but are not limited, to clopidogrel (PLAVIX®), ticlopidine

20 (TICLID®), prasugrel (EFFIENT®), ticagrelor (BRILINTA®), cangrelor (KENGREAL®) and elinogrel. Non-limiting examples of PDE inhibitors include dipyridamole (PERSANTINE®) and cilostazol (PLETAL®).

[0153] Examples of NSAIDs include, but are not limited to, acetylsalicylic acid, celecoxib (CELEBREX®), diclofenac (VOLTAREN®, PENNSAID®, SOLARAZE®, ZIPSOR®,

25 CATAFLAM®, ZORVOLEX®), diflunisal (DOLOBID®), etodolac (LODINE SR®, ECCOXOLAC®), ibuprofen (BRUFEN®, ADVIL®, MOTRIN®), indomethacin (INDOCIN®), ketoprofen (ORUDIS®), ketorolac (TORADOL®, ACULAR®, SPRIX®), nabumetone (RELAFEN®), naproxen (AFLAXEN®, ALEVE®, ANAPROX®, NAPRELAN®), oxaprozin (DAYPRO®, DAYRUN®, DURAPROX®), piroxicam

30 (FELDENE®), salsalate (MONO-GESIC®, SALFLEX®, DISALCID®, SALSITAB®),

sulindac (CLINORIL®), tolmetin (TOLECTIN®), prasugrel (EFFIENT®), ticagrelor (BRILINTA®) and cangrelor (KENGREAL®).

[0154] In some embodiments, the anti-CD154 antibody may be administered in combination with one or more supplemental agents including but not limited to immunosuppressive drugs, immunomodulatory drugs, and monoclonal and/or polyclonal antibodies. The anti-CD154 antibody may be administered simultaneously with the one or more supplemental agents. In some embodiments, the anti-CD154 antibody is administered sequentially with the one or more supplemental agents. Optionally, the anti-CD154 antibody is administered prior to the one or more supplemental agents. The anti-CD154 antibody may be administered subsequent to the one or more supplemental agents. In some embodiments, the anti-CD154 antibody is administered in the same composition as the one or more supplemental agents. Optionally, the anti-CD154 antibody and the one or more supplemental agents are administered in separate compositions. Examples of such one or more supplemental agents include, but not limited to, anti-CD2 antibodies, anti-CD3 antibodies, anti-CD4 antibodies, anti-CD28 antibodies, anti-CD52 antibodies, anti-C5 antibodies, mTOR inhibitors, calcineurin inhibitors, antiviral drugs, and fusion peptides that bind to and block the function of CD28. Non-limiting examples of fusion peptides that bind to and block the function of CD28 include abatacept and belatacept (NULOJIX®). For example, the anti-CD52 antibody may be alemtuzumab (CAMPATH®). Optionally, the anti-C5 antibody is eculizumab (SOLIRIS®).

[0155] Non-limiting examples of immunosuppressive drug or immunomodulatory drugs include cyclosporine A, tacrolimus (FK-506), doxorubicin (ADRIAMYCIN®), azathioprine (IMURAN®), busulfan (BUSULFEX®), cyclophosphamide (CYTOXAN®), fludarabine, 5-fluorouracil, methotrexate (OTREXUP®, RASUVO®, RHEUMATREX®, TREXALL™), mycophenolate mofetil (CELLCEPT®), mizoribine (BREDININ™), leflunomide, a nonsteroidal anti-inflammatory, adrenocortical steroids, rapamycin (RAPAMUNE®), deoxyspergualin, FTY720, muromonab-CD3 (ORTHOCLONE OKT3®), alemtuzumab (CAMPATH®, MABCAMPATH®, CAMPATH-1H®, LEMTRADA®), basiliximab (SIMULECT®), daclizumab (ZINBRYTA®), eculizumab (SOLIRIS®), rituximab (RITUXAN®, MABTHERA®), bortezomib (VELCADE®, CHEMOBORT®, BORTECAD®), sipilizumab, anti-thymocyte globulin (THYMOGLOBULIN®, ATGAM®), leronlimab, siltuximab (SYLVANT®), sarilumab (KEVZARA®), tocilizumab

(ACTEMRA®), bevacizumab (AVASTIN®), ranibizumab (LUCENTIS®), aflibercept (EYLEA®) and inhibitors of Bruton's tyrosine kinase (BTK), including zanubrutinib (BRUKINSA®), acalabrutinib (CALQUENCE®) and ibrutinib (IMBRUVICA®).

[0156] Examples of mTOR inhibitors include, but are not limited to, rapamycin (Rapamune®), everolimus (AFINITOR®), temsirolimus (TORISEL®), ridaforolimus, and deforolimus. Examples of calcineurin inhibitors include, but are not limited to, cyclosporine (NEORAL®, SANDIMMUNE®, GENGRAF®, RESTASIS®), tacrolimus (FK506, ENVARSUS®, HECORIA®, PROGRAF®, PROTOPIC®, ASTRAGRAF®), and pimecrolimus (ELIDEL®).

10 EXAMPLES

[0157] The following examples are offered for illustrative purposes only and do not limit the scope of the present disclosure or paragraphs in any way. Indeed, various modifications of the disclosure in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the paragraphs.

15 Example 1. Induction of Tolerance

[0158] To determine efficacy of anti-CD154 to induce tolerance, heterotopic kidney allotransplant experiments are performed on cynomolgus monkeys according to the regimen described in Figure 1. Briefly, transplant recipients are conditioned for transplant by total body irradiation of 1.5 Gy twice (6 days and 5 days before transplantation), thymic irradiation of 7 Gy one day before transplantation and administration of 50 mg/kg/day anti T-cell antibody [horse anti-thymocyte globulin (Atgam)] thrice (2 days before, one day before and the day of transplantation). On Day 0, the transplant recipients receive a kidney transplant and a bone marrow (containing hematopoietic stem cells) transplant. Transplant recipients are given an initial dose of 20 mg/kg anti-CD154 monoclonal antibody (mAb) (e.g., TNX02, TNX05, TNX06, etc.) within 24 hours of transplantation. Subsequent doses of the anti-CD154 antibody (20mg/kg) are then given at post operation day (POD) 3, 7, 14, 21, 28, 42, 56, 70, and 84 and monthly thereafter until POD 180 or graft rejection. Full necropsies are performed at POD 180 or at the time of graft failure to determine level of thromboembolism in all animals.

[0159] Kidney allograft survival is regularly monitored by urine volume, blood chemistry measurements (twice a week) and ultrasound examination of the kidney graft. Kidney biopsies

are performed at regularly scheduled intervals following transplant, *e.g.*, POD 42 and 84. Transplant recipients demonstrating elevation of serum creatinine by more than 50% of the baseline or change in the renal blood flow are further biopsied to evaluate health of the grafted tissue. Any animal with creatinine levels greater than 6mg/dl is considered graft rejection and results in graft explantation and necropsy. Histology is performed on hearts of all animals at time of graft rejection or POD 180 (whichever occurred first). Any incidence of thrombosis in the renal allograft or other sites is measured and analyzed to determine the level of rejection and inversely the immune tolerance exhibited by the recipient.

[0160] The immune response of the transplant recipient is continuously measured and monitored. Baseline serum and peripheral blood lymphocyte are archived. Then, post-operative serum and peripheral blood lymphocyte are collected to determine T-cell phenotype analyzed by Fluorescence Activated Cell Sorting (FACS) for markers such as CD3, CD4, CD8, CD25, CD45, CD127, and FoxP3. Blood is also drawn for serum and immune cells collected on POD 7, 14, 21, 30, 60, 90 and monthly until graft rejection or the experimental endpoint POD 180.

Table 1. Sequences of humanized anti-CD154 antibodies.

SEQ ID	Description	Sequences
Fc (CH2-CH3) WITH AND WITHOUT TERMINAL LYSINE AND WITH/WITHOUT HINGE		
Fc domain, no terminal lysine		
1	TNX01 IgG1 Fc (N297Q)	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS VMHEALHNHYTQKSLSLSPG
2	TNX02 IgG1 Fc (wildtype)	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS VMHEALHNHYTQKSLSLSPG
3	TNX03 IgG1 Fc (N297G)	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS VMHEALHNHYTQKSLSLSPG

4	TNX04 TNX11 TNX12 TNX13 IgG1 Fc (P238S)	APELLGGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPG
5	TNX05 TNX14 IgG4 Fc (L235A)	APEFAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYV DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGL PSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCS VMHEALHNHYTQKSLSLSPG
6	TNX10 IgG1 Fc (L234A, L235A)	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPG
7	IgG1 Fc (P238S, N297Q)	APELLGGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPG
8	TNX06 Wildtype IgG4 Fc	APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYV DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGL PSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCS VMHEALHNHYTQKSLSLSPG
9	Wildtype IgG2 Fc	APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVD GMEVHNAKTKPREEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLP APIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPG
237	TNX07 IgG4 Fc (S228P)	APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYV DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGL PSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCS VMHEALHNHYTQKSLSLSPG
238	TNX08 IgG4 Fc (L235E)	APEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYV DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGL PSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCS VMHEALHNHYTQKSLSLSPG
239	TNX09 IgG4 Fc (F234A, L235A)	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYV DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGL PSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCS VMHEALHNHYTQKSLSLSPG

Fc domain +terminal lysine		
10	TNX01 IgG1 Fc (N297Q)	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS VMHEALHNHYTQKSLSLSPGK
11	TNX02 IgG1 Fc (wildtype)	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS VMHEALHNHYTQKSLSLSPGK
12	TNX03 IgG1 Fc (N297G)	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS VMHEALHNHYTQKSLSLSPGK
13	TNX04 TNX11 TNX12 TNX13 IgG1 Fc (P238S)	APELLGGSSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS VMHEALHNHYTQKSLSLSPGK
14	TNX05 TNX14 IgG4 Fc (L235A)	APEFAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYV DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGL PSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQQGNVFCSS VMHEALHNHYTQKSLSLSPGK
15	TNX10 IgG1 Fc (L234A, L235A)	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS VMHEALHNHYTQKSLSLSPGK
16	IgG1 Fc (P238S, N297Q)	APELLGGSSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS VMHEALHNHYTQKSLSLSPGK
17	TNX06 Wildtype IgG4 Fc	APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYV DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGL PSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQQGNVFCSS VMHEALHNHYTQKSLSLSPGK
18	Wildtype IgG2 Fc	APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVD GMEVHNAKTKPREEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLP APIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPMLDSDGSFFLYSKLTVDKSRWQQGNVFCSSV MHEALHNHYTQKSLSLSPGK

240	TNX08 IgG4 Fc (L235E)	APEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVTLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPG
241	TNX09 IgG4 Fc (F234A, L235A)	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVTLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPG
Fc region, no terminal lysine		
19	TNX01 IgG1 <u>hinge</u> -Fc (N297Q)	<u>EPKSCDKTHTCPPCP</u> APPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVTLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
20	TNX02 IgG1 <u>hinge</u> -Fc (wildtype)	<u>EPKSCDKTHTCPPCP</u> APPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVTLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
21	TNX03 IgG1 <u>hinge</u> -Fc (N297G)	<u>EPKSCDKTHTCPPCP</u> APPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGSTYRVVSVLTVTLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
22	TNX04 IgG1 <u>hinge</u> -Fc (C220S, C226S, C229S, P238S)	<u>EPKSSDKTHTSPSPS</u> APPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVTLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
23	TNX05 TNX14 <u>hinge</u> -Fc IgG4 (S228P, L235A)	<u>ESKYGPPCPPCP</u> APPEFAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVTLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPG
24	TNX10 IgG1 <u>hinge</u> -Fc (L234A, L235A)	<u>EPKSCDKTHTCPPCP</u> APPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVTLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
25	IgG1 <u>hinge</u> -Fc (P238S)	<u>EPKSCDKTHTCPPCP</u> APPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVTLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

26	IgG1 <u>hinge</u> -Fc (P238S, N297Q)	<u>EPKSCDKTHTCP</u> PCPAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG
27	TNX06 Wildtype <u>hinge</u> -IgG4 Fc	<u>ESKYGPPCP</u> SCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFCFSVMHEALHNHYTQKSLSLSPG
28	Wildtype <u>hinge</u> -IgG2 Fc	<u>ERKCCVECP</u> PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGMEVHNAKTKPREEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG
29	IgG1 <u>hinge</u> -Fc (C220S, C226S, C229S, P238S, N297Q)	<u>EPKSSDKTHTSPP</u> SPAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG
30	IgG1 <u>hinge</u> -Fc (C220S, C226S, C229S)	<u>EPKSSDKTHTSPP</u> SPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG
31	IgG1 <u>hinge</u> -Fc (C220S, N297Q)	<u>EPKSSDKTHTCP</u> PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG
32	IgG1 <u>short-hinge</u> -Fc (C226S, C229S, P238S)	<u>THTSPP</u> SPAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG
33	IgG1 <u>short-hinge</u> -Fc (C226S, C229S)	<u>THTSPP</u> SPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG
34	IgG1 <u>short-hinge</u> -Fc (C226S, C229S, P238S, N297Q)	<u>THTSPP</u> SPAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG

35	IgG1 <u>short-hinge</u> -Fc (C226S, C229S, N297Q)	<u>THTSPSP</u> PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMEALHNHYTQKSLSLSPG
36	IgG1 <u>short-hinge</u> -Fc (N297Q)	<u>THTCPPC</u> PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMEALHNHYTQKSLSLSPG
37	TNX11 IgG1 <u>hinge</u> -Fc (C226S, C229S, P238S)	<u>EPKSCDKTHTSPSP</u> PAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ VSLTCLVKGFYPSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPG
242	TNX07 IgG4 <u>hinge</u> -Fc (S228P)	<u>ESKYGPPCPPC</u> PAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSL TCLVKGFYPSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDK SRWQEGNVFSCSVMEALHNHYTQKSLSLSLG
243	TNX08 IgG4 <u>hinge</u> -Fc (L235E)	<u>ESKYGPPCPPC</u> PAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSL TCLVKGFYPSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDK SRWQEGNVFSCSVMEALHNHYTQKSLSLSLG
244	TNX09 IgG4 <u>hinge</u> - Fc (F234A, L235A)	<u>ESKYGPPCPPC</u> PAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSL TCLVKGFYPSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDK SRWQEGNVFSCSVMEALHNHYTQKSLSLSLG
245	TNX12 IgG1 <u>hinge</u> -Fc (C229S, P238S)	<u>EPKSCDKTHTCPPS</u> PAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ VSLTCLVKGFYPSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPG
246	TNX13 IgG1 <u>hinge</u> -Fc (C226S, P238S)	<u>EPKSCDKTHTSPPC</u> PAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ VSLTCLVKGFYPSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPG
Fc region + terminal lysine		
38	TNX01 IgG1 <u>hinge</u> -Fc (N297Q)	<u>EPKSCDKTHTCPPC</u> PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ VSLTCLVKGFYPSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK

39	TNX02 IgG1 <u>hinge</u> -Fc (wildtype)	<u>EPKSCDKTHTCPPCP</u> APPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVHLQDWNLGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
40	TNX03 IgG1 <u>hinge</u> -Fc (N297G)	<u>EPKSCDKTHTCPPCP</u> APPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGSTYRVVSVLTVHLQDWNLGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
41	TNX04 IgG1 <u>hinge</u> -Fc (C220S, C226S, C229S, P238S)	<u>EPKSCDKTHTSPSP</u> APPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVHLQDWNLGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
42	TNX05 <u>hinge</u> - Fc IgG4 (S228P, L235A)	<u>ESKYGPPCP</u> CPAPEFAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVHLQDWNLGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLSLGK
43	TNX10 IgG1 <u>hinge</u> -Fc (L234A, L235A)	<u>EPKSCDKTHTCPPCP</u> APAEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVHLQDWNLGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
44	IgG1 <u>hinge</u> -Fc (P238S)	<u>EPKSCDKTHTCPPCP</u> APPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVHLQDWNLGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
45	IgG1 <u>hinge</u> -Fc (P238S, N297Q)	<u>EPKSCDKTHTCPPCP</u> APPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVHLQDWNLGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
46	TNX06 Wildtype <u>hinge</u> -IgG4 Fc	ESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVHLQDWNLGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLSLGK
47	Wildtype <u>hinge</u> -IgG2 Fc	<u>ERKCCVECP</u> CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGMEVHNAKTKPREEQFNSTFRVSVLTVVHQLDNLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK

48	IgG1 <u>hinge</u> -Fc (C220S, C226S, C229S, P238S, N297Q)	<u>EPKSSDKTHTSPSP</u> PAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
49	IgG1 <u>hinge</u> -Fc (C220S, C226S, C229S)	<u>EPKSSDKTHTSPSP</u> PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
50	IgG1 <u>hinge</u> -Fc (C220S, N297Q)	<u>EPKSSDKTHTCP</u> PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
51	IgG1 <u>short-hinge</u> -Fc (C226S, C229S, P238S)	<u>THTSPSP</u> PAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
52	IgG1 <u>short-hinge</u> -Fc (C226S, C229S)	<u>THTSPSP</u> PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
53	IgG1 <u>short-hinge</u> -Fc (C226S, C229S, P238S, N297Q)	<u>THTSPSP</u> PAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
54	IgG1 <u>short-hinge</u> -Fc (C226S, C229S, N297Q)	<u>THTSPSP</u> PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
55	IgG1 <u>short-hinge</u> -Fc (N297Q)	<u>THTCP</u> PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
56	TNX11 IgG1 <u>hinge</u> -Fc (C226S, C229S, P238S)	<u>EPKSCDKTHTSPSP</u> PAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

247	TNX08 IgG4 <u>hinge</u> -Fc (S228P, L235E)	<u>ESKYGPPCP</u> PCPAPEF <u>EGG</u> PSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVHLQDWLNG KEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDK SRWQEGNVFSCSVMEALHNHYTQKSLSLSPGK
248	TNX09 IgG4 <u>hinge</u> -Fc (S228P, F234A, L235A)	<u>ESKYGPPCP</u> PCPAPEA <u>AGG</u> PSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVHLQDWLNG KEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDK SRWQEGNVFSCSVMEALHNHYTQKSLSLSPGK
249	TNX12 IgG1 <u>hinge</u> -Fc (C229S, P238S)	<u>EPKSCDKTHT</u> CPSPAPPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVHLQDW LNGKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSRDELTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
250	TNX13 IgG1 <u>hinge</u> -Fc (C226S, P238S)	<u>EPKSCDKTHT</u> SPPCAPPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVHLQDW LNGKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSRDELTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
251	TNX14 IgG4 <u>hinge</u> -Fc (L115T, S228P, L235A)	<u>ESKYGPPCP</u> PCPAPEF <u>AGG</u> PSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVHLQDWLNG KEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDK SRWQEGNVFSCSVMEALHNHYTQKSLSLSPGK
Heavy and light chain components (CDRs, VH, VL CH1, CH2, CH3)		
57	CDR H1	SYMY
58	CDR H2	EINPSNGDTNFNEKFKS
59	CDR H3	SDGRNDMDS
60	CDR L1	ISCRASQRVSSSTYSYMH
61	CDR L2	YASNLES
62	CDR L3	QHSWEIPPT
63	VH full (with <u>leader</u>)	<u>MPLLLLLPL</u> WAGALAQVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIG ~~EINPSNGDTNFNEKFKS~~ KATLTVDKSASTAYME LSSLRSEDTAVYYCTR <u>SDGRNDMDS</u> WGQGT <u>L</u> TVTVSS
64	VH full (no leader)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGQGLEWIG EINPSNGDTNFNEKFKS ~~KATLTVDKSASTAYME~~ LSSLRSEDTAVYYCTR <u>SDGRNDMDS</u> WGQGT <u>L</u> TVTVSS
252	VH full (with <u>leader</u>) (L115T)	<u>MPLLLLLPL</u> WAGALAQVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIG ~~EINPSNGDTNFNEKFKS~~ KATLTVDKSASTAYME LSSLRSEDTAVYYCTR <u>SDGRNDMDS</u> WGQGT <u>T</u> TVTVSS

253	VH full (no leader) (L115T)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGT ^T VTVSS
65	VL full (with leader)	<u>MRLPAQLLGLLMLWVSGSGDI</u> VLTSQSPATLSVSPGERATISCRASQRV SSSTYSYMHWYQQKPGQP ^P KLLIKYASNLES ^G VPARFSGSGSGTDFTLT ISSVEPEDFATYYC <u>QHSWEI</u> ^P PTFGGGTKLEIK
66	VL full (no leader)	DIVLTQSPATLSVSPGERATISCRASQRVSSSTYSYMHWYQQKPGQP ^P K LLIKYASNLES ^G VPARFSGSGSGTDFTLTISSVEPEDFATYYC <u>QHSWEI</u> ^P PTFGGGTKLEIK
67	IgG1 CH1 (wildtype) (118-215 EU Numbering)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK ^K V
68	IgG1 CH2 (wildtype) (231-340)	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAK
69	IgG1 CH3 (wildtype) (341-446)	GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTFPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQ KSLSLSPGK
70	IgG2 CH1 (wildtype)	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSNFGTQTYTCNV ^D HKPSNTKVDKTV
71	IgG2 CH2 (wildtype) (231-339 EU)	APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVD GVEVHNAKTKPREEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLP APIEKTISKTK
72	IgG2 CH3 (wildtype) (340-446 EU)	GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDISVEWESNGQPEN NYKTTFPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQ KSLSLSPGK
73	IgG4 CH1 (wildtype)	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGKTYTCNV ^D HKPSNTKVDKRV
74	IgG4 CH2 (wildtype) (231-339 EU)	APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYV DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGL PSSIEKTISKAK
75	IgG4 CH3 (wildtype) (341-447 EU)	GQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTFPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQ KSLSLSL ^G K
HINGES		
76	IgG1 hinge (216-230)	EPKSCDKTHTCPPCP
77	IgG1 hinge (C229S)	EPKSCDKTHTCPPSP
78	IgG1 hinge (C226S)	EPKSCDKTHTSPPCP

79	IgG1 hinge (C220S)	EPKSSDKTHTCPPCP
80	IgG1 hinge (C220S, C229S)	EPKSSDKTHTCPPSP
81	IgG1 hinge (C226S, C229S)	EPKSCDKTHTSPPSP
82	IgG1 hinge (C220S, C226S)	EPKSSDKTHTSPPCP
83	IgG1 hinge-Fc (C220S, C226S, C229S)	EPKSSDKTHTSPPSP
84	IgG1 short- hinge-Fc (C226S, C229S)	THTSPPSP
85	IgG1 short- hinge-Fc	THTCPPCP
86	IgG1 short- hinge-Fc (C226S)	THTSPPCP
87	IgG1 short- hinge-Fc (C229S)	THTCPPSP
88	IgG4 hinge- Fc (S228P)	ESKYGPCCPPCP
89	Wildtype hinge-IgG4 Fc (216-230)	ESKYGPCCPSCP
90	Wildtype hinge-IgG2 Fc (216-230)	ERKCCVECPPCP
Heavy chain constant domains (ASTlinker-CH1-hinge-CH2-CH3) with and without terminal lysine residue		
ASTlinker-CH1-hinge-CH2-CH3 without terminal K		
91	TNX01 CH1- CH2-CH3 IgG1 (N297Q)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTPVSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG

92	TNX02 CH1-CH2-CH3 IgG1 (wt)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG
93	TNX03 CH1-CH2-CH3 IgG1 (N297G)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG
94	TNX04 CH1-CH2-CH3 IgG1 (C220S, C226S, C229S, P238S)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSDKTHSTPPSPAPPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG
95	TNX05 CH1-CH2-CH3 IgG4 (S228P, L235A)	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTI SKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCFSVMHEALHNHYTQKSLSLSLG
96	TNX06 CH1-CH2-CH3 IgG4 Wild Type	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTI SKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCFSVMHEALHNHYTQKSLSLSLG
97	CH1-CH2-CH3 IgG2 Wild Type	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVTSSNFGTQTYTCNVDHKPSNTKVDKTV ERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGMEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG
98	CH1-CH2-CH3 IgG1 (Δ E216-K222 IN HINGE) (C226S, C229S, P238S)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV THTSPSPAPPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG

99	CH1-CH2-CH3 IgG1 (C220S, C226S, C229S, P238S, N297Q)	<u>A</u> STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSSDKTHTSPSPAPPELLGGSSVFLFPPKPKDTLMISRTPEVTCVTV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
100	CH1-CH2-CH3 IgG1 (ΔE216-K222 IN HINGE) (C226S, C229S, P238S, N297Q)	<u>A</u> STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVPSSSLGTQTYICNVNHKPSNTKVDKKV THTSPSPAPPELLGGSSVFLFPPKPKDTLMISRTPEVTCVTVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPG
101	CH1-CH2-CH3 IgG1 (C220S, C226S, C229S, P238S, N297G)	<u>A</u> STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSSDKTHTSPSPAPPELLGGSSVFLFPPKPKDTLMISRTPEVTCVTV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
102	CH1-CH2-CH3 IgG1 (ΔE216-K222 IN HINGE) (C226S, C229S, P238S, N297G)	<u>A</u> STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVPSSSLGTQTYICNVNHKPSNTKVDKKV THTSPSPAPPELLGGSSVFLFPPKPKDTLMISRTPEVTCVTVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPG
103	TNX10 CH1- CH2-CH3 IgG1 (L234A, L235A)	<u>A</u> STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVTV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
104	TNX11 CH1- CH2-CH3 IgG1 (C226S, C229S, P238S)	<u>A</u> STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTSPSPAPPELLGGSSVFLFPPKPKDTLMISRTPEVTCVTV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

254	TNX07 CH1-CH2-CH3 IgG4 (S228P)	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLSPG
255	TNX08 CH1-CH2-CH3 IgG4 (S228P, L235E)	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLSPG
256	TNX09 CH1-CH2-CH3 IgG4 (S228P, F234A, L235A)	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLSPG
257	TNX12 IgG1 CH1-CH2-CH3 IgG1 (C229S, P238S)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVESKYGPPCPPCPAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMEALHNHYTQKSLSLSPG
258	TNX13 IgG1 VH-CH1-CH2-CH3 IgG1 (C226S, P238S)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVESKYGPPCPPCPAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMEALHNHYTQKSLSLSPG
259	TNX14 VH-CH1-CH2-CH3 IgG4 (L115T, S228P, L235A)	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLSPG
ASTlinker-CH1-hinge-CH2-CH3 with terminal K		
105	TNX01 CH1-CH2-CH3 IgG1 (N297Q)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVESKYGPPCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMEALHNHYTQKSLSLSPG

106	TNX02 CH1-CH2-CH3 IgG1 (wt)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
107	TNX03 CH1-CH2-CH3 IgG1 (N297G)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
108	TNX04 CH1-CH2-CH3 IgG1 (C220S, C226S, C229S, P238S)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSDKTHTSPSPAPPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
109	TNX05 CH1-CH2-CH3 IgG4 (S228P, L235A)	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVDHKPSNTKVDKRV ESKYGPPCPPCPAPEFAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTI SKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCFSVMHEALHNHYTQKSLSLSLGK
110	TNX06 CH1-CH2-CH3 IgG4 Wild Type	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVDHKPSNTKVDKRV ESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTI SKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCFSVMHEALHNHYTQKSLSLSLGK
111	CH1-CH2-CH3 IgG2 Wild Type	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVTSSNFGTQTYTCNVDHKPSNTKVDKTV ERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGMEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLSDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
112	CH1-CH2-CH3 IgG1 (Δ E216-K222 IN HINGE) (C226S, C229S, P238S)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV THTSPSPAPPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

