(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
16 July 2020 (16.07.2020)

(10) International Publication Number
WO 2020/146902 A3

(51) International Patent Classification:
C07K 16/18 (2006.01) *A61P 13/12* (2006.01)
A61P 35/00 (2006.01) *A61P 13/08* (2006.01)
C07K 14/71 (2006.01) *A61P 7/00* (2006.01)

(21) International Application Number: PCT/US2020/013410

(22) International Filing Date: 13 January 2020 (13.01.2020)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
62/791,661 11 January 2019 (11.01.2019) US
PCT/US2019/019566 26 February 2019 (26.02.2019) US
PCT/US2019/021556 11 March 2019 (11.03.2019) US

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(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, WS, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Declarations under Rule 4.17:
— *of inventorship (Rule 4.17(iv))*

Published:
— *with international search report (Art. 21(3))*
— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*

(88) Date of publication of the international search report:
27 August 2020 (27.08.2020)

WO 2020/146902 A3

(54) Title: ANTI-VARIABLE MUC1* ANTIBODIES AND USES THEREOF

(57) Abstract: The present application discloses an antibody, or fragment thereof, for the diagnosis, treatment or prevention of cancers wherein the antibody specifically binds to the PSMGFR peptide (SEQ ID NO:2) or a fragment thereof of the peptide.

ANTI-VARIABLE MUC1* ANTIBODIES AND USES THEREOF

BACKGROUND OF THE INVENTION

[0001] **1. Field of the Invention:**

[0002] The present application relates to human, humanized and non-human anti-MUC1* antibodies and methods of making and using them. The present application also relates to using an immune cell transfected or transduced with a cleavage enzyme for the treatment of cancer. The present invention also relates to using an immune cell transfected or transduced with a CAR and another protein for the treatment of cancer.

[0003] **2. General Background and State of the Art:**

[0004] We previously discovered that a cleaved form of the MUC1 (SEQ ID NO:1) transmembrane protein is a growth factor receptor that drives the growth of over 75% of all human cancers. The cleaved form of MUC1, which we called MUC1* (pronounced muk 1 star), is a powerful growth factor receptor. Cleavage and release of the bulk of the extracellular domain of MUC1 unmasks a binding site for activating ligands dimeric NME1, NME6, NME7, $NME7_{AB}$, NME7-X1 or NME8. It is an ideal target for cancer drugs as it is aberrantly expressed on over 75% of all cancers and is likely overexpressed on an even higher percentage of metastatic cancers (Mahanta et al. (2008) A Minimal Fragment of MUC1 Mediates Growth of Cancer Cells. PLoS ONE 3(4): e2054. doi:10.1371/ journal.pone.0002054; Fessler et al. (2009), “MUC1* is a determinant of trastuzumab (Herceptin) resistance in breast cancer cells,” Breast Cancer Res Treat. 118(1):113-124). After MUC1 cleavage most of its extracellular domain is shed from the cell surface. The remaining portion has a truncated extracellular domain that comprises most or all of the primary growth factor receptor sequence called PSMGFR (SEQ ID NO:2).

[0005] Antibodies are increasingly used to treat human diseases. Antibodies generated in non-human species have historically been used as therapeutics in humans, such as horse antibodies. More recently, antibodies are engineered or selected so that they contain mostly, or all, human sequences in order to avoid a generalized rejection of the foreign antibody. The process of engineering recognition fragments of a non-human antibody into a human antibody is generally called ‘humanizing’. The amount of non-human sequences that are used to replace the human antibody sequences determines whether they are called chimeric, humanized or fully human.

[0006] Alternative technologies exist that enable generation of humanized or fully human antibodies. These strategies involve screening libraries of human antibodies or antibody fragments and identifying those that bind to the target antigen, rather than immunizing an animal with the antigen. Another approach is to engineer the variable region(s) of an antibody into an antibody-like molecule. Another approach involves immunizing a humanized animal. The present invention is intended to also encompass these approaches for use with recognition fragments of antibodies that the inventors have determined bind to the extracellular domain of MUC1*.

[0007] In addition to treating patients with an antibody, cancer immunotherapies have recently been shown to be effective in the treatment of blood cancers. One cancer immunotherapy, called CAR T (chimeric antigen receptor T cell) therapy, engineers a T cell so that it expresses a chimeric receptor having an extra cellular domain that recognizes a tumor antigen, a transmembrane domain and cytoplasmic tail comprising T cell signaling and co-stimulatory components (Dai H, Wang Y, Lu X, Han W. (2016) Chimeric Antigen Receptors Modified T-Cells for Cancer Therapy. J Natl Cancer Inst. 108(7): djv439). Such receptor is composed of a single chain antibody fragment (scFv) that recognizes a tumor antigen, linked to a T cell transmembrane, signaling domain and co-stimulatory domain or domains. Upon binding of the receptor to a cancer associated antigen, a signal is transmitted resulting in T-cell activation, propagation and the targeted killing of the cancer cells. In practice, T cells are isolated from a patient or donor and transduced with a CAR, expanded and then injected back into the patient. If from a donor, the immune cells may be mutated or engineered such that they do not induce graft versus host disease in the recipient. When the CAR T cells bind to the antigen on a cancer cell, the CAR T cells attack the cancer cells and then expand that population of T cells.

[0008] Thus far, CAR T therapies have been very successful in the treatment of blood cancers but as yet have not shown efficacy against solid tumors in humans. Because most blood cancers are B cell malignancies, the CAR T cells can just eliminate all of the patient's B cells without causing serious harm to the patient. There is no B cell equivalent in solid tumors. Most tumor associated antigens are also expressed on normal tissues; they are just expressed at a higher level in cancerous tissues. Thus, the challenge is to develop an antibody that recognizes an epitope on a tumor associated antigen that is somehow different in the context of the tumor compared to normal tissue. To further minimize the risk of off-tumor/on-target killing of normal tissues, the antibody should recognize and bind to cancerous tissues at least two-times more than normal tissues. Antibodies that are not so cancer selective may be used therapeutically if they are inducibly expressed at the tumor site.

[0009] Another cancer therapy that incorporates cancer selective antibodies is Bi-specific T cell Engagers, also called BiTEs. The BiTE approach attempts to eliminate the CAR T associated risk of off-tumor/on-target effects. Unlike CAR T, BiTEs are bispecific antibodies that should not pose any greater risk than regular antibody-based therapies. However, unlike typical anti-cancer antibodies that bind to and block a cancer antigen, BiTEs are designed to bind to an antigen on the tumor cell and simultaneously bind to an antigen on an immune cell, such as a T cell. In this way, a BiTE recruits the T cell to the tumor. BiTEs are engineered proteins that simultaneously bind to a cancer associated antigen and a T-cell surface protein such as CD3-epsilon. BiTEs are antibodies made by genetically linking the scFv's of an antibody that binds to a T cell antigen, like anti-CD3-epsilon to a scFv of a therapeutic monoclonal antibody that binds to a cancer antigen (Patrick A. Baeuerle, and Carsten Reinhardt (2009) Bispecific T-cell engaging antibodies for cancer therapy. Cancer Res. 69(12):4941-4944). A drawback of BiTE technology is that, unlike CAR T cells, they do not expand in the patient, so have limited persistence.

[0010] Yet another cancer therapy that incorporates cancer selective antibodies is antibody drug conjugate, also called ADC, technology. In this case, a toxin, or a precursor to a toxin, is linked to a cancer selective antibody. Unlike CAR T cells that use the CD8 positive T cell's natural killing to kill cancer cells, ADCs carry a toxic payload to the tumor. Drawbacks of ADCs include the potential of delivering the toxic payload to normal cells and that most ADCs require binding to a cell surface molecule which then gets internalized after binding, with an approximate 10,000 surface molecule required for resultant cell death.

SUMMARY OF THE INVENTION

[0011] In one aspect, the present invention is directed to a non-human, human or humanized anti-MUC1* antibody or antibody fragment or antibody-like protein that binds to a region on extracellular domain of MUC1 isoform or cleavage product that is devoid of the tandem repeat domains. The non-human, human or humanized anti-MUC1* antibody or antibody fragment or antibody-like protein may specifically bind to

[0012] (i) PSMGFR region of MUC1;

[0013] (ii) PSMGFR peptide;

[0014] (iii) a peptide having amino acid sequence of QFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA (N-10) (SEQ ID NO:3)

[0015] (iv) a peptide having amino acid sequence of

[0016] ASRYNLTISDVSVSDVPFPFSAQSGA (N-19) (SEQ ID NO:4)

[0017] (v) a peptide having amino acid sequence of

[0018] NLTISDVSVSDVPFPFSAQSGA (N-23) (SEQ ID NO:5)

[0019] (vi) a peptide having amino acid sequence of

[0020] ISDVSVSDVPFPFSAQSGA (N-26) (SEQ ID NO:6)

[0021] (vii) a peptide having amino acid sequence of

[0022] SVSDVPFPFSAQSGA (N-30) (SEQ ID NO:7)

[0023] (viii) a peptide having amino acid sequence of

[0024] QFNQYKTEAASRYNLTISDVSVSDVPFPFS (N-10/C-5) (SEQ ID NO:8)

[0025] (ix) a peptide having amino acid sequence of

[0026] ASRYNLTISDVSVSDVPFPFS (N-19/C-5) (SEQ ID NO:9)

[0027] (x) a peptide having amino acid sequence of

[0028] FPFSAQSGA (SEQ ID NO:10)

[0029] The non-human, human or humanized antibody may be IgG1, IgG2, IgG3, IgG4 or IgM. The human or humanized antibody fragment or antibody-like protein may be scFv or scFv-Fc.

[0030] The murine, camelid, human or humanized antibody, antibody fragment or antibody-like protein as in above may comprise a heavy chain variable region and light chain variable region which is derived from mouse monoclonal MNC2, MNE6, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, and H11 antibody, and has at least 80%, 90% or 95% or 98% sequence identity to the mouse monoclonal MNC2, MNE6, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, and H11 antibody. The heavy chain variable region of CDR1 and CDR2 may have at least 90% or 95% or 98% sequence identity to the particularly indicated antibody heavy chain variable region sequence set forth in the present application in the sequence listing, and the light chain variable region of CDR1 and CDR2 may have at least 90% or 95% or 98% sequence identity to the particularly indicated antibody heavy chain variable region sequence set forth in the present application in the sequence listing section. The heavy chain variable region of CDR3 may have at least 80% or 85% or 90% sequence identity to the particularly indicated antibody heavy chain variable region sequence set forth in the present application in the sequence listing, and the light chain variable region of CDR3 may have at least 80% or 85% or 90% sequence identity to the particularly indicated antibody heavy chain variable region sequence set forth in the present application in the sequence listing section.

[0031] The murine, camelid, human or humanized antibody, antibody fragment or antibody-like protein according to above may include complementarity determining regions (CDRs) in the heavy chain variable region and light chain variable region having at least 90% or 95% or 98% sequence identity to the particularly indicated antibody heavy chain CDR1, CDR2 or CDR3 region and light chain CDR1, CDR2 or CDR3 region sequences set forth in the present application in the sequence listing section.

[0032] In another aspect, the present invention is directed to an anti-MUC1* extracellular domain antibody or anti-N-10 antibody, which may be any of the antibodies described above, comprised of sequences represented by humanized IgG2 heavy chain, or humanized IgG1 heavy chain, paired with humanized Kappa light chain, or humanized Lambda light chain. The humanized IgG2 heavy chain may be SEQ ID NOS:53, humanized IgG1 heavy chain may be SEQ ID NO:57, humanized Kappa light chain may be SEQ ID NO:108, and humanized Lambda light chain may be SEQ ID NO:112, or a sequence having 90%, 95% or 98% sequence identity thereof.

[0033] In another aspect, the invention is directed to an anti-MUC1* extracellular domain antibody or anti-N-10 antibody comprised of sequences of a humanized MN-C2 represented by humanized IgG1 heavy chain, humanized IgG2 heavy chain, paired with humanized Lambda light chain, and humanized Kappa light chain.

[0034] In another aspect, the invention is directed to an anti-MUC1* extracellular domain antibody or anti-N-10 antibody comprised of sequences of a humanized MNC2, MNE6, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, or H11 represented by humanized IgG1 heavy chain or humanized IgG2 heavy chain, paired with humanized Lambda light chain, or humanized Kappa light chain.

[0035] In another aspect, the invention is directed to an antibody that is "like" MNC2, MNE6, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, or H11 in that they have the same or very similar pattern of binding to subsets of peptides derived from the PSMGFR peptide, also do not recognize a linear epitope, competitively inhibit the binding of NME1 or $NME7_{AB}$ to MUC1*, recognize a MUC1 transmembrane cleavage product produced by cleavage by MMP9 or contain CDR sequences that are at least 80% homologous to the MN-E6, MN-C2, MN-18G12, MN-20A10, MN-25E6, MN-28F9, MN-5C6F3, MN-3C2B1, and MN-1E4 CDR consensus sequences.

[0036] In another aspect, the invention is directed to an antibody that binds to the extra cellular domain of a MUC1 that is devoid of the tandem repeat domain, which may be a cleavage product. In one aspect of the invention, the antibody binds to a peptide having the sequence of QFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA (N-10). In one aspect of the invention, the antibody binds to a peptide having the sequence of ASRYNLTISDVSVSDVPFPFSAQSGA (N-19). In one aspect of the invention, the antibody binds to a peptide having the sequence of SVSDVPFPFSAQSGA (N-30). In one aspect of the invention, the antibody binds to a peptide having the sequence of FPFSAQSGA (N-36). Examples of such antibodies include but are not limited to monoclonal antibodies MNC2, MNE6, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, and H11. The heavy chain and light chain complementary determining region sequences for these antibodies are set forth in the present application in the sequence listing section.

[0037] In one aspect of the invention, one or more of these antibodies is administered to a patient diagnosed with or at risk of developing a cancer. The antibody may be human or humanized. The antibody may be murine or camelid. The antibody may be bivalent or monovalent. The antibody may be a fragment, including a single chain fragment, scFv, of one of the antibodies. The antibody or antibody fragment may be administered directly to the patient or incorporated into a bispecific antibody, a bispecific T cell engager , BiTE, or an antibody drug conjugate, ADC. The antibody or antibody fragment may be incorporated into a T cell receptor, TCR. The sequence of the antibody or antibody fragment may be incorporated into a chimeric antigen receptor, a "CAR", or other similar entity, then introduced into an immune cell, *ex vivo*, then administered to a patient diagnosed with or at risk of developing a cancer. The immune cell, which may be a T cell or natural killer cell, may be derived from a donor or from the patient. In one aspect the immune cell is derived from a stem cell that has been directed to differentiate to that immune cell type in vitro. In one aspect, the antibody or a CAR containing sequences of the antibody may be expressed off of an inducible promoter. In one case the antibody or the CAR is expressed upon activation of the T cell or other immune cell. In one instance, the antibody or the CAR of the invention is expressed off of an NFAT response element. In another instance, CAR recognition of a target tumor cell activates the immune cell, leading to NFAT inducible expression of a cytokine, such as IL-12 or IL-18, or expression of a checkpoint inhibitor such as a PD1 inhibitor or a PDL-1 inhibitor. In yet another aspect, CAR recognition of a target tumor cell activates the immune cell, leading to NFAT inducible expression of a second CAR that contains sequences of a second antibody.

[0038] In another aspect, the invention is directed to a murine, camelid, human, humanized anti-MUC1* antibody or antibody fragment or antibody-like protein that binds to the N-10 peptide, according to above, which inhibits the binding of NME protein to MUC1*. The NME may be NME1, NME6, $NME7_{AB}$, NME7-X1, NME7 or NME8.

[0039] In yet another aspect, the invention is directed to a single chain variable fragment (scFv) comprising a heavy and light chain variable regions connected via a linker, further comprising CDRs of antibodies that bind to MUC1* extracellular domain. The CDRs may be derived from MNC2, MNE6, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, and H11. The scFv may be one that possesses the SEQ ID NOS:233, 235 and 237 (MN-E6); SEQ ID NOS:239, 241, and 243 (MN-C2)

[0040] In still another aspect, the invention is directed to a chimeric antigen receptor (CAR) comprising a scFv or a humanized variable region that binds to the extracellular domain of a MUC1 that is devoid of tandem repeats, a linker molecule, a transmembrane domain and a cytoplasmic domain. The single chain antibody fragment may bind to

[0041] (i) PSMGFR region of MUC1;

[0042] (ii) PSMGFR peptide;

[0043] (iii) a peptide having amino acid sequence of QFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA (N-10) (SEQ ID NO:3)

[0044] (iv) a peptide having amino acid sequence of

[0045] ASRYNLTISDVSVSDVPFPFSAQSGA (N-19) (SEQ ID NO:4)

[0046] (v) a peptide having amino acid sequence of

[0047] NLTISDVSVSDVPFPFSAQSGA (N-23) (SEQ ID NO:5)

[0048] (vi) a peptide having amino acid sequence of

[0049] ISDVSVSDVPFPFSAQSGA (N-26) (SEQ ID NO:6)

[0050] (vii) a peptide having amino acid sequence of

[0051] SVSDVPFPFSAQSGA (N-30) (SEQ ID NO:7)

[0052] (viii) a peptide having amino acid sequence of

[0053] QFNQYKTEAASRYNLTISDVSVSDVPFPFS (N-10/C-5) (SEQ ID NO:8)

[0054] (ix) a peptide having amino acid sequence of

[0055] ASRYNLTISDVSVSDVPFPFS (N-19/C-5) (SEQ ID NO:9)

[0056] (x) a peptide having amino acid sequence of

[0057] FPFSAQSGA (N-36) (SEQ ID NO:10)

[0058] In the CAR as described above, portions of any of the variable regions set forth and described above, or combination thereof may be used in the extracellular domain of the CAR. The CAR also comprises a transmembrane region and a cytoplasmic tail that comprises sequence motifs that signal immune system activation. The extracellular domain may be comprised of murine, camelid, human, non-human, or humanized single chain antibody fragments of an MNC2, MNE6, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, and H11. Additional antibodies from which single chain antibody fragments may made include but are not limited to monoclonal antibodies that are like MNC2, MNE6, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, and H11 in that they have the same or very similar pattern of binding to subsets of peptides derived from the PSMGFR peptide, may not recognize a linear epitope or competitively inhibit the binding of NME1 or $NME7_{AB}$ to MUC1*, or recognize a MUC1 transmembrane cleavage product produced by cleavage by MMP9 or contain CDR sequences that are at least 80% homologous to the MNC2, MNE6, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, and H11 CDR consensus sequences.