113	CH1-CH2-CH3 IgG1 (C220S, C226S, C229S, P238S, N297Q)	<u>A</u> STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSSDKTHTSPSPAPPELLGGSSVFLFPPKPKDTLMISRTPEVTCVTV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
114	CH1-CH2-CH3 IgG1 (ΔE216-K222 IN HINGE) (C226S, C229S, P238S, N297Q)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV THTSPSPAPPELLGGSSVFLFPPKPKDTLMISRTPEVTCVTVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPG
115	CH1-CH2-CH3 IgG1 (C220S, C226S, C229S, P238S, N297G)	<u>A</u> STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSSDKTHTSPSPAPPELLGGSSVFLFPPKPKDTLMISRTPEVTCVTV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
116	CH1-CH2-CH3 IgG1 (ΔE216-K222 IN HINGE) (C226S, C229S, P238S, N297G)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV THTSPSPAPPELLGGSSVFLFPPKPKDTLMISRTPEVTCVTVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK
117	TNX10 CH1- CH2-CH3 IgG1 (L234A, L235A)	<u>A</u> STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVTV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
118	TNX11 CH1- CH2-CH3 IgG1 (C226S, C229S, P238S)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTSPSPAPPELLGGSSVFLFPPKPKDTLMISRTPEVTCVTV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

260	TNX07 CH1-CH2-CH3 IgG4 (S228P)	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLSPGK
261	TNX08 CH1-CH2-CH3 IgG4 (S228P, L235E)	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLSPGK
262	TNX09 CH1-CH2-CH3 IgG4 (S228P, F234A, L235A)	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLSPGK
263	TNX12 IgG1 CH1-CH2-CH3 IgG1 (C229S, P238S)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPSPAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
264	TNX13 IgG1 VH-CH1-CH2-CH3 IgG1 (C226S, P238S)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTSPPCPAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
265	TNX14 VH-CH1-CH2-CH3 IgG4 (L115T, S228P, L235A)	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLSPGK

Full length heavy chain with and without leader; with and without terminal lysine residue		
Heavy chain full length sequences with <u>leader</u> and no terminal K		
119	TNX01 VH-CH1-CH2-CH3 IgG1 (N297Q)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYMYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSEDTAVYYCTRSDGRNDMDSWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPG
120	TNX02 VH-CH1-CH2-CH3 IgG1 (wt)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYMYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSEDTAVYYCTRSDGRNDMDSWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPG
121	TNX03 VH-CH1-CH2-CH3 IgG1 (N297G)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYMYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSEDTAVYYCTRSDGRNDMDSWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPG
122	TNX04 VH-CH1-CH2-CH3 IgG1 (C220S, C226S, C229S, P238S)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYMYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSEDTAVYYCTRSDGRNDMDSWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSSDKTHTSPPSPAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPG
123	TNX05 VH-CH1-CH2-CH3 IgG4 (S228P, L235A)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYMYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSEDTAVYYCTRSDGRNDMDSWGQGTTLTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVDHKPSNTKVDKRVESKYGPCCPCCPAPEFAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLG

124	TNX06 VH-CH1-CH2-CH3 IgG4 Wild Type	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSED ^T AVYYCT ^R SDGRND ^M DSWGQ ^G TLTV ^S SSAST ^K GPSV ^F FLAP CSRSTSESTAALGCLVKDYFPEPVT ^S WNSGALT ^S GVHT ^F PAVLQSSGL YSLSSVVTVPSSSLGT ^K TYTCNV ^D HKPSNT ^K VDKRVESKYGP ^P CPSCPA PEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDV ^S QEDPEVQFNWYVD GVEVHNAKTKPREEQFNSTYRVVSVLT ^V LHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPS ^Q EEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSPG
125	VH-CH1-CH2-CH3 IgG2 Wild Type	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSED ^T AVYYCT ^R SDGRND ^M DSWGQ ^G TLTV ^S SSAST ^K GPSV ^F FLAP CSRSTSESTAALGCLVKDYFPEPVT ^S WNSGALT ^S GVHT ^F PAVLQSSGL YSLSSVVTVTSSNFGTQTYTCNV ^D HKPSNT ^K VDKTVERKCCVECP ^P CPA PPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDV ^S SHEDPEVQFNWYVDG MEVHNAKTKPREEQFNSTFRVSVLT ^V VHQDWLNGKEYKCKVSNKGLPA PIEKTISKAKGQPREPQVYTLPPS ^R EEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPMLDSDGSFFLYSKLTVDKSRWQQGNV ^F SCSVM HEALHNHYTQKSLSLSPG
126	VH-CH1-CH2-CH3 IgG1 (ΔE216-K222 IN HINGE) (C226S, C229S, P238S)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSED ^T AVYYCT ^R SDGRND ^M DSWGQ ^G TLTV ^S SSAST ^K GPSV ^F FLAP SSKSTSGGTAALGCLVKDYFPEPVT ^S WNSGALT ^S GVHT ^F PAVLQSSGL YSLSSVVTVPSSSLGTQTYICNV ^N HKPSNT ^K VDKKV ^T HTSPSPAPELL GGSSVFLFPPKPKDTLMISRTPEVTCVVDV ^S SHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLT ^V LHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPS ^R DELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNV ^F SCSVMHEA LHNHYTQKSLSLSPG
127	VH-CH1-CH2-CH3 IgG1 (C220S, C226S, C229S, P238S, N297Q)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSED ^T AVYYCT ^R SDGRND ^M DSWGQ ^G TLTV ^S SSAST ^K GPSV ^F FLAP SSKSTSGGTAALGCLVKDYFPEPVT ^S WNSGALT ^S GVHT ^F PAVLQSSGL YSLSSVVTVPSSSLGTQTYICNV ^N HKPSNT ^K VDKKVEPKSSDKTHTSP SPAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVDV ^S SHEDPEVKFNW YVDGVEVHNAKTKPREEQYQSTYRVVSVLT ^V LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPS ^R DELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNV ^F SCSVMHEA LHNHYTQKSLSLSPG
128	VH-CH1-CH2-CH3 IgG1 (ΔE216-K222 IN HINGE) (C226S, C229S, P238S, N297Q)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSED ^T AVYYCT ^R SDGRND ^M DSWGQ ^G TLTV ^S SSAST ^K GPSV ^F FLAP SSKSTSGGTAALGCLVKDYFPEPVT ^S WNSGALT ^S GVHT ^F PAVLQSSGL YSLSSVVTVPSSSLGTQTYICNV ^N HKPSNT ^K VDKKV ^T HTSPSPAPELL GGSSVFLFPPKPKDTLMISRTPEVTCVVDV ^S SHEDPEVKFNWYVDGVEV HNAKTKPREEQYQSTYRVVSVLT ^V LHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPS ^R DELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNV ^F SCSVMHEA LHNHYTQKSLSLSPG

129	VH-CH1-CH2-CH3 IgG1 (C220S, C226S, C229S, P238S, N297G)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSEDTAVYYCTRSDGRNDMDSWGQGT ^L LVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSSDKTHTSPP SPAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQY ^G STYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPG
130	VH-CH1-CH2-CH3 IgG1 (ΔE216-K222 IN HINGE) (C226S, C229S, P238S, N297G)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSEDTAVYYCTRSDGRNDMDSWGQGT ^L LVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVTHTSPPSPAPELL GGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQY ^G STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPG
131	TNX10 VH-CH1-CH2-CH3 IgG1 (L234A, L235A)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSEDTAVYYCTRSDGRNDMDSWGQGT ^L LVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPC CPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQY ^N STYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPG
132	TNX11 VH-CH1-CH2-CH3 IgG1 (C226S, C229S, P238S)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSEDTAVYYCTRSDGRNDMDSWGQGT ^L LVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTSPP SPAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQY ^N STYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPG
266	TNX07 VH-CH1-CH2-CH3 IgG4 (S228P)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSEDTAVYYCTRSDGRNDMDSWGQGT ^L LVTVSSASTKGPSVFPLAP CSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVTPSSSLGTQTYTCNVDHKPSNTKVDKRVESKYGPCCPCPA PEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVD GVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLG

267	TNX08 VH-CH1-CH2-CH3 IgG4 (S228P, L235E)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSEDTAVYYCTRS DGRNDMDSWGQGT LVT VSSASTKGPSVFPLAP CSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLG TKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPA PEFEGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVD GVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLGLG
268	TNX09 VH-CH1-CH2-CH3 IgG4 (S228P, F234A, L235A)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSEDTAVYYCTRS DGRNDMDSWGQGT LVT VSSASTKGPSVFPLAP CSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLG TKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPA PEAAGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVD GVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLGLG
269	TNX12 IgG1 VH-CH1-CH2-CH3 IgG1 (C229S, P238S)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSEDTAVYYCTRS DGRNDMDSWGQGT LVT VSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLG TQTYICNV NHKPSNTKVDKKEPKSCDKTHTCP SPAPELLGGSSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPG
270	TNX13 IgG1 VH-CH1-CH2-CH3 IgG1 (C226S, P238S)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSEDTAVYYCTRS DGRNDMDSWGQGT LVT VSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLG TQTYICNV NHKPSNTKVDKKEPKSCDKTHTSPP CPAPELLGGSSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPG
271	TNX14 VH-CH1-CH2-CH3 IgG4 (L115T, S228P, L235A)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSEDTAVYYCTRS DGRNDMDSWGQGT TTVTVSSASTKGPSVFPLAP CSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLG TKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPA PEFAGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVD GVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLGLG
Heavy chain full length sequences above with <u>leader</u> and terminal K		

133	TNX01 VH-CH1-CH2-CH3 IgG1 (N297Q)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSEDTAVYYCTRS DGRNDMDSWGQGT LVT VSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDDKVEPKSCDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK
134	TNX02 VH-CH1-CH2-CH3 IgG1 (wt)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSEDTAVYYCTRS DGRNDMDSWGQGT LVT VSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDDKVEPKSCDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK
135	TNX03 VH-CH1-CH2-CH3 IgG1 (N297G)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSEDTAVYYCTRS DGRNDMDSWGQGT LVT VSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDDKVEPKSCDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK
136	TNX04 VH-CH1-CH2-CH3 IgG1 (C220S, C226S, C229S, P238S)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSEDTAVYYCTRS DGRNDMDSWGQGT LVT VSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDDKVEPKSSDKTHTSPP SPAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK
137	TNX05 VH-CH1-CH2-CH3 IgG4 (S228P, L235A)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSEDTAVYYCTRS DGRNDMDSWGQGT LVT VSSASTKGPSVFPLAP CSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYTCNVDHKPSNTKVDDKRVESKYGPCCPCPA PEFAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVD GVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSI EKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGK

138	TNX06 VH-CH1-CH2-CH3 IgG4 Wild Type	<u>MPLLLLLPLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSEDTAVYYCTRS DGRNDMDSWGQGT LVT VSSASTKGPSVFPLAP CSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYTCNV D HKPSNTKVDKRVESKYGP C PSCPA PEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVD GVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSPGK
139	VH-CH1-CH2-CH3 IgG2 Wild Type	<u>MPLLLLLPLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSEDTAVYYCTRS DGRNDMDSWGQGT LVT VSSASTKGPSVFPLAP CSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVTSSNFGTQTYTCNV D HKPSNTKVDKTVERKCCVECPPCA PPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDG MEVHNAKTKPREEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPMLDS DGSFFLYSKLTVDKSRWQQGNVFS CSVM HEALHNHYTQKSLSLSPGK
140	VH-CH1-CH2-CH3 IgG1 (ΔE216-K222 IN HINGE) (C226S, C229S, P238S)	<u>MPLLLLLPLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSEDTAVYYCTRS DGRNDMDSWGQGT LVT VSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKTHTSPSPAPELL GGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEA LHNHYTQKSLSLSPGK
141	VH-CH1-CH2-CH3 IgG1 (C220S, C226S, C229S, P238S, N297Q)	<u>MPLLLLLPLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSEDTAVYYCTRS DGRNDMDSWGQGT LVT VSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKEPKSSDKTHTSP SPAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK
142	VH-CH1-CH2-CH3 IgG1 (ΔE216-K222 IN HINGE) (C226S, C229S, P238S, N297Q)	<u>MPLLLLLPLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSEDTAVYYCTRS DGRNDMDSWGQGT LVT VSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKTHTSPSPAPELL GGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEA LHNHYTQKSLSLSPGK

143	VH-CH1-CH2-CH3 IgG1 (C220S, C226S, C229S, P238S, N297G)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKF ~~K~~ SKATLTVDKSASTAYME LSSLRSEDTAVYYCTRSDGRNDMDSWGQGT ~~L~~ VTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSSDKTHTSPP SPAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK
144	VH-CH1-CH2-CH3 IgG1 (ΔE216-K222 IN HINGE) (C226S, C229S, P238S, N297G)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKF ~~K~~ SKATLTVDKSASTAYME LSSLRSEDTAVYYCTRSDGRNDMDSWGQGT ~~L~~ VTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVTHTSPPSPAPELL GGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK
145	TNX10 VH-CH1-CH2-CH3 IgG1 (L234A, L235A)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKF ~~K~~ SKATLTVDKSASTAYME LSSLRSEDTAVYYCTRSDGRNDMDSWGQGT ~~L~~ VTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCP CPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK
146	TNX11 VH-CH1-CH2-CH3 IgG1 (C226S, C229S, P238S)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKF ~~K~~ SKATLTVDKSASTAYME LSSLRSEDTAVYYCTRSDGRNDMDSWGQGT ~~L~~ VTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTSPP SPAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK
272	TNX07 VH-CH1-CH2-CH3 IgG4 (S228P)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKF ~~K~~ SKATLTVDKSASTAYME LSSLRSEDTAVYYCTRSDGRNDMDSWGQGT ~~L~~ VTVSSASTKGPSVFPLAP CSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYTCNV ~~D~~ HKPSNTKVDKRVESKYGPCCPCPA PEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVD GVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSI ~~E~~ KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLGLK

273	TNX08 VH-CH1-CH2-CH3 IgG4 (S228P, L235E)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSED ~~T~~ AVYYCTRSDGRNDMDSWGQGT ~~L~~ TVTVSSASTKGPSVFPLAP CSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVTPSSSLG ~~T~~ KTYTCNV ~~D~~ HKPSNTKVDKRVESKYGPPCPCPCPA PEFEGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVD GVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYK ~~T~~ TPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSL ~~S~~ LGK
274	TNX09 VH-CH1-CH2-CH3 IgG4 (S228P, F234A, L235A)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSED ~~T~~ AVYYCTRSDGRNDMDSWGQGT ~~L~~ TVTVSSASTKGPSVFPLAP CSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVTPSSSLG ~~T~~ KTYTCNV ~~D~~ HKPSNTKVDKRVESKYGPPCPCPCPA PEAAGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVD GVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYK ~~T~~ TPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSL ~~S~~ LGK
275	TNX12 IgG1 VH-CH1-CH2-CH3 IgG1 (C229S, P238S)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSED ~~T~~ AVYYCTRSDGRNDMDSWGQGT ~~L~~ TVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVTPSSSLG ~~T~~ QTYICNVNHKPSNTKVDKKEPKSCDKTHTCPCP SPAPELLGGSSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYK ~~T~~ TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK
276	TNX13 IgG1 VH-CH1-CH2-CH3 IgG1 (C226S, P238S)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSED ~~T~~ AVYYCTRSDGRNDMDSWGQGT ~~L~~ TVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVTPSSSLG ~~T~~ QTYICNVNHKPSNTKVDKKEPKSCDKTHTSPP CPAPELLGGSSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYK ~~T~~ TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK
277	TNX14 VH-CH1-CH2-CH3 IgG4 (L115T, S228P, L235A)	<u>MPLLLLLLPLLWAGALA</u> QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYY MYWVKQAPGQGLEWIGEINPSNGDTNFNEKFKSKATLTVDKSASTAYME LSSLRSED ~~T~~ AVYYCTRSDGRNDMDSWGQGT ~~T~~ TVTVSSASTKGPSVFPLAP CSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVTPSSSLG ~~T~~ KTYTCNV ~~D~~ HKPSNTKVDKRVESKYGPPCPCPCPA PEFAGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVD GVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYK ~~T~~ TPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSL ~~S~~ LGK

Full-length heavy chain sequences without leader and no terminal K		
147	TNX01 VH-CH1-CH2-CH3 IgG1 (N297Q)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGGGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSED ~~T~~ AVYYCTR SDGRNDMDSWGQGT ~~L~~ VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVT ~~V~~ SWNSGALTSGVHTFPAVLQSSGLYSLSSV ~~V~~ TPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP ~~P~~ CPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYQSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK ~~T~~ ISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV ~~F~~ SCSV ~~M~~ HEALHNHYTQKS LSLSPG
148	TNX02 VH-CH1-CH2-CH3 IgG1 (wt)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGGGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSED ~~T~~ AVYYCTR SDGRNDMDSWGQGT ~~L~~ VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVT ~~V~~ SWNSGALTSGVHTFPAVLQSSGLYSLSSV ~~V~~ TPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP ~~P~~ CPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK ~~T~~ ISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV ~~F~~ SCSV ~~M~~ HEALHNHYTQKS LSLSPG
149	TNX03 VH-CH1-CH2-CH3 IgG1 (N297G)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGGGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSED ~~T~~ AVYYCTR SDGRNDMDSWGQGT ~~L~~ VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVT ~~V~~ SWNSGALTSGVHTFPAVLQSSGLYSLSSV ~~V~~ TPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP ~~P~~ CPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK ~~T~~ ISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV ~~F~~ SCSV ~~M~~ HEALHNHYTQKS LSLSPG
150	TNX04 VH-CH1-CH2-CH3 IgG1 (C220S, C226S, C229S, P238S)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGGGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSED ~~T~~ AVYYCTR SDGRNDMDSWGQGT ~~L~~ VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVT ~~V~~ SWNSGALTSGVHTFPAVLQSSGLYSLSSV ~~V~~ TPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSSDKTHTSP ~~P~~ SPAPELLGGSSVFLFP PKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK ~~T~~ ISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV ~~F~~ SCSV ~~M~~ HEALHNHYTQKS LSLSPG
151	TNX05 VH-CH1-CH2-CH3 IgG4 (S228P, L235A)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGGGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSED ~~T~~ AVYYCTR SDGRNDMDSWGQGT ~~L~~ VTVSSASTKGPSVFPLAPCSRSTSESTAALGCLV KDYFPEPVT ~~V~~ SWNSGALTSGVHTFPAVLQSSGLYSLSSV ~~V~~ TPSSSLGT KTYTCNV ~~D~~ HKPSNTKVDKRVESKYGP ~~P~~ CP ~~P~~ CPAPEFAGGSPVFLFP ~~P~~ PKP KDTLMISRTPEVTCVVDVSD ~~E~~ PEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEK ~~T~~ ISKAKGQPRE PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSRLTVDKSRWQEGNV ~~F~~ SCSV ~~M~~ HEALHNHYTQKSLSL SLG

152	TNX06 VH-CH1-CH2-CH3 IgG4 Wild Type	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGQGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGTLLTVSSASTKGPSVFPLAPCSRSTSESTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGT KTYTCNV ~~VD~~ HKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPRE PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSL SLG
153	VH-CH1-CH2-CH3 IgG2 Wild Type	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGQGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGTLLTVSSASTKGPSVFPLAPCSRSTSESTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSNFGT QTYTCNV ~~VD~~ HKPSNTKVDKTV ~~ER~~ KCCVECP ~~CP~~ APPVAGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGMEVHNAKTKPREEQFN STFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSL PG
154	VH-CH1-CH2-CH3 IgG1 (ΔE216-K222 IN HINGE) (C226S, C229S, P238S)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGQGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGT QTYICNVNHKPSNTKVDKKTHTSPSPAPELLGGSSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSL SPG
155	VH-CH1-CH2-CH3 IgG1 (C220S, C226S, C229S, P238S, N297Q)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGQGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGT QTYICNVNHKPSNTKVDKKEPKSSDKTHTSPSPAPELLGGSSVFLFPP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYQSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPG
156	VH-CH1-CH2-CH3 IgG1 (ΔE216-K222 IN HINGE) (C226S, C229S, P238S, N297Q)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGQGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGT QTYICNVNHKPSNTKVDKKTHTSPSPAPELLGGSSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTY RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSL SPG

157	VH-CH1-CH2-CH3 IgG1 (C220S, C226S, C229S, P238S, N297G)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGQGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGTTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSSDKTHTSPSPAPELLGGSSVFLFP PKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKS LSLSPG
158	VH-CH1-CH2-CH3 IgG1 (ΔE216-K222 IN HINGE) (C226S, C229S, P238S, N297G)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGQGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGTTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVHTHTSPSPAPELLGGSSVFLFPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYSTY RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVL DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG
159	TNX10 VH-CH1-CH2-CH3 IgG1 (L234A, L235A)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGQGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGTTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGSPVFLFP PKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKS LSLSPG
160	TNX11 VH-CH1-CH2-CH3 IgG1 (C226S, C229S, P238S)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGQGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGTTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHTSPSPAPELLGGSSVFLFP PKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKS LSLSPG
278	TNX07 VH-CH1-CH2-CH3 IgG4 (S228P)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGQGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGTTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVESKYGPCCPPCPAPEFLGGPSVFLFPKPK KDTLMI SRTPEVTCVVVDVQEDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPRE PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSRLTVDKSRWQEGNVFCFSVMHEALHNHYTQKSLSL SLG

279	TNX08 VH-CH1-CH2-CH3 IgG4 (S228P, L235E)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGQGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGT ^L LVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLV KDYFPEPVT ^S WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGT KTYTCNV ^D HKPSNTKVDKRVESKYGPPCPPCPAPEFEGGPSVFLFPPKP KDTLMI ^S RTP ^E VT ^C VVDV ^S QEDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLT ^V LHQDWLNGKEYKCKVSNKGLPSSIEKTI ^S SKAKGQPRE PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSL SLG
280	TNX09 VH-CH1-CH2-CH3 IgG4 (S228P, F234A, L235A)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGQGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGT ^L LVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLV KDYFPEPVT ^S WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGT KTYTCNV ^D HKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKP KDTLMI ^S RTP ^E VT ^C VVDV ^S QEDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLT ^V LHQDWLNGKEYKCKVSNKGLPSSIEKTI ^S SKAKGQPRE PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSL SLG
281	TNX12 IgG1 VH-CH1-CH2-CH3 IgG1 (C229S, P238S)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGQGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGT ^L LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVT ^S WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNV ^N HKPSNTKVDKKEPKSCDKTHTCPPAPPELLGGSSVFLFPP PKPKDTLMI ^S RTP ^E VT ^C VVDV ^S HEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLT ^V LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPG
282	TNX13 IgG1 VH-CH1-CH2-CH3 IgG1 (C226S, P238S)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGQGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGT ^L LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVT ^S WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNV ^N HKPSNTKVDKKEPKSCDKTHTSPPCPAPELLGGSSVFLFPP PKPKDTLMI ^S RTP ^E VT ^C VVDV ^S HEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLT ^V LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPG
283	TNX14 VH-CH1-CH2-CH3 IgG4 (L115T, S228P, L235A)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGQGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGT ^T TVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLV KDYFPEPVT ^S WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGT KTYTCNV ^D HKPSNTKVDKRVESKYGPPCPPCPAPEFAGGPSVFLFPPKP KDTLMI ^S RTP ^E VT ^C VVDV ^S QEDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLT ^V LHQDWLNGKEYKCKVSNKGLPSSIEKTI ^S SKAKGQPRE PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSL SLG
Full-length heavy chain sequences without leader and with terminal K		

161	TNX01 VH-CH1-CH2-CH3 IgG1 (N297Q)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGGGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGT ^L LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVT ^S WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS ^S SLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP ^C PCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYQSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI ^S SKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV ^F SCSV ^M MHEALHNHYTQKS LSLSPGK
162	TNX02 VH-CH1-CH2-CH3 IgG1 (wt)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGGGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGT ^L LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVT ^S WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS ^S SLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP ^C PCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI ^S SKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV ^F SCSV ^M MHEALHNHYTQKS LSLSPGK
163	TNX03 VH-CH1-CH2-CH3 IgG1 (N297G)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGGGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGT ^L LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVT ^S WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS ^S SLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP ^C PCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI ^S SKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV ^F SCSV ^M MHEALHNHYTQKS LSLSPGK
164	TNX04 VH-CH1-CH2-CH3 IgG1 (C220S, C226S, C229S, P238S)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGGGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGT ^L LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVT ^S WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS ^S SLGT QTYICNVNHKPSNTKVDKKVEPKSSDKTHTSP ^P SPAPELLGGSSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI ^S SKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV ^F SCSV ^M MHEALHNHYTQKS LSLSPGK
165	TNX05 VH-CH1-CH2-CH3 IgG4 (S228P, L235A)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGGGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGT ^L LVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLV KDYFPEPVT ^S WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS ^S SLGT KTYTCNV ^D HKPSNTKVDKRVESKYGP ^C PCPAPEFAGG ^P SVFLFP ^P PKP KDTLMISRTPEVTCVVVDVSD ^E PEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTI ^S SKAKGQPRE PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSRLTVDKSRWQEGNV ^F SCSV ^M MHEALHNHYTQKSLSL SLGK

166	TNX06 VH-CH1-CH2-CH3 IgG4 Wild Type	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGQGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGT ¹ LVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLV KDYFPEPVT ² VS ³ WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGT KTYTCNV ⁴ DHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFLFPPKPK KDTLMISRTPEVTCVVVDVSD ⁵ QEDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTI ⁶ SKAKGQPRE PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSL SLGK
167	VH-CH1-CH2-CH3 IgG2 Wild Type	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGQGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGT ¹ LVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLV KDYFPEPVT ² VS ³ WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSNFGT QTYTCNV ⁴ DHKPSNTKVDKTV ⁵ ERKCCVECP ⁶ PCAPPVAGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGMEVHNAKTKPREEQFN STFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
168	VH-CH1-CH2-CH3 IgG1 (ΔE216-K222 IN HINGE) (C226S, C229S, P238S)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGQGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGT ¹ LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVT ² VS ³ WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGT QTYICNV ⁴ NHKPSNTKVDKKTHTSPSPAPPELLGGSSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
169	VH-CH1-CH2-CH3 IgG1 (C220S, C226S, C229S, P238S, N297Q)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGQGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGT ¹ LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVT ² VS ³ WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGT QTYICNV ⁴ NHKPSNTKVDKKEPKSSDKTHTSPSPAPPELLGGSSVFLFPP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYQSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSL LSLSPGK
170	VH-CH1-CH2-CH3 IgG1 (ΔE216-K222 IN HINGE) (C226S, C229S, P238S, N297Q)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGQGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGT ¹ LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVT ² VS ³ WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGT QTYICNV ⁴ NHKPSNTKVDKKTHTSPSPAPPELLGGSSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTY RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK

171	VH-CH1-CH2-CH3 IgG1 (C220S, C226S, C229S, P238S, N297G)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGT ¹ LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVT ² VS ³ WNSGALTSGVHTFPAVLQSSGLYSLSSVTV ⁴ PSSSLGT QTYICNVNHKPSNTKVDKKVEPKSSDKTHTSPSPAPELLGGSSVFLFP PKPKDTLMI ⁵ SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYGSTYRVVSVLT ⁶ VLHQDWLNGKEYKCKVSNKALPAPIEK ⁷ TISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV ⁸ FSCSV ⁹ MHEALHNHYTQKS LSLSPGK
172	VH-CH1-CH2-CH3 IgG1 (ΔE216-K222 IN HINGE) (C226S, C229S, P238S, N297G)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGT ¹ LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVT ² VS ³ WNSGALTSGVHTFPAVLQSSGLYSLSSVTV ⁴ PSSSLGT QTYICNVNHKPSNTKVDKKVHTHTSPSPAPELLGGSSVFLFPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGSTY RVVSVLT ⁶ VLHQDWLNGKEYKCKVSNKALPAPIEK ⁷ TISKAKGQPREPQVY TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVL DSDGSFFLYSKLTVDKSRWQQGNV ⁸ FSCSV ⁹ MHEALHNHYTQKSLSLSPGK
173	TNX10 VH-CH1-CH2-CH3 IgG1 (L234A, L235A)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGT ¹ LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVT ² VS ³ WNSGALTSGVHTFPAVLQSSGLYSLSSVTV ⁴ PSSSLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP ⁵ PCPAPEAAGGSPVFLFP PKPKDTLMI ⁵ SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLT ⁶ VLHQDWLNGKEYKCKVSNKALPAPIEK ⁷ TISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV ⁸ FSCSV ⁹ MHEALHNHYTQKS LSLSPGK
174	TNX11 VH-CH1-CH2-CH3 IgG1 (C226S, C229S, P238S)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGT ¹ LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVT ² VS ³ WNSGALTSGVHTFPAVLQSSGLYSLSSVTV ⁴ PSSSLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHTSPSPAPELLGGSSVFLFP PKPKDTLMI ⁵ SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLT ⁶ VLHQDWLNGKEYKCKVSNKALPAPIEK ⁷ TISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV ⁸ FSCSV ⁹ MHEALHNHYTQKS LSLSPGK
284	TNX08 VH-CH1-CH2-CH3 IgG4 (S228P, L235E)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGGLEWIG EINPSNGDTNFNEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGT ¹ LVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLV KDYFPEPVT ² VS ³ WNSGALTSGVHTFPAVLQSSGLYSLSSVTV ⁴ PSSSLGT KTYTCNV ⁵ DHKPSNTKVDKRVESKYGP ⁶ PCPPCPAPEFEGGSPVFLFPKPK KDTLMI ⁵ SRTPEVTCVVVDV ⁶ SQEDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLT ⁶ VLHQDWLNGKEYKCKVSNKGLPSSIEK ⁷ TISKAKGQPRE PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSRLTVDKSRWQEGNV ⁸ FSCSV ⁹ MHEALHNHYTQKSLSL SLGK