[0059] In the CARs as described above, the extracellular domain may include a murine, camelid, human, non-human or humanized single chain antibody fragments of an MN-E6 scFv set forth as SEQ ID NOS: 233, 235, or 237), MN-C2 scFv (SEQ ID NOS:239, 241, or 243), or 20A10 scFv as set forth as SEQ ID NOS:1574-1575, 25E6 scFv as set forth as SEQ ID NOS:1598-1599.

[0060] In any of the CARs described above, the cytoplasmic tail may be comprised of one or more of signaling sequence motifs CD3-zeta, CD27, CD28, 4-1BB, OX40, CD30, CD40, ICAm-1, LFA-1, ICOS, CD2, CD5, or CD7. In any of the CARs described above, the cytoplasmic tails may include mutations that dampen signaling. Such mutations include but are not limited to Tyrosines that are mutated to inhibit phosphorylation and signaling (Salter et al, 2018). In any of the CARs described above, the ITAMs of CD3-zeta may be mutated to inhibit or dampen signaling (Feucht et al 2019). In any of the CARs described above, the CD3 of the cytoplasmic tail may comprise mutations in the ITAMs including those referred to as 1XX. In any of the CARs described above, the T cell may be engineered to overexpress c-Jun as a method to inhibit T cell exhaustion (Lynn et al 2019).

[0061] In any of the CARs described above, the sequence may be CAR MN-E6 CD28/CD3z (SEQ ID NOS:298); CAR MN-E6 4-1BB/CD3z (SEQ ID NOS:301); CAR MN-E6 OX40/CD3z (SEQ ID NOS:617); CAR MN-E6 CD28/4-1BB/CD3z (SEQ ID NOS:304); CAR MN-E6 CD28/OX40/CD3z (SEQ ID NOS:619); CAR MN-C2 CD3z (SEQ ID NOS:607); CAR MN-C2 CD28/CD3z SEQ ID NOS:609); CAR MN-C2 4-1BB/CD3z (SEQ ID NOS:611 and SEQ ID NOS: 719); CAR MN-C2 OX40/CD3z (SEQ ID NOS:613); CAR MN-C2 CD28/4-1BB/CD3z (SEQ ID NOS: 307); CAR MN-C2 CD28/OX40/CD3z (SEQ ID NOS:615) or CAR MN-C3 4-1BB/CD3z (SEQ ID NOS: 601).

[0062] In another aspect, the invention is directed to a composition that includes at least two CARs with different extracellular domain units transfected into the same cell, which may be an immune cell, which may be derived from the patient requiring treatment for a cancer. The expression of the second CAR may be inducible and driven by the recognition of a target by the first CAR. The nucleic acid encoding the second CAR may be linked to an inducible promoter. The expression of the second CAR may be induced by an event that occurs specifically when the immune cell mounts an immune response to a target tumor cell. The antibody fragments of one or both of the CARs may direct the cell to a MUC1* positive tumor. The antibody fragments of the first and second CARs may bind to a MUC1* that is produced when MUC1 is cleaved by two different cleavage enzymes. Expression of the second CAR by the inducible promoter may be induced when the antibody fragment of the first CAR engages or binds to a MUC1 or MUC1* on the tumor. One way to do this is to induce expression of the second CAR when, or shortly after, an NFAT protein is expressed or translocated to the nucleus. For example, a sequence derived from an NFAT promoter region is put upstream of the gene for the second CAR. In this way, when the transcription factors that bind to the promoter of the NFAT protein are present in sufficient concentration to bind to and induce transcription of the NFAT protein, they will also bind to that same promoter that is engineered in front of the sequence for transcription of the second CAR. The NFAT protein may be NFAT1 also known as NFATc2, NFAT2 also known as NFATc or NFATc1, NFAT3 also known as NFATc4, NFAT4 also known as NFATc3, or NFAT5. In one aspect of the invention, the NFAT is NFATc1, NFATc3 or NFATc2. In one aspect of the invention, the NFAT is NFAT2 also known as NFATc1. SEQ ID NO:646 shows nucleic acid sequence of the upstream transcriptional regulatory region for NFAT2. The recognition unit of the second CAR may be an antibody fragment or a peptide, wherein the recognition units may bind to NME7, PD-1, PDL-1, or a checkpoint inhibitor.

[0063] The at least two CARs may have one CAR that does not have a tumor antigen targeting recognition unit and the other CAR does have a tumor antigen targeting recognition unit. In another aspect of the invention, one of the extracellular domain recognition units may bind to MUC1* extracellular domain. In another aspect of the invention, one of the extracellular domain recognition units may be an antibody fragment and the other is a peptide, which may be devoid of transmembrane and signaling motifs; the peptide may be a single chain antibody fragment or antibody. In another aspect of the invention, one of the recognition units may bind PD-1 or PDL-1. In another aspect of the invention, one extra cellular domain recognition unit is an anti-MUC1* antibody, antibody fragment or scFv chosen from the group consisting of MNC2, MNE6, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, and H11. The other recognition unit may be a CAR or may be an anti-NME7 antibody.

[0064] In another aspect, the invention is directed to a cell comprising a CAR with an extracellular domain that binds to the extra cellular domain of a MUC1 molecule that is devoid of tandem repeats. In another aspect, the invention is directed to a cell comprising a CAR with an extracellular domain that binds to a MUC1* transfected or transduced cell. The cell that includes the CAR may be an immune system cell, preferably a T cell, a natural killer cell (NK), a dendritic cell or mast cell.

[0065] In another aspect, the invention is directed to an engineered antibody-like protein.

[0066] In another aspect, the invention is directed to a method for treating a disease in a subject comprising administering an antibody according to any claim above, to a person suffering from the disease, wherein the subject expresses MUC1 aberrantly. The disease may be cancer, such as breast cancer, ovarian cancer, pancreatic cancer, lung cancer, colon cancer, gastric cancer or esophageal cancer.

[0067] In another aspect, the invention is directed to an antibody, antibody fragment or scFv comprising variable domain fragments derived from an antibody that binds to an extracellular domain of MUC1 isoform or cleavage product that is devoid of the tandem repeat domains. In a preferred embodiment, the antibody or antibody fragment binds to the N-10 peptide. The variable domain fragments may be derived from mouse monoclonal antibody MN-E6 (SEQ ID NO:13 and 66) or from the humanized MN-E6 (SEQ ID NO: 39 and 94), or from MN-E6 scFv (SEQ ID NO: 233, 235 and 237). Or, the variable domain fragments may be derived from mouse monoclonal antibody MN-C2 (SEQ ID NO: 119 and 169) or from the humanized MN-C2 (SEQ ID NO: 145 and 195), or from MN-C2 scFv (SEQ ID NO: 239, 241 and 243). Or, the variable domain may be derived from monoclonal antibodies MN-18G12, MN-20A10, MN-25E6, MN-28F9, MN-5C6F3, MN-3C2B1, or MN-1E4. The heavy chain and light chain complementary determining region sequences for these antibodies are also set forth in the sequence listing herein.

[0068] In another aspect, the invention is directed to a method for the treatment of a person diagnosed with, suspected of having or at risk of developing a MUC1 or MUC1* positive cancer involving administering to the person an effective amount of the antibody, antibody fragment or scFv described above, wherein the species may be murine, camelid, human or humanized.

[0069] In another aspect, the invention is directed to a polypeptide comprising at least two different scFv sequences, wherein one of the scFv sequences is a sequence that binds to extracellular domain of MUC1 isoform or cleavage product that is devoid of the tandem repeat domains. The polypeptide may bind to

[0070] (i) PSMGFR region of MUC1;

[0071] (ii) PSMGFR peptide;

[0072] (iii) a peptide having amino acid sequence of QFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA (N-10) (SEQ ID NO:3)

[0073] (iv) a peptide having amino acid sequence of

[0074] ASRYNLTISDVSVSDVPFPFSAQSGA (N-19) (SEQ ID NO:4)

[0075] (v) a peptide having amino acid sequence of

[0076] NLTISDVSVSDVPFPFSAQSGA (N-23) (SEQ ID NO:5)

[0077] (vi) a peptide having amino acid sequence of

[0078] ISDVSVSDVPFPFSAQSGA (N-26) (SEQ ID NO:6)

[0079] (vii) a peptide having amino acid sequence of

[0080] SVSDVPFPFSAQSGA (N-30) (SEQ ID NO:7)

[0081] (viii) a peptide having amino acid sequence of

[0082] QFNQYKTEAASRYNLTISDVSVSDVPFPFS (N-10/C-5) (SEQ ID NO:8)

[0083] (ix) a peptide having amino acid sequence of

[0084] ASRYNLTISDVSVSDVPFPFS (N-19/C-5) (SEQ ID NO:9)

[0085] (x) a peptide having amino acid sequence of

[0086] FPFSAQSGA (N-36) (SEQ ID NO:10)

[0087] The polypeptide may bind to a receptor on an immune cell, such as T cell, and in particular, CD3 on T-cell.

[0088] In another aspect, the invention is directed to a method of detecting presence of a cell that expresses MUC1* aberrantly, comprising contacting a sample of cells with the scFv-Fc described above and detecting for the presence of the binding of scFv-Fc to the cell. The cell may be cancer cell.

[0089] In another aspect, the invention is directed to a method for testing a subject's cancer for suitability of treatment with a composition comprising antibodies of the invention, which may be murine, camelid, human or humanized, or fragments thereof, or portions of the variable regions of antibodies MNC2, MNE6, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, or H11, comprising the steps of contacting a bodily specimen from the patient, in vitro, ex-vivo, or in vivo, with the antibody and determining that the patient exhibits aberrant expression of MUC1* compared to normal tissue or specimen. The antibody used in these diagnostics may be conjugated to an imaging agent.

[0090] In another aspect, the invention is directed to a method of treating a subject suffering from a disease comprising, exposing T cells from the subject, or from a donor, to MUC1* peptides wherein through various rounds of maturation, T cells develop MUC1* specific receptors, creating adapted T cells, and expanding and administering the adapted T cells to the donor patient who is diagnosed with, suspected of having, or is at risk of developing a MUC1* positive cancer. The MUC1* peptide is chosen from among the group:

[0091] (i) PSMGFR region of MUC1;

[0092] (ii) PSMGFR peptide;

[0093] (iii) a peptide having amino acid sequence of QFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA (N-10)

[0094] (iv) a peptide having amino acid sequence of

[0095] ASRYNLTISDVSVSDVPFPFSAQSGA (N-19)

[0096] (v) a peptide having amino acid sequence of

[0097] NLTISDVSVSDVPFPFSAQSGA (N-23)

[0098] (vi) a peptide having amino acid sequence of

[0099] ISDVSVSDVPFPFSAQSGA (N-26)

[00100] (vii) a peptide having amino acid sequence of

[00101] SVSDVPFPFSAQSGA (N-30)

[00102] (viii) a peptide having amino acid sequence of

[00103] QFNQYKTEAASRYNLTISDVSVSDVPFPFS (N-10/C-5)

[00104] (ix) a peptide having amino acid sequence of

[00105] ASRYNLTISDVSVSDVPFPFS (N-19/C-5)

[00106] (x) a peptide having amino acid sequence of

[00107] FPFSAQSGA (N-36)

[00108] In one aspect of the invention, the antibody that is administered to a patient for the treatment or prevention of a MUC1 or MUC1* positive cancer is selected for its ability to bind to the N-10 peptide of the PSMGFR. The antibody can be administered alone, as a monovalent antibody, as an scFv, or a fragment of the antibody can be incorporated into a CAR, a BiTE or an ADC.

[00109] In one aspect of the invention, the antibody that is administered to a patient for the treatment or prevention of a MUC1 or MUC1* positive cancer is selected for its inability to recognize a linear epitope of MUC1 or MUC1*. The antibody can be administered alone, as a monovalent antibody, as an scFv, or a fragment of the antibody can be incorporated into a CAR, a BiTE or an ADC.

[00110] In one aspect of the invention, the antibody that is administered to a patient for the treatment or prevention of a MUC1 or MUC1* positive cancer is selected for its ability to recognize the MUC1 transmembrane cleavage product after it has been cleaved by MMP9. The antibody can be administered alone, as a monovalent antibody, as an scFv, or a fragment of the antibody can be incorporated into a CAR, a BiTE or an ADC.

[00111] In one aspect of the invention, the antibody that is administered to a patient for the treatment or prevention of a MUC1 or MUC1* positive cancer is selected for its ability to competitively inhibit the binding of $NME7_{AB}$ or NME7-X1 to the extra cellular domain of a MUC1 that is devoid of tandem repeats. The antibody can be administered alone, as a monovalent antibody, as an scFv, or a fragment of the antibody can be incorporated into a CAR, a BiTE or an ADC.

[00112] In another aspect, the invention is directed to a method of treating cancer in a patient comprising administering to the patient the immune cell of any of the above, in combination with a checkpoint inhibitor.

[00113] In the method above, any of the antibodies, or variable regions thereof, set forth in the following may be used: MNC2, MNE6, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, or H11.

[00114] In the method above, any of the variable regions set forth in the following may be used:

[00115] (i) an anti-MUC1* extracellular domain antibody or anti-N-10 antibody comprised of sequences of a humanized MN-E6 represented by humanized IgG2 heavy chain, or humanized IgG1 heavy chain, paired with humanized Kappa light chain, or humanized Lambda light chain;

[00116] (ii) an antibody of (i), wherein the humanized IgG2 heavy chain is SEQ ID NOS:53, humanized IgG1 heavy chain is SEQ ID NO:57, humanized Kappa light chain is SEQ ID NO:108, and humanized Lambda light chain is SEQ ID NO:112, or a sequence having 90%, 95% or 98% sequence identity thereof;

[00117] (iii) an anti-MUC1* extracellular domain antibody or anti-N-10 antibody comprised of sequences of a humanized MN-C2 represented by humanized IgG1 heavy chain, humanized IgG2 heavy chain, paired with humanized Lambda light chain, and humanized Kappa light chain;

[00118] (iv) an antibody of (iii), wherein the humanized IgG1 heavy chain MN-C2 (SEQ ID NOS:159) or IgG2 heavy chain (SEQ ID NOS:164) paired with Lambda light chain (SEQ ID NO:219) or Kappa light chain (SEQ ID NO:213), or a sequence having 90%, 95% or 98% sequence identity thereof;

[00119] In the method above, in the CAR, the extracellular domain may be comprised of humanized single chain antibody fragments of MNC2, MNE6, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, or H11. The extracellular domain may be comprised of humanized single chain antibody fragments of an MN-E6 scFv set forth as SEQ ID NOS: 233, 235, or 237), MN-C2 scFv (SEQ ID NOS:239, 241, or 243). In the CAR, the cytoplasmic tail may be comprised of one or more of signaling sequence motifs CD3-zeta, CD27, CD28, 4-1BB, OX40, CD30, CD40, ICAm-1, LFA-1, ICOS, CD2, CD5, or CD7.

[00120] The method above may include at least two CARs with different extracellular domain units transfected into the same cell. One of the extracellular domain recognition units may bind to MUC1* extracellular domain. One of the extracellular domain recognition units may bind to PD-1. One of the extracellular domain recognition units may be an antibody fragment and the other may be a peptide or an anti-MUC1* antibody fragment.

[00121] The method may include an immune cell transfected or transduced with a plasmid encoding a CAR and a plasmid encoding a non-CAR species that is expressed from an inducible promoter. The non-CAR species may be expressed from an inducible promoter that is activated by elements of an activated immune cell. The non-CAR species may be expressed from an NFAT inducible promoter. The NFAT may be NFATc1, NFATc3 or NFATc2. The cleavage enzyme may be MMP2, MMP3, MMP9, MMP13, MMP14, MMP16, ADAM10, ADAM17, or ADAM28, or a catalytically active fragment thereof. The non-CAR species may be a cytokine. The cytokine may be IL-7, IL-12, IL-15 or IL-18.

[00122] The present invention is directed to an antibody, or fragment thereof, for the diagnosis, treatment or prevention of cancers wherein the antibody specifically binds to the PSMGFR peptide (SEQ ID NO:2) or a fragment thereof of the peptide.

[00123] The antibody binds to the N-10 peptide (SEQ ID NO:3), N-19 peptide (SEQ ID NO:4), N-23 peptide (SEQ ID NO:5), N-26 peptide (SEQ ID NO:6), N-30 peptide (SEQ ID NO:7), N-10/C-5 peptide (SEQ ID NO:8), N-19/C-5 peptide (SEQ ID NO:9), or C-5 peptide (SEQ ID NO:825).

[00124] The antibody interacts with a peptide comprising conformational epitope SVSDV (SEQ ID NO:1751) and FPSA (SEQ ID NO:1747) within N-26 sequence ISDVSVSDVPFPFSAQSGA (SEQ ID NO:6), wherein mutation or deletion of FPFS (SEQ ID NO:1747) destroys binding of the antibody or fragment thereof to the N-26 peptide.

[00125] The antibody interacts with a peptide comprising conformational epitope ASRYNLT (SEQ ID NO:1745), SVSDV (SEQ ID NO:1751), and FPSA (SEQ ID NO:1747) within the N-19 sequence

ASRYNLT ISDVSVSDVPFPFSAQSGA (SEQ ID NO:4), wherein mutation or deletion of ASRYNLT (SEQ ID NO:1745) destroys binding of the antibody or fragment thereof to the N-26 peptide.

[00126] The antibody does not bind to the C-10 peptide (SEQ ID NO:825).

[00127] The antibody binds to the N-10 peptide (SEQ ID NO:3), but not to the C-10 peptide (SEQ ID NO:825).

[00128] The antibody inhibits interaction between NME7$_{AB}$ and MUC1*.

[00129] The antibody inhibits interaction between NME7$_{AB}$ and PSMGFR peptide (SEQ ID NO:2).

[00130] The antibody inhibits interaction between NME7$_{AB}$ and N-10 peptide (SEQ ID NO:3), N-19 peptide (SEQ ID NO:4), N-23 peptide (SEQ ID NO:5), N-26 peptide (SEQ ID NO:6), N-30 peptide (SEQ ID NO:7), N-10/C-5 peptide (SEQ ID NO:8), N-19/C-5 peptide (SEQ ID NO:9), or C-5 peptide (SEQ ID NO:825).

[00131] The antibody recognizes a MUC1 transmembrane enzymatic cleavage product.

[00132] In the above, the cleavage enzyme is MMP14 or MMP9 or a catalytically active fragment thereof of the enzyme.

[00133] The antibody binds to PSMGFR (SEQ ID NO:2) or fragment thereof in which presence of an amino acid sequence within PSMGFR (SEQ ID NO:2) induces binding of the antibody to the PSMGFR.

[00134] The amino acid sequence of the binding conformationally inducing peptide is present in N-10 peptide (SEQ ID NO:3).

[00135] The antibody does not bind to a linear form of the binding conformationally inducing peptide sequence wherein the linear form of the peptide is a denatured form.

[00136] The binding conformationally inducing peptide sequence is in the N-26 peptide sequence ISDVSVSDVPFPFSAQSGA (SEQ ID NO:6), wherein mutation or deletion of FPFS (SEQ ID NO:1747) destroys binding of the antibody or fragment thereof to the N-26 peptide.

[00137] The binding conformationally inducing peptide sequence is located within the N-19 sequence ASRYNLTISDVSVSDVPFPFSAQSGA (SEQ ID NO:4), wherein mutation or deletion of ASRYNLT (SEQ ID NO:1745) destroys binding of the antibody or fragment thereof to the N-19 peptide.

[00138] The binding inducing peptide sequence may be located within the N-26 sequence ISDVSVSDVPFPFSAQSGA (SEQ ID NO:6), wherein mutation or deletion within FPFS (SEQ ID NO:1747) destroys binding of the antibody or fragment thereof to PSMGFR.

[00139] The antibodies may have a consensus sequence.

[00140] heavy chain CDR1 comprises consensus sequence at least 90% identical to sequence: F or I at position 1, T at position 2, F at position 3, S at position 4, T, G, or R at position 5, Y at position 6, A, G or T at position 7, M at position 8 and S at position 9;

[00141] heavy Chain CDR2 comprises consensus sequence at least 90% identical to sequence: T at position 1, I or S at position 2, I or S at position 3, G or R at position 5, G or A at position 6, T or I at position 9, Y at position 10, Y at position 11, P or S at position12 and DSVKG for positions 13-17;

[00142] heavy chain CDR3 comprises consensus sequence at least 90% identical to sequence:_ G, L, or N at position 2, G or T at position 4, Y at position 7, D or E at position 12, A at position 14, and Y at position 15;

[00143] light chain CDR1 comprises consensus sequence at least 90% identical to sequence: K or R at position 1, A or S at position 2, S at position 3, K or Q at position 4, S at position 5, L or V at position 6, L at position 7, T or S at position 10, Y at position 15, and I, L or M at position 16;

[00144] light Chain CDR2 comprises consensus sequence at least 90% identical to sequence: L or W, or S at position 1, A or T at position 2, S at position 3, N or T at position 4, L or R at position 5, E or A at position 6, and S at position 7; and

[00145] light chain CDR3 comprises consensus sequence at least 90% identical to sequence: Q at position 1, H or Q at position 2, S, Q or R at position 3, R, S or Y at position 4, E, L, or S at position 5, L or S at position 6, P or S at position 7, F or L at position 8 and T at position 9.

[00146] An antibody binding conformationally inducing peptide is within the N-26 sequence ISDVSVSDVPFPFSAQSGA (SEQ ID NO:6), wherein mutation or deletion within FPFS (SEQ ID NO:1747), SVSDV (SEQ ID NO:1751), or ASRYNLT (SEQ ID NO:1745) destroys binding of the antibody or fragment thereof to PSMGFR.

[00147] The antibody may have a further consensus sequence,

[00148] wherein

[00149] heavy chain CDR1 comprises consensus sequence at least 90% identical to sequence: F or I at position 1, T or A at position 2, F at position 3, S at position 4, T, G, or R at position 5, Y or F at position 6, A, G or T at position 7, M at position 8 and S at position 9;

[00150] heavy Chain CDR2 comprises consensus sequence at least 90% identical to sequence: T or A at position 1, I or S at position 2, I or S at position 3, N, S, T or G at position 4, G or R at position 5, G or A at position 6, G, T, or D at position 7, Y, K, H or S at position 8, T or I at position 9, Y or F at position 10, Y at position 11, P or S at position12 and D at position 13, S or T at position 14, V or L at position 15 and KG for positions 16-17;

[00151] heavy chain CDR3 comprises consensus sequence at least 90% identical to sequence: G, L, or N at position 2, G, T, or Y at position 3, G or T at position 4, Y at position 7, Y, A, or G at position 10, M, D or F at position 11, D or E at position 12 and AY at position 14-15;

[00152] light chain CDR1 comprises consensus sequence _ at least 90% identical to sequence: K or R at position 1, A or S at position 2, S or R at position 3, S, Y, I or V at position 8, T or S at position 10, G, S, D, or Q at position 12, V, Y, K or N at position 13, N, S, or T at position 14, Y or F at position 15, and I, L or M at position 16;

[00153] light Chain CDR2 comprises consensus sequence at least 90% identical to sequence: A, T or V at position 2, S at position 3, N, T, or K at position 4, L or R at position 5, E, A, F or D at position 6, and S at position 7; and

[00154] light chain CDR3 comprises consensus sequence at least 90% identical to sequence: Q, F or W at position 1, H or Q at position 2, R, S, T, Y or N at position 4, E, L, S or H at position 5, L, S, V, D or Y at position 6, P or S at position 7, and T at position 9.

[00155] The antibody above which may be MNC2, having

[00156] heavy chain CDR1 comprises consensus sequence FTFSGYAMS;

[00157] heavy Chain CDR2 comprises consensus sequence TISSGGTYIYYPDSVKG;

[00158] heavy chain CDR3 comprises consensus sequence -LGGDNYYEYFDV--;

[00159] light chain CDR1 comprises consensus sequence RASKS--VSTSGYSYMH;

[00160] light Chain CDR2 comprises consensus sequence LASNLES; and

[00161] light chain CDR3 comprises consensus sequence QHSRELPFT.

[00162] MNE6, having

[00163] heavy chain CDR1 comprises consensus sequence FTFSRYGMS;

[00164] heavy Chain CDR2 comprises consensus sequence TISGGGTYIYYPDSVKG;

[00165] heavy chain CDR3 comprises consensus sequence DNYGRNYDYGMDY--;

[00166] light chain CDR1 comprises consensus sequence -------SATSSVSYIH;

[00167] light Chain CDR2 comprises consensus sequence STSNLAS; and

[00168] light chain CDR3 comprises consensus sequence QQRSSSPFT.

[00169] B2, having

[00170] heavy chain CDR1 comprises consensus sequence FAFSTFAMS;

[00171] heavy Chain CDR2 comprises consensus sequence AISNGGGYTYYPDTLKG;

[00172] heavy chain CDR3 comprises consensus sequence ----RYYDLYFDL--;

[00173] light chain CDR1 comprises consensus sequence RSSQNIV-HSNGNTYLE;

[00174] light Chain CDR2 comprises consensus sequence KVSNRFS; and

[00175] light chain CDR3 comprises consensus sequence FQDSHVPLT.

[00176] B7, having

[00177] heavy chain CDR1 comprises consensus sequence FTFSRYGMS;

[00178] heavy Chain CDR2 comprises consensus sequence TISSGGTYIYYPDSVKG;

[00179] heavy chain CDR3 comprises consensus sequence DNYGSSYDYAMDY--;

[00180] light chain CDR1 comprises consensus sequence RSSQTIV-HSNGNTYLE;

[00181] light Chain CDR2 comprises consensus sequence KVSNRFS; and

[00182] light chain CDR3 comprises consensus sequence FQDSHVPLT.

[00183] B9, having

[00184] heavy chain CDR1 comprises consensus sequence FTFSRYGMS;

[00185] heavy Chain CDR2 comprises consensus sequence TISSGGTYIYYPDSVKG;

[00186] heavy chain CDR3 comprises consensus sequence DNYGSSYDYAMDY--;

[00187] light chain CDR1 comprises consensus sequence -------SASSSVSYMH;

[00188] light Chain CDR2 comprises consensus sequence TTSNLAS; and

[00189] light chain CDR3 comprises consensus sequence QQRSSYPF-.

[00190] 8C7F3, having

[00191] heavy chain CDR1 comprises consensus sequence FTFSTYAMS;

[00192] heavy Chain CDR2 comprises consensus sequence AISNGGGYTYYPDSLKG;

[00193] heavy chain CDR3 comprises consensus sequence ----RYYDHYFDY--;

[00194] light chain CDR1 comprises consensus sequence --RASESVATYGNNFMQ;

[00195] light Chain CDR2 comprises consensus sequence LASTLDS; and

[00196] light chain CDR3 comprises consensus sequence QQNNEDPPT.

[00197] H11, having

[00198] heavy chain CDR1 comprises consensus sequence FAFSTFAMS;

[00199] heavy Chain CDR2 comprises consensus sequence AISNGGGYTYYPDTLKG;

[00200] heavy chain CDR3 comprises consensus sequence ----RYYDLYFDL--;

[00201] light chain CDR1 comprises consensus sequence RSSQNIV-HSNGNTYLE;

[00202] light Chain CDR2 comprises consensus sequence KVSNRFS; and

[00203] light chain CDR3 comprises consensus sequence FQDSHVPLT.

[00204] B12, having

[00205] heavy chain CDR1 comprises consensus sequence SYGVH;

[00206] heavy Chain CDR2 comprises consensus sequence VIWPGGSTNYNSTLMSRM;

[00207] heavy chain CDR3 comprises consensus sequence DRTPRVGAWFAY; and

[00208] light chain CDR1 comprises consensus sequence RASESVATYGNNFMQ;

[00209] light Chain CDR2 comprises consensus sequence LASTLDS; and

[00210] light chain CDR3 comprises consensus sequence QQNNEDPPT.

[00211] 20A10, having

[00212] heavy chain CDR1 comprises consensus sequence FTFSTYAMS;

[00213] heavy Chain CDR2 comprises consensus sequence -SIGRAGSTYYSDSVKG;

[00214] heavy chain CDR3 comprises consensus sequence ---GPIYNDYDEFAY;

[00215] light chain CDR1 comprises consensus sequence KSSQSVLYSSNQKNYLA;

[00216] light Chain CDR2 comprises consensus sequence WASTRES; and

[00217] light chain CDR3 comprises consensus sequence HQYLSSLT.

[00218] 3C2B1, having

[00219] heavy chain CDR1 comprises consensus sequence ITFSTYTMS;

[00220] heavy Chain CDR2 comprises consensus sequence TISTGGDKTYYSDSVKG;

[00221] heavy chain CDR3 comprises consensus sequence -GTTAMYYYAMDY;

[00222] light chain CDR1 comprises consensus sequence RASKS---ISTSDYNYIH ;

[00223] light Chain CDR2 comprises consensus sequence LASNLES; and

[00224] light chain CDR3 comprises consensus sequence QHSRELPLT.

[00225]

[00226] In another aspect, the invention is directed to an antibody, or fragment thereof, for the diagnosis, treatment or prevention of cancers that requires presence of antibody binding conformationally inducing peptide ASRYNLT (SEQ ID NO:1745) of PSMGFR (SEQ ID NO:2). The antibody may be 25E6, having

[00227] heavy chain CDR1 comprises consensus sequence FTFSSYGMS;

[00228] heavy Chain CDR2 comprises consensus sequence TISNGGRHTFYPDSVKG;

[00229] heavy chain CDR3 comprises consensus sequence QTGTEGWFAY;

[00230] light chain CDR1 comprises consensus sequence KSSQSLLDSDGKTYLN;

[00231] light Chain CDR2 comprises consensus sequence LVSKLDS _; and

[00232] light chain CDR3 comprises consensus sequence WQGTHFPQT.

[00233]

[00234] In another aspect, the invention is directed to an antibody, or fragment thereof, for the diagnosis, treatment or prevention of cancers that requires presence of antibody binding conformationally inducing peptide SVSDV (SEQ ID NO:1761) of PSMGFR (SEQ ID NO:2). The antibody may be 5C6F3, having

[00235] heavy chain CDR1 comprises consensus sequence FTFSTYAMS ;

[00236] heavy Chain CDR2 comprises consensus sequence AISNGGGYTYYPDSLKG;

[00237] heavy chain CDR3 comprises consensus sequence RYYDHYFDY;

[00238] light chain CDR1 comprises consensus sequence RSSQTIVHSNGNTYLE;

[00239] light Chain CDR2 comprises consensus sequence KVSNRFS; and

[00240] light chain CDR3 comprises consensus sequence FQDSHVPLT.

[00241] The antibody or fragment thereof according all of the above may be murine, camelid, human or humanized. The antibody fragment may be scFv or scFv-Fc, which variable regions thereof may be murine, camelid, human or humanized.

[00242] In another aspect, the invention is directed to a chimeric antigen receptor (CAR) comprising the antibody fragments of above, and may further comprise mutations in the co-stimulatory domain or CD3-zeta signaling domain. Tyrosines may be mutated in CD28 or 4-1BB. CD3-zeta may contani 1XX mutations.

[00243] In another aspect, the invention is directed to an immune cell comprising the CAR of above. Immune cell may be T cell, NK cell, dendritic cell, or mast cell.

[00244] In another aspect, the invention is directed to a cell composition expressed in a cell comprising a CARs of above, and second entity having a biological recognition unit that has a specificity that is different from that of the CAR. The second entity may bind PD-1, PDL-1, or other checkpoint inhibitor, or NME7, or a cytokine such as IL-12 or IL-18, or c-Jun.

[00245] In yet another aspect, the invention is directed to an immune cell engineered to express a nucleic encoding a CAR of above and a nucleic acid encoding a second entity as in any of the claims above wherein the second entity expressed from an inducible promoter. The second entity may be expressed from an inducible promoter that is activated by elements of an activated immune cell. The second entity may be expressed from an NFAT inducible promoter. NFAT may be NFATc1, NFATc3 or NFATc2. The second entity may be a cytokine such as IL-7, IL-15, or IL-18. The nucleic acids encoding the second entity may be inserted into a Foxp3 promoter or enhancer region, wherein the cytokine is IL-18. The cytokine may be expressed from an NFAT inducible promoter.

[00246] In another aspect, the invention is directed to a BiTE construct comprising the antibody fragment of above.

[00247] In yet another aspect, the invention is directed to an antibody drug conjugate (ADC) comprising the antibody or antibody fragment of above.

[00248] The present invention is directed to an antibody or fragment thereof that specifically binds to PSMGFR (SEQ ID NO:2) and N-10 (SEQ ID NO:3); and

[00249] does not bind to full-length MUC1;

[00250] does not bind to C-10 (SEQ ID NO:825);

[00251] competitively inhibits binding of NME1 or NME7$_{AB}$ to MUC1* extra cellular domain or a PSMGFR peptide;

[00252] recognizes a MUC1* generated by cleavage by a cleavage enzyme;

[00253] recognizes a conformational epitope and not a linear epitope; or

[00254] is cancer selective by immunohistochemistry on tissues.

[00255] Four of the criteria (i) – (vi) may be satisfied. Five of the criteria (i) – (vi) may be satisfied. Six of the criteria (i) – (vi) may be satisfied. At least criteria (vi) may be satisfied. Cleavage enzyme may be MMP-9.

[00256] In all of the above, the cancer may be breast cancer, pancreatic cancer, ovarian cancer, lung cancer, colon cancer, gastric cancer or esophageal cancer.

[00257] The present invention is also directed to a method of diagnosing, treating or preventing cancer by administering the antibodies and fragments disclosed herein to a cancer patient in need thereof that has been identified as expressing MUC1 aberrantly and expressing truncated MUC1, such as MUC1*.

[00258] These and other objects of the invention will be more fully understood from the following description of the invention, the referenced drawings attached hereto and the claims appended hereto.

BRIEF DESCRIPTION OF THE DRAWINGS

[00259] The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawings will be provided by the Office upon request and payment of the necessary fee.

[00260] The present invention will become more fully understood from the detailed description given herein below, and the accompanying drawings which are given by way of illustration only, and thus are not limitative of the present invention, and wherein;

[00261] **Figures 1A-1D** show cell growth assay graphs of MUC1* positive cells treated with either bivalent 'bv' anti-MUC1* antibody, monovalent 'mv' or Fab, NM23-H1 dimers or

NME7-AB. Bivalent anti-MUC1* antibodies stimulate growth of cancer cells whereas the monovalent Fab inhibits growth (Fig. 1A-1B). Classic bell-shaped curve indicates ligand induced dimerization stimulates growth. Dimeric NM23-H1, aka NME1, stimulates growth of MUC1* positive cancer cells but siRNA to suppress MUC1 expression eliminate its effect (Fig. 1C). NME7-AB also stimulates the growth of MUC1* positive cells (Fig. 1D).