285	TNX09 VH-CH1-CH2-CH3 IgG4 (S228P, F234A, L235A)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPQGGLLEWIG EINPSNGDTNFNEKF ~~K~~ SKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGT ~~L~~ TVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLV KDYFPEPVT ~~V~~ SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGT KTYTCNV ~~D~~ HKPSNTKVDKR ~~V~~ ESKYGPPCP ~~P~~ CPAPEAAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLT ~~V~~ LHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPRE PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSL SLGK
286	TNX12 IgG1 VH-CH1-CH2-CH3 IgG1 (C229S, P238S)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPQGGLLEWIG EINPSNGDTNFNEKF ~~K~~ SKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGT ~~L~~ TVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVT ~~V~~ SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP ~~P~~ SPAPELLGGSSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLT ~~V~~ LHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK
287	TNX13 IgG1 VH-CH1-CH2-CH3 IgG1 (C226S, P238S)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPQGGLLEWIG EINPSNGDTNFNEKF ~~K~~ SKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGT ~~L~~ TVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVT ~~V~~ SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHTSP ~~P~~ CPAPELLGGSSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLT ~~V~~ LHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK
288	TNX14 VH-CH1-CH2-CH3 IgG4 (L115T, S228P, L235A)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPQGGLLEWIG EINPSNGDTNFNEKF ~~K~~ SKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMDSWGQGT ~~T~~ TVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLV KDYFPEPVT ~~V~~ SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGT KTYTCNV ~~D~~ HKPSNTKVDKR ~~V~~ ESKYGPPCP ~~P~~ CPAPEFAGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLT ~~V~~ LHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPRE PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSL SLGK

Heavy chain DNA sequences corresponding WITH LEADER, no terminal K		
175	TNX01 VH-CH1-CH2-CH3 IgG1 (N297Q) (no terminal K)	ATGCCACTGCTGCTGCTGCTGCCACTGCTGTGGGCTGGCGCTCTGGCTC AGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGGTGAAGCCAGGCGCCTC TGTGAAGCTGTCTTCAAGGCTAGCGGCTACATCTTCACCTCCTACTAT <u>ATGTATTGGGTGAAGCAGGCTCCTGGACAGGGACTGGAGTGGATCGGCG</u> <u>AGATCAACCCATCTAATGGCGACACCAACTTCAATGAGAAGTTTAAGTC</u> CAAGGCTACCCCTGACAGTGGATAAGTCCGCCCTCTACAGCCTACATGGAG CTGTCCAGCCTGAGAAGCGAGGACACCGCCGTGTACTATTGCACAAGGT CTGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCACCCCTGGTGAC AGTGTCTTCCGCTTCTACCAAGGGCCCTTCCGTGTTTCCACTGGCTCCA AGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTGA AGGACTATTTCCCTGAGCCAGTGACAGTGAGCTGGAACCTCTGGCGCTCT GACCTCCGGCGTGACACATTTCCAGCCGTGCTGCAGTCCAGCGGCCCTG TACAGCCTGTCTTCCGTGGTGACCGTGCCAAGCTCTTCCCTGGGCACCC AGACATATATCTGCAACGTGAATCATAAGCCCTCTAATACAAAGGTGGA CAAGAAGGTGGAGCCCAAGTCTTGTGATAAAACACATACTTGCCCCCT TGTCTGCACCAGAACTGCTGGGAGGACCTAGCGTGTTCTGTTTCCAC CCAAGCCAAAAGACACCCTGATGATTAGTAGAACCCCTGAGGTCACATG CGTGGTTCGTGGACGTGAGCCACGAGGACCCCGAGGTGAAGTTCAACTGG TACGTGGACGGCGTGGAGGTGCACAATGCTAAGACCAAGCCAGAGAGG AGCAGTACCAGAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGCTGCA TCAGGATTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAAG GCTCTGCCCCGCCCTATCGAGAAGACCATCTCTAAGGCTAAGGGCCAGC CTAGGGAGCCACAGGTGTACACACTGCCCCCTTCCCGGGACGAGCTGAC CAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCAGC GATATCGCCGTGGAGTGGGAGTCTAATGGCCAGCCTGAGAACAATTACA AGACCACACCACCGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATTTC CAAGCTGACCGTGATAAAGAGCCGCTGGCAGCAGGGCAACGTGTTTTCT TGTTCCTGTATGCACGAGGCCCTGCACAATCATTACACACAGAAGAGCC TGTCTCTGTCCCCTGGC

176	TNX02 VH-CH1-CH2-CH3 IgG1 (wt) (no terminal K)	ATGCCCCCTGCTGCTGCTGCTGCCTCTGCTGTGGGCTGGCGCTCTGGCTC AGGTGCAGCTGGTGCAGTCCGGAGCTGAGGTGGTGAAGCCAGGAGCCTC TGTGAAGCTGTCCTGCAAGGCTAGCGGCTACATCTTCACCAGCTACTAT ATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGCG AGATCAACCCTTCTAATGGCGACACCAACTTCAATGAGAAGTTTAAGTC CAAGGCTACCCTGACAGTGGATAAGTCCGCCTCTACAGCCTACATGGAG CTGTCCAGCCTGAGGTCTGAGGACACCGCCGTGTACTATTGCACAAGGT CTGATGGCCGGAACGACATGGATTCTGGGGCCAGGGCACCTGGTGAC AGTGTCTTCCGCTTCTACCAAGGGACCATCCGTGTTTCCACTGGCTCCA AGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTGA AGGACTATTTCCCAGAGCCCGTGACAGTGAGCTGGAACCTGGCGCTCT GACCAGCGGCGTGACACATTTCCAGCCGTGCTGCAGTCCAGCGGCCCTG TACTCTCTGTCTTCCGTGGTGACCGTGCCCTAGCTCTTCCCTGGGCACCC AGACATATATCTGCAACGTGAATCACAAGCCTAGCAATACAAAGGTGGA CAAGAAGGTGGAGCCAAAGTCTTGTGATAAGACCCATACATGCCCCCT TGTCTGCTCCAGAGCTGCTGGGAGGACCATCCGTGTTCTGTTTCCAC CCAAGCCCAAGGACACCCTGATGATCTCCAGAACCCTGAGGTGACATG CGTGGTGGTGGACGTGAGCCACGAGGACCCCGAGGTGAAGTTCAACTGG TACGTGGATGGCGTGGAGGTGCATAATGCCAAGACCAAGCCTAGAGAGG AGCAGTACAATAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGTGCA CCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCTAATAAG GCTCTGCCCCGCCCTATCGAGAAGACCATCTCCAAGGCTAAGGGCCAGC CTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGAC CAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCAAGC GATATCGCCGTGGAGTGGGAGTCTAATGGCCAGCCCAGAACCAATTACA AGACCACACCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATTC CAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTTTCT TGTTCCTGATGCATGAGGCTCTGCACAATCATTACACACAGAAGAGCC TGTCTCTGTCCCCAGGC
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177	TNX03 VH-CH1-CH2-CH3 IgG1 (N297G) (no terminal K)	ATGCCCCCTGCTGCTGCTGCTGCCTCTGCTGTGGGCTGGCGCTCTGGCTC AGGTGCAGCTGGTGCCAGTCCGGAGCTGAGGTGGTGAAGCCAGGAGCCTC TGTGAAGCTGTCCTGCAAGGCTAGCGGCTACATCTTCACCAGCTACTAT ATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGCG AGATCAACCCTTCTAATGGCGACACCAACTTCAATGAGAAGTTTAAGTC CAAGGCTACCCTGACAGTGGATAAGTCCGCCTCTACAGCCTACATGGAG CTGTCCAGCCTGAGGTCTGAGGACACCGCCGTGTACTATTGCACAAGGT CTGATGGCCGGAACGACATGGATTCTGGGGCCAGGGCACCTGGTGAC AGTGTCTTCCGCTTCTACCAAGGGACCATCCGTGTTTCCACTGGCTCCA AGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTGA AGGACTATTTCCCAGAGCCCGTGACAGTGAGCTGGAACCTGGCGCTCT GACCAGCGGCGTGACACATTTCCAGCCGTGCTGCAGTCCAGCGGCCCTG TACTCTCTGTCTTCCGTGGTGACCGTGCCCTAGCTCTTCCCTGGGCACCC AGACATATATCTGCAACGTGAATCACAAGCCTAGCAATACAAAGGTGGA CAAGAAGGTGGAGCCAAAGTCTTGTGATAAGACCCATACATGCCCCCT TGTCTGCTCCAGAGCTGCTGGGAGGACCATCCGTGTTCTGTTTCCAC CCAAGCCAAGGACACCCTGATGATCTCCAGAACCCTGAGGTGACATG CGTGGTGGTGGACGTGAGCCACGAGGACCCCGAGGTGAAGTTCAACTGG TACGTGGATGGCGTGGAGGTGCATAATGCCAAGACCAAGCCTAGAGAGG AGCAGTACGGCAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGTGCA CCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCTAATAAG GCTCTGCCCCGCCCTATCGAGAAGACCATCTCCAAGGCTAAGGGCCAGC CTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGAC CAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCAAGC GATATCGCCGTGGAGTGGGAGTCTAATGGCCAGCCCAGAACCAATTACA AGACCACACCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATTC CAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTTTCT TGTTCCTGATGCATGAGGCTCTGCACAATCATTACACACAGAAGAGCC TGTCTCTGTCCCCAGGC
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178	TNX04 VH-CH1-CH2-CH3 IgG1 (C220S, C226S, C229S, P238S) (no terminal K)	ATGCCCTGCTGCTGCTGCTGCCTCTGCTGTGGGCTGGCGCTCTGGCTC AGGTGCAGCTGGTGCAGAGCGGAGCTGAGGTGGTGAAGCCAGGAGCCTC TGTGAAGCTGTCTTCAAGGCTAGCGGCTACATCTTCACCTCTTACTAT ATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGCG AGATCAACCCTTCTAATGGCGACACCAACTTCAATGAGAAGTTTAAAGTC CAAGGCTACCCTGACAGTGGATAAGTCTGCTTCCACAGCCTACATGGAG CTGTCCAGCCTGAGGTCCGAGGACACCGCGTGTACTATTGCACAAGGT CTGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCACCTGGTGAC AGTGTCTTCCGCTTCTACCAAGGGACCATCCGTGTTTCCACTGGCTCCA AGCTCTAAGAGCACCTCTGGAGGAACAGCCGCTCTGGGATGTCTGGTGA AGGACTATTTCCCAGAGCCCGTGACAGTGTCTTGGAACTCCGGCGCTCT GACCTCTGGCGTGACACATTTCTGCCGTGCTGCAGTCCAGCGGCTG TACTCCCTGTCTTCCGTGGTGACCGTGCCAAGCTCTTCCCTGGGCACCC AGACATATATCTGCAACGTGAATCACAAGCCTTCCAATACAAAGGTGGA CAAGAAGGTGGAGCCAAAGAGCTCTGATAAGACCCATACAAGCCCCCT TCTCCTGCTCCAGAGCTGCTGGGAGGCTCCAGCGTGTTCCTGTTCCAC CCAAGCCAAAGGACACCCTGATGATCAGCAGAACCCCCGAGGTGACATG CGTGGTGGTGGACGTGTCTCACGAGGACCCCGAGGTGAAGTTCAACTGG TACGTGGATGGCGTGGAGGTGCATAATGCCAAGACCAAGCCTAGAGAGG AGCAGTACAATAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGTGCA CCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCCAATAAG GCTCTGCCCCGCCCTATCGAGAAGACCATCAGCAAGGCTAAGGGCCAGC CTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGAC CAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCAAGC GATATCGCCGTGGAGTGGGAGTCTAATGGCCAGCCCAGAACAAATTACA AGACCACACCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATTTC CAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTTTCC TGACGCTGATGCATGAGGCTCTGCACAATCATTAACACAGAAGTCTC TGTCCCTGAGCCCTGGC
179	TNX05 VH-CH1-CH2-CH3 IgG4 (S228P, L235A) (no terminal K)	ATGCCCTGCTGCTGCTGCTGCCTCTGCTGTGGGCTGGCGCTCTGGCTC AGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGGTGAAGCCTGGAGCTAG CGTGAAGCTGTCTTGAAGGCTTCCGGCTACATCTTCACCTCTTACTAT ATGTATTGGGTGAAGCAGGCTCCTGGACAGGGCCTGGAGTGGATCGGCG AGATCAACCCATCCAATGGCGACACAACTTCAATGAGAAGTTTAAAGAG CAAGGCTACCCTGACAGTGGATAAGTCCGCTCTACCGCTACATGGAG CTGTCCAGCCTGAGGAGCGAGGACACAGCCGTGTACTATTGTACCAGGA GCGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCACACTGGTGAC CGTGTCTTCCGCTAGCACAAAGGGACCATCCGTGTTCCACTGGCTCCA TGCTCCAGGAGCACATCTGAGTCCACCGCCGCTCTGGGCTGTCTGGTGA AGGACTATTTCCCTGAGCCAGTGACCGTGTCTTGGAAATAGCGGCGCTCT GACATCCGGAGTGACACCTTTCCAGCCGTGCTGCAGAGCTCTGGCCTG TACAGCCTGTCCAGCGTGGTGACAGTGCCTTCTTCCAGCCTGGGCACCA AGACATATACCTGCAACGTGGACCATAAGCCATCTAATACCAAGGTGGA TAAGAGAGTGGAGTCCAAGTACGGACCACCTTGCCCAACCTGTCCAGCT CCTGAGTTCTGCTGGAGGACCATCCGTGTTCTGTTTCTCCAAAGCCCA AGGACACCCTGATGATCTCTCGCACACCAGAGGTGACCTGCGTGGTGGT GGACGTGTCCAGGAGGACCCCGAGGTGCAGTTCAACTGGTACGTGGAT GGCGTGGAGGTGCACAATGCTAAGACCAAGCCAGGGAGGAGCAGTTTA ACTCCACATACCGGGTGGTGAGCGTGTGACCGTGTGCTGCATCAGGATTG GCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAAGGGCCTGCCT TCTTCCATCGAGAAGACAATCTCTAAGGCTAAGGGCCAGCCTCGGGAGC CACAGGTGTACACCCTGCCCCCTAGCCAGGAGGAGATGACAAAGAACCA GGTGTCTCTGACCTGTCTGGTGAAGGGCTTCTATCCCTCCGACATCGCC GTGGAGTGGGAGAGCAATGGCCAGCCTGAGAACAATTACAGACCACAC CACCCGTGCTGGACTCTGATGGCTCCTTCTTTCTGTATTCTAGACTGAC CGTCGATAAGTCCCGCTGGCAGGAGGGCAACGTGTTTGTAGCTGCTGTG ATGCACGAGGCCCTGCACAATCATTAACCCAGAAGTCCCTGAGCCTGT CTCTGGGC

289	TNX06 VH-CH1-CH2-CH3 IgG4 (wild type) (no terminal K)	ATGCCTCTGCTGCTGCTGCTGCCTCTGCTGTGGGCCGGTGCTCTGGCTC AGGTCCAGCTGGTCCAGTCAGGGGCTGAAGTGGTCAAACCCGGCGCCAG CGTGAAGCTGTCTTGAAGGCTTCCGGCTACATCTTCACCAGCTACTAT ATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGCG AGATCAACCCTTCCAATGGCGACACAACTTCAATGAGAAGTTTAAGAG CAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACCGCTTACATGGAG CTGTCCAGCCTGAGGTCTGAGGACACAGCCGTGTACTATTGTACCAGGA GCGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCACACTGGTGAC CGTGTCTTCCGCCAGCACAAAGGGCCCTTCCGTGTTCCCCCTGGCTCCT TGCTCCAGGAGCACATCTGAGTCCACCGCCGCTCTGGGCTGTCTGGTGA AGGACTACTTCCCAGAGCCCGTGACCGTGTCTGGAATAGCGGCGCCCT GACATCCGGAGTGACACCTTTCCAGCTGTGCTGCAGAGCTCTGGCCTG TACAGCCTGTCCAGCGTGGTGACAGTGCCCTCTTCCAGCCTGGGCACCA AGACATATACCTGCAACGTGGACCATAAGCCTTCTAATACCAAGGTGGA TAAGAGAGTGGAGTCCAAGTACGGACCACCTTGCCCTAGCTGTCTGTCT CCAGAGTTCTTGGGAGGACCTTCCGTGTTCTGTTTCCACCAAGCCAA AGGACACACTGATGATCTCTCGCACACCTGAGGTGACCTGCGTGGTGGT GGACGTGTCCCAGGAGGGACCCCGAGGTGCAGTTCAACTGGTACGTGGA TGGCGTGGAGGTGCACAATGCTAAGACCAAGCCAAGGGAGGAGCAGTTT AACTCCACATACCGGGTGGTGAGCGTGCTGACCGTGCTGCATCAGGATT GGCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAAGGGCCTGCC CTCTTCCATCGAGAAGACAATCTCTAAGGCTAAGGGACAGCCAAGGGAG CCACAGGTGTACACCCTGCCTCCAAGCCAGGAGGAGATGACAAAGAACC AGGTGTCTCTGACCTGTCTGGTGAAGGGCTTCTATCCATCTGACATCGC TGTGGAGTGGGAGTCCAATGGCCAGCCCGAGAACAATTACAGACCACA CCCCCTGTGCTGGACTCTGATGGCTCCTTCTTTCTGTATTCTAGACTGA CCGTGGATAAGTCCCGCTGGCAGGAGGGCAACGTGTTCTCCTGCTCTGT GATGCACGAAGCACTGCACAATCATTACACTCAGAAGAGCCTGTCACTG TCCCTGGGC
290	TNX07 VH-CH1-CH2-CH3 IgG4 (S228P) (no terminal K)	ATGCCTCTGCTGCTGCTGCTGCCTCTGCTGTGGGCCGGTGCTCTGGCTC AGGTCCAGCTGGTCCAGTCAGGGGCTGAAGTGGTCAAACCCGGCGCCAG CGTGAAGCTGTCTTGAAGGCTTCCGGCTACATCTTCACCAGCTACTAT ATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGCG AGATCAACCCTTCCAATGGCGACACAACTTCAATGAGAAGTTTAAGAG CAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACCGCTTACATGGAG CTGTCCAGCCTGAGGTCTGAGGACACAGCCGTGTACTATTGTACCAGGA GCGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCACACTGGTGAC CGTGTCTTCCGCCAGCACAAAGGGCCCTTCCGTGTTCCCCCTGGCTCCT TGCTCCAGGAGCACATCTGAGTCCACCGCCGCTCTGGGCTGTCTGGTGA AGGACTACTTCCCAGAGCCCGTGACCGTGTCTGGAATAGCGGCGCCCT GACATCCGGAGTGACACCTTTCCAGCTGTGCTGCAGAGCTCTGGCCTG TACAGCCTGTCCAGCGTGGTGACAGTGCCCTCTTCCAGCCTGGGCACCA AGACATATACCTGCAACGTGGACCATAAGCCTTCTAATACCAAGGTGGA TAAGAGAGTGGAGTCCAAGTACGGACCACCTTGCCCTCCCTGTCTGTCT CCAGAGTTCTTGGGAGGACCTTCCGTGTTCTGTTTCCACCAAGCCAA AGGACACACTGATGATCTCTCGCACACCTGAGGTGACCTGCGTGGTGGT GGACGTGTCCCAGGAGGACCCCGAGGTGCAGTTCAACTGGTACGTGGAT GGCGTGGAGGTGCACAATGCTAAGACCAAGCCAAGGGAGGAGCAGTTTA ACTCCACATACCGGGTGGTGAGCGTGCTGACCGTGCTGCATCAGGATTG GCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAAGGGCCTGCCC TCTTCCATCGAGAAGACAATCTCTAAGGCTAAGGGACAGCCAAGGGAGC CACAGGTGTACACCCTGCCTCCAAGCCAGGAGGAGATGACAAAGAACCA GGTGTCTCTGACCTGTCTGGTGAAGGGCTTCTATCCATCTGACATCGCT GTGGAGTGGGAGTCCAATGGCCAGCCCGAGAACAATTACAGACCACAC CCCCCTGTGCTGGACTCTGATGGCTCCTTCTTTCTGTATTCTAGACTGAC CGTGGATAAGTCCCGCTGGCAGGAGGGCAACGTGTTCTCCTGCTCTGTG ATGCACGAAGCACTGCACAATCATTACACTCAGAAGAGCCTGTCACTGT CCCTGGGC

291	TNX08 VH-CH1-CH2-CH3 (IgG4 S228P/L235E) (no terminal K)	ATGCCTCTGCTGCTGCTGCTGCCTCTGCTGTGGGCCGGTGCTCTGGCTC AGGTCCAGCTGGTCCAGTCAGGGGCTGAAGTGGTCAAACCCGGCGCCAG CGTGAAGCTGTCTTGCAAGGCTTCCGGCTACATCTTCACCAGCTACTAT ATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGCG AGATCAACCCTTCCAATGGCGACACAACTTCAATGAGAAGTTTAAGAG CAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACCGCTTACATGGAG CTGTCCAGCCTGAGGTCTGAGGACACAGCCGTGTACTATTGTACCAGGA GCGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCACACTGGTGAC CGTGTCTTCCGCCAGCACAAAGGGCCCTTCCGTGTTCCCCCTGGCTCCT TGCTCCAGGAGCACATCTGAGTCCACCGCCGCTCTGGGCTGTCTGGTGA AGGACTACTTCCCAGAGCCCGTGACCGTGTCTGGAATAGCGGCGCCCT GACATCCGGAGTGACACCTTTCCAGCTGTGCTGCAGAGCTCTGGCCTG TACAGCCTGTCCAGCGTGGTGACAGTGCCCTCTTCCAGCCTGGGCACCA AGACATATACCTGCAACGTGGACCATAAGCCTTCTAATACCAAGGTGGA TAAGAGAGTGGAGTCCAAGTACGGACCACCTTGCCCTCCCTGTCTGTCT CCAGAGTTCGAGGAGGACCTTCCGTGTTCTGTTTCCACCAAGCCAA AGGACACACTGATGATCTCTCGCACACCTGAGGTGACCTGCGTGGTGGT GGACGTGTCCCAGGAGGACCCCGAGGTGCAGTTCAACTGGTACGTGGAT GGCGTGGAGGTGCACAATGCTAAGACCAAGCCAAGGGAGGAGCAGTTTA ACTCCACATACCGGGTGGTGAGCGTGCTGACCGTGCTGCATCAGGATTG GCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAAGGGCCTGCC TCTTCCATCGAGAAGACAATCTTAAGGCTAAGGGACAGCCAAGGGAGC CACAGGTGTACACCCTGCCTCCAAGCCAGGAGGAGATGACAAAGAACCA GGTGTCTCTGACCTGTCTGGTGAAGGGCTTCTATCCATCTGACATCGCT GTGGAGTGGGAGTCCAATGGCCAGCCCGAGAACAATTACAGACCACAC CCCCGTGTGCTGGACTCTGATGGCTCCTTCTTTCTGTATTCTAGACTGAC CGTGGATAAGTCCCGCTGGCAGGAGGGCAACGTGTTCTCCTGCTCTGTG ATGCACGAAGCACTGCACAATCATTACACTCAGAAGAGCCTGTCACTGT CCCTGGGC
292	TNX09 VH-CH1-CH2-CH3 IgG4 (S228P/F234A/L235A) (no terminal K)	ATGCCTCTGCTGCTGCTGCTGCCTCTGCTGTGGGCCGGTGCTCTGGCTC AGGTCCAGCTGGTCCAGTCAGGGGCTGAAGTGGTCAAACCCGGCGCCAG CGTGAAGCTGTCTTGCAAGGCTTCCGGCTACATCTTCACCAGCTACTAT ATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGCG AGATCAACCCTTCCAATGGCGACACAACTTCAATGAGAAGTTTAAGAG CAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACCGCTTACATGGAG CTGTCCAGCCTGAGGTCTGAGGACACAGCCGTGTACTATTGTACCAGGA GCGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCACACTGGTGAC CGTGTCTTCCGCCAGCACAAAGGGCCCTTCCGTGTTCCCCCTGGCTCCT TGCTCCAGGAGCACATCTGAGTCCACCGCCGCTCTGGGCTGTCTGGTGA AGGACTACTTCCCAGAGCCCGTGACCGTGTCTGGAATAGCGGCGCCCT GACATCCGGAGTGACACCTTTCCAGCTGTGCTGCAGAGCTCTGGCCTG TACAGCCTGTCCAGCGTGGTGACAGTGCCCTCTTCCAGCCTGGGCACCA AGACATATACCTGCAACGTGGACCATAAGCCTTCTAATACCAAGGTGGA TAAGAGAGTGGAGTCCAAGTACGGACCACCTTGCCCTCCCTGTCTGTCT CCAGAGGCCCGGAGGACCTTCCGTGTTCTGTTTCCACCAAGCCAA AGGACACACTGATGATCTCTCGCACACCTGAGGTGACCTGCGTGGTGGT GGACGTGTCCCAGGAGGACCCCGAGGTGCAGTTCAACTGGTACGTGGAT GGCGTGGAGGTGCACAATGCTAAGACCAAGCCAAGGGAGGAGCAGTTTA ACTCCACATACCGGGTGGTGAGCGTGCTGACCGTGCTGCATCAGGATTG GCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAAGGGCCTGCC TCTTCCATCGAGAAGACAATCTTAAGGCTAAGGGACAGCCAAGGGAGC CACAGGTGTACACCCTGCCTCCAAGCCAGGAGGAGATGACAAAGAACCA GGTGTCTCTGACCTGTCTGGTGAAGGGCTTCTATCCATCTGACATCGCT GTGGAGTGGGAGTCCAATGGCCAGCCCGAGAACAATTACAGACCACAC CCCCGTGTGCTGGACTCTGATGGCTCCTTCTTTCTGTATTCTAGACTGAC CGTGGATAAGTCCCGCTGGCAGGAGGGCAACGTGTTCTCCTGCTCTGTG ATGCACGAAGCACTGCACAATCATTACACTCAGAAGAGCCTGTCACTGT CCCTGGGC