[00262] **Figures 2A-2I** show results of ELISA assays. MUC1* peptides PSMGFR, PSMGFR minus 10 amino acids from the N-terminus aka N-10, or PSMGFR minus 10 amino acids from the C-terminus, aka C-10 are immobilized on the plate and the following are assayed for binding: NME7-AB (Fig. 2A), MN-C2 monoclonal antibody (Fig. 2B), MN-E6 monoclonal antibody (Fig. 2C), or dimeric NME1 (Fig. 2D). These assays show that NME1, NME7-AB and monoclonal antibodies MN-C2 and MN-E6 all require the first membrane proximal 10 amino acids of the MUC1* extracellular domain to bind. MUC1* peptides PSMGFR minus 10 amino acids from the N-terminus aka N-10, or PSMGFR minus 10 amino acids from the C-terminus, aka C-10, are immobilized on the plate and the following are assayed for binding: MN-C3 (Fig. 2E) and MN-C8 (Fig. 2F). Fig. 2G shows the amino acid sequence of the PSMGFR peptide. Fig. 2H shows the amino acid sequence of the N-10 peptide. Fig. 2I shows the amino acid sequence of the C-10 peptide.

[00263] **Figures 3A-3C** show results of competitive ELISA assays. The PSMGFR MUC1* peptide is immobilized on the plate and dimeric NM23-H1, aka NME1, is added either alone or after the MN-E6 antibody has been added (Fig. 3A). The same experiment was performed wherein NM23-H7, NME7-AB, is added alone or after MN-E6 has been added (Fig. 3B). Results show that MN-E6 competitively inhibits the binding of MUC1* activating ligands NME1 and NME7. In a similar experiment (Fig. 3C), PSMGFR or PSMGFR minus 10 amino acids from the N-terminus, aka N-10, is immobilized on the plate. Dimeric NM23-H1 is then added. Anti-MUC1* antibodies MN-E6, MN-C2, MN-C3 or MN-C8 are then tested for their ability to compete off the NM23-H1. Results show that although all three antibodies bind to the PSMGFR peptides, MN-E6 and MN-C2 competitively inhibit binding of the MUC1* activating ligands.

[00264] **Figures 4A-4F** show FACS scans of anti-MUC1* antibody huMN-C2scFv binding specifically to MUC1* positive cancer cells and MUC1* transfected cells but not MUC1* or MUC1 negative cells. ZR-75-1, aka 1500, MUC1* positive breast cancer cells were stained with 1:2 or 1:10 dilutions of the 1.5 ug/ml humanized MN-C2. After two washes, cells were stained with secondary antibody, Anti-Penta-His antibody conjugated to Alexa 488 (Qiagen) dilutions of 1:200 (Fig. 4A), 1:50 (Fig. 4B), or 1:10 (Fig. 4C) to detect the 6x His tag on the huMN-C2 scFv. Fig. 4A shows huMN-C2 binding to ZR-75-1 breast cancer cells where secondary antibody is added at a 1:200 dilution. Fig. 4B shows huMN-C2 binding to ZR-75-1 breast cancer cells where secondary antibody is added at a 1:50 dilution. Fig. 4C shows huMN-C2 binding to ZR-75-1 breast cancer cells where secondary antibody is added at a 1:10 dilution. Flow cytometric analysis revealed a concentration-dependent shift of a subset of cells, indicating specific binding, which is unseen in the absence of the MN-C2 scFv (Fig. 4A-4C). Fig. 4D shows anti-MUC1* antibody MN-E6 staining of MUC1 negative HCT-116 colon cancer cells transfected with the empty vector, single cell clone #8. Fig. 4E shows anti-MUC1* antibody MN-E6 staining of HCT-116 colon cancer cells transfected with MUC1* single cell clone #10. Fig. 4F shows anti-MUC1* antibody MN-E6 staining of ZR-75-1, aka 1500, MUC1* positive breast cancer cells. As the FACS scans show, both MN-C2 and MN-E6 only stain MUC1* positive cells and not MUC1 or MUC1* negative cells.

[00265] **Figure 5** shows a graph of an ELISA in which surface is coated with either the MUC1* PSMGFR peptide or a control peptide. Humanized MN-C2 scFv is then incubated with the surface, washed and detected according to standard methods. The ELISA shows that the huMN-C2 scFv binds to the MUC1* peptide with an EC-50 of about 333nM.

[00266] **Figures 6A-6B** show graphs of cancer cell growth inhibition by MUC1* antibody variable region fragment humanized MN-C2 scFv. hMN-C2 scFv potently inhibited the growth of ZR-75-1, aka 1500, MUC1* positive breast cancer cells (Fig. 6A) and T47D MUC1* positive breast cancer cells (Fig. 6B) with approximately the same EC-50 as the *in vitro* ELISAs.

[00267] **Figures 7A-7B** show graphs of tumor growth in immune compromised mice that have been implanted with human tumors then treated with anti-MUC1* antibody MN-E6 Fab or mock treatment. Female nu/nu mice implanted with 90-day estrogen pellets were implanted with 6 million T47D human breast cancer cells that had been mixed 50/50 with Matrigel. Mice bearing tumors that were at least 150 mm^3 and had three successive increases in tumor volume were selected for treatment. Animals were injected sub cutaneously twice per week with 80 mg/kg MN-E6 Fab and an equal number of mice fitting the same selection criteria were injected with vehicle alone (Fig. 7A). Male NOD/SCID mice were implanted with 6 million DU-145 human prostate cancer cells that had been mixed 50/50 with Matrigel. Mice bearing tumors that were at least 150 mm^3 and had three successive increases in tumor volume were selected for treatment. Animals were injected sub-cutaneously every 48 hours with 160 mg/kg MN-E6 Fab and an equal number of mice fitting the same selection criteria were injected with vehicle alone (Fig. 7B). Tumors were measured independently by two researchers twice per week and recorded. Statistics were blindly calculated by independent statistician, giving a P value of 0.0001 for each. Anti-MUC1* Fab inhibited breast cancer growth and prostate cancer growth. Treatment had no effect on weight, bone marrow cell type or number.

[00268] **Figure 8** shows a graph of an ELISA wherein the surface was immobilized with either PSMGFR peptide, PSMGFR minus 10 amino acids from the N-terminus or minus 10 amino acids from the C-terminus. The huMN-E6 scFv-Fc bound to the PSMGFR peptide and to the PSMGFR N-10 peptide but not to the PSMGFR C-10 peptide. The parent MN-E6 antibody and the humanized MN-E6 require the C-terminal 10 amino acids of PSMGFR for binding.

[00269] **Figures 9A-9B** show graphs of ELISAs wherein the assay plate surface was immobilized with either PSMGFR peptide, PSMGFR minus 10 amino acids from the N-terminus or minus 10 amino acids from the C-terminus. The MN-C3 antibody variants were then assayed for binding to the various MUC1* peptides. Fig. 9A shows purified mouse monoclonal MN-C3 antibody; and Figure 9B shows the humanized MN-C3 scFv-Fc. ELISAs show binding to the PSMGFR peptide as well as to certain deletion peptides.

[00270] **Figures 10A-10J.** Figs. 10A10B are photographs of breast cancer tissue arrays. Fig. 10A was stained with VU4H5 which recognizes MUC1-FL (full length); Fig. 10B was stained with mouse monoclonal antibody MN-C2 which recognizes cancerous MUC1*. Following automated staining (Clarient Diagnostics), the tissue staining was scored using Allred scoring method which combines an intensity score and a distribution score. Figs. 10C10F are color coded graphs showing the score calculated for MUC1 full-length staining for each patient's tissue. Figs. 10G10J are color coded graphs showing the score calculated for MUC1* staining for each patient's tissue.

[00271] **Figures 11A-11J.** Figs. 11A11B are photographs of breast cancer tissue arrays. Fig. 11A was stained with VU4H5 which recognizes MUC1-FL (full length); Fig. 11B was stained with mouse monoclonal antibody MN-C2 which recognizes cancerous MUC1*. Following automated staining (Clarient Diagnostics), the tissue staining was scored using Allred scoring method which combines an intensity score and a distribution score. Figs. 11C-11F are color coded graphs showing the score calculated for MUC1 full-length staining for each patient's tissue. Figs. 11G-11J are color coded graphs showing the score calculated for MUC1* staining for each patient's tissue.

[00272] **Figures 12A-12H** show photographs of normal breast and breast cancer tissues stained with humanized MN-E6-scFv-Fc biotinylated anti-MUC1* antibody at 2.5 ug/mL, then stained with a secondary streptavidin HRP antibody. Fig. 12A is a normal breast tissue. Figs. 12B-12D are breast cancer tissues from patients as denoted in the figure. Figs. 12E-12H are photographs of the corresponding serial sections that were stained with the secondary antibody alone.

[00273] **Figures 13A-13F** show photographs of normal breast and breast cancer tissues stained with humanized MN-E6-scFv-Fc biotinylated anti-MUC1* antibody at 2.5 ug/mL, then stained with a secondary streptavidin HRP antibody. Fig. 13A is a normal breast tissue. Figs. 13B-13C are breast cancer tissues from patients as denoted in the figure. Figs. 13D-13F are photographs of the corresponding serial sections that were stained with the secondary antibody alone.

[00274] **Figures 14A-14H** show photographs of breast cancer tissues stained with MN-E6 anti-MUC1* antibody at 10 ug/mL, then stained with a rabbit anti mouse secondary HRP antibody. Figs. 14A-14D are breast cancer tissues from patient #300. Figs. 14E-14H are breast cancer tissues from metastatic patient #291.

[00275] **Figures 15A-15F** show photographs of normal lung and lung cancer tissues stained with humanized MN-E6-scFv-Fc biotinylated anti-MUC1* antibody at 2.5 ug/mL, then stained with a secondary streptavidin HRP antibody. Fig. 15A is a normal lung tissue. Figs. 15B15C are lung cancer tissues from patients as denoted in the figure. Figs. 15D-15F are photographs of the corresponding serial sections that were stained with the secondary antibody alone.

[00276] **Figures 16A-16F** show photographs of normal lung and lung cancer tissues stained with humanized MN-E6-scFv-Fc biotinylated anti-MUC1* antibody at 2.5 ug/mL, then stained with a secondary streptavidin HRP antibody. Fig. 16A is a normal lung tissue. Figs. 16B16C are lung cancer tissues from patients as denoted in the figure. Figs. 16D-16F are photographs of the corresponding serial sections that were stained with the secondary antibody alone.

[00277] **Figures 17A-17F** show photographs of normal lung and lung cancer tissues stained with humanized MN-E6-scFv-Fc biotinylated anti-MUC1* antibody at 25 ug/mL, then stained with a secondary streptavidin HRP antibody. Fig. 17A is a normal lung tissue. Figs. 17B-17C are lung cancer tissues from patients as denoted in the figure. Figs. 17D-17F are photographs of the corresponding serial sections that were stained with the secondary antibody alone.

[00278] **Figures 18A-18F** show photographs of normal lung and lung cancer tissues stained with humanized MN-E6-scFv-Fc biotinylated anti-MUC1* antibody at 25 ug/mL, then stained with a secondary streptavidin HRP antibody. Fig. 18A is a normal lung tissue. Figs. 18B-18C are lung cancer tissues from patients as denoted in the figure. Figs. 18D-18F are photographs of the corresponding serial sections that were stained with the secondary antibody alone.

[00279] **Figures 19A-19D** show photographs of normal small intestine and cancerous small intestine tissues stained with humanized MN-E6-scFv-Fc biotinylated anti-MUC1* antibody at 5 ug/mL, then stained with a secondary streptavidin HRP antibody. Fig. 19A is a normal small intestine tissue. Fig. 19B is small intestine cancer from patient as denoted in the figure. Figs. 19C-19D are photographs of the corresponding serial sections that were stained with the secondary antibody alone.

[00280] **Figures 20A-20H** show photographs of normal small intestine tissues stained with humanized MN-E6-scFv-Fc anti-MUC1* antibody at 50 ug/mL, then stained with a secondary goat-anti-human HRP antibody. Figs. 20A-20D are normal small intestine tissue. Figs. 20E-20H are photographs of the corresponding serial sections that were stained with the secondary antibody alone.

[00281] **Figures 21A-21H** show photographs of cancerous small intestine tissues stained with humanized MN-E6-scFv-Fc anti-MUC1* antibody at 50 ug/mL, then stained with a secondary goat-anti-human HRP antibody. Figs. 21A-21D are cancerous small intestine tissue from a patient as denoted in figure. Figs. 21E-21H are photographs of the corresponding serial sections that were stained with the secondary antibody alone.

[00282] **Figures 22A-22H** show photographs of cancerous small intestine tissues stained with humanized MN-E6-scFv-Fc anti-MUC1* antibody at 50 ug/mL, then stained with a secondary goat-anti-human HRP antibody. Figs. 22A-22D are cancerous small intestine tissue from a patient as denoted in figure. Figs. 22E-22H are photographs of the corresponding serial sections that were stained with the secondary antibody alone.

[00283] **Figures 23A-23H** show photographs of normal colon tissues stained with humanized MN-E6-scFv-Fc anti-MUC1* antibody at 50 ug/mL, then stained with a secondary goat-anti-human HRP antibody. Figs. 23A-23D are normal colon. Figs. 23E-23H are photographs of the corresponding serial sections that were stained with the secondary antibody alone.

[00284] **Figures 24A-24H** show photographs of colon cancer tissues stained with humanized MN-E6-scFv-Fc anti-MUC1* antibody at 50 ug/mL, then stained with a secondary goat-anti-human HRP antibody. Figs. 24A-24D are colon cancer tissue from a metastatic patient as denoted in figure. Figs. 24E-24H are photographs of the corresponding serial sections that were stained with the secondary antibody alone.

[00285] **Figures 25A-25H** show photographs of colon cancer tissues stained with humanized MN-E6-scFv-Fc anti-MUC1* antibody at 50 ug/mL, then stained with a secondary goat-anti-human HRP antibody. Figs. 25A-25D are colon cancer tissue from a Grade 2 patient as denoted in figure. Figs. 25E-25H are photographs of the corresponding serial sections that were stained with the secondary antibody alone.

[00286] **Figures 26A-26H** show photographs of colon cancer tissues stained with humanized MN-E6-scFv-Fc anti-MUC1* antibody at 50 ug/mL, then stained with a secondary goat-anti-human HRP antibody. Figs. 26A-26D are colon cancer tissue from a metastatic patient as denoted in figure. Figs. 26E-26H are photographs of the corresponding serial sections that were stained with the secondary antibody alone.

[00287] **Figures 27A-27H** show photographs of prostate cancer tissues stained with humanized MN-E6-scFv-Fc anti-MUC1* antibody at 50 ug/mL, then stained with a secondary goat-anti-human HRP antibody. Figs. 27A-27D are prostate cancer tissue from a patient as denoted in figure. Figs. 27E-27H are photographs of the corresponding serial sections that were stained with the secondary antibody alone.

[00288] **Figures 28A-28H** show photographs of prostate cancer tissues stained with humanized MN-E6-scFv-Fc anti-MUC1* antibody at 50 ug/mL, then stained with a secondary goat-anti-human HRP antibody. Figs. 28A-28D are prostate cancer tissue from a patient as denoted in figure. Figs. 28E-28H are photographs of the corresponding serial sections that were stained with the secondary antibody alone.

[00289] **Figures 29A-29H** show photographs of prostate cancer tissues stained with humanized MN-E6-scFv-Fc anti-MUC1* antibody at 50 ug/mL, then stained with a secondary goat-anti-human HRP antibody. Figs. 29A-29D are prostate cancer tissue from a patient as denoted in figure. Figs. 29E-29H are photographs of the corresponding serial sections that were stained with the secondary antibody alone.

[00290]

[00291] **Figures 30A-30F** show photographs of a triple negative breast cancer array stained with anti-MUC1* antibody huMNC2scFv. The first score shown is the Allred score and the second is the tumor grade. The percentage of the array that scored zero, weak, medium or strong is graphed as a pie chart**.** Fig. 30A shows the pie chart of score of anti-MUC1* antibody staining. Fig. 30B shows a photograph of the array stained with the antibody. Figs. 30C-30D show magnified photographs of two of the breast cancer specimens from the array. Figs. 30E-30F show more magnified photographs of the portion of the specimen that is marked by a box.

[00292] **Figures 31A-31F** show photographs of an ovarian cancer array stained with anti-MUC1* antibody huMNC2scFv. The first score shown is the Allred score and the second is the tumor grade. The percentage of the array that scored zero, weak, medium or strong is graphed as a pie chart. Fig. 31A shows the pie chart of score of anti-MUC1* antibody staining. Fig. 31B shows a photograph of the array stained with the antibody. Figs. 31C-31D show magnified photographs of two of the breast cancer specimens from the array. Figs. 31E-31F show more magnified photographs of the portion of the specimen that is marked by a box.

[00293] **Figures 32A-32F** show photographs of a pancreatic cancer array stained with anti-MUC1* antibody huMNC2scFv. The first score shown is the Allred score and the second is the tumor grade. The percentage of the array that scored zero, weak, medium or strong is graphed as a pie chart. Fig. 32A shows the pie chart of score of anti-MUC1* antibody staining. Fig. 32B shows a photograph of the array stained with the antibody. Figs. 32C-32D show magnified photographs of two of the breast cancer specimens from the array. Figs. 32E-32F show more magnified photographs of the portion of the specimen that is marked by a box.

[00294] **Figures 33A-33F** show photographs of a lung cancer array stained with anti-MUC1* antibody huMNC2scFv. The first score shown is the Allred score and the second is the tumor grade. The percentage of the array that scored zero, weak, medium or strong is graphed as a pie chart. Fig. 33A shows the pie chart of score of anti-MUC1* antibody staining. Fig. 33B shows a photograph of the array stained with the antibody. Figs. 33C-33D show magnified photographs of two of the breast cancer specimens from the array. Figs. 33E-33F show more magnified photographs of the portion of the specimen that is marked by a box.

[00295] **Figures 34A-34I** show photographs of normal tissues stained with anti-MUC1* antibody huMNC2scFv.

[00296] **Figures 35A-35D** show FACS scans of cells expressing either no MUC1, MUC1* or full-length MUC1, wherein the cells were probed with either MNC2 or VU4H5. Fig. 35A shows MUC1 negative HCT-116 colon cancer cells probed with antibody MNC2. Fig. 35B shows HCT cells that have been transfected with MUC1* wherein the extra cellular domain is just the sequence of the PSMGFR peptide wherein the cells are probed with antibody MNC2. Fig. 35C shows HCT-MUC1-18 cells which are a cleavage resistant single cell clone of HCT cells transfected with full-length MUC1, also referred to herein as HCT-MUC1-41TR, and cells were probed with antibody MNC2. Fig. 35D shows HCT-MUC1-18 cells probed with antibody VU4H5 which is an antibody that recognizes the hundreds of tandem repeats epitopes in full-length MUC1. As can be seen in the figures, MNC2 recognizes an ectopic epitope that is not accessible in full-length MUC1.

[00297] **Figures 36A-36D** show Western blots and corresponding FACs analysis of HCT-116 cells which are a MUC1 negative colon cancer cell line, that were then stably transfected with either MUC1* or MUC1 full-length. The single cell clones that are shown are HCT-MUC1-41TR, and HCT-MUC1*. Fig. 36A shows a Western blot of the parent cell line HCT-116, HCT-MUC1-41TR and HCT-MUC1* wherein the gel has been probed with a rabbit polyclonal antibody, SDIX, that only recognizes cleaved MUC1. A visible band between 25 and 35kDa can be readily seen in Lane 6, loaded with HCT-MUC1*, whereas there is only a faint band in Lanes 4 and 5, showing that only a small amount of MUC1 is cleaved in the HCT-MUC1-41Tr cells. There is no cleaved MUC1 present in the parent cell line HCT-116 loaded into Lanes 2 and 3. Fig. 36B is a Western blot that was probed with a mouse monoclonal antibody VU4H5 that recognizes the tandem repeats of full-length MUC1. As can be seen, only HCT-MUC1-41TR contains full-length MUC1. Fig. 36C shows FACS scans showing that HCT-MUC1* is 95.7% positive for SDIX which only binds to MUC1* and essentially not at all for MUC1 full-length. Fig. 36D shows FACS scans that show that HCT-MUC1-41TR cells are 95% positive for full-length MUC1 and only about 11% positive for the cleaved form, MUC1*.

[00298] **Figure 37A-37C** shows western blots and a bar graph of FACS analysis assessing the ability of MNC2to recognize a full-length MUC1 after it has been cleaved by MMP9. Fig. 37A shows a Western blot of HCT-MUC1-18 cells, which are a cleavage resistant cell line, to which was added cleavage enzyme MMP9. The cell lysate fraction was run on a gel and probed with a polyclonal anti-PSMGFR antibody. The photo shows that in a dose dependent manner, MMP9 cleaved MUC1 to MUC1*, the ~25kDa species. Fig. 37B shows the Western blot of the conditioned media from the same experiment. The photo shows that the addition of cleavage enzyme MMP9, in a dose dependent manner, increased the release of the tandem repeat domain into the conditioned media. Fig. 37C shows FACS analysis of the experiment. The graphs show that the addition of MMP9, in a dose dependent manner, increased recognition of the cleavage product by anti-MUC1* antibody MNC2 and decreased the recognition of the full-length MUC1 which contains the tandem repeat domain.

[00299] **Figure 38** shows a photograph of a Western blot in which HCT-MUC1-18 cells, labeled here as HCT-18, a cleavage resistant single cell clone of HCT cells transfected with full-length MUC1, are treated with varying amounts of a catalytically active ADAM17 or MMP14. Shed MUC1 tandem repeat domain of full-length MUC1 is immunoprecipitated from the conditioned media, and run on a gel that is then probed with VU4H5 that binds to the tandem repeat epitopes. As can be seen, MMP14 also efficiently cleaves MUC1 full-length and sheds the tandem repeat containing extra cellular domain into the conditioned media. Cleavage enzyme ADAM17 did not cleave MUC1.

[00300] **Figure 39A-39B** shows fluorescence activated cell sorting (FACS) measurements of human CD34+ hematopoietic stem cells of human bone marrow stained with anti-MUC1* monoclonal antibodies MNC3, MNC2, MNE6 or an isotype control antibody. The histogram of the FACS assay and the bar graph showing the data show that the MUC1* positive cells of the bone marrow are recognized by one anti-MUC1* antibody, MNC3 but not by MNE6 or MNC2. All three antibodies bind to the PSMGFR peptide. The great difference in the specificity of these antibodies suggests that MNC3 recognizes a MUC1*-like form created when MUC1 is cleaved by an enzyme that is different from MMP9.

[00301] **Figure 40A-40G** shows the details of FACS analysis of the hematopoietic stem cells probed with either MNC3 or MNE6. Fig. 40A shows the FACS scatter plot of total bone marrow cells. Fig. 40B shows the FACS scatter plot of the CD34+ cells. Fig. 40C shows the FACS histogram of the CD34+ cells. Fig. 40D shows the FACS scatter plot of the earliest hematopoietic stem cells, which are CD34+/CD38-, stained with either MNC3 or MNE6. Fig. 40E shows the histogram of the experiment. Fig. 40F shows the histogram overlay of MNC3 binding to CD34+/CD38- cells versus MNE6. Fig. 40G shows the bar graph of that FACS experiment.

[00302] **Figure 41A-42H** shows the details of FACS analysis of CD34+/CD38$^{-/lo}$ hematopoietic stem cells probed with a polyclonal anti-PSMGFR antibody SDIX, MNE6 or MNC2. Fig. 41A shows the FACS scatter plot of the CD34+/CD38$^{-/lo}$ population of cells. Fig. 41E shows a table of the detailed analysis. Fig. 41B shows the FACS scatter plot of the CD34+/CD38$^{-/lo}$ population of cells probed with the anti-PSMGFR polyclonal antibody SDIX. Fig. 41F shows a table of the detailed analysis. Fig. 41C shows the FACS scatter plot of the CD34+/CD38$^{-/lo}$ population of cells probed with MNE6. Fig. 41G shows a table of the detailed analysis. Fig. 41D shows the FACS scatter plot of the CD34+/CD38$^{-/lo}$ population of cells probed with MNC2. Fig. 41H shows a table of the detailed analysis.

[00303] **Figure 42A-42H** shows photographs of DU145 prostate cancer cells or T47D breast cancer cells that have been treated with either the Fab of anti-MUC1* antibody MNC2, MNE6, MNC3 or MNC8. The images show that cancer specific antibodies MNC2 and MNE6 effectively kill prostate and breast cancer cells while the monoclonal antibodies MNC3 and MNC8 do not.

[00304] **Figure 43** shows a graph of a PCR experiment comparing expression of a wide range of cleavage enzymes expressed in different cells lines, wherein the values have been normalized to those expressed in breast cancer cell line T47D. Cell lines that are compared are prostate cancer cell line DU145, HCT-MUC1-41TR that is a MUC1 negative colon cancer cell line transfected with a MUC1 whose extracellular domain is truncated after 41 tandem repeat units and that is not cleaved to the MUC1* form, T47D breast cancer cell line and CD34+ bone marrow cells.

[00305] **Figure 43** shows a graph of a PCR experiment in which the expression levels of various cleavage enzymes are measured in DU145 prostate cancer cells, HCT116+MUC1FL, also known as HCT-MUC1-18 a cell line expressing full-length MUC1, T47D breast cancer cells, and CD34+ hematopoietic stem cells of the bone marrow. The fold expression is relative to the expression of each cleavage enzyme in T47D breast cancer cells, set as 1.

[00306] **Figure 44** shows the graph of the PCR experiment of Figure 43 but with the Y-axis maximum set to 5.

[00307] **Figures 45A-45P** show photographs of a CAR T co-culture assay in which the targeting antibody fragment of the CAR is huMNC2scFv wherein CAR44 has a CD8 transmembrane domain, followed by 41BB-3zeta and CAR50 has a CD4 transmembrane domain, followed by 41BB-3zeta. The target cancer cells are: HCT-FLR which is HCT-116 cells transfected with MUC1*$_{45}$ and HCT-MUC1-41TR, which is a stable single cell clone HCT-116 cell line that expresses MUC1 with an extracellular domain truncated after 41 tandem repeats and that does not get cleaved to the MUC1* form on its own. The HCT-MUC1-41TR cancer cells were also incubated with conditioned media from cells transfected with MMP9 or ADAM17 before co-culture with the CAR T cells. Conditioned media of the MMP9 or ADAM17 expressing cells were also incubated with APMA which is an activator of those cleavage enzymes. The images shown are an overlay of the 4X bright field image and the fluorescent image of the same showing cancer cells dyed with a red CMTMR lipophilic dye. Figs. 45A, 45E, 45I, 45M show photographs of cells co-cultured with untransduced human T cells. Figs. 45B, 45F, 45J, 45N show photographs of cells co-cultured with human T cells transduced with anti-MUC1* CAR44 at an MOI of 10. Figs. 45C, 45G, 45K, 45O show photographs of cells co-cultured with human T cells transduced with anti-MUC1* CAR50 at an MOI of 10. Figs. 45D, 45H, 45L, 45P show photographs of cells co-cultured with human T cells transduced with anti-MUC1* CAR44 at an MOI of 50, which increases transduction efficiency. Figs. 45B, 45C, 45D show that both CAR44 and CAR50 transduced T cells recognized MUC1* expressed in these cancer cells, bound to them, induced clustering and killed many cancer cells. Figs. 45F, 45G, 45H show that neither CAR44 nor CAR50 transduced T cells recognize full-length MUC1 expressed in HCT-MUC1-41TR cancer cells. There is no T cell induced clustering and the number of cancer cells has not decreased. Figs. 45J, 45K, 45L show that activated MMP9 has cleaved full-length MUC1 to a MUC1* form that is recognized by both CAR44 and CAR50 transduced T cells. There is clearly visible CAR T cell induced clustering and a decrease in the number of cancer cells as they are killed. Figs. 45N, 45O, 45P show that activated ADAM17 has either not cleaved MUC1 or cleaved it at a position not recognized by MNC2. Neither huMNC2-CAR44 nor huMNC2-CAR50 transduced T cells recognized these cancer cells.

[00308] **Figure 46A-46T** shows photographs of a CAR T co-culture assay in which the targeting antibody fragment of the CAR is MNC2 scFv wherein CAR44 has a CD8 transmembrane domain, followed by 41BB-3zeta and CAR50 has a CD4 transmembrane domain, followed by 41BB-3zeta. The target cancer cells are breast cancer T47D cells that were also incubated with conditioned media from cells transfected with MMP2, MMP9 or ADAM17 before co-culture with the MNC2-CAR T cells. In some cases, the conditioned media of the MMP2 and MMP9 expressing cells were also incubated with APMA, which is an activator of these cleavage enzymes. The images shown are an overlay of the 4X bright field image and the fluorescent image of the same showing cancer cells dyed with a red CMTMR lipophilic dye. As can be seen, the MNC2-CAR T cells only bind to and attack the target cancer cells that express the cleaved form, MUC1*.

[00309] **Figures 47A-47I** show photographs of cancer cells co-cultured with anti-MUC1* CAR T cells, wherein some of the cancer cells were pre-incubated with activated MMP9 prior to co-culture with the CAR T cells. The cancer cells shown in Figs. 47A-47C are MUC1 negative colon cancer cell line HCT-116 that have been stably transfected to express MUC1*. The cancer cells shown in Figs. 47D-47F are MUC1 positive breast cancer cell line T47Ds that express high levels of both MUC1 full-length and MUC1*. The cancer cells shown in Figs. 47G-47I are MUC1 positive breast cancer cell line T47Ds that were pre-incubated with activated MMP9. The cells shown in Figs. 47A, 47D and 47G were co-cultured with untransduced human T cells and are the controls. The cells shown in Figs. 47B, 47E and 47H were co-cultured with human T cells that were transduced with huMNC2-CAR44 at an MOI of 10, wherein MOI stands for multiplicity of infection and the higher the MOI the more CARs are expressed on the T cells. The cells shown in Figs. 47C, 47F and 47I were co-cultured with human T cells that were transduced with huMNC2-CAR44 at an MOI of 50. As can be seen in the photographs, the CAR44 T cells bind to the target MUC1* positive cancer cells, surrounding and killing them. Comparing the photograph Fig. 47I with the others, it can be seen that the cells that were pre-incubated with MMP9 become much more susceptible to CAR T killing when the antibody targeting head of the CAR recognizes MUC1*. It also demonstrates that MUC1 cleaved by MMP9 is recognized by huMNC2scFv.

[00310] **Figure 48** shows an xCelligence graph of T47D breast cancer cells in co-culture with either untransduced T cells, as a control, or huMNC2-CAR44 T cells over a 45 hour period. After 18 hours of cancer cell growth, a catalytic sub-unit MMP9 was added to some of the cells. At 25 hours, T cells were added. As can be seen, huMNC2-CAR44 T cell killing is greatly improved when the T47D cells are pre-incubated with cleavage enzyme MMP9. In the xCelligence system, target cancer cells, which are adherent, are plated onto electrode array plates. Adherent cells insulate the electrode and increase the impedance. The number of adherent cancer cells is directly proportional to impedance. T cells are not adherent and do not contribute to impedance. Therefore, increasing impedance reflects growth of cancer cells and decreasing impedance reflects killing of cancer cells.

[00311] **Figure 49** shows an xCelligence graph of DU145 prostate cancer cells in co-culture with either untransduced T cells, as a control, or huMNC2-CAR44 T cells over a 45 hour period. After 18 hours of cancer cell growth, a catalytic sub-unit MMP9 was added to some of the cells. At 25 hours, T cells were added. As can be seen, huMNC2-CAR44 T cell killing is not affected by pre-incubation with cleavage enzyme MMP9. DU145 cancer cells express a significantly lower amount of MUC1 which includes the full-length form as well as MUC1*. The lower density of MUC1 full-length does not sterically hinder T cell access to the membrane proximal MUC1*.

[00312] **Figure 50** shows a bar graph of a PCR experiment measuring the amount of MUC1 expressed by a panel of cell lines and primary cells, comprised of normal cells as well as cancer cells.

[00313] **Figure 51A-51B** shows a bar graph of an ELISA assay measuring the amount of interferon gamma, IFN-g, secreted by huMNC2-CAR44 human T cells after co-culture with the normal cells or the HCT-MUC1* cancer cells for 72 hours. Fig. 51A shows the results of the experiment where the CAR44 T cell to target cell ratio was 1:1. Fig. 51B shows the results of the experiment where the CAR44 T cell to target cell ratio was 0.5:1.

[00314] **Figure 52A-52B** shows a bar graph of an ELISA assay measuring the amount of interleukin-2, IL-2, secreted by huMNC2-CAR44 human T cells after co-culture with the normal cells or the HCT-MUC1* cancer cells for 72 hours. Fig. 52A shows the results of the experiment where the CAR44 T cell to target cell ratio was 1:1. Fig. 52B shows the results of the experiment where the CAR44 T cell to target cell ratio was 0.5:1.

[00315] **Figure 53A-53J** shows bar graphs of FACS analysis of live versus dead markers and photographs of normal cells versus cancer cells after co-culture with huMNC2-CAR44 T cells. Fig. 53A.1 shows the bar graph of FACS analysis of live versus dead cells after HCT-MUC1* cancer cells were co-cultured with huMNC2-CAR44 T cells. Fig. 53A.2 and Fig. 53A.3 show the photographs of the experiment described in Fig. 53A.1. Fig. 53B.1 shows the bar graph of FACS analysis of live versus dead cells after MCF-12A normal breast cells were co-cultured with huMNC2-CAR44 T cells. Fig. 53B.2 and Fig. 53B.3 show the photographs of the experiment described in Fig. 53B.1. Fig. 53C.1 shows the bar graph of FACS analysis of live versus dead cells after THLE-3 normal liver cells were co-cultured with huMNC2-CAR44 T cells. Fig. 53C.2 and Fig. 53C.3 show the photographs of the experiment described in Fig. 53C.1. Fig. 53D.1 shows the bar graph of FACS analysis of live versus dead cells after T/G HA-HSMC normal heart cells were co-cultured with huMNC2-CAR44 T cells. Fig. 53D.2 and Fig. 53D.3 show the photographs of the experiment described in Fig. 53D.1. Fig. 53E.1 shows the bar graph of FACS analysis of live versus dead cells after Hs1.Tes normal testes cells were co-cultured with huMNC2-CAR44 T cells. Fig. 53E.2 and Fig. 53E.3 show the photographs of the experiment described in Fig. 53E.1. Fig. 53F.1 shows the bar graph of FACS analysis of live versus dead cells after HEK-293 MUC1 negative cells were co-cultured with huMNC2-CAR44 T cells. Fig. 53F.2 and Fig. 53F.3 show the photographs of the experiment described in Fig. 53F.1. Fig. 53G.1 shows the bar graph of FACS analysis of live versus dead cells after HRCE normal kidney cells were co-cultured with huMNC2-CAR44 T cells. Fig. 53G.2 and Fig. 53G.3 show the photographs of the experiment described in Fig. 53G.1. Fig. 53H.1 shows the bar graph of FACS analysis of live versus dead cells after CCD-18Lu normal lung cells were co-cultured with huMNC2-CAR44 T cells. Fig. 53H.2 and Fig. 53H.3 show the photographs of the experiment described in Fig. 53H.1. Fig. 53I.1 shows the bar graph of FACS analysis of live versus dead cells after HBEC-5i normal brain cells were co-cultured with huMNC2-CAR44 T cells. Fig. 53I.2 and Fig. 53I.3 show the photographs of the experiment described in Fig. 53I.1. Fig. 53J.1 shows the bar graph of FACS analysis of live versus dead cells after Hs.738.St/Int normal stomach and intestine cells were co-cultured with huMNC2-CAR44 T cells. Fig. 53J.2 and Fig. 53J.3 show the photographs of the experiment described in Fig. 53J.1.