293	TNX10 VH-CH1-CH2-CH3 IgG1 (L234A/L235A) (no terminal K)	ATGCCTCTGCTGCTGCTGCTGCCTCTGCTGTGGGCCGGTGCCCTGGCTC AGGTCCAGCTGGTCCAGTCAGGTGCCGAAGTGGTCAAGCCCGGCGCCTC TGTGAAGCTGTCTGCAAGGCTAGCGGCTACATCTTCACCTCCTACTAT ATGTATTGGGTGAAGCAGGCTCCTGGACAGGGCCTGGAGTGGATCGGCG AGATCAACCCATCTAATGGCGACACCAACTTCAATGAGAAGTTTAAATC CAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACAGCTTACATGGAG CTGTCCAGCCTGAGGAGCGAGGACACCGCCGTGTACTATTGCACAAGGT CTGATGGCCGGAACGACATGGATTCTGGGGCCAGGGCACCTGGTGAC AGTGTCTTCCGCCCTTACCAAGGGCCCTTCCGTGTTTCCACTGGCTCCC AGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTGA AGGACTACTTCCCAGAGCCCGTGACAGTGAGCTGGAACCTGGCGCCCT GACCAGCGGAGTGACACATTTCTGCTGTGCTGCAGTCCAGCGGCCCTG TACTCTCTGTCTTCCGTGGTGACCGTGCCAAGCTCTTCCCTGGGCACCC AGACATATATCTGCAACGTGAATCACAAGCCAAGCAATACAAAGGTGGA CAAGAAGGTGGAGCCCAAGTCTTGTGATAAGACCCATACATGCCCCCT TGTCTGCTCCAGAGGCTGCTGGAGGACCATCCGTGTTCTTCCAC CCAAGCCTAAGGACACCCTGATGATCTCCAGAACCCAGAGGTGACATG CGTGGTGGTGGACGTGAGCCACGAGGACCCCGAGGTGAAGTTCAACTGG TACGTGGATGGCGTGGAGGTGCATAATGCTAAGACCAAGCCAAGAGAGG AGCAGTACAACAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGTGCA TCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCTAATAAG GCCCTGCCCCGCTCCTATCGAGAAGACCATCTCCAAGGCCAAGGGCCAGC CTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGAC CAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCCAGC GATATCGCTGTGGAGTGGGAGTCTAATGGCCAGCCTGAGAACAAATTACA AGACCACACCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATTC CAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTCTCC TGTTCCGTCTATGCACGAGGCACTGCACAATCATTACACCCAGAAGTCAC TGTCCTGTGCTACCAGGA
294	TNX11 VH-CH1-CH2-CH3 IgG1 (C226S, C229S, P238S) (no terminal K)	ATGCCTCTGCTGCTGCTGCTGCCTCTGCTGTGGGCCGGTGCCCTGGCTC AGGTCCAGCTGGTCCAGTCAGGTGCCGAAGTGGTCAAGCCCGGCGCCTC TGTGAAGCTGTCTGCAAGGCTAGCGGCTACATCTTCACCTCCTACTAT ATGTATTGGGTGAAGCAGGCTCCTGGACAGGGCCTGGAGTGGATCGGCG AGATCAACCCATCTAATGGCGACACCAACTTCAATGAGAAGTTTAAATC CAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACAGCTTACATGGAG CTGTCCAGCCTGAGGAGCGAGGACACCGCCGTGTACTATTGCACAAGGT CTGATGGCCGGAACGACATGGATTCTGGGGCCAGGGCACCTGGTGAC AGTGTCTTCCGCCCTTACCAAGGGCCCTTCCGTGTTTCCACTGGCTCCC AGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTGA AGGACTACTTCCCAGAGCCCGTGACAGTGAGCTGGAACCTGGCGCCCT GACCAGCGGAGTGACACATTTCTGCTGTGCTGCAGTCCAGCGGCCCTG TACTCTCTGTCTTCCGTGGTGACCGTGCCAAGCTCTTCCCTGGGCACCC AGACATATATCTGCAACGTGAATCACAAGCCAAGCAATACAAAGGTGGA CAAGAAGGTGGAGCCCAAGTCTTGTGATAAGACCCATACATccCCCCCT TccCCTGCTCCAGAGCTGCTGGGAGGAAGCTCCGTGTTCTGTTTCCAC CCAAGCCTAAGGACACCCTGATGATCTCCAGAACCCAGAGGTGACATG CGTGGTGGTGGACGTGAGCCACGAGGACCCCGAGGTGAAGTTCAACTGG TACGTGGATGGCGTGGAGGTGCATAATGCTAAGACCAAGCCAAGAGAGG AGCAGTACAACAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGTGCA TCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCTAATAAG GCCCTGCCCCGCTCCTATCGAGAAGACCATCTCCAAGGCCAAGGGCCAGC CTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGAC CAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCCAGC GATATCGCTGTGGAGTGGGAGTCTAATGGCCAGCCTGAGAACAAATTACA AGACCACACCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATTC CAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTCTCC TGTTCCGTCTATGCACGAGGCACTGCACAATCATTACACCCAGAAGTCAC TGTCCTGTGCTACCAGGA

295	TNX12 VH-CH1-CH2-CH3 IgG1 (C229S, P238S) (no terminal K)	ATGCCTCTGCTGCTGCTGCTGCCTCTGCTGTGGGCCGGTGCCCTGGCTC AGGTCCAGCTGGTCCAGTCAGGTGCCGAAGTGGTCAAGCCCGGCGCCTC TGTGAAGCTGTCTGCAAGGCTAGCGGCTACATCTTCACCTCCTACTAT ATGTATTGGGTGAAGCAGGCTCCTGGACAGGGCCTGGAGTGGATCGGCG AGATCAACCCATCTAATGGCGACACCAACTTCAATGAGAAGTTTAAAGTC CAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACAGCTTACATGGAG CTGTCCAGCCTGAGGAGCGAGGACACCGCCGTGTACTATTGCACAAGGT CTGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCACCTGGTGAC AGTGTCTTCCGCCCTCTACCAAGGGCCCTTCCGTGTTTCCACTGGCTCCC AGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTGA AGGACTACTTCCCAGAGCCCGTGACAGTGAGCTGGAACCTGGCGCCCT GACCAGCGGAGTGACACATTTCTGCTGTGCTGCAGTCCAGCGGCCCTG TACTCTCTGTCTTCCGTGGTGACCGTGCCAAGCTCTTCCCTGGGCACCC AGACATATATCTGCAACGTGAATCACAAGCCAAGCAATACAAAGGTGGA CAAGAAGGTGGAGCCCAAGTCTTGTGATAAGACCCATACATGCCCCCT TCCCCTGCTCCAGAGCTGCTGGGAGGAAGcTCCGTGTTCTGTTTCCAC CCAAGCCTAAGGACACCCTGATGATCTCCAGAACCCAGAGGTGACATG CGTGGTGGTGGACGTGAGCCACGAGGACCCCGAGGTGAAGTTCAACTGG TACGTGGATGGCGTGGAGGTGCATAATGCTAAGACCAAGCCAAGAGAGG AGCAGTACAACAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGTGCA TCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCTAATAAG GCCCTGCCCCGCTCCTATCGAGAAGACCATCTCCAAGGCCAAGGGCCAGC CTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGAC CAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCCAGC GATATCGCTGTGGAGTGGGAGTCTAATGGCCAGCCTGAGAACAAATTACA AGACCACACCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATTTC CAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTCTCC TGTTCCGTATGCACGAGGCACTGCACAATCATTACACCCAGAAGTCAC TGTCACTGTACCAGGA
296	TNX13 VH-CH1-CH2-CH3 IgG1 (C226S, P238S) (no terminal K)	ATGCCTCTGCTGCTGCTGCTGCCTCTGCTGTGGGCCGGTGCCCTGGCTC AGGTCCAGCTGGTCCAGTCAGGTGCCGAAGTGGTCAAGCCCGGCGCCTC TGTGAAGCTGTCTGCAAGGCTAGCGGCTACATCTTCACCTCCTACTAT ATGTATTGGGTGAAGCAGGCTCCTGGACAGGGCCTGGAGTGGATCGGCG AGATCAACCCATCTAATGGCGACACCAACTTCAATGAGAAGTTTAAAGTC CAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACAGCTTACATGGAG CTGTCCAGCCTGAGGAGCGAGGACACCGCCGTGTACTATTGCACAAGGT CTGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCACCTGGTGAC AGTGTCTTCCGCCCTCTACCAAGGGCCCTTCCGTGTTTCCACTGGCTCCC AGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTGA AGGACTACTTCCCAGAGCCCGTGACAGTGAGCTGGAACCTTGGCGCCCT GACCAGCGGAGTGACACATTTCTGCTGTGCTGCAGTCCAGCGGCCCTG TACTCTCTGTCTTCCGTGGTGACCGTGCCAAGCTCTTCCCTGGGCACCC AGACATATATCTGCAACGTGAATCACAAGCCAAGCAATACAAAGGTGGA CAAGAAGGTGGAGCCCAAGTCTTGTGATAAGACCCATACATCCCCCCT TGCCCTGCTCCAGAGCTGCTGGGAGGAAGCTCCGTGTTCTGTTTCCAC CCAAGCCTAAGGACACCCTGATGATCTCCAGAACCCAGAGGTGACATG CGTGGTGGTGGACGTGAGCCACGAGGACCCCGAGGTGAAGTTCAACTGG TACGTGGATGGCGTGGAGGTGCATAATGCTAAGACCAAGCCAAGAGAGG AGCAGTACAACAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGTGCA TCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCTAATAAG GCCCTGCCCCGCTCCTATCGAGAAGACCATCTCCAAGGCCAAGGGCCAGC CTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGAC CAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCCAGC GATATCGCTGTGGAGTGGGAGTCTAATGGCCAGCCTGAGAACAAATTACA AGACCACACCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATTTC CAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTCTCC TGTTCCGTATGCACGAGGCACTGCACAATCATTACACCCAGAAGTCAC TGTCACTGTACCAGGA

297	TNX14 VH-CH1-CH2-CH3 IgG4 (L115T, S228P, L235A) (no terminal K)	ATGCCTCTGCTGCTGCTGCTGCCTCTGCTGTGGGCCGGTGCTCTGGCTC AGGTCCAGCTGGTCCAGTCAGGGGCTGAAGTGGTCAAACCCGGCGCCAG CGTGAAGCTGTCTTGCAAGGCTTCCGGCTACATCTTCACCAAGCTACTAT ATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGCG AGATCAACCCCTTCCAATGGCGACACAACTTCAATGAGAAGTTTAAGAG CAAGGCCACCCGTGACAGTGGATAAGAGCGCCTCTACCGCTTACATGGAG CTGTCCAGCCTGAGGTCTGAGGACACAGCCGTGTACTATTGTACCAGGA GCGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCACAACAGTGAC CGTGTCTTCCGCCAGCACAAAGGGCCCTTCCGTGTTCCCCCTGGCTCCT TGCTCCAGGAGCACATCTGAGTCCACCGCCGCTCTGGGCTGTCTGGTGA AGGACTACTTCCCAGAGCCCGTGACCGTGTCTGGAATAGCGGCGCCCT GACATCCGGAGTGACACCTTTCCAGCTGTGCTGCAGAGCTCTGGCCTG TACAGCCTGTCCAGCGTGGTGACAGTGCCCTCTTCCAGCCTGGGCACCA AGACATATACCTGCAACGTGGACCATAAGCCTTCTAATACCAAGGTGGA TAAGAGAGTGGAGTCCAAGTACGGACCACCTTGCCCTCCTTGTCTGTCT CCAGAGTTTCGCCGAGGACCTTCCGTGTTCTGTTTCCACCCAAGCCAA AGGACACACTGATGATCTCTCGCACACCTGAGGTGACCTGCGTGGTGGT GGACGTGTCCCAGGAGGACCCCGAGGTGCAGTTCAACTGGTACGTGGAT GGGCTGGAGGTGCACAATGCTAAGACCAAGCCAAGGGAGGAGCAGTTTA ACTCCACATACCGGGTGGTGAGCGTGCTGACCGTGCTGCATCAGGATTG GCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAAGGGCCTGCC TCTTCCATCGAGAAGACAATCTTAAGGCTAAGGGACAGCCAAGGGAGC CACAGGTGTACACCTGCCTCCAAGCCAGGAGGAGATGACAAAGAACCA GGTGTCTCTGACCTGTCTGGTGAAGGGCTTCTATCCATCTGACATCGCT GTGGAGTGGGAGTCCAATGGCCAGCCCAGAACCAATTACAGACCACAC CCCCTGTGCTGGACTCTGATGGCTCCTTCTTCTGTATTCTAGACTGAC CGTGGATAAGTCCCGCTGGCAGGAGGGCAACGTGTTCTCCTGCTCTGTG ATGCACGAAGCACTGCACAATCATTACACTCAGAAGAGCCTGTCACTGT CCCTGGGC
Heavy chain DNA sequences WITHOUT LEADER; no terminal K		
180	TNX01 VH-CH1-CH2-CH3 IgG1 (N297Q) (no terminal K)	CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGGTGAAGCCAGGCGCCT CTGTGAAGCTGTCTTGCAAGGCTAGCGGCTACATCTTCACCTCCTACTA TATGTATTGGGTGAAGCAGGCTCCTGGACAGGGACTGGAGTGGATCGGC GAGATCAACCCATCTAATGGCGACACCAACTTCAATGAGAAGTTTAAGT CCAAGGCTACCCTGACAGTGGATAAGTCCGCCTCTACAGCCTACATGGA GCTGTCCAGCCTGAGAAGCGAGGACACCGCCGTGTACTATTGCACAAGG TCTGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCACCCTGGTGA CAGTGTCTTCCGCTTCTACCAAGGGCCCTTCCGTGTTTCCACTGGCTCC AAGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTGA AAGGACTATTTCCCTGAGCCAGTGACAGTGAGCTGGAACCTCTGGCGCTC TGACCTCCGGCGTGACACATTTCCAGCCGTGCTGCAGTCCAGCGGCCT GTACAGCCTGTCTTCCGTGGTGACCGTGCCAAGCTCTTCCCTGGGCACC CAGACATATATCTGCAACGTGAATCATAAGCCCTCTAATACAAAGGTGG ACAAGAAGGTGGAGCCCAAGTCTTGTGATAAAACACATACTTGCCCCC TTGTCTGACCCAGAACTGCTGGGAGGACCTAGCGTGTTCCTGTTTCCA CCCAAGCCAAAAGACACCCTGATGATTAGTAGAACCCTGAGGTACAT GCGTGGTCTGTGGACGTGAGCCACGAGGACCCCGAGGTGAAGTTCAACTG GTACGTGGACGGCGTGGAGGTGCACAATGCTAAGACCAAGCCAGAGAG GAGCAGTACCAGAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGCTGC ATCAGGATTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAA GGCTCTGCCCCGCCCTATCGAGAAGACCATCTTAAGGCTAAGGGCCAG CCTAGGGAGCCACAGGTGTACACACTGCCCCCTTCCGGGACGAGCTGA CCAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCCAG CGATATCGCCGTGGAGTGGGAGTCTAATGGCCAGCCTGAGAACAATTAC AAGACCACACCACCGTGCTGGACTCCGATGGCAGCTTCTTCTGTATT CCAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTTTT TTGTTCCGTGATGCACGAGGCCCTGCACAATCATTACACACAGAAGAGC CTGTCTCTGTCCCCTGGC

181	TNX02 VH-CH1-CH2-CH3 IgG1 (wt) (no terminal K)	CAGGTGCAGCTGGTGCAGTCCGGAGCTGAGGTGGTGAAGCCAGGAGCCT CTGTGAAGCTGTCTTGCAAGGCTAGCGGCTACATCTTCACCAGCTACTA TATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGC GAGATCAACCCCTTCTAATGGCGACACCAACTTCAATGAGAAGTTTAAGT CCAAGGCTACCCTGACAGTGGATAAGTCCGCCTCTACAGCCTACATGGA GCTGTCCAGCCTGAGGTCTGAGGACACCGCCGTGTAATTTGCACAAGG TCTGATGGCCGGAACGACATGGATTCTGTTGGGCGCAGGGCACCCTGGTGA CAGTGTCTTCCGCTTCTACCAAGGGACCATCCGTGTTTCCACTGGCTCC AAGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTG AAGGACTATTTCCAGAGCCCGTGACAGTGAGCTGGAACCTCTGGCGCTC TGACCAGCGGCGTGACACATTTCCAGCCGTGCTGCAGTCCAGCGGCCT GTACTCTCTGTCTTCCGTGGTGACCGTGCCCTAGCTCTTCCCTGGGCACC CAGACATATATCTGCAACGTGAATCACAAGCCTAGCAATACAAAGGTGG ACAAGAAGGTGGAGCCAAAGTCTTGTGATAAGACCCATACATGCCCCC TTGTCTGCTCCAGAGCTGCTGGGAGGACCATCCGTGTTCTGTTTCCA CCCAAGCCCAAGGACACCCTGATGATCTCCAGAACCCTGAGGTGACAT GCGTGGTGGTGGACGTGAGCCACGAGGACCCCGAGGTGAAGTTCAACTG GTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACCAAGCCTAGAGAG GAGCAGTACAATAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGCTGC ACCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCTAATAA GGCTCTGCCCCGCCCTATCGAGAAGACCATCTCCAAGGCTAAGGGCCAG CCTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGA CCAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCAAG CGATATCGCCGTGGAGTGGGAGTCTAATGGCCAGCCCGAGAACAATTAC AAGACCACACCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATT CCAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTTTC TTGTTCCGTGATGCATGAGGCTCTGCACAATCATTACACACAGAAGAGC CTGTCTCTGTCCCCAGGC
182	TNX03 VH-CH1-CH2-CH3 IgG1 (N297G) (no terminal K)	CAGGTGCAGCTGGTGCAGTCCGGAGCTGAGGTGGTGAAGCCAGGAGCCT CTGTGAAGCTGTCTTGCAAGGCTAGCGGCTACATCTTCACCAGCTACTA TATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGC GAGATCAACCCCTTCTAATGGCGACACCAACTTCAATGAGAAGTTTAAGT CCAAGGCTACCCTGACAGTGGATAAGTCCGCCTCTACAGCCTACATGGA GCTGTCCAGCCTGAGGTCTGAGGACACCGCCGTGTAATTTGCACAAGG TCTGATGGCCGGAACGACATGGATTCTGTTGGGCGCAGGGCACCCTGGTGA CAGTGTCTTCCGCTTCTACCAAGGGACCATCCGTGTTTCCACTGGCTCC AAGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTG AAGGACTATTTCCAGAGCCCGTGACAGTGAGCTGGAACCTCTGGCGCTC TGACCAGCGGCGTGACACATTTCCAGCCGTGCTGCAGTCCAGCGGCCT GTACTCTCTGTCTTCCGTGGTGACCGTGCCCTAGCTCTTCCCTGGGCACC CAGACATATATCTGCAACGTGAATCACAAGCCTAGCAATACAAAGGTGG ACAAGAAGGTGGAGCCAAAGTCTTGTGATAAGACCCATACATGCCCCC TTGTCTGCTCCAGAGCTGCTGGGAGGACCATCCGTGTTCTGTTTCCA CCCAAGCCCAAGGACACCCTGATGATCTCCAGAACCCTGAGGTGACAT GCGTGGTGGTGGACGTGAGCCACGAGGACCCCGAGGTGAAGTTCAACTG GTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACCAAGCCTAGAGAG GAGCAGTACGGCAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGCTGC ACCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCTAATAA GGCTCTGCCCCGCCCTATCGAGAAGACCATCTCCAAGGCTAAGGGCCAG CCTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGA CCAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCAAG CGATATCGCCGTGGAGTGGGAGTCTAATGGCCAGCCCGAGAACAATTAC AAGACCACACCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATT CCAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTTTC TTGTTCCGTGATGCATGAGGCTCTGCACAATCATTACACACAGAAGAGC CTGTCTCTGTCCCCAGGC

183	TNX04 VH-CH1-CH2-CH3 IgG1 (C220S, C226S, C229S, P238S) (no terminal K)	CAGGTGCAGCTGGTGCAGAGCGGAGCTGAGGTGGTGAAGCCAGGAGCCTCTGTGAAGCTGTCTTGCAAGGCTAGCGGCTACATCTTCACCTCTTACTATATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGCAGATCAACCCCTTCTAATGGCGACACCAACTTCAATGAGAAGTTTAAGTCCAAGGCTACCCTGACAGTGGATAAGTCTGCTTCCACAGCCTACATGGA GCTGTCCAGCCTGAGGTCCGAGGACACCGCCGTGTACTATTGCACAAGGTCTGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCACCCTGGTGA CAGTGTCTTCCGCTTCTACCAAGGGACCATCCGTGTTTCCACTGGCTCC AAGCTCTAAGAGCACCTCTGGAGGAACAGCCGCTCTGGGATGTCTGGTG AAGGACTATTTCCAGAGCCCGTGACAGTGTCTTGGAACCTCCGGCGCTCTGACCTCTGGCGTGACACATTTCTGCGGTGCTGCAGTCCAGCGGCCTGTACTCCCTGTCTTCCGTGGTGACCGTGCCAAAGCTCTTCCCTGGGCACC CAGACATATATCTGCAACGTGAATCACAAGCCTTCCAATACAAAGGTGGACAAGAAGGTGGAGCCAAAGAGCTCTGATAAGACCCATACAAAGCCCCCTTCTCCTGTCTCCAGAGCTGCTGGGAGGCTCCAGCGTGTCTCTGTTTCCA CCCAAGCCAAAGGACACCCTGATGATCAGCAGAACCCCGAGGTGACATGCGTGGTGGTGGACGTGTCTCACGAGGACCCCGAGGTGAAGTTCAACTGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACCAAGCCTAGAGAG GAGCAGTACAATAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGTCTGCCAGGACTGGCTGAACCGCAAGGAGTATAAGTGCAAGGTGTCCAATAAGGCTCTGCCCCGCCCTATCGAGAAGACCATCAGCAAGGCTAAGGGCCAG CCTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGACCAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCAAGCGATATCGCCGTGGAGTGGGAGTCTAATGGCCAGCCCGAGAACAATTAC AAGACCACACCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATTCCAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTTTCTGTAGCGTGATGCATGAGGCTCTGCACAATCATTACACACAGAAGTCTCTGTCCCTGAGCCCTGGC
184	TNX05 VH-CH1-CH2-CH3 IgG4 (S228P, L235A) (no terminal K)	CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGGTGAAGCCTGGAGCTAGCGTGAAGCTGTCTTGCAAGGCTTCCGCTACATCTTCACCTCCTACTATATGTATTGGGTGAAGCAGGCTCCTGGACAGGGCCTGGAGTGGATCGGC GAGATCAACCCATCCAATGGCGACACAACTTCAATGAGAAGTTTAAAGAGCAAGGCTACCCTGACAGTGGATAAGTCCGCTCTACCGCTACATGGA GCTGTCCAGCCTGAGGAGCGAGGACACAGCCGTGTACTATTGTACCAGGAGCGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCACACTGGTGA CCGTGTCTTCCGCTAGCACAAAGGGACCATCCGTGTTCCACTGGCTCC ATGCTCCAGGAGCACATCTGAGTCCACCGCCGCTCTGGGCTGTCTGGTG AAGGACTATTTCCCTGAGCCAGTGACCGTGTCTTGGGAATAGCGGCGCTCTGACATCCGGAGTGCACACCTTTCCAGCCGTGCTGCAGAGCTCTGGCCTGTACAGCCTGTCCAGCGTGGTGACAGTGCCTTCTTCCAGCCTGGGCACC AAGACATATACCTGCAACGTGGACCATAAGCCATCTAATACCAAGGTGGATAAGAGAGTGGAGTCCAAGTACGGACACCTTGCCACCATGTCCAGCTCCTGAGTTCGCTGGAGGACCATCCGTGTTCTGTTTCCAAAGCCC AAGGACACCCTGATGATCTCTCGCACACCAGAGGTGACCTGCGTGGTGGTGGACGTGTCCCAGGAGGACCCGAGGTGCAGTTCAACTGGTACGTGGA TGGCGTGGAGGTGCACAATGCTAAGACCAAGCCCAGGGAGGAGCAGTTTAACTCCACATACCGGGTGGTGAAGCGTGTGACCGTGTCTGCATCAGGATT GGCTGAACCGCAAGGAGTATAAGTGCAAGGTGAGCAATAAGGGCCTGCC TTCTTCCATCGAGAAGACAATCTCTAAGGCTAAGGGCCAGCCTCGGGAGCCACAGGTGTACACCTGCCCCCTAGCCAGGAGGAGATGACAAAGAACC AGGTGTCTCTGACCTGTCTGGTGAAGGGCTTCTATCCCTCCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCTGAGAACAATTACAAGACCACA CCACCCGTGCTGGACTCTGATGGCTCCTTCTTCTGTATTCTAGACTGACCGTCGATAAGTCCCGCTGGCAGGAGGGCAACGTGTTTAGCTGCTCTGTGATGCACGAGGCCCTGCACAATCATTACACCCAGAAGTCCCTGAGCCTGTCTCTGGGC

298	TNX06 VH-CH1-CH2-CH3 IgG4 (wild type) (no terminal K)	CAGGTCCAGCTGGTCCAGTCAGGGGCTGAAGTGGTCAAACCCGGCGCCA GCGTGAAGCTGTCTTGCAAGGCTTCCGGCTACATCTTCACCAGCTACTA TATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGC GAGATCAACCCCTTCCAATGGCGACACAACTTCAATGAGAAGTTTAAGA GCAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACCGCTTACATGGA GCTGTCCAGCCTGAGGTCTGAGGACACAGCCGTGTACTATTGTACCAGG AGCGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCAGCTGGTGA CCGTGTCTTCCGCCAGCACAAAGGGCCCTTCCGTGTTCCCCCTGGCTCC TTGCTCCAGGAGCACATCTGAGTCCACCGCCGCTCTGGGCTGTCTGGTG AAGGACTACTTCCCAGAGCCCGTGACCGTGTCTGGAATAGCGGCGCCC TGACATCCGGAGTGACACCTTTCAGCTGTGCTGCAGAGCTCTGGCCT GTACAGCCTGTCCAGCGTGGTGACAGTGCCCTCTTCAGCCTGGGCACC AAGACATATACCTGCAACGTGGACCATAAGCCTTCTAATACCAAGGTGG ATAAGAGAGTGGAGTCCAAGTACGGACCACCTTGCCCTAGCTGTCTGC TCCAGAGTTCTTGGGAGGACCTTCCGTGTTCTGTTCACCCAAGCCA AAGGACACACTGATGATCTCTCGCACACCTGAGGTGACCTGCGTGGTGG TGGACGTGTCCCAGGAGGACCCGAGGTGCAGTTCAACTGGTACGTGGA TGGCGTGGAGGTGCACAATGCTAAGACCAAGCCAAGGGAGGAGCAGTTT AACTCCACATACCGGGTGGTGAGCGTGCTGACCGTGCTGCATCAGGATT GGCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAAGGGCCTGCC CTCTTCCATCGAGAAGACAATCTCTAAGGCTAAGGGACAGCCAAGGGAG CCACAGGTGTACACCCTGCCTCCAAGCCAGGAGGAGATGACAAAGAACC AGGTGTCTCTGACCTGTCTGGTGAAGGGCTTCTATCCATCTGACATCGC TGTGGAGTGGGAGTCCAATGGCCAGCCCGAGAACAATTACAAGACCACA CCCCCTGTGCTGGACTCTGATGGCTCCTTCTTCTGTATTCTAGACTGA CCGTGGATAAGTCCCGCTGGCAGGAGGGCAACGTGTTCTCTGCTCTGT GATGCACGAAGCACTGCACAATCATTACACTCAGAAGAGCCTGTCACTG TCCCTGGGC
299	TNX07 VH-CH1-CH2-CH3 IgG4 (S228P) (no terminal K)	CAGGTCCAGCTGGTCCAGTCAGGGGCTGAAGTGGTCAAACCCGGCGCCA GCGTGAAGCTGTCTTGCAAGGCTTCCGGCTACATCTTCACCAGCTACTA TATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGC GAGATCAACCCCTTCCAATGGCGACACAACTTCAATGAGAAGTTTAAGA GCAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACCGCTTACATGGA GCTGTCCAGCCTGAGGTCTGAGGACACAGCCGTGTACTATTGTACCAGG AGCGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCAGCTGGTGA CCGTGTCTTCCGCCAGCACAAAGGGCCCTTCCGTGTTCCCCCTGGCTCC TTGCTCCAGGAGCACATCTGAGTCCACCGCCGCTCTGGGCTGTCTGGTG AAGGACTACTTCCCAGAGCCCGTGACCGTGTCTGGAATAGCGGCGCCC TGACATCCGGAGTGACACCTTTCAGCTGTGCTGCAGAGCTCTGGCCT GTACAGCCTGTCCAGCGTGGTGACAGTGCCCTCTTCAGCCTGGGCACC AAGACATATACCTGCAACGTGGACCATAAGCCTTCTAATACCAAGGTGG ATAAGAGAGTGGAGTCCAAGTACGGACCACCTTGCCCTCCCTGTCTGC TCCAGAGTTCTTGGGAGGACCTTCCGTGTTCTGTTCACCCAAGCCA AAGGACACACTGATGATCTCTCGCACACCTGAGGTGACCTGCGTGGTGG TGGACGTGTCCCAGGAGGACCCGAGGTGCAGTTCAACTGGTACGTGGA TGGCGTGGAGGTGCACAATGCTAAGACCAAGCCAAGGGAGGAGCAGTTT AACTCCACATACCGGGTGGTGAGCGTGCTGACCGTGCTGCATCAGGATT GGCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAAGGGCCTGCC CTCTTCCATCGAGAAGACAATCTCTAAGGCTAAGGGACAGCCAAGGGAG CCACAGGTGTACACCCTGCCTCCAAGCCAGGAGGAGATGACAAAGAACC AGGTGTCTCTGACCTGTCTGGTGAAGGGCTTCTATCCATCTGACATCGC TGTGGAGTGGGAGTCCAATGGCCAGCCCGAGAACAATTACAAGACCACA CCCCCTGTGCTGGACTCTGATGGCTCCTTCTTCTGTATTCTAGACTGA CCGTGGATAAGTCCCGCTGGCAGGAGGGCAACGTGTTCTCTGCTCTGT GATGCACGAAGCACTGCACAATCATTACACTCAGAAGAGCCTGTCACTG TCCCTGGGC