[00316] **Figure 54** shows photographs of a breast cancer tissue array (CB – insert array number) in which for each patient there is a specimen from the primary tumor plus a specimen from that patient's metastasis. As can be seen in the figure, most often the metastasis expresses more MUC1* than the primary tumor.

[00317] **Figures 55A-55H** show the cytotoxic effect of huMNC2-CAR44 T cells on MUC1* positive DU145 prostate cancer cells as measured by a variety of assays. Fig. 55A is a fluorescent photograph of untransduced T cells co-cultured with the prostate cancer cells, wherein granzyme B is stained with a red fluorophore. Fig. 55B shows merging of DAPI and granzyme B. Fig. 55C is a fluorescent photograph of huMNC2-CAR44 T cells co-cultured with the prostate cancer cells, wherein granzyme B is stained with a red fluorophore**. Fig. 55D** shows merging of DAPI and granzyme B. Fig. 55E is a FACS scan for fluorescently labeled granzyme B for untransduced T cells incubated with the cancer cells. Fig. 55F is a FACS scan showing a positive increase in fluorescently labeled granzyme B for huMNC2-CAR44 T cells incubated with the cancer cells. Fig. 55G is a graph of the mean fluorescent intensity. Fig. 55H is an xCELLigence scan tracking the real-time killing of DU145 cancer cells by huMNC2-CAR44 T cells (blue trace) but not by untransduced T cells (green).

[00318] **Figures 56A-56H** show the cytotoxic effect of huMNC2-CAR44 T cells on MUC1* positive CAPAN-2 pancreatic cancer cells as measured by a variety of assays. Fig. 56A is a fluorescent photograph of untransduced T cells co-cultured with the pancreatic cancer cells, wherein granzyme B is stained with a red fluorophore. Fig. 56B shows merging of DAPI and granzyme B. Fig. 56C is a fluorescent photograph of huMNC2-CAR44 T cells co-cultured with the pancreatic cancer cells, wherein granzyme B is stained with a red fluorophore. Fig. 56D shows merging of DAPI and granzyme B. Fig. 56E is a FACS scan for fluorescently labeled granzyme B for untransduced T cells incubated with the cancer cells. Fig. 56F is a FACS scan showing a positive increase in fluorescently labeled granzyme B for huMNC2-CAR44 T cells incubated with the cancer cells. Fig. 56G is a graph of the mean fluorescent intensity. Fig. 56H is an xCELLigence scan tracking the real-time killing of CAPAN-2 cancer cells by huMNC2-CAR44 T cells (blue trace) but not by untransduced T cells (green).

[00319] **Figures 57A-57C** show xCELLigence scans tracking the real-time killing of MUC1* positive cancer cells, but not MUC1* negative cells, by huMNC2-CAR44 T cells. Fig. 57A shows that huMNC2-CAR44 T cells effectively kill HCT colon cancer cells that have been stably transfected with MUC1*. Fig. 57B shows that huMNC2-CAR44 T cells have almost no effect on HCT-MUC1-41TR, which is a MUC1 negative cancer cell that has been stably transfected with a MUC1 full-length. In this cell line only about 10% of the cells have MUC1 cleaved to MUC1*. Fig. 57C shows that huMNC2-CAR44 T cells have no effect on HCT-116 cells, which is a MUC1 negative colon cancer cell line.

[00320] **Figure 58A- 58F** shows photographs NOD/SCID/GAMMA mice in an IVIS instrument measuring photon emission from tumor cells after mice were treated with nothing, PBS, untransduced human T cells or huMNC2-CAR44 T cells. Mice had been injected sub-cutaneously with HCT-MUC1* tumor cells that had been made Luciferase positive. Ten (10) minutes before the IVIS photographs were taken, the mice were injected into the intraperitoneal (ip) space with the Luciferase substrate, Luciferin. Fig. 58A shows the tumor bearing mice that had only been treated with phosphate buffered saline, PBS. Fig. 58B shows the tumor bearing mice that had only been treated with untransduced T cells. Fig. 58C shows the tumor bearing mice that had been treated with a single dose of huMNC2-CAR44 T cells. Fig. 58D shows color scale of the images. Fig. 58E shows Kaplan-Meier survival curves of the experiment. Fig. 58F shows a table detailing the molecular makeup of the human T cells that were isolated from the mouse blood after sacrifice.

[00321] **Figure 59A- 59C** shows photographs NOD/SCID/GAMMA mice in an IVIS instrument measuring photon emission from tumor cells after mice were treated with nothing, PBS or huMNC2-CAR44 T cells. Mice had been injected sub-cutaneously with T47D-wt breast cancer cells or T47D+more MUC1*, which is a mixed population of cells wherein 95% of the cells were T47D cells that had been stably transfected with even more MUC1*. Both T47D-wt and T47D plus more MUC1* cells had been made Luciferase positive. Ten (10) minutes before the IVIS photographs were taken, the mice were injected into the intraperitoneal (ip) space with the Luciferase substrate, Luciferin. Fig. 59A shows the tumor bearing mice that had only been treated with phosphate buffered saline, PBS. Fig. 59B shows the T47D-wt tumor bearing mice that had been treated with two (2) doses of huMNC2-CAR44 T cells. Fig. T90.1C shows the T47D-MUC1* tumor bearing mice that had been treated with two (2) doses of huMNC2-CAR44 T cells.

[00322] **Figure 60A- 60C** shows photographs NOD/SCID/GAMMA mice in an IVIS instrument measuring photon emission from tumor cells after mice were treated with nothing, PBS, untransduced T cells or huMNC2-CAR44 T cells. Mice had been injected sub-cutaneously with a mixed population of 70% T47D-wt breast cancer cells and 30% T47D cells that had been transfected with even more MUC1*. Both cell types had been made Luciferase positive. Ten (10) minutes before the IVIS photographs were taken, the mice were injected into the intraperitoneal (ip) space with the Luciferase substrate, Luciferin. Fig. 60A shows the tumor bearing mice that had only been treated with phosphate buffered saline, PBS. Fig. 60B shows tumor bearing mice that had only been treated with untransduced T cells. Fig. 60C shows the tumor bearing mice that had been treated with two (2) doses of huMNC2-CAR44 T cells.

[00323] Figures 61A-61J show fluorescent photographs of mice taken on an IVIS instrument. NSG (NOD/SCID/GAMMA) immune compromised mice that on Day 0 were sub-cutaneously injected into the flank with 500K human BT-20 cells which are a MUC1* positive triple negative breast cancer cell line. The cancer cells had been stably transfected with Luciferase. Tumors were allowed to engraft. On Day 6 after IVIS measurement, animals were given a one-time injection of 10 million of either human T cells transduced with huMNC2-scFv-CAR44 or untransduced T cells. 5 million T cells were injected intra-tumor and 5 million were injected into the tail vein. 10 minutes prior to IVIS photographs, mice were IP injected with Luciferin, which fluoresces after cleavage by Luciferase, thus making tumor cells fluoresce. Figs. 61A, 61D, 61G show photographs of mice that were treated with huMNC2-scFv-CAR44 T cells that had been pre-stimulated by co-culturing for 24 hours with 4μm beads to which was attached a synthetic MUC1*, PSMGFR peptide 24 hours prior to administration: Protocol 1. Figs. 61B, 61E, 61H show photographs of mice that were treated with huMNC2-scFv-CAR44 T cells that had been pre-stimulated by twice co-culturing for 24 hours with MUC1* positive cancer cells 24 hours prior to administration: Protocol 2. Figs. 61C, 61F, 61I show photographs of mice that were treated with untransduced human T cells. Fig. 61J is a color scale relating fluorescence in photons/second to color.

[00324] Figures 62A-62M show fluorescent photographs of mice taken on an IVIS instrument. NSG (NOD/SCID/GAMMA) immune compromised mice that on Day 0 were injected into the intraperitoneal cavity (IP) with 500K human SKOV-3 cells which are a MUC1* positive ovarian cancer cell line. The cancer cells had been stably transfected with Luciferase. Tumors were allowed to engraft. On Day 4, animals were injected into the intraperitoneal space with 10M either human T cells transduced with huMNC2-scFv-CAR44, untransduced T cells or PBS. On Day 11, animals were injected again except that half the cells were injected into the tail vein and the other half was IP injected. Animals were imaged by IVIS on Days 3, 7, 10 and 15. 10 minutes prior to IVIS photographs, mice were IP injected with Luciferin, which fluoresces after cleavage by Luciferase, thus making tumor cells fluoresce. Figs. 62A, 62D, 62G, and 62J show photographs of mice that were treated with huMNC2-scFv-CAR44 T cells that had been pre-stimulated by co-culturing for 24 hours with 1μm beads to which was attached a synthetic MUC1*, PSMGFR peptide 24 hours prior to administration. Figs. 62B, 62E, 62H, and 62K show photographs of mice that were treated with untransduced human T cells. Figs. 62C, 62F, 62I, and

62L show photographs of mice that were treated with PBS. Figs. 62A, 62B and 62C are IVIS images taken Day 3 prior to CAR T, T cell or PBS administration. Figs. 62D, 62E and 62F show IVIS images of animals on Day 7, just four (4) days after treatment. Figs. 62G, 62H, and 62I show IVIS images of animals on Day 10. Figs. 62J, 62K, and 62L show IVIS images of animals on Day 15 Fig. 62M is the IVIS color scale relating fluorescence in photons/second to color.

[00325] **Figure 63** shows a graph of an ELISA binding assay in which various monoclonal antibodies are tested for their ability to bind to the PSMGFR peptide, the N-10, C-10, N+20/C-27, or the N+9/C-9 peptide, wherein the concentration of the antibody was at 10ug/mL or 1ug/mL. Note that anti-MUC1* monoclonal antibodies C2 and E6, which have been demonstrated to be cancer specific, bind to the PSMGFR peptide, still bind if the 10 N-terminal amino acids are missing, but do not bind if the 10 or 9 C-terminal amino acids are missing.

[00326] **Figure 64A-64B** shows a graph of an ELISA binding assay. The antibodies being tested were derived from animals immunized with the PSMGFR peptide. The first selection criteria was to confirm that the antibodies bound to the immunizing PSMGFR peptide. Fig. 64A shows a graph of an ELISA of selected antibodies that were further tested to determine their ability to bind to the PSMGFR peptide, the N-10, the C-10, N+20/C-27, or N+9/C-9 peptide. All the antibodies except 18B4 were able to bind to the N-10 peptide. 18B4 recognized N+20/C-27 but not the N-10 peptide, implying that its cognate epitope lies within the GTINVHDVET sequence. All except 20A10 and C2 showed some binding to the C-10 and N+9/C-9 peptide, showing that both 20A10 and C2 require the 10 membrane proximal amino acids for binding. C2, which requires the 10 membrane proximal amino acids for binding has been demonstrated to be cancer specific. Fig. 64B shows the sequences of the various peptides. The color of the bars for each antibody in the ELISA graph are color coded to match the deductive cognate sequence, or a portion thereof, of that antibody.

[00327] **Figure 65A-65B** shows a graph of an ELISA binding assay in which various monoclonal antibodies are tested for their ability to bind to the PSMGFR peptide, the N-10, the C-10, N+20/C-27, or N+9/C-9 peptide. The antibodies being tested were derived from animals immunized with the N+20/C-27 peptide. The first selection criteria was to confirm that the antibodies bound to the immunizing N+20/C-27 peptide. Fig. 65A shows a graph of ELISA binding assay that tests the ability of each antibody to bind to various peptides. Although these antibodies were raised against the N+20/C-27 peptide, all but one, 45C11, still bind to the

PSMGFR peptide. The binding of 45C11 is weak but deductive reasoning shows that the cognate epitope must lie within the SNIKFRPGSVV sequence. 1E4 was able to bind to the N+20/C-27 peptide, the PSMGFR and the N-10 peptide, consistent with the idea that its epitope must lie within the QFNQYKTE sequence. Fig. 65B shows the sequences of the various peptides. The color of the bars for each antibody in the ELISA graph are color coded to match the deductive cognate sequence, or a portion thereof, of that antibody.

[00328] **Figure 66A-66B** shows a graph of an ELISA binding assay in which various monoclonal antibodies are tested for their ability to bind to the PSMGFR peptide, the N-10, the C-10, N+20/C-27, or N+9/C-9 peptide. The antibodies being tested were derived from animals immunized with the N+9/C-9 peptide. The first selection criteria was to confirm that the antibodies bound to the immunizing N+9/C-9 peptide. Fig. 66A shows a graph of the ELISA assay. All but one, 39H5, were only able to bind to the immunizing peptide, N+9/C-9. 39H5 showed very weak binding to the PSMGFR and N-10 peptide, consistent with the idea that at least a portion of its cognate epitope must lie within the QFNQYKTE sequence. Fig. 66B shows the sequences of the various peptides. The color of the bars for each antibody in the ELISA graph are color coded to match the deductive cognate sequence, or a portion thereof, of that antibody.

[00329] **Figure 67A-67D** shows results of ELISA assays to further define antibody epitopes within the MUC1 or MUC1* extra cellular domain. The antibodies shown in this figure were all generated by immunizing animals with the PSMGFR peptide. Binding assays tested antibodies for their ability to bind to peptides N-19, N-26, N-30, N-10/C-5, N-19/C-5, PSMGFR, N-10 and C-10, which are all subsets of the PSMGFR peptide and numbering refers back to the PSMGFR peptide. Fig. 67A shows the binding of the various antibodies to the various peptides. Fig. 67B shows the sequence of the PSMGFR peptide that has been extended 20 amino acids at the N-terminus. Fig. 67C shows the sequences of the PSMGFR-derived subset peptides. Fig. 67D shows the sequences that comprise all or part of the epitope that is essential for antibody recognition.

[00330] **Figure 68A-68D** shows results of ELISA assays to further define antibody epitopes within the MUC1 or MUC1* extra cellular domain. The antibodies shown in this figure were all generated by immunizing animals with the N+20/C-27 peptide. Binding assays tested antibodies for their ability to bind to peptides N-19, N-26, N-30, N-10/C-5, N-19/C-5, PSMGFR, N-10 and

C-10, which are all subsets of the PSMGFR peptide and numbering refers back to the PSMGFR peptide. Fig. 68A shows the binding of the various antibodies to the various peptides. Fig. 68B shows the sequence of the PSMGFR peptide that has been extended 20 amino acids at the N-terminus. Fig. 68C shows the sequences of the PSMGFR-derived subset peptides. Fig. 68D shows the sequences that comprise all or part of the epitope that is essential for antibody recognition.

[00331] **Figures 69A-69D** show results of ELISA assays to further define antibody epitopes within the MUC1 or MUC1* extra cellular domain. The antibodies shown in this figure were all generated by immunizing animals with the N+9/C-9 peptide. Binding assays tested antibodies for their ability to bind to peptides N-19, N-26, N-30, N-10/C-5, N-19/C-5, PSMGFR, N-10 and C-10, which are all subsets of the PSMGFR peptide and numbering refers back to the PSMGFR peptide. Fig. 69A shows the binding of the various antibodies to the various peptides. Fig. 69B shows the sequence of the PSMGFR peptide that has been extended 20 amino acids at the N-terminus. Fig. 69C shows the sequences of the PSMGFR-derived subset peptides. Fig. 69D shows the sequences that comprise all or part of the epitope that is essential for antibody recognition.

[00332] **Figure 70** shows a graph of an ELISA displacement assay. In this experiment, a multi-well plate was coated with the PSMGFR peptide. Recombinant $NME7_{AB}$ was allowed to bind to the surface-immobilized PSMGFR peptide. Various antibodies were added, followed by a wash step. The amount of $NME7_{AB}$ that remained attached to the PSMGFR coated plate, after antibody competition, was measured by detecting a tag on the $NME7_{AB}$. As a control, anti-$NME7_{AB}$ antibodies were also tested for their ability to displace $NME7_{AB}$ from the PSMGFR.

[00333] **Figure 71A-71H** shows photographs of Western blots in which antibodies are tested for their ability to bind to a linear epitope in full-length MUC1 or MUC1*. Fig. 71A-71D shows testing of antibodies for ability to bind to a MUC1 negative cell line, HCT-116, or engineered cell lines HCT-MUC1-18, which is a cleavage resistant clone that expresses full-length MUC1, or HCT-MUC1*, which is engineered to express only the PSMGFR sequence in its extra cellular domain. Fig. 71E-71H shows testing of antibodies for ability to bind to breast cancer cell lines T47D or 1500 aka ZR-75-1. Fig. 71A and Fig. 71E show MNC2, a monoclonal antibody raised against PSMGFR peptide that binds to N-10 but not C-10 variants of the PSMGFR peptide. Fig. 71B and Fig. 71F show MNE6, a monoclonal antibody raised against PSMGFR peptide that binds to N-10 but not C-10 variants of the PSMGFR peptide. Fig. 71C and Fig. 71G show SDIX, a polyclonal antibody raised against PSMGFR peptide and which binds to the PSMGFR peptide. Fig. 71D and Fig. 71H show VU4H5, a commercially available monoclonal antibody that binds to the tandem repeats of full-length MUC1. As can be seen, neither MNC2 nor MNE6 bind linear epitopes of MUC1 species.

[00334] **Figure 72A-72P** shows photographs of Western blots in which antibodies are tested for their ability to bind to a linear epitope in full-length MUC1 or MUC1*. All these antibodies were raised against the PSMGFR peptide and bind to the PSMGFR peptide. Fig. 72A-72H shows testing of antibodies for ability to bind to a MUC1 negative cell line, HCT-116, or engineered cell lines HCT-MUC1-18, which is a cleavage resistant clone that expresses full-length MUC1, or HCT-MUC1*, which is engineered to express only the PSMGFR sequence in its extra cellular domain. Fig. 72I-72P shows testing of antibodies for ability to bind to breast cancer cell lines T47D or 1500 aka ZR-75-1. Fig. 72A and Fig. 72I show 20A10. Fig. 72B and Fig. 72J show 25E6. Fig. 72C and Fig. 72K show 18B4. Fig. 72D and Fig. 72L show 18G12. Fig. 72E and Fig. 72M show 28F9. Fig. 72F and Fig. 72N show 3C2B1. Fig. 72G and Fig. 72O show 5C6F3. Fig. 72H and Fig. 72P show 5C6F3 wherein the blot has been exposed for a longer time period to render more visible the MUC1* specific bands. As can be seen, antibodies 25E6, 18B4 and to a degree 5C6F3 recognize linear epitopes but 20A10, 3C2B1, 18G12 and 28F9 do not.

[00335] **Figure 73A-73J** shows photographs of Western blots in which antibodies are tested for their ability to bind to a linear epitope in full-length MUC1 or MUC1*. All these antibodies were raised against the N+20/C-27 variant of the PSMGFR peptide and bind to the N+20/C-27 peptide. Fig. 73A-73E shows testing of antibodies for ability to bind to a MUC1 negative cell line, HCT-116, or engineered cell lines HCT-MUC1-18, which is a cleavage resistant clone that expresses full-length MUC1, or HCT-MUC1*, which is engineered to express only the PSMGFR sequence in its extra cellular domain. Fig. 73F-73J shows testing of antibodies for ability to bind to breast cancer cell lines T47D or 1500 aka ZR-75-1. Fig. 73A and Fig. 73F show 1E4. Fig. 73B and Fig. 73G show 45C11. Fig. 73C and Fig. 73H show 31A1. Fig. 73D and Fig. 73I show 32C1. Fig. 73E and Fig. 73J show 29H1. As can be seen, antibodies 31A1 and 32C1 recognize linear epitopes.

[00336] **Figure 74A-74H** shows photographs of Western blots in which antibodies are tested for their ability to bind to a linear epitope in full-length MUC1 or MUC1*. All these antibodies were raised against the N+9/C-9 variant of the PSMGFR peptide and bind to the N+9/C-9 peptide. Fig. 74A-74D shows testing of antibodies for ability to bind to a MUC1 negative cell line, HCT-116, or engineered cell lines HCT-MUC1-18, which is a cleavage resistant clone that expresses full-length MUC1, or HCT-MUC1*, which is engineered to express only the PSMGFR sequence in its extra cellular domain. Fig. 74E-74H shows testing of antibodies for ability to bind to breast cancer cell lines T47D or 1500 aka ZR-75-1. Fig. 74A and Fig. 74E show 8A9. Fig. 74B and Fig. 74F show 17H6. Fig. 74C and Fig. 74G show 3C5. Fig. 74D and Fig. 74H show 39H5.

[00337] **Figure 75A-75P** show graphs of FACS analysis. HCT-MUC1-18 cells, which express full-length MUC1, were incubated with a catalytically active MMP9 or MMP2 for 24 hours, incubated with an antibody of the invention and then analyzed by FACS to see if the antibody bound to the MMP9 or the MMP2 cleaved form of MUC1. Note that the first bar of each graph shows that none of the antibodies binds to full-length MUC1 in the absence of cleavage. Each bar graph is labeled with both the name of the antibody used in that assay and its cognate epitope. The order of the graphs from right to left corresponds to the distance the from the cell surface of the antibody's cognate epitope. Fig. 75A shows antibody 1E4. Fig. 75B shows antibody 28F9. Fig. 75C shows antibody 18G12. Fig. 75D shows antibody 25E6. Fig. 75E shows antibody 20A10. Fig. 75F shows antibody 3C5. Fig. 75G shows antibody 29H1. Fig. 75H shows antibody 32C1. Fig. 75I shows antibody 31A1. Fig. 75J shows antibody 18B4. Fig. 75K shows antibody 45C11. Fig. 75L shows antibody 8A9. Fig. 75M shows antibody 17H6. Fig. 75N shows antibody 39H5. Fig. 75O shows antibody 3C2B1. Fig. 75P shows antibody 5C6F3.

[00338] **Figure 76A-76J** show graphs of FACS analyses of reference antibodies MNC2, "C2", and VU4H5 binding to either the MUC1-negative cell line HCT-116, HCTs transfected with MUC1*, "HCT-MUC1*", a cleavage resistant single cell clone of HCTs transfected with MUC1 full-length, "HCT-MUC1-18", and MNC2 binding to breast cancer cells line T47D or breast cancer cell line 1500 also known as ZR-75-1. MNC2 binds to an ectopic binding site on the extra cellular domain of MUC1*, within the membrane proximal portion of the PSMGFR sequence. The MNC2 binding site is only available after cleavage and release of the bulk of the extra cellular domain comprising the tandem repeat domain. VU4H5 binds to hundreds of repeating epitopes in the tandem repeat domain. Fig. 76A-76E show percent binding and Fig. 76F-76J show Mean Fluorescent Intensity or MFI.

[00339] **Figure 77A-77N** show graphs of FACS analyses of reference antibody MNC2, “C2”, binding to a panel of cancer cell lines that are MUC1* positive, with the exception of MDA-MB-231, which expresses MUC1 and MUC1* at a level that is so low that it is often used as a negative control. MNC2 binds to an ectopic binding site on the extra cellular domain of MUC1*, within the membrane proximal portion of the PSMGFR sequence. The MNC2 binding site is only available after cleavage and release of the bulk of the extra cellular domain comprising the tandem repeat domain. Fig. 77A-77G show percent binding and Fig. 77H-77N show Mean Fluorescent Intensity or MFI. Fig. 77A and 77H show the antibodies binding to lung cancer cell line NCI-H292. Fig. 77B and 77I show the antibodies binding to lung cancer cell line NCI-H1975. Fig. 77C and 77J show the antibodies binding to ovarian cancer cell line SKOV-3. Fig. 77D and 77K show the antibodies binding to pancreatic cancer cell line HPAF-II. Fig. 77E and 77L show the antibodies binding to pancreatic cancer cell line Capan-1. Fig. 77F and 77M show the antibodies binding to prostate cancer cell line DU145. Fig. 77G and 77N show the antibodies binding to breast cancer cell line MDA-MB-231, which is nearly MUC1 and MUC1* negative.

[00340] **Figure 78A-78C** shows a color coded schematic of the basic PSMGFR sequence that has been extended or deleted at both the N- and C-termini. Antibodies of the invention were tested against this subset of peptides to further refine the epitopes to which each antibody binds or the critical amino acids within the epitope to which each antibody binds. Fig. 78A is an aligned schematic of the various subsets of peptides. Fig. 78B lists the antibodies that bind to each of the color coded sequences. Fig. 78C lists the cancer cell lines that each antibody recognizes.

[00341] **Figure 79A-79I** shows color coded graphs that resulted from FACS analyses of each antibody binding to T47D breast cancer cells and their respective cognate sequences within the N-terminally extended PSMGFR sequence. Fig. 79A-79D are FACS graphs showing the percent cells that were recognized by each antibody. Fig. 79E-79H are FACS graphs showing the Mean Fluorescence Intensity, MFI, of each antibody. Fig. 79A and Fig. 79E show the FACS graph of antibodies that were generated by immunizing with the PSMGFR peptide. Fig. 79B and Fig. 79F show the FACS graph of antibodies that were generated by immunizing with the N+20/C-27 peptide. Fig. 79C and Fig. 79G show the FACS graph of antibodies that were generated by immunizing with the N+9/C-9 peptide. Fig. 79D and Fig.79H also show the FACS graph of antibodies that were generated by immunizing with the PSMGFR peptide. Fig. 79I shows the PSMGFR sequence that is extended at the N-terminus by 20 amino acids.

[00342] **Figure 80A-80I** shows color coded graphs that resulted from FACS analyses of each antibody binding to 1500, also known as ZR-75-1, breast cancer cells and their respective cognate sequences within the N-terminally extended PSMGFR sequence. Fig. 80A-80C are FACS graphs showing the percent cells that were recognized by each antibody. Fig. 80D-80F are FACS graphs showing the Mean Fluorescence Intensity, MFI, of each antibody. Fig. 80A, Fig. 80E Fig. 80D and Fig. 80H show the FACS graph of antibodies that were generated by immunizing with the PSMGFR peptide. Fig. 80B and Fig. 80F show the FACS graph of antibodies that were generated by immunizing with the N+20/C-27 peptide. Fig. 80C and Fig. 80G show the FACS graph of antibodies that were generated by immunizing with the N+9/C-9 peptide. Fig. 80I shows the PSMGFR sequence that is extended at the N-terminus by 20 amino acids.

[00343] **Figure 81A-81G** shows color coded graphs that resulted from FACS analyses of each antibody binding to NCI-H292 lung cancer cells and their respective cognate sequences within the N-terminally extended PSMGFR sequence. Fig. 81A-81C are FACS graphs showing the percent cells that were recognized by each antibody. Fig. 81D-81F are FACS graphs showing the Mean Fluorescence Intensity, MFI, of each antibody. Fig. 81A and Fig. 81D show the FACS graph of antibodies that were generated by immunizing with the PSMGFR peptide. Fig. 81B and Fig. 81E show the FACS graph of antibodies that were generated by immunizing with the N+20/C-27 peptide. Fig. 81C and Fig. 81F show the FACS graph of antibodies that were generated by immunizing with the N+9/C-9 peptide. Fig. 81G shows the PSMGFR sequence that is extended at the N-terminus by 20 amino acids.

[00344] **Figure 82A-82G** shows color coded graphs that resulted from FACS analyses of each antibody binding to NCI-H1975 lung cancer cells and their respective cognate sequences within the N-terminally extended PSMGFR sequence. Fig. 82A-82C are FACS graphs showing the percent cells that were recognized by each antibody. Fig. 82D-82F are FACS graphs showing the Mean Fluorescence Intensity, MFI, of each antibody. Fig. 82A and Fig. 82D show the FACS graph of antibodies that were generated by immunizing with the PSMGFR peptide. Fig. 82B and Fig. 82E show the FACS graph of antibodies that were generated by immunizing with the N+20/C-27 peptide. Fig. 82C and Fig. 82F show the FACS graph of antibodies that were generated by immunizing with the N+9/C-9 peptide. Fig. 82G shows the PSMGFR sequence that is extended at the N-terminus by 20 amino acids.

[00345] **Figure 83A-83G** shows color coded graphs that resulted from FACS analyses of each antibody binding to SKOV-3 ovarian cancer cells and their respective cognate sequences within the N-terminally extended PSMGFR sequence. Fig. 83A-83C are FACS graphs showing the percent cells that were recognized by each antibody. Fig. 83D-83F are FACS graphs showing the Mean Fluorescence Intensity, MFI, of each antibody. Fig. 83A and Fig. 83D show the FACS graph of antibodies that were generated by immunizing with the PSMGFR peptide. Fig. 83B and Fig. 83E show the FACS graph of antibodies that were generated by immunizing with the N+20/C-27 peptide. Fig. 83C and Fig. 83F show the FACS graph of antibodies that were generated by immunizing with the N+9/C-9 peptide. Fig. 83G shows the PSMGFR sequence that is extended at the N-terminus by 20 amino acids.

[00346] **Figure 84A-84G** shows color coded graphs that resulted from FACS analyses of each antibody binding to DU145 prostate cancer cells and their respective cognate sequences within the N-terminally extended PSMGFR sequence. Fig. 84A-84C are FACS graphs showing the percent cells that were recognized by each antibody. Fig. 84D-84F are FACS graphs showing the Mean Fluorescence Intensity, MFI, of each antibody. Fig. 84A and Fig. 84D show the FACS graph of antibodies that were generated by immunizing with the PSMGFR peptide. Fig. 84B and Fig. 84E show the FACS graph of antibodies that were generated by immunizing with the N+20/C-27 peptide. Fig. 84C and Fig. 84F show the FACS graph of antibodies that were generated by immunizing with the N+9/C-9 peptide. Fig. 84G shows the PSMGFR sequence that is extended at the N-terminus by 20 amino acids.

[00347] **Figure 85A-85G** shows color coded graphs that resulted from FACS analyses of each antibody binding to HPAF-II pancreatic cancer cells and their respective cognate sequences within the N-terminally extended PSMGFR sequence. Fig. 85A-85C are FACS graphs showing the percent cells that were recognized by each antibody. Fig. 85D-85F are FACS graphs showing the Mean Fluorescence Intensity, MFI, of each antibody. Fig. 85A and Fig. 85D show the FACS graph of antibodies that were generated by immunizing with the PSMGFR peptide. Fig. 85B and Fig. 85E show the FACS graph of antibodies that were generated by immunizing with the N+20/C-27 peptide. Fig. 85C and Fig. 85F show the FACS graph of antibodies that were generated by immunizing with the N+9/C-9 peptide. Fig. 85G shows the PSMGFR sequence that is extended at the N-terminus by 20 amino acids.

[00348] **Figure 86A-86G** shows color coded graphs that resulted from FACS analyses of each antibody binding to Capan-1 pancreatic cancer cells and their respective cognate sequences within the N-terminally extended PSMGFR sequence. Fig. 86A-86C are FACS graphs showing the percent cells that were recognized by each antibody. Fig. 86D-86F are FACS graphs showing the Mean Fluorescence Intensity, MFI, of each antibody. Fig. 86A and Fig. 86D show the FACS graph of antibodies that were generated by immunizing with the PSMGFR peptide. Fig. 86B and Fig. 86E show the FACS graph of antibodies that were generated by immunizing with the N+20/C-27 peptide. Fig. 86C and Fig. 86F show the FACS graph of antibodies that were generated by immunizing with the N+9/C-9 peptide. Fig. 86G shows the PSMGFR sequence that is extended at the N-terminus by 20 amino acids.

[00349] **Figure 87A-87G** shows color coded graphs that resulted from FACS analyses of each antibody binding to MDA-MB-231 breast cancer cells, which are nearly MUC1 negative, and their respective cognate sequences within the N-terminally extended PSMGFR sequence. Fig. 87A-87C are FACS graphs showing the percent cells that were recognized by each antibody. Fig. 87D-87F are FACS graphs showing the Mean Fluorescence Intensity, MFI, of each antibody. Fig. 87A and Fig. 87D show the FACS graph of antibodies that were generated by immunizing with the PSMGFR peptide. Fig. 87B and Fig. 87E show the FACS graph of antibodies that were generated by immunizing with the N+20/C-27 peptide. Fig. 87C and Fig. 87F show the FACS graph of antibodies that were generated by immunizing with the N+9/C-9 peptide. Fig. 87G shows the PSMGFR sequence that is extended at the N-terminus by 20 amino acids.

[00350] **Figure 88A-88L** show photographs of normal liver tissue specimens, each from the same donor but stained with a different antibody of the invention. Fig. 88A-88F show the entire tissue core. Fig. 88G-88L show the 40X magnification of a particular area of the tissue. The tissues are ordered from right to left with antibodies that bind to the most membrane proximal, that is to say most C-terminal portion of the PSMGFR peptide, on the right and antibodies that bind to the most N-terminal portions of the MUC1 extra cellular domain, even beyond the PSMGFR region, on the left. As can be seen in the figure, the most cancer-specific antibodies are those that bind to the more membrane proximal portions of the PSMGFR sequence and antibodies that bind to the most distal, N-terminal portions lose cancer specificity, with those antibodies that bind to epitopes outside of the PSMGFR having lost all cancer specificity.

[00351] **Figure 89A-89H** show photographs of normal heart tissue specimens, stained with different antibodies of the invention. Fig. 89A-89D show the entire tissue core. Fig. 89E-89HL show the 40X magnification of a particular area of the tissue. Fig. 89A and Fig. 89E show staining with MNC2-scFv. Fig. 89B and Fig. 89F show staining with MNE6. Fig. 89C and Fig. 89G show staining with 20A10. Fig. 89D and Fig. 89H show staining with 3C2B1. These antibodies bind to an epitope that comprises all or part of the sequence FPFS or PFPFSAQSGA. All these antibodies are all able to bind to the PSMGFR peptide, bind to the N-10 peptide but do not bind to the C-10 peptide. In addition, these antibodies disrupt the binding of NME7$_{AB}$ to the MUC1* extra cellular domain as exemplified by the PSMGFR peptide. Further, these antibodies recognize a MUC1 cleavage product when the cleavage enzyme is MMP9. As can be seen in the figure, these antibodies show no binding to normal heart tissue.

[00352] **Figure 90A-90D** show photographs of normal heart tissue specimens, stained with different antibodies of the invention. Fig. 90A-90B show the entire tissue core. Fig. 90C-90D show the 40X magnification of a particular area of the tissue. Fig. 90A and Fig. 90C show staining with MNC3. Fig. 90B and Fig. 90D show staining with 25E6. These antibodies bind to an epitope that comprises all or part of the sequence ASRYNLT. These antibodies are all able to bind to the PSMGFR peptide, bind to the N-10 peptide but also bind to the C-10 peptide.

[00353] **Figure 91A-91B** show photographs of normal heart tissue specimens, stained with an antibody of the invention 1E4. Fig. 91A show the entire tissue core. Fig. 91B show the 40X magnification of a particular area of the tissue. Antibody 1E4 binds to an epitope that comprises all or part of the sequence QFNQYKTEA. Antibody 1E4 can bind to the N-10 peptide but also binds to the C-10 peptide. As can be seen in the figure, 1E4 binds to normal heart tissue.

[00354] **Figure 92A-92H** show photographs of normal heart tissue specimens, stained with different antibodies of the invention. Fig. 92A-92D show the entire tissue core. Fig. 92E-92HL show the 40X magnification of a particular area of the tissue. Fig. 92A and Fig. 92E show staining with 18B4. Fig. 92B and Fig. 92F show staining with 31A1. Fig. 92C and Fig. 92G show staining with 32C1. Fig. 92D and Fig. 92H show staining with 29H1. These antibodies bind to an epitope that comprises all or part of the sequence GTINVHDVET, which is the most N-terminal part of the PSMGFR peptide. None of these antibodies are able to bind to the N-10 peptide. As can be seen in the figure, all of these antibodies except 18B4 show bind to normal heart tissue.