300	TNX08 VH-CH1-CH2-CH3 (IgG4 S228P/L235E) (no terminal K)	CAGGTCCAGCTGGTCCAGTCAGGGGCTGAAGTGGTCAAACCCGGCGCCA GCGTGAAGCTGTCTTGCAAGGCTTCCGGCTACATCTTCACCAGCTACTA TATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGC GAGATCAACCCTTCCAATGGCGACACAACTTCAATGAGAAGTTTAAGA GCAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACCGCTTACATGGA GCTGTCCAGCCTGAGGTCTGAGGACACAGCCGTGTACTATTGTACCAGG AGCGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCAGCTGGTGA CCGTGTCTTCCGCCAGCACAAAGGGCCCTTCCGTGTTCCCCCTGGCTCC TTGCTCCAGGAGCACATCTGAGTCCACCGCCGCTCTGGGCTGTCTGGTG AAGGACTACTTCCCAGAGCCCGTGACCGTGTCTGGAATAGCGGCGCCC TGACATCCGGAGTGACACCTTTCAGCTGTGCTGCAGAGCTCTGGCCT GTACAGCCTGTCCAGCGTGGTGACAGTGCCCTCTTCAGCCTGGGCACC AAGACATATACCTGCAACGTGGACCATAAGCCTTCTAATACCAAGGTGG ATAAGAGAGTGGAGTCCAAGTACGGACCACCTTGCCCTCCCTGTCTGC TCCAGAGTTCGAGGGAGGACCTTCCGTGTTCTGTTCACCCAAGCCA AAGGACACACTGATGATCTCTCGCACACCTGAGGTGACCTGCGTGGTGG TGGACGTGTCCCAGGAGGACCCGAGGTGCAGTTCAACTGGTACGTGGA TGGCGTGGAGGTGCACAATGCTAAGACCAAGCCAAGGGAGGAGCAGTTT AACTCCACATACCGGGTGGTGAGCGTGCTGACCGTGCTGCATCAGGATT GGCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAAGGGCCTGCC CTCTTCCATCGAGAAGACAATCTCTAAGGCTAAGGGACAGCCAAGGGAG CCACAGGTGTACACCCTGCCTCCAAGCCAGGAGGAGATGACAAAGAACC AGGTGTCTCTGACCTGTCTGGTGAAGGGCTTCTATCCATCTGACATCGC TGTGGAGTGGGAGTCCAATGGCCAGCCCGAGAACAATTACAAGACCACA CCCCCTGTGCTGGACTCTGATGGCTCCTTCTTCTGTATTCTAGACTGA CCGTGGATAAGTCCCGCTGGCAGGAGGGCAACGTGTTCTCTGCTCTGT GATGCACGAAGCACTGCACAATCATTACACTCAGAAGAGCCTGTCACTG TCCCTGGGC
301	TNX09 VH-CH1-CH2-CH3 IgG4 (S228P/F234A/L235A) (no terminal K)	CAGGTCCAGCTGGTCCAGTCAGGGGCTGAAGTGGTCAAACCCGGCGCCA GCGTGAAGCTGTCTTGCAAGGCTTCCGGCTACATCTTCACCAGCTACTA TATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGC GAGATCAACCCTTCCAATGGCGACACAACTTCAATGAGAAGTTTAAGA GCAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACCGCTTACATGGA GCTGTCCAGCCTGAGGTCTGAGGACACAGCCGTGTACTATTGTACCAGG AGCGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCAGCTGGTGA CCGTGTCTTCCGCCAGCACAAAGGGCCCTTCCGTGTTCCCCCTGGCTCC TTGCTCCAGGAGCACATCTGAGTCCACCGCCGCTCTGGGCTGTCTGGTG AAGGACTACTTCCCAGAGCCCGTGACCGTGTCTGGAATAGCGGCGCCC TGACATCCGGAGTGACACCTTTCAGCTGTGCTGCAGAGCTCTGGCCT GTACAGCCTGTCCAGCGTGGTGACAGTGCCCTCTTCAGCCTGGGCACC AAGACATATACCTGCAACGTGGACCATAAGCCTTCTAATACCAAGGTGG ATAAGAGAGTGGAGTCCAAGTACGGACCACCTTGCCCTCCCTGTCTGC TCCAGAGGCCGCGGAGGACCTTCCGTGTTCTGTTCACCCAAGCCA AAGGACACACTGATGATCTCTCGCACACCTGAGGTGACCTGCGTGGTGG TGGACGTGTCCCAGGAGGACCCGAGGTGCAGTTCAACTGGTACGTGGA TGGCGTGGAGGTGCACAATGCTAAGACCAAGCCAAGGGAGGAGCAGTTT AACTCCACATACCGGGTGGTGAGCGTGCTGACCGTGCTGCATCAGGATT GGCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAAGGGCCTGCC CTCTTCCATCGAGAAGACAATCTCTAAGGCTAAGGGACAGCCAAGGGAG CCACAGGTGTACACCCTGCCTCCAAGCCAGGAGGAGATGACAAAGAACC AGGTGTCTCTGACCTGTCTGGTGAAGGGCTTCTATCCATCTGACATCGC TGTGGAGTGGGAGTCCAATGGCCAGCCCGAGAACAATTACAAGACCACA CCCCCTGTGCTGGACTCTGATGGCTCCTTCTTCTGTATTCTAGACTGA CCGTGGATAAGTCCCGCTGGCAGGAGGGCAACGTGTTCTCTGCTCTGT GATGCACGAAGCACTGCACAATCATTACACTCAGAAGAGCCTGTCACTG TCCCTGGGC

302	TNX10 VH-CH1-CH2-CH3 IgG1 (L234A/L235A) (no terminal K)	CAGGTCCAGCTGGTCCAGTCAGGTGCCGAAGTGGTCAAGCCCGGCGCCT CTGTGAAGCTGTCTTGCAAGGCTAGCGGCTACATCTTCACCTCCTACTA TATGTATTGGGTGAAGCAGGCTCCTGGACAGGGCCTGGAGTGGATCGGC GAGATCAACCCATCTAATGGCGACACCAACTTCAATGAGAAGTTTAAGT CCAAGGCCACCCCTGACAGTGGATAAGAGCGCCTCTACAGCTTACATGGA GCTGTCCAGCCTGAGGAGCGAGGACACCGCCGTGTACTATTGCACAAGG TCTGATGGCCGGAACGACATGGATTCTGTTGGGCCAGGGCACCTGGTGA CAGTGTCTTCCGCCTCTACCAAGGGCCCTTCCGTGTTTCCACTGGCTCC CAGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTG AAGGACTACTTCCCAGAGCCCGTGACAGTGAGCTGGAACCTCTGGCGCCC TGACCAGCGGAGTGACACATTTCTGTGTGTGTGACAGTCCAGCGCCT GTACTCTCTGTCTTCCGTGGTGACCGTGCCAAGCTCTTCCCTGGGCACC CAGACATATATCTGCAACGTGAATCACAAGCCAAGCAATACAAAGGTGG ACAAGAAGGTGGAGCCCAAGTCTTGTGATAAGACCCATACATGCCCCC TTGTCTGTCTCCAGAGGCTGTGGAGGACCATCCGTGTTCTGTTCCTCA CCCAAGCCTAAGGACACCCCTGATGATCTCCAGAACCCAGAGGTGACAT GCGTGGTGGTGGACGTGAGCCACGAGGACCCGAGGTGAAGTTCAACTG GTACGTGGATGGCGTGGAGGTGCATAATGCTAAGACCAAGCCAAGAGAG GAGCAGTACAACAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGCTGC ATCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCTAATAA GGCCCTGCCCCGCTCCTATCGAGAAGACCATCTCCAAGGCCAAGGGCCAG CCTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGA CCAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCCAG CGATATCGCTGTGGAGTGGGAGTCTAATGGCCAGCCTGAGAACAATTAC AAGACCACACCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATT CCAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTCTC CTGTTCCGTCTATGCACGAGGCACTGCACAATCATTACACCCAGAAGTCA CTGTCACTGTCAACAGGA
303	TNX11 VH-CH1-CH2-CH3 IgG1 (C226S, C229S, P238S) (no terminal K)	CAGGTCCAGCTGGTCCAGTCAGGTGCCGAAGTGGTCAAGCCCGGCGCCT CTGTGAAGCTGTCTTGCAAGGCTAGCGGCTACATCTTCACCTCCTACTA TATGTATTGGGTGAAGCAGGCTCCTGGACAGGGCCTGGAGTGGATCGGC GAGATCAACCCATCTAATGGCGACACCAACTTCAATGAGAAGTTTAAGT CCAAGGCCACCCCTGACAGTGGATAAGAGCGCCTCTACAGCTTACATGGA GCTGTCCAGCCTGAGGAGCGAGGACACCGCCGTGTACTATTGCACAAGG TCTGATGGCCGGAACGACATGGATTCTGTTGGGCCAGGGCACCTGGTGA CAGTGTCTTCCGCCTCTACCAAGGGCCCTTCCGTGTTTCCACTGGCTCC CAGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTG AAGGACTACTTCCCAGAGCCCGTGACAGTGAGCTGGAACCTCTGGCGCCC TGACCAGCGGAGTGACACATTTCTGTGTGTGTGACAGTCCAGCGGCCCT GTACTCTCTGTCTTCCGTGGTGACCGTGCCAAGCTCTTCCCTGGGCACC CAGACATATATCTGCAACGTGAATCACAAGCCAAGCAATACAAAGGTGG ACAAGAAGGTGGAGCCCAAGTCTTGTGATAAGACCCATACATccccCCCC TTccCCTGTCTCCAGAGCTGTGGGAGGAAGCTCCGTGTTCTGTTCCTCA CCCAAGCCTAAGGACACCCCTGATGATCTCCAGAACCCAGAGGTGACAT GCGTGGTGGTGGACGTGAGCCACGAGGACCCGAGGTGAAGTTCAACTG GTACGTGGATGGCGTGGAGGTGCATAATGCTAAGACCAAGCCAAGAGAG GAGCAGTACAACAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGCTGC ATCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCTAATAA GGCCCTGCCCCGCTCCTATCGAGAAGACCATCTCCAAGGCCAAGGGCCAG CCTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGA CCAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCCAG CGATATCGCTGTGGAGTGGGAGTCTAATGGCCAGCCTGAGAACAATTAC AAGACCACACCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATT CCAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTCTC CTGTTCCGTCTATGCACGAGGCACTGCACAATCATTACACCCAGAAGTCA CTGTCACTGTCAACAGGA

304	TNX12 VH-CH1-CH2-CH3 IgG1 (C229S, P238S) (no terminal K)	CAGGTCCAGCTGGTCCAGTCAGGTGCCGAAGTGGTCAAGCCCGGCGCCT CTGTGAAGCTGTCTTGCAAGGCTAGCGGCTACATCTTCACCTCCTACTA TATGTATTGGGTGAAGCAGGCTCCTGGACAGGGCCTGGAGTGGATCGGC GAGATCAACCCATCTAATGGCGACACCAACTTCAATGAGAAGTTTAAGT CCAAGGCCACCCCTGACAGTGGATAAGAGCGCCTCTACAGCTTACATGGA GCTGTCCAGCCTGAGGAGCGAGGACACCGCCGTGTACTATTGCACAAGG TCTGATGGCCGGAACGACATGGATTCTCTGGGGCCAGGGCACCCTGGTGA CAGTGTCTTCCGCCTCTACCAAGGGCCCTTCCGTGTTTCCACTGGCTCC CAGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTG AAGGACTACTTCCCAGAGCCCGTGACAGTGAGCTGGAACCTCTGGCGCCC TGACCAGCGGAGTGACACATTTCTGTGTGTGTGACAGTCCAGCGGCCT GTACTCTCTGTCTTCCGTGGTGACCGTGCCAAGCTCTTCCCTGGGCACC CAGACATATATCTGCAACGTGAATCACAAGCCAAGCAATACAAAGGTGG ACAAGAAGGTGGAGCCCAAGTCTTGTGATAAGACCCATACATGCCCCC TTCCCTGTCTCCAGAGCTGTCTGGGAGGAAGCTCCGTGTTCTGTTCCTCA CCCAAGCCTAAGGACACCCTGATGATCTCCAGAACCCAGAGGTGACAT GCGTGGTGGTGGACGTGAGCCACGAGGACCCGAGGTGAAGTCAACTG GTACGTGGATGGCGTGGAGGTGCATAATGCTAAGACCAAGCCAAGAGAG GAGCAGTACAACAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGCTGC ATCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCTAATAA GGCCCTGCCCCGTCTATCGAGAAGACCATCTCCAAGGCCAAGGGCCAG CCTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGA CCAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCCAG CGATATCGCTGTGGAGTGGGAGTCTAATGGCCAGCCTGAGAACAATTAC AAGACCACACCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATT CCAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTCTC CTGTTCCGTGATGCACGAGGCACTGCACAATCATTACCCAGAAGTCA CTGTCACTGTCAACAGGA
305	TNX13 VH-CH1-CH2-CH3 IgG1 (C226S, P238S) (no terminal K)	CAGGTCCAGCTGGTCCAGTCAGGTGCCGAAGTGGTCAAGCCCGGCGCCT CTGTGAAGCTGTCTTGCAAGGCTAGCGGCTACATCTTCACCTCCTACTA TATGTATTGGGTGAAGCAGGCTCCTGGACAGGGCCTGGAGTGGATCGGC GAGATCAACCCATCTAATGGCGACACCAACTTCAATGAGAAGTTTAAGT CCAAGGCCACCCCTGACAGTGGATAAGAGCGCCTCTACAGCTTACATGGA GCTGTCCAGCCTGAGGAGCGAGGACACCGCCGTGTACTATTGCACAAGG TCTGATGGCCGGAACGACATGGATTCTCTGGGGCCAGGGCACCCTGGTGA CAGTGTCTTCCGCCTCTACCAAGGGCCCTTCCGTGTTTCCACTGGCTCC CAGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTG AAGGACTACTTCCCAGAGCCCGTGACAGTGAGCTGGAACCTCTGGCGCCC TGACCAGCGGAGTGACACATTTCTGTGTGTGTGACAGTCCAGCGGCCT GTACTCTCTGTCTTCCGTGGTGACCGTGCCAAGCTCTTCCCTGGGCACC CAGACATATATCTGCAACGTGAATCACAAGCCAAGCAATACAAAGGTGG ACAAGAAGGTGGAGCCCAAGTCTTGTGATAAGACCCATACATCCCCC TTGCCCTGTCTCCAGAGCTGTCTGGGAGGAAGCTCCGTGTTCTGTTCCTCA CCCAAGCCTAAGGACACCCTGATGATCTCCAGAACCCAGAGGTGACAT GCGTGGTGGTGGACGTGAGCCACGAGGACCCGAGGTGAAGTCAACTG GTACGTGGATGGCGTGGAGGTGCATAATGCTAAGACCAAGCCAAGAGAG GAGCAGTACAACAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGCTGC ATCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCTAATAA GGCCCTGCCCCGTCTATCGAGAAGACCATCTCCAAGGCCAAGGGCCAG CCTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGA CCAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCCAG CGATATCGCTGTGGAGTGGGAGTCTAATGGCCAGCCTGAGAACAATTAC AAGACCACACCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATT CCAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTCTC CTGTTCCGTGATGCACGAGGCACTGCACAATCATTACCCAGAAGTCA CTGTCACTGTCAACAGGA

306	TNX14 VH-CH1-CH2-CH3 IgG4 (L115T, S228P, L235A) (no terminal K)	CAGGTCCAGCTGGTCCAGTCAGGGGCTGAAGTGGTCAAACCCGGCGCCA GCGTGAAGCTGTCTTGCAAGGCTTCCGGCTACATCTTCACCAGCTACTA TATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGC GAGATCAACCCCTTCCAATGGCGACACAACTTCAATGAGAAGTTTAAGA GCAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACCGCTTACATGGA GCTGTCCAGCCTGAGGTCTGAGGACACAGCCGTGTACTATTGTACCAGG AGCGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCACAACAGTGA CCGTGTCTTCCGCCAGCACAAAGGGCCCTTCCGTGTTCCCCCTGGCTCC TTGCTCCAGGAGCACATCTGAGTCCACCGCCGCTCTGGGCTGTCTGGTG AAGGACTACTTCCCAGAGCCCGTGACCGTGTCTGGAATAGCGGCGCCC TGACATCCGGAGTGACACCTTCCAGCTGTGCTGCAGAGCTCTGGCCT GTACAGCCTGTCCAGCGTGGTGACAGTGCCCTCTTCCAGCCTGGGCACC AAGACATATACCTGCAACGTGGACCATAAGCCTTCTAATACCAAGGTGG ATAAGAGAGTGGAGTCCAAGTACGGACCACCTTGCCCTCCTTGTCTGC TCCAGAGTTCGCCGGAGGACCTTCCGTGTTCTGTTTCCACCCAAGCCA AAGGACACACTGATGATCTCTCGCACACCTGAGGTGACCTGCGTGGTGG TGGACGTGTCCCAGGAGGACCCGAGGTGCAGTTCAACTGGTACGTGGA TGGCGTGGAGGTGCACAATGCTAAGACCAAGCCAAGGGAGGAGCAGTTT AACTCCACATACCGGGTGGTGAGCGTGCTGACCGTGCTGCATCAGGATT GGCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAAGGGCCTGCC CTCTTCCATCGAGAAGACAATCTCTAAGGCTAAGGGACAGCCAAGGGAG CCACAGGTGTACACCCTGCCCTCCAAGCCAGGAGGAGATGACAAAGAACC AGGTGTCTCTGACCTGTCTGGTGAAGGGCTTCTATCCATCTGACATCGC TGTGGAGTGGGAGTCCAATGGCCAGCCCGAGAACAATTACAAGACCACA CCCCCTGTGCTGGACTCTGATGGCTCCTTCTTCTGTATTCTAGACTGA CCGTGGATAAGTCCCGCTGGCAGGAGGGCAACGTGTTCTCTGCTCTGT GATGCACGAAGCACTGCACAATCATTACACTCAGAAGAGCCTGTCACTG TCCCTGGGC
Heavy chain DNA sequences WITHOUT LEADER; with terminal K		
185	TNX01 VH-CH1-CH2-CH3 IgG1 (N297Q) (with terminal K)	CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGGTGAAGCCAGGCGCCT CTGTGAAGCTGTCTTGCAAGGCTAGCGGCTACATCTTCACCTCCTACTA TATGTATTGGGTGAAGCAGGCTCCTGGACAGGGACTGGAGTGGATCGGC GAGATCAACCCATCTAATGGCGACACCACTTCAATGAGAAGTTTAAGT CCAAGGCTACCCTGACAGTGGATAAGTCCGCCCTCTACAGCCTACATGGA GCTGTCCAGCCTGAGAAGCGAGGACACCGCCGTGTACTATTGCACAAGG TCTGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCACCCTGGTGA CAGTGTCTTCCGCTTCTACCAAGGGCCCTTCCGTGTTTCCACTGGCTCC AAGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTG AAGGACTATTTCCCTGAGCCAGTGACAGTGAGCTGGAACCTTGGCGCTC TGACCTCCGGCGTGACACATTTCCAGCCGTGCTGCAGTCCAGCGGCCCT GTACAGCCTGTCTTCCGTGGTGACCGTGCCAAGCTCTTCCCTGGGCACC CAGACATATATCTGCAACGTGAATCATAAGCCCTCTAATACAAAGGTGG ACAAGAAGGTGGAGCCCAAGTCTTGTGATAAAACACATACTTGCCCCC TTGTCTTGCACCAGAACTGCTGGGAGGACCTAGCGTGTTCTGTTTCCA CCCAAGCCAAAAGACACCCTGATGATTAGTAGAACCCCTGAGGTACAT GCGTGGTCTGTGGACGTGAGCCACGAGGACCCCGAGGTGAAGTTCAACTG GTACGTGGACGGCGTGGAGGTGCACAATGCTAAGACCAAGCCAGAGAG GAGCAGTACCAGAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGCTGC ATCAGGATTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAA GGCTCTGCCCCGCCCTATCGAGAAGACCATCTCTAAGGCTAAGGGCCAG CCTAGGGAGCCACAGGTGTACACACTGCCCCCTTCCGGGACGAGCTGA CCAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCCAG CGATATCGCCGTGGAGTGGGAGTCTAATGGCCAGCCTGAGAACAATTAC AAGACCACACCACCGTGCTGGACTCCGATGGCAGCTTCTTCTGTATT CCAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTTT TTGTTCCGTGATGCACGAGGCCCTGCACAATCATTACACACAGAAGAGC CTGTCTCTGTCCCTGGCAAG

186	TNX02 VH-CH1-CH2-CH3 IgG1 (wt) (with terminal K)	CAGGTGCAGCTGGTGCAGTCCGGAGCTGAGGTGGTGAAGCCAGGAGCCT CTGTGAAGCTGTCTTGCAAGGCTAGCGGCTACATCTTCACCAGCTACTA TATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGC GAGATCAACCCCTTCTAATGGCGACACCAACTTCAATGAGAAGTTTAAGT CCAAGGCTACCCTGACAGTGGATAAGTCCGCCTCTACAGCCTACATGGA GCTGTCCAGCCTGAGGTCTGAGGACACCGCCGTGTAATTTGCACAAGG TCTGATGGCCGGAACGACATGGATTCTGTTGGGCCAGGGCACCCTGGTGA CAGTGTCTTCCGCTTCTACCAAGGGACCATCCGTGTTTCCACTGGCTCC AAGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTG AAGGACTATTTCCAGAGCCCGTGACAGTGAGCTGGAACCTCTGGCGCTC TGACCAGCGGCGTGACACATTTCCAGCCGTGCTGCAGTCCAGCGGCCT GTACTCTCTGTCTTCCGTGGTGACCGTGCCCTAGCTCTTCCCTGGGCACC CAGACATATATCTGCAACGTGAATCACAAGCCTAGCAATACAAAGGTGG ACAAGAAGGTGGAGCCAAAGTCTTGTGATAAGACCCATACATGCCCCC TTGTCCTGCTCCAGAGCTGCTGGGAGGACCATCCGTGTTCTGTTTCCA CCCAAGCCCAAGGACACCCTGATGATCTCCAGAACCCTGAGGTGACAT GCGTGGTGGTGGACGTGAGCCACGAGGACCCGAGGTGAAGTTCAACTG GTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACCAAGCCTAGAGAG GAGCAGTACAATAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGCTGC ACCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCTAATAA GGCTCTGCCCCCCCCTATCGAGAAGACCATCTCCAAGGCTAAGGGCCAG CCTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGA CCAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCAAG CGATATCGCCGTGGAGTGGGAGTCTAATGGCCAGCCCGAGAACAATTAC AAGACCACACCCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATT CCAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTTTC TTGTTCCGTGATGCATGAGGCTCTGCACAATCATTACACACAGAAGAGC CTGTCTCTGTCCCCAGGCAAG
187	TNX03 VH-CH1-CH2-CH3 IgG1 (N297G) (with terminal K)	CAGGTGCAGCTGGTGCAGTCCGGAGCTGAGGTGGTGAAGCCAGGAGCCT CTGTGAAGCTGTCTTGCAAGGCTAGCGGCTACATCTTCACCAGCTACTA TATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGC GAGATCAACCCCTTCTAATGGCGACACCAACTTCAATGAGAAGTTTAAGT CCAAGGCTACCCTGACAGTGGATAAGTCCGCCTCTACAGCCTACATGGA GCTGTCCAGCCTGAGGTCTGAGGACACCGCCGTGTAATTTGCACAAGG TCTGATGGCCGGAACGACATGGATTCTGTTGGGCCAGGGCACCCTGGTGA CAGTGTCTTCCGCTTCTACCAAGGGACCATCCGTGTTTCCACTGGCTCC AAGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTG AAGGACTATTTCCAGAGCCCGTGACAGTGAGCTGGAACCTCTGGCGCTC TGACCAGCGGCGTGACACATTTCCAGCCGTGCTGCAGTCCAGCGGCCT GTACTCTCTGTCTTCCGTGGTGACCGTGCCCTAGCTCTTCCCTGGGCACC CAGACATATATCTGCAACGTGAATCACAAGCCTAGCAATACAAAGGTGG ACAAGAAGGTGGAGCCAAAGTCTTGTGATAAGACCCATACATGCCCCC TTGTCCTGCTCCAGAGCTGCTGGGAGGACCATCCGTGTTCTGTTTCCA CCCAAGCCCAAGGACACCCTGATGATCTCCAGAACCCTGAGGTGACAT GCGTGGTGGTGGACGTGAGCCACGAGGACCCCGAGGTGAAGTTCAACTG GTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACCAAGCCTAGAGAG GAGCAGTACGGCAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGCTGC ACCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCTAATAA GGCTCTGCCCCCCCCTATCGAGAAGACCATCTCCAAGGCTAAGGGCCAG CCTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGA CCAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCAAG CGATATCGCCGTGGAGTGGGAGTCTAATGGCCAGCCCGAGAACAATTAC AAGACCACACCCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATT CCAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTTTC TTGTTCCGTGATGCATGAGGCTCTGCACAATCATTACACACAGAAGAGC CTGTCTCTGTCCCCAGGCAAG

188	TNX04 VH-CH1-CH2-CH3 IgG1 (C220S, C226S, C229S, P238S) (with terminal K)	CAGGTGCAGCTGGTGCAGAGCGGAGCTGAGGTGGTGAAGCCAGGAGCCTCTGTGAAGCTGTCTTGCAAGGCTAGCGGCTACATCTTCACCTCTTACTATATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGCAGATCAACCCCTTCTAATGGCGACACCAACTTCAATGAGAAGTTTAAGTCCAAGGCTACCCTGACAGTGGATAAGTCTGCTTCCACAGCCTACATGGAGCTGTCCAGCCTGAGGTCCGAGGACACCGCCGTGTACTATTGCACAAGGTCTGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCACCTGGTGAAGGTCTTCCGCTTCTACCAAGGGACCATCCGTGTTTCCACTGGCTCCAAGCTCTAAGAGCACCTCTGGAGGAACAGCCGCTCTGGGATGTCTGGTG AAGGACTATTTCCAGAGCCCGTGACAGTGTCTTGGAACCTCCGGCGCTCTGACCTCTGGCGTGCACACATTTCTGCGGTGCTGCAGTCCAGCGGCCTGTACTCCCTGTCTTCCGTGGTGACCGTGCCAAAGCTCTTCCCTGGGCACCAGACATATATCTGCAACGTGAATCACAAGCCTTCCAATACAAAGGTGGACAAGAAGGTGGAGCCAAAGAGCTCTGATAAGACCCATACAAAGCCCCCTTCTCCTGCTCCAGAGCTGCTGGGAGGCTCCAGCGTGTTCCTGTTTCCA CCAAGCCAAAGGACACCCTGATGATCAGCAGAACCCCGAGGTGACATGCGTGGTGGTGGACGTGTCTCACGAGGACCCCGAGGTGAAGTTCAACTGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACCAAGCCTAGAGAGAGCAGTACAATAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGTCTGCCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCCAATAAGGCTCTGCCCCCCCTATCGAGAAGACCATCAGCAAGGCTAAGGGCCAGCCTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGCCAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCAAGCGATATCGCCGTGGAGTGGGAGTCTAATGGCCAGCCGAGAACCAATTACAAGACCACACCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATTCCAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTTTCTGTAGCGTGATGCATGAGGCTCTGCACAATCATTACACACAGAAGTCTCTGTCCCTGAGCCCTGGCAAG
189	TNX05 VH-CH1-CH2-CH3 IgG4 (S228P, L235A) (with terminal K)	CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGGTGAAGCCTGGAGCTAGCGTGAAGCTGTCTTGCAAGGCTTCCGCTACATCTTCACCTCCTACTATATGTATTGGGTGAAGCAGGCTCCTGGACAGGGCCTGGAGTGGATCGGCAGATCAACCCATCCAATGGCGACACAACTTCAATGAGAAGTTTAAGAGCAAGGCTACCCTGACAGTGGATAAGTCCGCTCTACCGCTACATGGAGCTGTCCAGCCTGAGGAGCGAGGACACAGCCGTGTACTATTGTACCAGGAGCGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCACACTGGTGA CCGTGTCTTCCGCTAGCACAAAGGGACCATCCGTGTTCCCACTGGCTCCATGCTCCAGGAGCACATCTGAGTCCACCGCCGCTCTGGGCTGTCTGGTG AAGGACTATTTCCCTGAGCCAGTGACCGTGTCTTGGGAATAGCGCGCTCTGACATCCGGAGTGCACACCTTTCCAGCCGTGCTGCAGAGCTCTGGCCTGTACAGCCTGTCCAGCGTGGTGACAGTGCCTTCTTCCAGCCTGGGCACC AAGACATATACCTGCAACGTGGACCATAAGCCATCTAATACCAAGGTGGATAAGAGAGTGGAGTCCAAGTACGGACACCTTGCCACCATGTCCAGCTCCTGAGTTCGCTGGAGGACCATCCGTGTTCTGTTTCCAAAGCCC AAGGACACCCTGATGATCTCTCGCACACCAGAGGTGACCTGCGTGGTGGTGGACGTGTCCCAGGAGGACCCGAGGTGCAGTTCAACTGGTACGTGGA TGGCGTGGAGGTGCACAATGCTAAGACCAAGCCCAGGGAGGAGCAGTTTAACTCCACATACCGGGTGGTGAGCGTGCTGACCGTGCTGCATCAGGATTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAAGGGCCTGCC TTCTTCCATCGAGAAGACAATCTCTAAGGCTAAGGGCCAGCCTCGGGAGCCACAGGTGTACACCTGCCCTAGCCAGGAGGAGATGACAAAGAACCAGGTGTCTGACCTGTCTGGTGAAGGGCTTCTATCCCTCCGACATCGC CGTGGAGTGGGAGAGCAATGGCCAGCCTGAGAACCAATTACAAGACCACA CCACCCGTGCTGGACTCTGATGGCTCCTTCTTCTGTATTCTAGACTGACCGTCGATAAGTCCCGCTGGCAGGAGGGCAACGTGTTTAGCTGCTCTGTGATGCACGAGGCCCTGCACAATCATTACACCCAGAAGTCCCTGAGCCTGTCTTGGGCAAG

307	TNX06 VH-CH1-CH2-CH3 IgG4 (wild type) (with terminal K)	CAGGTCCAGCTGGTCCAGTCAGGGGCTGAAGTGGTCAAACCCGGCGCCA GCGTGAAGCTGTCTTGCAAGGCTTCCGGCTACATCTTCACCAGCTACTA TATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGC GAGATCAACCCTTCCAATGGCGACACAACTTCAATGAGAAGTTTAAGA GCAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACCGCTTACATGGA GCTGTCCAGCCTGAGGTCTGAGGACACAGCCGTGTACTATTGTACCAGG AGCGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCAGCTGGTGA CCGTGTCTTCCGCCAGCACAAAGGGCCCTTCCGTGTTCCCCCTGGCTCC TTGCTCCAGGAGCACATCTGAGTCCACCGCCGCTCTGGGCTGTCTGGTG AAGGACTACTTCCCAGAGCCCGTGACCGTGTCTGGAATAGCGGCGCCC TGACATCCGGAGTGACACCTTTCAGCTGTGCTGCAGAGCTCTGGCCT GTACAGCCTGTCCAGCGTGGTGACAGTGCCCTCTTCAGCCTGGGCACC AAGACATATACCTGCAACGTGGACCATAAGCCTTCTAATACCAAGGTGG ATAAGAGAGTGGAGTCCAAGTACGGACCACCTTGCCCTAGCTGTCTGC TCCAGAGTTCTTGGGAGGACCTTCCGTGTTCTGTTCACCCAAGCCA AAGGACACACTGATGATCTCTCGCACACCTGAGGTGACCTGCGTGGTGG TGGACGTGTCCCAGGAGGACCCGAGGTGCAGTTCAACTGGTACGTGGA TGGCGTGGAGGTGCACAATGCTAAGACCAAGCCAAGGGAGGAGCAGTTT AACTCCACATACCGGGTGGTGAGCGTGCTGACCGTGCTGCATCAGGATT GGCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAAGGGCCTGCC CTCTTCCATCGAGAAGACAATCTCTAAGGCTAAGGGACAGCCAAGGGAG CCACAGGTGTACACCCTGCCTCCAAGCCAGGAGGAGATGACAAAGAACC AGGTGTCTCTGACCTGTCTGGTGAAGGGCTTCTATCCATCTGACATCGC TGTGGAGTGGGAGTCCAATGGCCAGCCCGAGAACAATTACAAGACCACA CCCCCTGTGCTGGACTCTGATGGCTCCTTCTTCTGTATTCTAGACTGA CCGTGGATAAGTCCCGCTGGCAGGAGGGCAACGTGTTCTCTGCTCTGT GATGCACGAAGCACTGCACAATCATTACACTCAGAAGAGCCTGTCACTG TCCCTGGGCAAA
308	TNX07 VH-CH1-CH2-CH3 IgG4 (S228P) (with terminal K)	CAGGTCCAGCTGGTCCAGTCAGGGGCTGAAGTGGTCAAACCCGGCGCCA GCGTGAAGCTGTCTTGCAAGGCTTCCGGCTACATCTTCACCAGCTACTA TATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGC GAGATCAACCCTTCCAATGGCGACACAACTTCAATGAGAAGTTTAAGA GCAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACCGCTTACATGGA GCTGTCCAGCCTGAGGTCTGAGGACACAGCCGTGTACTATTGTACCAGG AGCGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCAGCTGGTGA CCGTGTCTTCCGCCAGCACAAAGGGCCCTTCCGTGTTCCCCCTGGCTCC TTGCTCCAGGAGCACATCTGAGTCCACCGCCGCTCTGGGCTGTCTGGTG AAGGACTACTTCCCAGAGCCCGTGACCGTGTCTGGAATAGCGGCGCCC TGACATCCGGAGTGACACCTTTCAGCTGTGCTGCAGAGCTCTGGCCT GTACAGCCTGTCCAGCGTGGTGACAGTGCCCTCTTCAGCCTGGGCACC AAGACATATACCTGCAACGTGGACCATAAGCCTTCTAATACCAAGGTGG ATAAGAGAGTGGAGTCCAAGTACGGACCACCTTGCCCTCCCTGTCTGC TCCAGAGTTCTTGGGAGGACCTTCCGTGTTCTGTTCACCCAAGCCA AAGGACACACTGATGATCTCTCGCACACCTGAGGTGACCTGCGTGGTGG TGGACGTGTCCCAGGAGGACCCGAGGTGCAGTTCAACTGGTACGTGGA TGGCGTGGAGGTGCACAATGCTAAGACCAAGCCAAGGGAGGAGCAGTTT AACTCCACATACCGGGTGGTGAGCGTGCTGACCGTGCTGCATCAGGATT GGCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAAGGGCCTGCC CTCTTCCATCGAGAAGACAATCTCTAAGGCTAAGGGACAGCCAAGGGAG CCACAGGTGTACACCCTGCCTCCAAGCCAGGAGGAGATGACAAAGAACC AGGTGTCTCTGACCTGTCTGGTGAAGGGCTTCTATCCATCTGACATCGC TGTGGAGTGGGAGTCCAATGGCCAGCCCGAGAACAATTACAAGACCACA CCCCCTGTGCTGGACTCTGATGGCTCCTTCTTCTGTATTCTAGACTGA CCGTGGATAAGTCCCGCTGGCAGGAGGGCAACGTGTTCTCTGCTCTGT GATGCACGAAGCACTGCACAATCATTACACTCAGAAGAGCCTGTCACTG TCCCTGGGCAAA

309	TNX08 VH-CH1-CH2-CH3 (IgG4 S228P/L235E) (with terminal K)	CAGGTCCAGCTGGTCCAGTCAGGGGCTGAAGTGGTCAAACCCGGCGCCA GCGTGAAGCTGTCTTGCAAGGCTTCCGGCTACATCTTCACCAGCTACTA TATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGC GAGATCAACCCTTCCAATGGCGACACAACTTCAATGAGAAGTTTAAGA GCAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACCGCTTACATGGA GCTGTCCAGCCTGAGGTCTGAGGACACAGCCGTGTACTATTGTACCAGG AGCGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCAGCTGGTGA CCGTGTCTTCCGCCAGCACAAAGGGCCCTTCCGTGTTCCCCCTGGCTCC TTGCTCCAGGAGCACATCTGAGTCCACCGCCGCTCTGGGCTGTCTGGTG AAGGACTACTTCCCAGAGCCCGTGACCGTGTCTGGAATAGCGGCGCCC TGACATCCGGAGTGACACCTTTCAGCTGTGCTGCAGAGCTCTGGCCT GTACAGCCTGTCCAGCGTGGTGACAGTGCCCTCTTCAGCCTGGGCACC AAGACATATACCTGCAACGTGGACCATAAGCCTTCTAATACCAAGGTGG ATAAGAGAGTGGAGTCCAAGTACGGACCACCTTGCCCTCCCTGTCTGC TCCAGAGTTCGAGGGAGGACCTTCCGTGTTCTGTTTCCACCCAAGCCA AAGGACACACTGATGATCTCTCGCACACCTGAGGTGACCTGCGTGGTGG TGGACGTGTCCCAGGAGGACCCGAGGTGCAGTTCAACTGGTACGTGGA TGGCGTGGAGGTGCACAATGCTAAGACCAAGCCAAGGGAGGAGCAGTTT AACTCCACATACCGGGTGGTGAGCGTGCTGACCGTGCTGCATCAGGATT GGCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAAGGGCCTGCC CTCTTCCATCGAGAAGACAATCTCTAAGGCTAAGGGACAGCCAAGGGAG CCACAGGTGTACACCCTGCCTCCAAGCCAGGAGGAGATGACAAAGAACC AGGTGTCTCTGACCTGTCTGGTGAAGGGCTTCTATCCATCTGACATCGC TGTGGAGTGGGAGTCCAATGGCCAGCCCGAGAACAATTACAAGACCACA CCCCCTGTGCTGGACTCTGATGGCTCCTTCTTCTGTATTCTAGACTGA CCGTGGATAAGTCCCGCTGGCAGGAGGGCAACGTGTTCTCTGCTCTGT GATGCACGAAGCACTGCACAATCATTACACTCAGAAGAGCCTGTCACTG TCCCTGGGCAAA
310	TNX09 VH-CH1-CH2-CH3 IgG4 (S228P/F234A/L235A) (with terminal K)	CAGGTCCAGCTGGTCCAGTCAGGGGCTGAAGTGGTCAAACCCGGCGCCA GCGTGAAGCTGTCTTGCAAGGCTTCCGGCTACATCTTCACCAGCTACTA TATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGC GAGATCAACCCTTCCAATGGCGACACAACTTCAATGAGAAGTTTAAGA GCAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACCGCTTACATGGA GCTGTCCAGCCTGAGGTCTGAGGACACAGCCGTGTACTATTGTACCAGG AGCGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCAGCTGGTGA CCGTGTCTTCCGCCAGCACAAAGGGCCCTTCCGTGTTCCCCCTGGCTCC TTGCTCCAGGAGCACATCTGAGTCCACCGCCGCTCTGGGCTGTCTGGTG AAGGACTACTTCCCAGAGCCCGTGACCGTGTCTGGAATAGCGGCGCCC TGACATCCGGAGTGACACCTTTCAGCTGTGCTGCAGAGCTCTGGCCT GTACAGCCTGTCCAGCGTGGTGACAGTGCCCTCTTCAGCCTGGGCACC AAGACATATACCTGCAACGTGGACCATAAGCCTTCTAATACCAAGGTGG ATAAGAGAGTGGAGTCCAAGTACGGACCACCTTGCCCTCCCTGTCTGC TCCAGAGGCCGCGGAGGACCTTCCGTGTTCTGTTTCCACCCAAGCCA AAGGACACACTGATGATCTCTCGCACACCTGAGGTGACCTGCGTGGTGG TGGACGTGTCCCAGGAGGACCCGAGGTGCAGTTCAACTGGTACGTGGA TGGCGTGGAGGTGCACAATGCTAAGACCAAGCCAAGGGAGGAGCAGTTT AACTCCACATACCGGGTGGTGAGCGTGCTGACCGTGCTGCATCAGGATT GGCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAAGGGCCTGCC CTCTTCCATCGAGAAGACAATCTCTAAGGCTAAGGGACAGCCAAGGGAG CCACAGGTGTACACCCTGCCTCCAAGCCAGGAGGAGATGACAAAGAACC AGGTGTCTCTGACCTGTCTGGTGAAGGGCTTCTATCCATCTGACATCGC TGTGGAGTGGGAGTCCAATGGCCAGCCCGAGAACAATTACAAGACCACA CCCCCTGTGCTGGACTCTGATGGCTCCTTCTTCTGTATTCTAGACTGA CCGTGGATAAGTCCCGCTGGCAGGAGGGCAACGTGTTCTCTGCTCTGT GATGCACGAAGCACTGCACAATCATTACACTCAGAAGAGCCTGTCACTG TCCCTGGGCAAA

311	TNX10 VH-CH1-CH2-CH3 IgG1 (L234A/L235A) (with terminal K) x = A or G	CAGGTCCAGCTGGTCCAGTCAGGTGCCGAAGTGGTCAAGCCCGGCGCCTCTGTGAAGCTGTCTTGCAAGGCTAGCGGCTACATCTTCACCTCCTACTATATGTATTGGGTGAAGCAGGCTCCTGGACAGGGCCTGGAGTGGATCGGCAGATCAACCCATCTAATGGCGACACCAACTTCAATGAGAAGTTTAAGTCCAAGGCCACCCGTGACAGTGGATAAGAGCGCCTCTACAGCTTACATGGA GCTGTCCAGCCTGAGGAGCGAGGACACCGCCGTGTACTATTGCACAAGG TCTGATGGCCGGAACGACATGGATTCTCTGGGGCCAGGGCACCCTGGTGA CAGTGTCTTCCGCCTCTACCAAGGGCCCTTCCGTGTTTCCACTGGCTCC CAGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTG AAGGACTACTTCCCAGAGCCCGTGACAGTGAGCTGGAACCTCTGGCGCCC TGACCAGCGGAGTGACACATTTCTGTGTGTGTGCTGACGTCCAGCGGCCT GTACTCTCTGTCTTCCGTGGTGACCGTGCCAAGCTCTTCCCTGGGCACC CAGACATATATCTGCAACGTGAATCACAAGCCAAGCAATACAAAGGTGG ACAAGAAGGTGGAGCCCAAGTCTTGTGATAAGACCCATACATGCCCCCC TTGTCTGTCTCCAGAGGCTGTCTGGAGGACCATCCGTGTTCTGTCTTCCA CCAAGCCCTAAGGACACCCTGATGATCTCCAGAACCCAGAGGTGACAT GCGTGGTGGTGGACGTGAGCCACGAGGACCCCGAGGTGAAGTTCAACTG GTACGTGGATGGCGTGGAGGTGCATAATGCTAAGACCAAGCCAAGAGAG GAGCAGTACAACAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGCTGC ATCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCTAATAA GGCCCTGCCCGCTCCTATCGAGAAGACCATCTCCAAGGCCAAGGGCCAG CCTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGA CCAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCCAG CGATATCGCTGTGGAGTGGGAGTCTAATGGCCAGCCTGAGAACCAATTAC AAGACCACACCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATT CCAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTCTC CTGTTCCGTCTATGCACGAGGCACTGCACAATCATTACACCCAGAAGTCA CTGTCACTGTCAACGAGGAAAx
312	TNX11 VH-CH1-CH2-CH3 IgG1 (C226S, C229S, P238S) (with terminal K) x = A or G	CAGGTCCAGCTGGTCCAGTCAGGTGCCGAAGTGGTCAAGCCCGGCGCCTCTGTGAAGCTGTCTTGCAAGGCTAGCGGCTACATCTTCACCTCCTACTATATGTATTGGGTGAAGCAGGCTCCTGGACAGGGCCTGGAGTGGATCGGCAGATCAACCCATCTAATGGCGACACCAACTTCAATGAGAAGTTTAAGTCCAAGGCCACCCGTGACAGTGGATAAGAGCGCCTCTACAGCTTACATGGA GCTGTCCAGCCTGAGGAGCGAGGACACCGCCGTGTACTATTGCACAAGG TCTGATGGCCGGAACGACATGGATTCTCTGGGGCCAGGGCACCCTGGTGA CAGTGTCTTCCGCCTCTACCAAGGGCCCTTCCGTGTTTCCACTGGCTCC CAGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTG AAGGACTACTTCCCAGAGCCCGTGACAGTGAGCTGGAACCTCTGGCGCCC TGACCAGCGGAGTGACACATTTCTGTGTGTGTGCTGACGTCCAGCGGCCT GTACTCTCTGTCTTCCGTGGTGACCGTGCCAAGCTCTTCCCTGGGCACC CAGACATATATCTGCAACGTGAATCACAAGCCAAGCAATACAAAGGTGG ACAAGAAGGTGGAGCCCAAGTCTTGTGATAAGACCCATACATccCCCC TTccCCTGTCTCCAGAGCTGTCTGGGAGGAAGTCCGTGTTCTGTCTTCCA CCAAGCCCTAAGGACACCCTGATGATCTCCAGAACCCAGAGGTGACAT GCGTGGTGGTGGACGTGAGCCACGAGGACCCCGAGGTGAAGTTCAACTG GTACGTGGATGGCGTGGAGGTGCATAATGCTAAGACCAAGCCAAGAGAG GAGCAGTACAACAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGCTGC ATCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCTAATAA GGCCCTGCCCGCTCCTATCGAGAAGACCATCTCCAAGGCCAAGGGCCAG CCTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGA CCAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCCAG CGATATCGCTGTGGAGTGGGAGTCTAATGGCCAGCCTGAGAACCAATTAC AAGACCACACCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATT CCAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTCTC CTGTTCCGTCTATGCACGAGGCACTGCACAATCATTACACCCAGAAGTCA CTGTCACTGTCAACGAGGAAAx

313	TNX12 VH-CH1-CH2-CH3 IgG1 (C229S, P238S) (with terminal K) x = A or G	CAGGTCCAGCTGGTCCAGTCAGGTGCCGAAGTGGTCAAGCCCGGCGCCTCTGTGAAGCTGTCTTGCAAGGCTAGCGGCTACATCTTCACCTCCTACTATATGTATTGGGTGAAGCAGGCTCCTGGACAGGGCCTGGAGTGGATCGGCAGATCAACCCATCTAATGGCGACACCAACTTCAATGAGAAGTTTAAGTCCAAGGCCACCCCTGACAGTGGATAAAGAGCGCCTCTACAGCTTACATGGAGCTGTCCAGCCTGAGGAGCGAGGACACCGCCGTGTACTATTGCACAAGGTCTGATGGCCGGAACGACATGGATTCTCTGGGGCCAGGGCACCCTGGTGAAGTGTCTTCCGCCTCTACCAAGGGCCCTTCCGTGTTTCCACTGGCTCCAGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTG AAGGACTACTTCCCAGAGCCCGTGACAGTGAGCTGGAACCTCTGGCGCCC TGACCAGCGGAGTGACACATTTCTGTGTGTGTGACAGTCCAGCGGCCTGTACTCTGTCTTCCGTGGTGACCGTGCCAAAGCTCTTCCCTGGGCACC CAGACATATATCTGCAACGTGAATCACAAGCCAAGCAATACAAAGGTGG ACAAGAAGGTGGAGCCCAAGTCTTGTGATAAGACCCATACATGCCCCCCTTCCCTGTCTCCAGAGCTGTCTGGGAGGAAGCTCCGTGTTCTGTCTTCCA CCAAGCCCTAAGGACACCCCTGATGATCTCCAGAACCCAGAGGTGACAT GCGTGGTGGTGGACGTGAGCCACGAGGACCCCGAGGTGAAGTTCAACTG GTACGTGGATGGCGTGGAGGTGCATAATGCTAAGACCAAGCCAAGAGAG GAGCAGTACAACAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGCTGC ATCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCTAATAA GGCCCTGCCCCGCTCCTATCGAGAAGACCATCTCCAAGGCCAAGGGCCAG CCTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGA CCAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCCAG CGATATCGCTGTGGAGTGGGAGTCTAATGGCCAGCCTGAGAACCAATTAC AAGACCACACCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATT CCAAGCTGACCGTGGATAAAGAGCCGCTGGCAGCAGGGCAACGTGTTCTC CTGTTCCGTCTATGCACGAGGCACTGCACAATCATTACACCCAGAAGTCA CTGTCACTGTCAACAGGAAAx
314	TNX13 VH-CH1-CH2-CH3 IgG1 (C226S, P238S) (with terminal K) x = A or G	CAGGTCCAGCTGGTCCAGTCAGGTGCCGAAGTGGTCAAGCCCGGCGCCTCTGTGAAGCTGTCTTGCAAGGCTAGCGGCTACATCTTCACCTCCTACTATATGTATTGGGTGAAGCAGGCTCCTGGACAGGGCCTGGAGTGGATCGGCAGATCAACCCATCTAATGGCGACACCAACTTCAATGAGAAGTTTAAGTCCAAGGCCACCCCTGACAGTGGATAAAGAGCGCCTCTACAGCTTACATGGAGCTGTCCAGCCTGAGGAGCGAGGACACCGCCGTGTACTATTGCACAAGGTCTGATGGCCGGAACGACATGGATTCTCTGGGGCCAGGGCACCCTGGTGAAGTGTCTTCCGCCTCTACCAAGGGCCCTTCCGTGTTTCCACTGGCTCCAGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTG AAGGACTACTTCCCAGAGCCCGTGACAGTGAGCTGGAACCTCTGGCGCCC TGACCAGCGGAGTGACACATTTCTGTGTGTGTGACAGTCCAGCGGCCTGTACTCTGTCTTCCGTGGTGACCGTGCCAAGCTCTTCCCTGGGCACC CAGACATATATCTGCAACGTGAATCACAAGCCAAGCAATACAAAGGTGG ACAAGAAGGTGGAGCCCAAGTCTTGTGATAAGACCCATACATCCCCCCTTGCCCTGTCTCCAGAGCTGTCTGGGAGGAAGTCCGTGTTCTGTCTTCCA CCAAGCCCTAAGGACACCCCTGATGATCTCCAGAACCCAGAGGTGACAT GCGTGGTGGTGGACGTGAGCCACGAGGACCCCGAGGTGAAGTTCAACTG GTACGTGGATGGCGTGGAGGTGCATAATGCTAAGACCAAGCCAAGAGAG GAGCAGTACAACAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGCTGC ATCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCTAATAA GGCCCTGCCCCGCTCCTATCGAGAAGACCATCTCCAAGGCCAAGGGCCAG CCTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGA CCAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCCAG CGATATCGCTGTGGAGTGGGAGTCTAATGGCCAGCCTGAGAACCAATTAC AAGACCACACCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATT CCAAGCTGACCGTGGATAAAGAGCCGCTGGCAGCAGGGCAACGTGTTCTC CTGTTCCGTCTATGCACGAGGCACTGCACAATCATTACACCCAGAAGTCA CTGTCACTGTCAACAGGAAAx

315	TNX14 VH-CH1-CH2-CH3 IgG4 (L115T, S228P, L235A) (with terminal K)	CAGGTCCAGCTGGTCCAGTCAGGGGCTGAAGTGGTCAAACCCGGCGCCA GCGTGAAGCTGTCTTGCAAGGCTTCCGGCTACATCTTCACCAGCTACTA TATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGC GAGATCAACCCCTTCCAATGGCGACACAACTTCAATGAGAAGTTTAAGA GCAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACCGTTACATGGA GCTGTCCAGCCTGAGGTCTGAGGACACAGCCGTGTACTATTGTACCAGG AGCGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCACAACAGTGA CCGTGTCTTCCGCCAGCACAAAGGGCCCTTCCGTGTTCCCCCTGGCTCC TTGCTCCAGGAGCACATCTGAGTCCACCGCCGCTCTGGGCTGTCTGGTG AAGGACTACTTCCCAGAGCCCGTGACCGTGTCTGGAATAGCGGCGCCC TGACATCCGGAGTGACACCTTCCAGCTGTGCTGCAGAGCTCTGGCCT GTACAGCCTGTCCAGCGTGGTGACAGTGCCCTCTTCCAGCCTGGGCACC AAGACATATACCTGCAACGTGGACCATAAGCCTTCTAATACCAAGGTGG ATAAGAGAGTGGAGTCCAAGTACGGACCACCTTGCCCTCCTTGTCTGC TCCAGAGTTCGCGGAGGACCTTCCGTGTTCTGTTTCCACCCAAGCCA AAGGACACACTGATGATCTCTCGCACACCTGAGGTGACCTGCGTGGTGG TGGACGTGTCCCAGGAGGACCCGAGGTGCAGTTCAACTGGTACGTGGA TGGCGTGGAGGTGCACAATGCTAAGACCAAGCCAAGGGAGGAGCAGTTT AACTCCACATACCGGGTGGTGAGCGTGCTGACCGTGCTGCATCAGGATT GGCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAAGGGCCTGCC CTCTTCCATCGAGAAGACAATCTCTAAGGCTAAGGGACAGCCAAGGGAG CCACAGGTGTACACCCTGCCCTCCAAGCCAGGAGGAGATGACAAAGAACC AGGTGTCTCTGACCTGTCTGGTGAAGGGCTTCTATCCATCTGACATCGC TGTGGAGTGGGAGTCCAATGGCCAGCCCGAGAACAATTACAAGACCACA CCCCCTGTGCTGGACTCTGATGGCTCCTTCTTCTGTATTCTAGACTGA CCGTGGATAAGTCCCGCTGGCAGGAGGGCAACGTGTTCTCTGCTCTGT GATGCACGAAGCACTGCACAATCATTACACTCAGAAGAGCCTGTCACTG TCCCTGGGCAAA
Heavy Chain DNA Sequences WITH LEADER; with terminal K		
190	TNX01 VH-CH1-CH2-CH3 IgG1 (N297Q) (with terminal K)	ATGCCACTGCTGCTGCTGCTGCCACTGCTGTGGGCTGGCGCTCTGGCTC AGGTGCAGCTGGTGAGTCTGGAGCTGAGGTGGTGAAGCCAGGCGCCTC TGTGAAGCTGTCTGCAAGGCTAGCGGCTACATCTTCACCTCCTACTAT ATGTATTGGGTGAAGCAGGCTCCTGGACAGGACTGGAGTGGATCGGCG AGATCAACCCATCTAATGGCGACACCAACTTCAATGAGAAGTTTAAGTC CAAGGCTACCCTGACAGTGGATAAGTCCGCCTCTACAGCCTACATGGAG CTGTCCAGCCTGAGAAGCGAGGACACCGCCGTGTACTATTGCACAAGGT CTGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCACCTGGTGAC AGTGTCTTCCGCTTCTACCAAGGGCCCTTCCGTGTTTCCACTGGCTCCA AGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTGA AGGACTATTTCCCTGAGCCAGTGACAGTGAGCTGGAACCTTGCGCTCT GACCTCCGGCGTGACACATTTCAGCCGTGCTGCAGTCCAGCGGCCCTG TACAGCCTGTCTTCCGTGGTGACCGTGCCAAGCTCTTCCCTGGGCACCC AGACATATATCTGCAACGTGAATCATAAGCCCTCTAATACAAAGGTGGA CAAGAAGGTGGAGCCCAAGTCTTGTGATAAAACATACTTGCCCCCT TGTCTGCACCAGAACTGCTGGGAGGACCTAGCGTGTTCTGTTTCCAC CCAAGCCAAAAGACACCCTGATGATTAGTAGAACCCTGAGGTACATG CGTGGTCTGTGGACGTGAGCCACGAGGACCCCGAGGTGAAGTTCAACTGG TACGTGGACGGCGTGGAGGTGCACAATGCTAAGACCAAGCCAGAGAGG AGCAGTACCAGAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGCTGCA TCAGGATTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAAG GCTCTGCCCCGCCCTATCGAGAAGACCATCTCTAAGGCTAAGGGCCAGC CTAGGGAGCCACAGGTGTACACACTGCCCCCTTCCCGGGACGAGCTGAC CAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCCAGC GATATCGCCGTGGAGTGGGAGTCTAATGGCCAGCCTGAGAACAAATTACA AGACCACACCACCGTGCTGGACTCCGATGGCAGCTTCTTCTGTATTCT CAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTTCT TGTTCCGTGATGCACGAGGCCCTGCACAATCATTACACACAGAAGAGCC TGTCTGTCTCCCTGGCAAG

191	TNX02 VH-CH1-CH2-CH3 IgG1 (wt) (with terminal K)	ATGCCCCCTGCTGCTGCTGCTGCCTCTGCTGTGGGCTGGCGCTCTGGCTC AGGTGCAGCTGGTGCAGTCCGGAGCTGAGGTGGTGAAGCCAGGAGCCTC TGTGAAGCTGTCTTCAAGGCTAGCGGCTACATCTTCACCAGCTACTAT ATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGCG AGATCAACCCTTCTAATGGCGACACCAACTTCAATGAGAAGTTTAAGTC CAAGGCTACCCTGACAGTGGATAAGTCCGCCTCTACAGCCTACATGGAG CTGTCCAGCCTGAGGTCTGAGGACACCGCCGTGTACTATTGCACAAGGT CTGATGGCCGGAACGACATGGATTCTGGGGCCAGGGCACCTGGTGAC AGTGTCTTCCGCTTCTACCAAGGGACCATCCGTGTTTCCACTGGCTCCA AGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTGA AGGACTATTTCCCAGAGCCCGTGACAGTGAGCTGGAACCTGGCGCTCT GACCAGCGGCGTGACACATTTCCAGCCGTGCTGCAGTCCAGCGGCCCTG TACTCTCTGTCTTCCGTGGTGACCGTGCCCTAGCTCTTCCCTGGGCACCC AGACATATATCTGCAACGTGAATCACAAGCCTAGCAATACAAAGGTGGA CAAGAAGGTGGAGCCAAAGTCTTGTGATAAGACCCATACATGCCCCCT TGTCTGCTCCAGAGCTGCTGGGAGGACCATCCGTGTTCTGTTTCCAC CCAAGCCCAAGGACACCCTGATGATCTCCAGAACCCTGAGGTGACATG CGTGGTGGTGGACGTGAGCCACGAGGACCCCGAGGTGAAGTTCAACTGG TACGTGGATGGCGTGGAGGTGCATAATGCCAAGACCAAGCCTAGAGAGG AGCAGTACAATAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGTGCA CCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCTAATAAG GCTCTGCCCCGCCCTATCGAGAAGACCATCTCCAAGGCTAAGGGCCAGC CTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGAC CAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCAAGC GATATCGCCGTGGAGTGGGAGTCTAATGGCCAGCCCAGAACCAATTACA AGACCACACCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATTC CAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTTTCT TGTTCCTGATGCATGAGGCTCTGCACAATCATTACACACAGAAGAGCC TGTCTCTGTCCCCAGGCAAG
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192	TNX03 VH-CH1-CH2-CH3 IgG1 (N297G) (with terminal K)	ATGCCCCCTGCTGCTGCTGCTGCCTCTGCTGTGGGCTGGCGCTCTGGCTC AGGTGCAGCTGGTGCAGTCCGGAGCTGAGGTGGTGAAGCCAGGAGCCTC TGTGAAGCTGTCCCTGCAAGGCTAGCGGCTACATCTTCACCAGCTACTAT ATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGCG AGATCAACCCTTCTAATGGCGACACCAACTTCAATGAGAAGTTTAAGTC CAAGGCTACCCTGACAGTGGATAAGTCCGCCTCTACAGCCTACATGGAG CTGTCCAGCCTGAGGTCTGAGGACACCGCCGTGTACTATTGCACAAGGT CTGATGGCCGGAACGACATGGATTCTGGGGCCAGGGCACCTGGTGAC AGTGTCTTCCGCTTCTACCAAGGGACCATCCGTGTTTCCACTGGCTCCA AGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTGA AGGACTATTTCCCAGAGCCCGTGACAGTGAGCTGGAACCTGGCGCTCT GACCAGCGGCGTGACACATTTCCAGCCGTGCTGCAGTCCAGCGGCCCTG TACTCTCTGTCTTCCGTGGTGACCGTGCCCTAGCTCTTCCCTGGGCACCC AGACATATATCTGCAACGTGAATCACAAGCCTAGCAATACAAAGGTGGA CAAGAAGGTGGAGCCAAAGTCTTGTGATAAGACCCATACATGCCCCCT TGTCTGCTCCAGAGCTGCTGGGAGGACCATCCGTGTTCTGTTTCCAC CCAAGCCAAGGACACCCTGATGATCTCCAGAACCCTGAGGTGACATG CGTGGTGGTGGACGTGAGCCACGAGGACCCCGAGGTGAAGTTCAACTGG TACGTGGATGGCGTGGAGGTGCATAATGCCAAGACCAAGCCTAGAGAGG AGCAGTACGGCAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGTGCA CCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCTAATAAG GCTCTGCCCCGCCCTATCGAGAAGACCATCTCCAAGGCTAAGGGCCAGC CTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGAC CAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCAAGC GATATCGCCGTGGAGTGGGAGTCTAATGGCCAGCCCAGAACCAATTACA AGACCACACCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATTC CAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTTTCT TGTTCCTGATGCATGAGGCTCTGCACAATCATTACACACAGAAGAGCC TGTCTCTGTCCCCAGGCAAG
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193	TNX04 VH-CH1-CH2-CH3 IgG1 (C220S, C226S, C229S, P238S) (with terminal K)	ATGCCCCCTGCTGCTGCTGCTGCCTCTGCTGTGGGCTGGCGCTCTGGCTC AGGTGCAGCTGGTGCAGAGCGGAGCTGAGGTGGTGAAGCCAGGAGCCTC TGTGAAGCTGTCTTCAAGGCTAGCGGCTACATCTTCACCTCTTACTAT ATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGCG AGATCAACCCTTCTAATGGCGACACCAACTTCAATGAGAAGTTTAAAGTC CAAGGCTACCCTGACAGTGGATAAGTCTGCTTCCACAGCCTACATGGAG CTGTCCAGCCTGAGGTCCGAGGACACCGCGTGTACTATTGCACAAGGT CTGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCACCTGGTGAC AGTGTCTTCCGCTTCTACCAAGGGACCATCCGTGTTTCCACTGGCTCCA AGCTCTAAGAGCACCTCTGGAGGAACAGCCGCTCTGGGATGTCTGGTGA AGGACTATTTCCCAGAGCCCGTGACAGTGTCTTGGAACTCCGGCGCTCT GACCTCTGGCGTGACACATTTCTGCCGTGCTGCAGTCCAGCGGCTG TACTCCCTGTCTTCCGTGGTGACCGTGCCAAGCTCTTCCCTGGGCACCC AGACATATATCTGCAACGTGAATCACAAGCCTTCCAATACAAAGGTGGA CAAGAAGGTGGAGCCAAAGAGCTCTGATAAGACCCATACAAGCCCCCT TCTCCTGCTCCAGAGCTGCTGGGAGGCTCCAGCGTGTTCCTGTTCCAC CCAAGCCAAAGGACACCCTGATGATCAGCAGAACCCCCGAGGTGACATG CGTGGTGGTGGACGTGTCTCACGAGGACCCCGAGGTGAAGTTCAACTGG TACGTGGATGGCGTGGAGGTGCATAATGCCAAGACCAAGCCTAGAGAGG AGCAGTACAATAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGTGCA CCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCCAATAAG GCTCTGCCCCGCCCTATCGAGAAGACCATCAGCAAGGCTAAGGGCCAGC CTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGAC CAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCAAGC GATATCGCCGTGGAGTGGGAGTCTAATGGCCAGCCCAGAACAAATTACA AGACCACACCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATTTC CAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTTTCC TGACGCTGATGCATGAGGCTCTGCACAATCATACACACAGAAGTCTC TGTCCCTGAGCCCTGGCAAG
194	TNX05 VH-CH1-CH2-CH3 IgG4 (S228P, L235A) (with terminal K)	ATGCCCCCTGCTGCTGCTGCTGCCTCTGCTGTGGGCTGGCGCTCTGGCTC AGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGGTGAAGCCTGGAGCTAG CGTGAAGCTGTCTTGAAGGCTTCCGGCTACATCTTCACCTCTTACTAT ATGTATTGGGTGAAGCAGGCTCCTGGACAGGGCCTGGAGTGGATCGGCG AGATCAACCCATCCAATGGCGACACAACTTCAATGAGAAGTTTAAAGAG CAAGGCTACCCTGACAGTGGATAAGTCCGCCTTACCGCTACATGGAG CTGTCCAGCCTGAGGAGCGAGGACACAGCCGTGTACTATTGTACCAGGA GCGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCACACTGGTGAC CGTGTCTTCCGCTAGCACAAAGGGACCATCCGTGTTCCACTGGCTCCA TGCTCCAGGAGCACATCTGAGTCCACCGCCGCTCTGGGCTGTCTGGTGA AGGACTATTTCCCTGAGCCAGTGACCGTGTCTTGGAAATAGCGGCGCTCT GACATCCGGAGTGACACCTTTCCAGCCGTGCTGCAGAGCTCTGGCCTG TACAGCCTGTCCAGCGTGGTGACAGTGCCTTCTTCCAGCCTGGGCACCA AGACATATACCTGCAACGTGGACCATAAGCCATCTAATACCAAGGTGGA TAAGAGAGTGGAGTCCAAGTACGGACCACCTTGCCCACCATGTCCAGCT CCTGAGTTCTGCTGGAGGACCATCCGTGTTCTGTTTCTCCAAAGCCCA AGGACACCCTGATGATCTCTCGCACACCAGAGGTGACCTGCGTGGTGGT GGACGTGTCCAGGAGGACCCCGAGGTGCAGTTCAACTGGTACGTGGAT GGCGTGGAGGTGCACAATGCTAAGACCAAGCCAGGGAGGAGCAGTTTA ACTCCACATACCGGGTGGTGAGCGTGTGACCGTGTGCTGCATCAGGATTG GCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAAGGGCCTGCCT TCTTCCATCGAGAAGACAATCTCTAAGGCTAAGGGCCAGCCTCGGGAGC CACAGGTGTACACCCTGCCCCCTAGCCAGGAGGAGATGACAAAAGAACCA GGTGTCTCTGACCTGTCTGGTGAAGGGCTTCTATCCCTCCGACATCGCC GTGGAGTGGGAGAGCAATGGCCAGCCTGAGAACAATTACAGACCACAC CACCCGTGCTGGACTCTGATGGCTCCTTCTTTCTGTATTCTAGACTGAC CGTCGATAAGTCCCGCTGGCAGGAGGGCAACGTGTTTGTAGCTGCTGTG ATGCACGAGGCCCTGCACAATCATACACCAGAAAGTCCCTGAGCCTGT CTCTGGGCAAG

316	TNX06 VH-CH1-CH2-CH3 IgG4 (wild type) (with terminal K)	ATGCCTCTGCTGCTGCTGCTGCCTCTGCTGTGGGCCGGTGCTCTGGCTC AGGTCCAGCTGGTCCAGTCAGGGGCTGAAGTGGTCAAACCCGGCGCCAG CGTGAAGCTGTCTTGAAGGCTTCCGGCTACATCTTCACCAGCTACTAT ATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGCG AGATCAACCCTTCCAATGGCGACACAACTTCAATGAGAAGTTTAAGAG CAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACCGCTTACATGGAG CTGTCCAGCCTGAGGTCTGAGGACACAGCCGTGTACTATTGTACCAGGA GCGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCACACTGGTGAC CGTGTCTTCCGCCAGCACAAAGGGCCCTTCCGTGTTCCCCCTGGCTCCT TGCTCCAGGAGCACATCTGAGTCCACCGCCGCTCTGGGCTGTCTGGTGA AGGACTACTTCCCAGAGCCCGTGACCGTGTCTGGAATAGCGGCGCCCT GACATCCGGAGTGACACCTTTCCAGCTGTGCTGCAGAGCTCTGGCCTG TACAGCCTGTCCAGCGTGGTGACAGTGCCCTCTTCCAGCCTGGGCACCA AGACATATACCTGCAACGTGGACCATAAGCCTTCTAATACCAAGGTGGA TAAGAGAGTGGAGTCCAAGTACGGACCACCTTGCCCTAGCTGTCTGTCT CCAGAGTTCTTGGGAGGACCTTCCGTGTTCTGTTTCCACCAAGCCAA AGGACACACTGATGATCTCTCGCACACCTGAGGTGACCTGCGTGGTGGT GGACGTGTCCCAGGAGGACCCCGAGGTGCAGTTCAACTGGTACGTGGAT GGCGTGGAGGTGCACAATGCTAAGACCAAGCCAAGGGAGGAGCAGTTTA ACTCCACATACCGGGTGGTGAGCGTGCTGACCGTGCTGCATCAGGATTG GCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAAGGGCCTGCC TCTTCCATCGAGAAGACAATCTTAAGGCTAAGGGACAGCCAAGGGAGC CACAGGTGTACACCCTGCCTCCAAGCCAGGAGGAGATGACAAAGAACCA GGTGTCTCTGACCTGTCTGGTGAAGGGCTTCTATCCATCTGACATCGCT GTGGAGTGGGAGTCCAATGGCCAGCCCAGAACCAATTACAGACCACAC CCCCGTGTGCTGGACTCTGATGGCTCCTTCTTTCTGTATTCTAGACTGAC CGTGGATAAGTCCCGCTGGCAGGAGGGCAACGTGTTCTCCTGCTCTGTG ATGCACGAAGCACTGCACAATCATTACACTCAGAAGAGCCTGTCACTGT CCCTGGGCAAA
317	TNX07 VH-CH1-CH2-CH3 IgG4 (S228P) (with terminal K)	ATGCCTCTGCTGCTGCTGCTGCCTCTGCTGTGGGCCGGTGCTCTGGCTC AGGTCCAGCTGGTCCAGTCAGGGGCTGAAGTGGTCAAACCCGGCGCCAG CGTGAAGCTGTCTTGAAGGCTTCCGGCTACATCTTCACCAGCTACTAT ATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGCG AGATCAACCCTTCCAATGGCGACACAACTTCAATGAGAAGTTTAAGAG CAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACCGCTTACATGGAG CTGTCCAGCCTGAGGTCTGAGGACACAGCCGTGTACTATTGTACCAGGA GCGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCACACTGGTGAC CGTGTCTTCCGCCAGCACAAAGGGCCCTTCCGTGTTCCCCCTGGCTCCT TGCTCCAGGAGCACATCTGAGTCCACCGCCGCTCTGGGCTGTCTGGTGA AGGACTACTTCCCAGAGCCCGTGACCGTGTCTGGAATAGCGGCGCCCT GACATCCGGAGTGACACCTTTCCAGCTGTGCTGCAGAGCTCTGGCCTG TACAGCCTGTCCAGCGTGGTGACAGTGCCCTCTTCCAGCCTGGGCACCA AGACATATACCTGCAACGTGGACCATAAGCCTTCTAATACCAAGGTGGA TAAGAGAGTGGAGTCCAAGTACGGACCACCTTGCCCTCCCTGTCTGTCT CCAGAGTTCTTGGGAGGACCTTCCGTGTTCTGTTTCCACCAAGCCAA AGGACACACTGATGATCTCTCGCACACCTGAGGTGACCTGCGTGGTGGT GGACGTGTCCCAGGAGGACCCCGAGGTGCAGTTCAACTGGTACGTGGAT GGCGTGGAGGTGCACAATGCTAAGACCAAGCCAAGGGAGGAGCAGTTTA ACTCCACATACCGGGTGGTGAGCGTGCTGACCGTGCTGCATCAGGATTG GCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAAGGGCCTGCC TCTTCCATCGAGAAGACAATCTTAAGGCTAAGGGACAGCCAAGGGAGC CACAGGTGTACACCCTGCCTCCAAGCCAGGAGGAGATGACAAAGAACCA GGTGTCTCTGACCTGTCTGGTGAAGGGCTTCTATCCATCTGACATCGCT GTGGAGTGGGAGTCCAATGGCCAGCCCAGAACCAATTACAGACCACAC CCCCGTGTGCTGGACTCTGATGGCTCCTTCTTTCTGTATTCTAGACTGAC CGTGGATAAGTCCCGCTGGCAGGAGGGCAACGTGTTCTCCTGCTCTGTG ATGCACGAAGCACTGCACAATCATTACACTCAGAAGAGCCTGTCACTGT CCCTGGGCAAA

318	TNX08 VH-CH1-CH2-CH3 (IgG4 S228P/L235E) (with terminal K)	ATGCCTCTGCTGCTGCTGCTGCCTCTGCTGTGGGCCGGTGCTCTGGCTC AGGTCCAGCTGGTCCAGTCAGGGGCTGAAGTGGTCAAACCCGGCGCCAG CGTGAAGCTGTCTTGCAAGGCTTCCGGCTACATCTTCACCAGCTACTAT ATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGCG AGATCAACCCTTCCAATGGCGACACAACTTCAATGAGAAGTTTAAGAG CAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACCGCTTACATGGAG CTGTCCAGCCTGAGGTCTGAGGACACAGCCGTGTACTATTGTACCAGGA GCGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCACACTGGTGAC CGTGTCTTCCGCCAGCACAAAGGGCCCTTCCGTGTTCCCCCTGGCTCCT TGCTCCAGGAGCACATCTGAGTCCACCGCCGCTCTGGGCTGTCTGGTGA AGGACTACTTCCCAGAGCCCGTGACCGTGTCTGGAATAGCGGCGCCCT GACATCCGGAGTGACACCTTTCCAGCTGTGCTGCAGAGCTCTGGCCTG TACAGCCTGTCCAGCGTGGTGACAGTGCCCTCTTCCAGCCTGGGCACCA AGACATATACCTGCAACGTGGACCATAAGCCTTCTAATACCAAGGTGGA TAAGAGAGTGGAGTCCAAGTACGGACCACCTTGCCCTCCCTGTCTGTCT CCAGAGTTCGAGGGAGGACCTTCCGTGTTCTGTTTCCACCAAGCCAA AGGACACACTGATGATCTCTCGCACACCTGAGGTGACCTGCGTGGTGGT GGACGTGTCCCAGGAGGACCCCGAGGTGCAGTTCAACTGGTACGTGGAT GGCGTGGAGGTGCACAATGCTAAGACCAAGCCAAGGGAGGAGCAGTTTA ACTCCACATACCGGGTGGTGAGCGTGCTGACCGTGCTGCATCAGGATTG GCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAAGGGCCTGCC TCTTCCATCGAGAAGACAATCTTAAGGCTAAGGGACAGCCAAGGGAGC CACAGGTGTACACCCTGCCTCCAAGCCAGGAGGAGATGACAAAGAACCA GGTGTCTCTGACCTGTCTGGTGAAGGGCTTCTATCCATCTGACATCGCT GTGGAGTGGGAGTCCAATGGCCAGCCCGAGAACAATTACAGACCACAC CCCTGTGCTGGACTCTGATGGCTCCTTCTTTCTGTATTCTAGACTGAC CGTGGATAAGTCCCGCTGGCAGGAGGGCAACGTGTTCTCCTGCTCTGTG ATGCACGAAGCACTGCACAATCATTACACTCAGAAGAGCCTGTCACTGT CCCTGGGCAAA
319	TNX09 VH-CH1-CH2-CH3 IgG4 (S228P/F234A/L235A) (with terminal K)	ATGCCTCTGCTGCTGCTGCTGCCTCTGCTGTGGGCCGGTGCTCTGGCTC AGGTCCAGCTGGTCCAGTCAGGGGCTGAAGTGGTCAAACCCGGCGCCAG CGTGAAGCTGTCTTGCAAGGCTTCCGGCTACATCTTCACCAGCTACTAT ATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGCG AGATCAACCCTTCCAATGGCGACACAACTTCAATGAGAAGTTTAAGAG CAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACCGCTTACATGGAG CTGTCCAGCCTGAGGTCTGAGGACACAGCCGTGTACTATTGTACCAGGA GCGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCACACTGGTGAC CGTGTCTTCCGCCAGCACAAAGGGCCCTTCCGTGTTCCCCCTGGCTCCT TGCTCCAGGAGCACATCTGAGTCCACCGCCGCTCTGGGCTGTCTGGTGA AGGACTACTTCCCAGAGCCCGTGACCGTGTCTGGAATAGCGGCGCCCT GACATCCGGAGTGACACCTTTCCAGCTGTGCTGCAGAGCTCTGGCCTG TACAGCCTGTCCAGCGTGGTGACAGTGCCCTCTTCCAGCCTGGGCACCA AGACATATACCTGCAACGTGGACCATAAGCCTTCTAATACCAAGGTGGA TAAGAGAGTGGAGTCCAAGTACGGACCACCTTGCCCTCCCTGTCTGTCT CCAGAGGCCCGGAGGACCTTCCGTGTTCTGTTTCCACCAAGCCAA AGGACACACTGATGATCTCTCGCACACCTGAGGTGACCTGCGTGGTGGT GGACGTGTCCCAGGAGGACCCCGAGGTGCAGTTCAACTGGTACGTGGAT GGCGTGGAGGTGCACAATGCTAAGACCAAGCCAAGGGAGGAGCAGTTTA ACTCCACATACCGGGTGGTGAGCGTGCTGACCGTGCTGCATCAGGATTG GCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAAGGGCCTGCC TCTTCCATCGAGAAGACAATCTTAAGGCTAAGGGACAGCCAAGGGAGC CACAGGTGTACACCCTGCCTCCAAGCCAGGAGGAGATGACAAAGAACCA GGTGTCTCTGACCTGTCTGGTGAAGGGCTTCTATCCATCTGACATCGCT GTGGAGTGGGAGTCCAATGGCCAGCCCGAGAACAATTACAGACCACAC CCCTGTGCTGGACTCTGATGGCTCCTTCTTTCTGTATTCTAGACTGAC CGTGGATAAGTCCCGCTGGCAGGAGGGCAACGTGTTCTCCTGCTCTGTG ATGCACGAAGCACTGCACAATCATTACACTCAGAAGAGCCTGTCACTGT CCCTGGGCAAA

320	TNX10 VH-CH1-CH2-CH3 IgG1 (L234A/L235A) (with terminal K) x = A or G	ATGCCTCTGCTGCTGCTGCTGCCTCTGCTGTGGGCCGGTGCCCTGGCTC AGGTCCAGCTGGTCCAGTCAGGTGCCGAAGTGGTCAAGCCCGGCGCCTC TGTGAAGCTGTCTGCAAGGCTAGCGGCTACATCTTCACCTCCTACTAT ATGTATTGGGTGAAGCAGGCTCCTGGACAGGGCCTGGAGTGGATCGGCG AGATCAACCCATCTAATGGCGACACCAACTTCAATGAGAAGTTTAAAGTC CAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACAGCTTACATGGAG CTGTCCAGCCTGAGGAGCGAGGACACCGCCGTGTACTATTGCACAAGGT CTGATGGCCGGAACGACATGGATTCTGGGGCCAGGGCACCTGGTGAC AGTGTCTTCCGCCCTTACCAAGGGCCCTTCCGTGTTTCCACTGGCTCCC AGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTGA AGGACTACTTCCCAGAGCCCGTGACAGTGAGCTGGAACCTGGCGCCCT GACCAGCGGAGTGACACATTTCTGCTGTGCTGCAGTCCAGCGGCCCTG TACTCTCTGTCTTCCGTGGTGACCGTGCCAAGCTCTTCCCTGGGCACCC AGACATATATCTGCAACGTGAATCACAAGCCAAGCAATACAAAGGTGGA CAAGAAGGTGGAGCCCAAGTCTTGTGATAAGACCCATACATGCCCCCT TGTCTGCTCCAGAGGCTGCTGGAGGACCATCCGTGTTCTTCCAC CCAAGCCTAAGGACACCCTGATGATCTCCAGAACCCAGAGGTGACATG CGTGGTGGTGGACGTGAGCCACGAGGACCCCGAGGTGAAGTTCAACTGG TACGTGGATGGCGTGAGGTGCATAATGCTAAGACCAAGCCAAGAGAGG AGCAGTACAACAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGTGCA TCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCTAATAAG GCCCTGCCCGCTCCTATCGAGAAGACCATCTCCAAGGCCAAGGGCCAGC CTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGAC CAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCCAGC GATATCGCTGTGGAGTGGGAGTCTAATGGCCAGCCTGAGAACAAATTACA AGACCACACCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATTC CAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTCTCC TGTTCCGTCTATGCACGAGGCACTGCACAATCATTACACCCAGAAGTCAC TGTCCTGTCTACCAGGAAAx
321	TNX11 VH-CH1-CH2-CH3 IgG1 (C226S, C229S, P238S) (with terminal K) x = A or G	ATGCCTCTGCTGCTGCTGCTGCCTCTGCTGTGGGCCGGTGCCCTGGCTC AGGTCCAGCTGGTCCAGTCAGGTGCCGAAGTGGTCAAGCCCGGCGCCTC TGTGAAGCTGTCTGCAAGGCTAGCGGCTACATCTTCACCTCCTACTAT ATGTATTGGGTGAAGCAGGCTCCTGGACAGGGCCTGGAGTGGATCGGCG AGATCAACCCATCTAATGGCGACACCAACTTCAATGAGAAGTTTAAAGTC CAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACAGCTTACATGGAG CTGTCCAGCCTGAGGAGCGAGGACACCGCCGTGTACTATTGCACAAGGT CTGATGGCCGGAACGACATGGATTCTGGGGCCAGGGCACCTGGTGAC AGTGTCTTCCGCCCTTACCAAGGGCCCTTCCGTGTTTCCACTGGCTCCC AGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTGA AGGACTACTTCCCAGAGCCCGTGACAGTGAGCTGGAACCTGGCGCCCT GACCAGCGGAGTGACACATTTCTGCTGTGCTGCAGTCCAGCGGCCCTG TACTCTCTGTCTTCCGTGGTGACCGTGCCAAGCTCTTCCCTGGGCACCC AGACATATATCTGCAACGTGAATCACAAGCCAAGCAATACAAAGGTGGA CAAGAAGGTGGAGCCCAAGTCTTGTGATAAGACCCATACATccCCCCCT TccCCTGCTCCAGAGCTGCTGGGAGGAAGCTCCGTGTTCTGTTTCCAC CCAAGCCTAAGGACACCCTGATGATCTCCAGAACCCAGAGGTGACATG CGTGGTGGTGGACGTGAGCCACGAGGACCCCGAGGTGAAGTTCAACTGG TACGTGGATGGCGTGAGGTGCATAATGCTAAGACCAAGCCAAGAGAGG AGCAGTACAACAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGTGCA TCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCTAATAAG GCCCTGCCCGCTCCTATCGAGAAGACCATCTCCAAGGCCAAGGGCCAGC CTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGAC CAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCCAGC GATATCGCTGTGGAGTGGGAGTCTAATGGCCAGCCTGAGAACAAATTACA AGACCACACCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATTC CAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTCTCC TGTTCCGTCTATGCACGAGGCACTGCACAATCATTACACCCAGAAGTCAC TGTCCTGTCTACCAGGAAAx

322	TNX12 VH-CH1-CH2-CH3 IgG1 (C229S, P238S) (with terminal K) x = A or G	ATGCCTCTGCTGCTGCTGCTGCCTCTGCTGTGGGCCGGTGCCCTGGCTC AGGTCCAGCTGGTCCAGTCAGGTGCCGAAGTGGTCAAGCCCGGCGCCTC TGTGAAGCTGTCTGCAAGGCTAGCGGCTACATCTTCACCTCCTACTAT ATGTATTGGGTGAAGCAGGCTCCTGGACAGGGCCTGGAGTGGATCGGCG AGATCAACCCATCTAATGGCGACACCAACTTCAATGAGAAGTTTAAAGTC CAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACAGCTTACATGGAG CTGTCCAGCCTGAGGAGCGAGGACACCGCCGTGTACTATTGCACAAGGT CTGATGGCCGGAACGACATGGATTCTCTGGGGCCAGGGCACCTGGTGAC AGTGTCTTCCGCCCTCTACCAAGGGCCCTTCCGTGTTTCCACTGGCTCCC AGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTGA AGGACTACTTCCCAGAGCCCGTGACAGTGAGCTGGAACCTGGCGCCCT GACCAGCGGAGTGACACATTTCTGCTGTGCTGCAGTCCAGCGGCCCTG TACTCTCTGTCTTCCGTGGTGACCGTGCCAAGCTCTTCCCTGGGCACCC AGACATATATCTGCAACGTGAATCACAAGCCAAGCAATACAAAGGTGGA CAAGAAGGTGGAGCCCAAGTCTTGTGATAAGACCCATACATGCCCCCT TCCCCTGCTCCAGAGCTGCTGGGAGGAAGcTCCGTGTTTCCGTCTTCCAC CCAAGCCTAAGGACACCCTGATGATCTCCAGAACCCAGAGGTGACATG CGTGGTGGTGGACGTGAGCCACGAGGACCCCGAGGTGAAGTTCAACTGG TACGTGGATGGCGTGGAGGTGCATAATGCTAAGACCAAGCCAAGAGAGG AGCAGTACAACAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGTGCA TCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCTAATAAG GCCCTGCCCCGCTCCTATCGAGAAGACCCTCTCAAGGCCAAGGGCCAGC CTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGAC CAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCCAGC GATATCGCTGTGGAGTGGGAGTCTAATGGCCAGCCTGAGAACAAATTACA AGACCACACCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATTTC CAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTCTCC TGTTCCGTCTATGCACGAGGCACTGCACAATCATTACACCCAGAAGTCAC TGTCCTGTCTACCAGGAAAx
323	TNX13 VH-CH1-CH2-CH3 IgG1 (C226S, P238S) (with terminal K) x = A or G	ATGCCTCTGCTGCTGCTGCTGCCTCTGCTGTGGGCCGGTGCCCTGGCTC AGGTCCAGCTGGTCCAGTCAGGTGCCGAAGTGGTCAAGCCCGGCGCCTC TGTGAAGCTGTCTGCAAGGCTAGCGGCTACATCTTCACCTCCTACTAT ATGTATTGGGTGAAGCAGGCTCCTGGACAGGGCCTGGAGTGGATCGGCG AGATCAACCCATCTAATGGCGACACCAACTTCAATGAGAAGTTTAAAGTC CAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACAGCTTACATGGAG CTGTCCAGCCTGAGGAGCGAGGACACCGCCGTGTACTATTGCACAAGGT CTGATGGCCGGAACGACATGGATTCTCTGGGGCCAGGGCACCTGGTGAC AGTGTCTTCCGCCCTCTACCAAGGGCCCTTCCGTGTTTCCACTGGCTCCC AGCTCTAAGTCCACCAGCGGAGGAACAGCCGCTCTGGGCTGTCTGGTGA AGGACTACTTCCCAGAGCCCGTGACAGTGAGCTGGAACCTGGCGCCCT GACCAGCGGAGTGACACATTTCTGCTGTGCTGCAGTCCAGCGGCCCTG TACTCTCTGTCTTCCGTGGTGACCGTGCCAAGCTCTTCCCTGGGCACCC AGACATATATCTGCAACGTGAATCACAAGCCAAGCAATACAAAGGTGGA CAAGAAGGTGGAGCCCAAGTCTTGTGATAAGACCCATACATCCCCCCT TGCCCTGCTCCAGAGCTGCTGGGAGGAAGCTCCGTGTTCTGTTTCCAC CCAAGCCTAAGGACACCCTGATGATCTCCAGAACCCAGAGGTGACATG CGTGGTGGTGGACGTGAGCCACGAGGACCCCGAGGTGAAGTTCAACTGG TACGTGGATGGCGTGGAGGTGCATAATGCTAAGACCAAGCCAAGAGAGG AGCAGTACAACAGCACCTATCGCGTGGTGTCTGTGCTGACAGTGTGCA TCAGGACTGGCTGAACGGCAAGGAGTATAAGTGCAAGGTGTCTAATAAG GCCCTGCCCCGCTCCTATCGAGAAGACCCTCTCAAGGCCAAGGGCCAGC CTAGGGAGCCACAGGTGTACACACTGCCTCCATCCCGGGACGAGCTGAC CAAGAACCAGGTGAGCCTGACATGTCTGGTGAAGGGCTTCTATCCCAGC GATATCGCTGTGGAGTGGGAGTCTAATGGCCAGCCTGAGAACAAATTACA AGACCACACCCCTGTGCTGGACTCCGATGGCAGCTTCTTTCTGTATTTC CAAGCTGACCGTGGATAAGAGCCGCTGGCAGCAGGGCAACGTGTTCTCC TGTTCCGTCTATGCACGAGGCACTGCACAATCATTACACCCAGAAGTCAC TGTCCTGTCTACCAGGAAAx

324	TNX14 VH-CH1-CH2-CH3 IgG4 (L115T, S228P, L235A) (with terminal K)	ATGCCTCTGCTGCTGCTGCTGCCTCTGCTGTGGGCCGGTGCTCTGGCTC AGGTCCAGCTGGTCCAGTCAGGGGCTGAAGTGGTCAAACCCGGCGCCAG CGTGAAGCTGTCTTGCAAGGCTTCCGGCTACATCTTCACCAAGCTACTAT ATGTATTGGGTGAAGCAGGCTCCAGGACAGGGCCTGGAGTGGATCGGCG AGATCAACCCTTCCAATGGCGACACAACTTCAATGAGAAGTTTAAGAG CAAGGCCACCCTGACAGTGGATAAGAGCGCCTCTACCGCTTACATGGAG CTGTCCAGCCTGAGGTCTGAGGACACAGCCGTGTACTATTGTACCAGGA GCGATGGCCGGAACGACATGGATTCTTGGGGCCAGGGCACAACAGTGAC CGTGTCTTCCGCCAGCACAAAGGGCCCTTCCGTGTTCCCCCTGGCTCCT TGCTCCAGGAGCACATCTGAGTCCACCGCCGCTCTGGGCTGTCTGGTGA AGGACTACTTCCCAGAGCCCGTGACCGTGTCTGGAATAGCGGCGCCCT GACATCCGGAGTGACACCTTTCCAGCTGTGCTGCAGAGCTCTGGCCTG TACAGCTGTCCAGCGTGGTGACAGTGCCCTCTTCCAGCCTGGGCACCA AGACATATACCTGCAACGTGGACCATAAGCCTTCTAATACCAAGGTGGA TAAGAGAGTGGAGTCCAAGTACGGACCACCTTGCCCTCCTTGTCTGTCT CCAGAGTTCGCGGAGGACCTTCCGTGTTCTGTTTCCACCAAGCCAA AGGACACACTGATGATCTCTCGCACACCTGAGGTGACCTGCGTGGTGGT GGACGTGTCCCAGGAGGACCCCGAGGTGCAGTTCAACTGGTACGTGGAT GGCGTGGAGGTGCACAATGCTAAGACCAAGCCAAGGGAGGAGCAGTTTA ACTCCACATACCGGGTGGTGAGCGTGCTGACCGTGCTGCATCAGGATTG GCTGAACGGCAAGGAGTATAAGTGCAAGGTGAGCAATAAGGGCCTGCC TCTTCCATCGAGAAGACAATCTTAAGGCTAAGGGACAGCCAAGGGAGC CACAGGTGTACACCCTGCCTCCAAGCCAGGAGGAGATGACAAAGAACCA GGTGTCTCTGACCTGTCTGGTGAAGGGCTTCTATCCATCTGACATCGCT GTGGAGTGGGAGTCCAATGGCCAGCCCAGAACCAATTACAGACCACAC CCCCGTGTCTGGACTCTGATGGCTCCTTCTTCTGTATTCTAGACTGAC CGTGGATAAGTCCCGCTGGCAGGAGGGCAACGTGTTCTCCTGCTCTGTG ATGCACGAAGCACTGCACAATCATTACACTCAGAAGAGCCTGTCACTGT CCCTGGGCAAA
Full light chain (VL-CL)		
195	VL-CL protein seq with leader	MRLPAQLLGLMLWVSGSSGDIVLTSQSPATLSVSPGERATISCRASQRV SSSTYSYMHWYQQKPGQPPKLLIKYASNLESVGPVRFSGSGSGTDFTLT ISSVEPEDFATYYCQHSWEIPTTFGGGTKEIKRTVAAPSVFIFPPSDE QLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
196	VL-CL protein seq without leader	DIVLTQSPATLSVSPGERATISCRASQRVSSSTYSYMHWYQQKPGQPPK LLIKYASNLESVGPVRFSGSGSGTDFTLTISSVEPEDFATYYCQHSWEI PPTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
197	VL-CL nucleotide seq with leader	ATGAGGCTGCCAGCTCAGCTGCTGGGACTGCTGATGCTGTGGGTGTCCG GCTCCAGCGCGACATCGTGCTGACCCAGAGCCAGCTACACTGTCCGT GTCCCCTGGAGAGAGGGCTACCATCAGCTGCAGGGCTTCTCAGCGGGTG TCTTCCAGCACATACAGCTATATGCACTGGTACCAGCAGAAGCCAGGCC AGCCCCCTAAGCTGCTGATCAAGTATGCCTCCAACCTGGAGAGCGGAGT GCCAGCTAGATTACAGCGGCTCTGGCTCCGGCACCGACTTTACCTGACA ATCTCTTCCGTGGAGCCTGAGGATTTGCCACATACTATTGCCAGCATT CTTGGGAGATCCCACCCACCTTTGGCGGCGGCACAAAGCTGGAGATCAA GAGAACCGTGGCCGCTCCTAGCGTGTTTCATCTTCTCCTCCATCTGACGAG CAGCTGAAGTCTGGCACCCTTCCGTGGTGTGCTGCTGAACAATTTCT ACCCACGCGAGGCCAAGGTGCAGTGAAGGTGGATAACGCTCTGCAGAG CGGCAATTCTCAGGAGTCCGTGACCGAGCAGGACAGCAAGGATTCTACA TATTCCTGAGCTCTACCCTGACACTGTCTAAGGCCGATTACGAGAAGC ACAAGGTGTATGCTTGCGAGGTGACCCATCAGGGCCTGTCCAGCCCAGT GACAAAGTCCTTTAATCGCGCGAGTGT

198	VL-CL nucleotide seq without leader	CATCGTGCTGACCCAGAGCCCAGCTACACTGTCCGTGTCCCCTGGAGAG AGGGCTACCATCAGCTGCAGGGCTTCTCAGCGGGTGTCTTCCAGCACAT ACAGCTATATGCACTGGTACCAGCAGAAGCCAGGCCAGCCCCCTAAGCT GCTGATCAAGTATGCCTCCAACCTGGAGAGCGGAGTGCCAGCTAGATT AGCGGCTCTGGCTCCGGCACCGACTTTACCCTGACAATCTTCCGTGG AGCCTGAGGATTTCCGCCACATACTATTGCCAGCATTCTTGGGAGATCCC ACCCACCTTTGGCGGCGGCACAAAGCTGGAGATCAAGAGAACCGTGGCC GCTCCTAGCGTGTTTCATCTTTCCTCCATCTGACGAGCAGCTGAAGTCTG GCACCGCTTCCGTGGTGTGCCTGCTGAACAATTTCTACCCACGCGAGGC CAAGGTGCAGTGAAGGTGGATAACGCTCTGCAGAGCGGCAATTCTCAG GAGTCCGTGACCGAGCAGGACAGCAAGGATTCTACATATTCCTGAGCT CTACCCTGACACTGTCTAAGGCCGATTACGAGAAGCACAAAGGTGTATGC TTGCGAGGTGACCCATCAGGGCCTGTCCAGCCAGTGACAAAGTCCTTT AATCGCGCGCAGTGT
Linkers		
199	L1	GGGS
200	L2	GGGS
201	L3	GGGS
202	L4	GGGS
203	L5	GGGS
204	L6	GSSG
205	L7	GSSG
206	L8	GSSG
207	L9	GSSG
208	L10	GSSG
209	L11	GSSG
210	L12	GSSG
211	L13	GSSG
212	L14	GSSG
213	L15	GSSG
214	L16	AS
215	L17	AST
216	L18	TVAAPS
217	L19	TVA
218	L20	ASTSGPS
219	L21	KESGSVSSEQLAQFRSLD
220	L22	EGKSSGSSESST
221	L23	GGGGG
222	L24	GGGGGGG
223	L25	GSAGSAAGSGEF
325	CT-Long	EPKSSDK
326	CT-Long	ASTEPKSSDK
Leader sequences		
224	Heavy chain leader sequence (AA)	MPLLLLLP ¹ LLWAGALA
225	Light chain leader sequence (AA)	MRLPAQL ¹ LLGLLMLWVSGSSG
226	Heavy chain leader sequence (NA)	ATGCCACTGCTGCTGCTGCTGCCACTGCTGTGGGCTGGCGCTCTGGCT
227	Light chain leader sequence (NA)	ATGAGGCTGCCAGCTCAGCTGCTGGGACTGCTGATGCTGTGGGTGTCCG GCTCCAGCGGCGA

Misc sequences		
228	EcoRI site sequence	GAATTCGGCCGGCCACC
229	BamHI site sequence	TAATGAACGCGTGGATCC
230	VD-CH2-CH3 (C220S, C226S, C229S, P238S) and terminal K Full Ab	EVQLLESGGGLVQPGGSLRLSCAASGFTFNWELMGWARQAPGKGLEWVS GIEGPGDVITYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCVK VGKDAKSDYRGQGLTVTVSSASTEPKSSDKTHTSPFSPAPPELLGGSSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYT QKSLSLSPGK
231	VD-CH2-CH3 (C220S, C226S, C229S, P238S) and terminal K Fc domain	APELLGGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCS VMHEALHNHYTQKSLSLSPGK
232	Fc region (C220S, C226S, C229S, P238S) and terminal K Fc region	EPKSSDKTHTSPFSPAPPELLGGSSVFLFPPKPKDTLMISRTPEVTCVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK
233	VH region	EVQLLESGGGLVQPGGSLRLSCAASGFTFNWELMGWARQAPGKGLEWVS GIEGPGDVITYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCVK VGKDAKSDYRGQGLTVTVSS
234	TNX07 IgG4 heavy chain with K (S228P)	QVQLVQSGAEVVKPGASVKLSCKASGYIFTSYYMYWVKQAPGQGLEWIG EINPSNGDTNFKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTR SDGRNDMSWGQGLTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGT KTYTCNVDPKPSNTKVDKRVE SKYGPPCPAPAEFLGGPSVFLFPPKPK KDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPRE PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSRLTVDKSRWQEGNV FSCSV MHEALHNHYTQKSLSL SLGK
235	TNX07 IgG4 Fc region (S228P) and terminal K	ESKYGPPCPAPAEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDK SRWQEGNV FSCSV MHEALHNHYTQKSLSLSLGK

236	IgG4 Fc region and terminal K Fc domain	APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYV DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGL PSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCS VMHEALHNHYTQKSLSLGLGK
Note that x = A or G in the listings above		

What is claimed:

1. A method of inducing immune tolerance in a transplant recipient, the method comprising administering to the recipient one or more doses of an isolated anti-CD154 antibody, transplanting into the recipient hematopoietic stem cells, and transplanting a donor organ, a donor tissue or donor cell into the recipient, wherein the hematopoietic stem cells produce immune cells that are tolerant of the donor organ, donor tissue or donor cell, thereby inducing immune tolerance in the recipient.
2. The method of claim 1, wherein the tolerance is central tolerance.
3. The method of claim 2, wherein the method further comprises depleting T cells in the thymus and/or bone marrow.
4. The method of claim 1, wherein the tolerance is peripheral tolerance.
5. The method of claim 4, wherein the method further comprises depleting T cells in the lymph nodes and/or peripheral tissue.
6. The method of claim 1, wherein the tolerance is organ-specific tolerance.
7. The method of claim 6, wherein the method further comprises depleting T cells from the heart, kidney, liver, lung, pancreas, intestines, islet cells, face, hand, arm, foot, leg or skin or a combination thereof.
8. The method of any one of claims 3, 5 and 7, wherein the T cells are depleted by a method selected from a group consisting of total body irradiation, administration of abatacept, administration of one or more BCL-2 inhibitors, administration of busulfan, administration of fludarabine phosphate, administration of cyclophosphamide, administration of one or more immunosuppressive T cell-depleting antibodies, administration of one or more anti- $\alpha\beta$ T cell receptor antibodies, and administration of one or more CD122 antagonists or a combination thereof.
9. The method of claim 8, wherein the one or more T cell-depleting antibodies are selected from the group consisting of anti-CD4, anti-CD8, anti-CD45, anti-CTLA4, anti-CD20, and anti-CD33 antibodies or a combination thereof.
10. The method of any one of claims 1-9, wherein the method results in mixed chimerism.

11. The method of any one of claims 1-10, wherein the anti-CD154 antibody is administered prior to, subsequently to or simultaneously with the transplantation of the hematopoietic stem cells.
12. The method of claim 1-11, wherein the anti-CD154 antibody is administered at a dose of 5-50 mg/kg.
13. The method of any one of claims 1-12, wherein the anti-CD154 antibody is administered subcutaneously, intravenously, intravitreally, orally, via inhalation, transdermally, or rectally.
14. The method of any one of claims 1-13, wherein the anti-CD154 antibody, comprises a human or humanized variable domain, wherein the variable domain comprises a heavy chain variable region (VH) and a light chain variable region (VL), and wherein the VH is operably linked to a human Fc domain with modified effector functions.
15. The method of claim 14, wherein one or more effector functions are reduced.
16. The method of claim 14 or 15, wherein one or more effector functions are eliminated.
17. The method of any one of claims 14-16, wherein the VH is operably linked to a human Fc region, wherein the human Fc region comprises a human hinge sequence and the human Fc domain, wherein the human hinge sequence is between the VH and the human Fc domain.
18. The method of claim 17, wherein the hinge comprises the amino acid sequence of any one of SEQ ID NOs: 76-90.
19. The method of any one of claims 14-18, wherein the Fc domain is derived from an IgG4 Fc (or crystallizable fragment) region.
20. The method of claim 19, wherein the Fc domain comprises one or more amino acid modifications that modifies effector functions.
21. The method of claim 20, wherein the antibody comprises an amino acid modification at any one of the positions selected from the group consisting of S228, L235, G237, E318, and N297 or a combination thereof, wherein the numbering of amino acid residues is according to the EU index as set forth in Edelman.
22. The method of claim 21, wherein the antibody comprises an amino acid modification selected from the group consisting of S228P, F234A, L235A, L235E, G237A, E318A, and N297Q or a combination thereof.

23. The method of any one of claims 14-18, wherein the Fc domain is derived from an IgG1 Fc (or crystallizable fragment) region and comprises one or more amino acid modifications that modifies effector functions.

24. The method of claim 23, wherein the antibody comprises an amino acid modification at any one of the positions selected from the group consisting of E216, R217, K218, C219, C220, C226, C229, P230, E233, L234, L235, G236, G237, P238, S239, V240, F241, K246, L251, T260, D265, V266, H268, W277, N297, E318, K322, P329, A330, P331, Q347, N348, T350, L351, K360, T366, N390, K392, T394, D399, S400, F405, Y407, K409, T411, or a combination thereof, wherein the numbering of amino acid residues is according to the EU index as set forth in Edelman.

25. The method of claim 24, wherein the antibody comprises an amino acid modification selected from the group consisting of C220S, C226S, C229S, P230S, E233P, L234A, L234F, L234V, L235A, L235E, L235V, G236E, G237A, P238S, D265S, D265A, H268Q, W277T, N297G, N297Q, N297D, N297A, E318A, K322A, P329G, P329A, A330S, P331S, Q347R, Q347E, Q347K, T350V, L351Y, K360D, K360E, T366A, T366I, T366L, T366M, T366V, N390R, N390K, N390D, K392V, K392M, K392R, K392L, K392F, K392E, T394W, D399R, D399W, D399K, S400E, S400D, S400R, S400K, F405A, F405I, F405M, F405T, F405S, F405V, F405W, Y407A, Y407I, Y407L, Y407V, K409F, K409I, K409S, K409W, T411N, T411R, T411Q, T411K, T411D, T411E, T411W, Δ E216-E222, K246R/L251E/T260R, InR234/235, InV235/236, InR236/237, InR237/238, InV238/239, InN238/239, InL238/239, InE238/239, InG238/239, InS239/240, InG240/241, InE240/241, InG240/241, InL238/239/P238Q, InE238/239/N348A, InS239/240/V266A, and InR237/238/G236A or a combination thereof.

26. The method of any one of claims 14-18, wherein the Fc domain is derived from an IgG2 Fc (or crystallizable fragment) crystallizable fragment region.

27. The method of claim 26, wherein the antibody comprises an amino acid modification at any one of the positions selected from the group consisting of V234, G237, P238, H268, V309, A330, and P331 or a combination thereof, wherein the numbering of amino acid residues is according to the EU index as set forth in Edelman.

28. The method of claim 27, wherein the antibody comprises an amino acid modification selected from the group consisting of V234A, G237A, P238S, H268Q, H268A, V309L, A330S, and P331S, or a combination thereof.

29. The method of any one of claims 14-18, wherein the Fc domain comprises the amino acid sequence selected from the group consisting of SEQ ID NOs: 3-9, 12-18, and 238-241.
30. The method according to claim 17, wherein the Fc region comprises the amino acid sequence selected from the group consisting of SEQ ID NOs: 21-37, 40-56, and 243-251.
31. The method of any one of claims 14-30, wherein the VH comprises:
- (a) a heavy chain CDR1 having the amino acid sequence of SEQ ID NO: 57,
 - (b) a heavy chain CDR2 having the amino acid sequence of SEQ ID NO: 58, and
 - (c) a heavy chain CDR3 having the amino acid sequence of SEQ ID NO: 59; and
- wherein the VL comprises:
- (a) a light chain CDR1 having the amino acid sequence of SEQ ID NO: 60,
 - (b) a light chain CDR2 having the amino acid sequence of SEQ ID NO: 61, and
 - (c) a light chain CDR3 having the amino acid sequence of SEQ ID NO: 62.
32. The method of any one of claims 14-31, wherein the VH comprises the amino acid sequence selected from the group consisting of SEQ ID NO: 63, 64, 252 and 253.
33. The antibody of any one of claims 14-32, wherein the VL comprises the amino acid sequence of SEQ ID NO: 65 or 66.
34. The method of any one of claims 17-33, wherein the antibody further comprises a CH1 domain, wherein the CH1 domain is operably linked to
- (a) the C-terminal end of the VH, and
 - (b) the N-terminal end of the hinge.
35. The method of claim 34, wherein the CH1 domain comprises an amino acid sequence that is at least 80% identical to the amino acid sequence of any one of SEQ ID NOs: 67, 70, and 73.
36. The method of any one of claims 14-35, wherein the antibody comprises a linker between the VH and the Fc domain.
37. The method of any one of claims 17-35, wherein the antibody comprises a linker between the VH and the hinge.

38. The method of claim 34 or 35, wherein the antibody comprises a linker between the VH and the CH1 domain.
39. The method of any one of claims 36-38, wherein the linker comprises the amino acid sequence of any one of SEQ ID NOs: 199-223 and 327-330.
40. The method of any one of claims 14-39, wherein the VH is operably linked to the amino acid sequence of any one of SEQ ID NOs: 3-9, 12-18, 21-37, 40-56, 238-241, and 243-251.
41. The method of any one of claims 14-40, wherein the heavy chain comprises the amino acid sequence of any one of SEQ ID NOs: 121-132, 135-146, 149, 151-160, 163, 165-174, 266-277, and 279-288.
42. The method of any one of claims 14-41, wherein the light chain comprises the amino acid sequence of SEQ ID NO: 195 or 196.
43. The method of any one of claims 14-42, wherein the antibody is monoclonal.
44. The method of any one of claims 14-43, wherein the antibody is chimeric.
45. The method of any one of claims 14-44, wherein the antibody is humanized.
46. The method of any one of claims 14-30, 34-40 and 43, wherein the antibody is human.
47. The method of any one of claims 14-46, wherein the binding of the antibody to human CD154 inhibits the interaction between human CD154 and human CD40.
48. The method of any one of claims 14-47, wherein the antibody blocks the activation of one or more of B cells, macrophages, dendritic cells, or endothelial cells by inhibiting binding of CD154 to CD40.
49. The method of any one of claims 14-48, wherein the antibody has one or more of the following effects when administered to a subject:
- (a) decreased risk of thrombosis or thromboembolic events compared to hu5c8 antibody;
 - (b) decreased activation of platelets expressing CD154;
 - (c) inhibition of CD154 shedding; and
 - (d) alteration of the expression or activity of downstream targets of CD154-CD40 signaling.
50. The method of any one of claims 14-49, wherein the antibody has a K_D of less than 50 pM for CD154, such as 5-25 pM or 9.5-23 pM.

51. The method of any one of claims 14-50, wherein the antibody does not comprise the amino acid sequence consisting of any one of SEQ ID NOs: 119, 120, 133, 134, 147, 148, 150, 161, 162, 164, 230, 234 and 278.
52. The method of any one of claims 1-51, wherein the transplant recipient is human.
53. The method of any one of claims 1-51, wherein the transplant recipient is non-human.
54. The method of claim 53, wherein the transplant recipient is a monkey.
55. The method of any one of claims 1-54, wherein the transplant is an allogeneic transplant, autologous transplant or a xenogeneic transplant.
56. The method of any one of claims 1-54, wherein the donor cell is an engineered cell or an ex-vivo expanded cell.
57. The method of claim 56, wherein one or more genes in the donor cell is modified using one or more techniques selected from a group consisting of transduction to express a cDNA, a CRISPR/Cas9 system, RNAi technology and retroviral technology.
58. The method of claim 56 or 57, wherein the donor cell is modified to express a chimeric antigen receptor (CAR) on its surface.
59. The method of any one of claims 55-58, wherein the donor cell is selected from a group consisting of a stem cell, a regulatory T cell, a CAR-T cell, a CAR-B cell, a tumor-infiltrating lymphocyte (TIL).
60. The method of any one of claims 1-59, wherein the method promotes a long-term survival of the donor organ, donor tissue or donor cell, wherein said long-term graft survival is selected from the group consisting of:
- (a) at least 6 months post-transplant;
 - (b) at least 1 year post-transplant; and
 - (c) at least 5 years post-transplant.
61. The method of any one of claims 1-60, wherein the anti-CD154 antibody is administered locally.
62. The method of any one of claims 1-60, wherein the anti-CD154 antibody is administered systemically.