[00355] **Figure 93A-93D** show photographs of normal heart tissue specimens, stained with antibodies of the invention. Fig. 93A-93B show the entire tissue core. Fig. 93C-93D show the 40X magnification of a particular area of the tissue. Fig. 93A and Fig. 93C show staining with antibody 8A9. Fig. 93B and Fig 93D show staining with antibody 17H6. Both antibodies bind to an epitope that that is outside of the PSMGFR region and comprises all or part of the sequence VQLTLAFRE. As can be seen in the figure, both antibodies show strong binding to normal heart tissue.

[00356] **Figure 94A-94B** show photographs of normal heart tissue specimens, stained with an antibody of the invention 45C11. Fig. 94A show the entire tissue core. Fig. 94B show the 40X magnification of a particular area of the tissue. Antibody 45C11 binds to an epitope that is outside of the PSMGFR region and comprises all or part of the sequence **SNIKFRPGSVV**. Antibody 45C11 cannot bind to the N-10 peptide. As can be seen in the figure, 45C11 binds strongly to normal heart tissue.

[00357] **Figure 95A-95H** show photographs of normal liver tissue specimens, stained with different antibodies of the invention. Fig. 95A-95D show the entire tissue core. Fig. 95E-95HL show the 40X magnification of a particular area of the tissue. Fig. 95A and Fig. 95E show staining with MNC2-scFv. Fig. 95B and Fig. 95F show staining with MNE6. Fig. 95C and Fig. 95G show staining with 20A10. Fig. 95D and Fig. 95H show staining with 3C2B1. These antibodies bind to an epitope that comprises all or part of the sequence FPFS or PFPFSAQSGA. All these antibodies are all able to bind to the PSMGFR peptide, bind to the N-10 peptide but do not bind to the C-10 peptide. In addition, these antibodies disrupt the binding of $NME7_{AB}$ to the MUC1* extra cellular domain as exemplified by the PSMGFR peptide. Further, these antibodies recognize a MUC1 cleavage product when the cleavage enzyme is MMP9. As can be seen in the figure, these antibodies show no binding to normal liver tissue.

[00358] **Figure 96A-96D** show photographs of normal liver tissue specimens, stained with different antibodies of the invention. Fig. 96A-96B show the entire tissue core. Fig. 96C-96D show the 40X magnification of a particular area of the tissue. Fig. 96A and Fig. 96C show staining with MNC3. Fig. 96B and Fig. 96D show staining with 25E6. These antibodies bind to an epitope that comprises all or part of the sequence ASRYNLT. These antibodies are all able to bind to the PSMGFR peptide, bind to the N-10 peptide but also bind to the C-10 peptide.

[00359] **Figure 97A-97B** show photographs of normal liver tissue specimens, stained with an antibody of the invention 1E4. Fig. 97A show the entire tissue core. Fig. 97B show the 40X magnification of a particular area of the tissue. Antibody 1E4 binds to an epitope that comprises all or part of the sequence QFNQYKTEA. Antibody 1E4 can bind to the N-10 peptide but also binds to the C-10 peptide. As can be seen in the figure, 1E4 binds to normal liver tissue.

[00360] **Figure 98A-98H** show photographs of normal liver tissue specimens, stained with different antibodies of the invention. Fig. 98A-98D show the entire tissue core. Fig. 98E-98H show the 40X magnification of a particular area of the tissue. Fig. 98A and Fig. 98E show staining with 18B4. Fig. 98B and Fig. 98F show staining with 31A1. Fig. 98C and Fig. 98G show staining with 32C1. Fig. 98D and Fig. 98H show staining with 29H1. These antibodies bind to an epitope that comprises all or part of the sequence GTINVHDVET, which is the most N-terminal part of the PSMGFR peptide. None of these antibodies are able to bind to the N-10 peptide. As can be seen in the figure, 32C1 shows some binding to normal liver and 29H1 shows extremely strong binding to normal liver tissue.

[00361] **Figure 99A-99D** show photographs of normal liver tissue specimens, stained with antibodies of the invention. Fig. 99A-99B show the entire tissue core. Fig. 99C-99D show the 40X magnification of a particular area of the tissue. Fig. 99A and Fig. 99C show staining with antibody 8A9. Fig. 99B and Fig. 99D show staining with antibody 17H6. Both antibodies bind to an epitope that that is outside of the PSMGFR region and comprises all or part of the sequence VQLTLAFRE. As can be seen in the figure, 8A9 shows strong binding to normal liver tissue. 17H6 is a weak antibody and it is possible that it was not used at a high enough concentration in this study.

[00362] **Figure 100A-100B** show photographs of normal liver tissue specimens, stained with an antibody of the invention 45C11. Fig. 100A show the entire tissue core. Fig. 100B show the 40X magnification of a particular area of the tissue. Antibody 45C11 binds to an epitope that is outside of the PSMGFR region and comprises all or part of the sequence **SNIKFRPGSVV**. Antibody 45C11 cannot bind to the N-10 peptide. As can be seen in the figure, 45C11 binds strongly to normal liver tissue.

[00363] **Figure 101A-101H** show photographs of normal lung tissue specimens, stained with different antibodies of the invention. Fig. 101A-101D show the entire tissue core. Fig. 101E-101H show the 40X magnification of a particular area of the tissue. Fig. 101A and Fig. 101E show staining with MNC2-scFv. Fig. 101B and Fig. 101F show staining with MNE6. Fig. 101C and Fig. 101G show staining with 20A10. Fig. 101D and Fig. 101H show staining with 3C2B1. These antibodies bind to an epitope that comprises all or part of the sequence FPFS or PFPFSAQSGA. All these antibodies are all able to bind to the PSMGFR peptide, bind to the N-10 peptide but do not bind to the C-10 peptide. In addition, these antibodies disrupt the binding of $NME7_{AB}$ to the MUC1* extra cellular domain as exemplified by the PSMGFR peptide. Further, these antibodies recognize a MUC1 cleavage product when the cleavage enzyme is MMP9. As can be seen in the figure, these antibodies show no binding to normal lung tissue.

[00364] **Figure 102A-102D** show photographs of normal lung tissue specimens, stained with different antibodies of the invention. Fig. 102A-102B show the entire tissue core. Fig. 102C-102D show the 40X magnification of a particular area of the tissue. Fig. 102A and Fig. 102C show staining with MNC3. Fig. 102B and Fig. 102D show staining with 25E6. These antibodies bind to an epitope that comprises all or part of the sequence ASRYNLT. These antibodies are all able to bind to the PSMGFR peptide, bind to the N-10 peptide but also bind to the C-10 peptide.

[00365] **Figure 103A-103B** show photographs of normal lung tissue specimens, stained with an antibody of the invention 1E4. Fig. 103A show the entire tissue core. Fig. 103B show the 40X magnification of a particular area of the tissue. Antibody 1E4 binds to an epitope that comprises all or part of the sequence QFNQYKTEA. Antibody 1E4 can bind to the N-10 peptide but also binds to the C-10 peptide.

[00366] **Figure 104A-104H** show photographs of normal lung tissue specimens, stained with different antibodies of the invention. Fig. 104A-104D show the entire tissue core. Fig. 104E-104H show the 40X magnification of a particular area of the tissue. Fig. 104A and Fig. 104E show staining with 18B4. Fig. 104B and Fig. 104F show staining with 31A1. Fig. 104C and Fig. 104G show staining with 32C1. Fig. 104D and Fig. 104H show staining with 29H1. These antibodies bind to an epitope that comprises all or part of the sequence GTINVHDVET, which is the most N-terminal part of the PSMGFR peptide. None of these antibodies are able to bind to the N-10 peptide. As can be seen in the figure, all these antibodies show strong binding to normal lung tissue.

[00367] **Figure 105A-105D** show photographs of normal lung tissue specimens, stained with antibodies of the invention. Fig. 105A-105B show the entire tissue core. Fig. 105C-105D show the 40X magnification of a particular area of the tissue. Fig. 105A and Fig. 105C show staining with antibody 8A9. Fig. 105B and Fig. 105D show staining with antibody 17H6. Both antibodies bind to an epitope that that is outside of the PSMGFR region and comprises all or part of the sequence VQLTLAFRE. As can be seen in the figure, 8A9 shows strong binding to normal lung tissue. 17H6 is a weak antibody and it is possible that it was not used at a high enough concentration in this study.

[00368] **Figure 106A-106B** show photographs of normal lung tissue specimens, stained with an antibody of the invention 45C11. Fig. 106A show the entire tissue core. Fig. 106B show the 40X magnification of a particular area of the tissue. Antibody 45C11 binds to an epitope that is outside of the PSMGFR region and comprises all or part of the sequence **SNIKFRPGSVV**. Antibody 45C11 cannot bind to the N-10 peptide. As can be seen in the figure, 45C11 binds to normal lung tissue.

[00369] **Figure 107A-107H** show photographs of normal bone marrow tissue specimens, stained with different antibodies of the invention. Fig. 107A-107D show the entire tissue core. Fig. 107E-107H show the 40X magnification of a particular area of the tissue. Fig. 107A and Fig. 107E show staining with MNC2-scFv. Fig. 107B and Fig. 107F show staining with MNE6. Fig. 107C and Fig. 107G show staining with 20A10. Fig. 107D and Fig. 107H show staining with 3C2B1. These antibodies bind to an epitope that comprises all or part of the sequence FPFS or PFPFSAQSGA. All these antibodies are all able to bind to the PSMGFR peptide, bind to the N-10 peptide but do not bind to the C-10 peptide. In addition, these antibodies disrupt the binding of $NME7_{AB}$ to the MUC1* extra cellular domain as exemplified by the PSMGFR peptide. Further, these antibodies recognize a MUC1 cleavage product when the cleavage enzyme is MMP9. As can be seen in the figure, these antibodies show no binding to normal bone marrow tissue.

[00370] **Figure 108A-108D** show photographs of normal bone marrow tissue specimens, stained with different antibodies of the invention. Fig. 108A-108B show the entire tissue core. Fig. 108C-108D show the 40X magnification of a particular area of the tissue. Fig. 108A and Fig. 108C show staining with MNC3. Fig. 108B and Fig. 108D show staining with 25E6. These antibodies bind to an epitope that comprises all or part of the sequence ASRYNLT. These antibodies are all able to bind to the PSMGFR peptide, bind to the N-10 peptide but also bind to the C-10 peptide.

[00371] **Figure 109A-109B** show photographs of normal bone marrow tissue specimens, stained with an antibody of the invention 1E4. Fig. 109A show the entire tissue core. Fig. 109B show the 40X magnification of a particular area of the tissue. Antibody 1E4 binds to an epitope that comprises all or part of the sequence QFNQYKTEA. Antibody 1E4 can bind to the N-10 peptide but also binds to the C-10 peptide. 1E4 binds to normal bone marrow.

[00372] **Figure 110A-110H** show photographs of normal bone marrow tissue specimens, stained with different antibodies of the invention. Fig. 110A-110D show the entire tissue core. Fig. 110E-110H show the 40X magnification of a particular area of the tissue. Fig. 110A and Fig. 110E show staining with 18B4. Fig. 110B and Fig. 110F show staining with 31A1. Fig. 110C and Fig. 110G show staining with 32C1. Fig. 110D and Fig. 110H show staining with 29H1. These antibodies bind to an epitope that comprises all or part of the sequence GTINVHDVET, which is the most N-terminal part of the PSMGFR peptide. None of these antibodies are able to bind to the N-10 peptide. As can be seen in the figure, all these antibodies show strong binding to normal bone marrow tissue.

[00373] **Figure 111A-111D** show photographs of normal bone marrow tissue specimens, stained with antibodies of the invention. Fig. 111A-111B show the entire tissue core. Fig. 111C-111D show the 40X magnification of a particular area of the tissue. Fig. 111A and Fig. 111C show staining with antibody 8A9. Fig. 111B and Fig. 111D show staining with antibody 17H6. Both antibodies bind to an epitope that that is outside of the PSMGFR region and comprises all or part of the sequence VQLTLAFRE. As can be seen in the figure, 8A9 shows strong binding to normal bone marrow tissue. 17H6 is a weak antibody and it is possible that it was not used at a high enough concentration in this study.

[00374] **Figure 112A-112B** show photographs of normal bone marrow tissue specimens, stained with an antibody of the invention 45C11. Fig. 112A show the entire tissue core. Fig. 112B show the 40X magnification of a particular area of the tissue. Antibody 45C11 binds to an epitope that is outside of the PSMGFR region and comprises all or part of the sequence **SNIKFRPGSVV**. Antibody 45C11 cannot bind to the N-10 peptide. As can be seen in the figure, 45C11 binds to normal bone marrow tissue.

[00375] **Figure 113A-113C** shows photographs, array map and description of FDA normal tissue array 1021 stained with the anti-PSMGFR antibody 20A10 at 0.25ug/mL. Fig. 113A shows photographs of the tissue micro array. Fig. 113B shows map of the array with abbreviated tissue descriptors. Fig. 113C detailed description of the tissue micro array with non-identifying donor data.

[00376] **Figure 114A-114X** shows photographs of specific tissues from FDA normal tissue array 1021 stained with the anti-PSMGFR antibody 20A10 at 0.25ug/mL, magnified to 6X and 20X. Fig. 114A and Fig. 114E are adrenal gland. Fig. 114B and Fig. 114F are breast. Fig. 114C and Fig. 114G are fallopian tube. Fig. 114D and Fig. 114H are kidney. Fig. 114I and Fig. 114M are heart muscle. Fig. 114J and Fig. 114N are liver. Fig. 114K and Fig. 114O are lung. Fig. 114L and Fig. 114P are ureter. Fig. 114Q and Fig. 114U are eye. Fig. 114R and Fig. 114V are cerebral cortex. Fig. 114S and Fig. 114W are bone marrow. Fig. 114T and Fig. 114X are skeletal muscle.

[00377] **Figure 115A-115C** shows photographs, array map and description of breast cancer tissue array 1141 stained with the anti-PSMGFR antibody 20A10 at 0.25ug/mL. Fig. 115A shows photographs of the tissue micro array. Fig. 115B shows map of the array with abbreviated tissue descriptors. Fig. 115C detailed description of the tissue micro array with non-identifying donor data.

[00378] **Figure 116A-116F** shows photographs of specific tissues from breast cancer tissue array 1141 stained with the anti-PSMGFR antibody 20A10 at 0.25ug/mL, magnified to 6X and 20X. Fig. 116A and Fig. 116D are photographs of a Grade 2 invasive ductal carcinoma. Fig. 116B and Fig. 116E are photographs of a Grade 2 invasive ductal carcinoma. Fig. 116C and Fig. 116F are photographs of a Grade 2 invasive ductal carcinoma.

[00379] **Figure 117A-117C** shows photographs, array map and description of pancreatic cancer tissue array PA805c stained with the anti-PSMGFR antibody 20A10 at 0.25ug/mL. Fig. 117A shows photographs of the tissue micro array. Fig. 117B shows map of the array with abbreviated tissue descriptors. Fig. 117C detailed description of the tissue micro array with non-identifying donor data.

[00380] **Figure 118A-118F** shows photographs of specific tissues from pancreatic cancer tissue array PA805c stained with the anti-PSMGFR antibody 20A10 at 0.25ug/mL, magnified to 6X and 20X. Fig. 118A and Fig. 118D are photographs of a Grade 2 papillary adenocarcinoma.

Fig. 118B and Fig. 118E are photographs of a Grade 2-3 ductal carcinoma. Fig. 118C and Fig. 118F are photographs of a Grade 3 invasive adenocarcinoma.

[00381] **Figure 119A-119C** shows photographs, array map and description of esophageal cancer tissue array BC001113 stained with the anti-PSMGFR antibody 20A10 at 0.25ug/mL. Fig. 119A shows photographs of the tissue micro array. Fig. 119B shows map of the array with abbreviated tissue descriptors. Fig. 119C detailed description of the tissue micro array with non-identifying donor data.

[00382] **Figure 120A-120F** shows photographs of specific tissues from esophageal cancer tissue array BC001113 stained with the anti-PSMGFR antibody 20A10 at 0.25ug/mL, magnified to 6X and 20X. Fig. 120A and Fig. 120D are photographs of the specimen at position A1. Fig. 120B and Fig. 120E are photographs of the specimen at position A7. Fig. 120C and Fig. 120F are photographs of the specimen at position A8.

[00383] **Figure 121A-121C** shows photographs, array map and description of FDA normal tissue array 1021 stained with the anti-PSMGFR antibody 3C2B1 at 20ug/mL. Fig. 121A shows photographs of the tissue micro array. Fig. 121B shows map of the array with abbreviated tissue descriptors. Fig. 121C detailed description of the tissue micro array with non-identifying donor data.

[00384] **Figure 122A-122X** shows photographs of specific tissues from FDA normal tissue array 1021 stained with the anti-PSMGFR antibody 3C2B1 at 20ug/mL, magnified to 6X and 20X. Fig. 122A and Fig. 122E are adrenal gland. Fig. 122B and Fig. 122F are breast. Fig. 122C and Fig. 122G are fallopian tube. Fig. 122D and Fig. 122H are kidney. Fig. 122I and Fig. 122M are heart muscle. Fig. 122J and Fig. 122N are liver. Fig. 122K and Fig. 122O are lung. Fig. 122L and Fig. 122P are ureter. Fig. 122Q and Fig. 122U are eye. Fig. 122R and Fig. 122V are cerebral cortex. Fig. 122S and Fig. 122W are bone marrow. Fig. 122T and Fig. 122X are skeletal muscle.

[00385] **Figure 123A-123C** shows photographs, array map and description of pancreatic cancer tissue array PA1003 stained with the anti-PSMGFR antibody 3C2B1 at 20ug/mL. Fig. 123A shows photographs of the tissue micro array. Fig. 123B shows map of the array with abbreviated tissue descriptors. Fig. 123C detailed description of the tissue micro array with non-identifying donor data.

[00386] **Figure 124A-124F** shows photographs of specific tissues from pancreatic cancer tissue array PA1003 stained with the anti-PSMGFR antibody 3C2B1 at 20ug/mL, magnified to 6X and 20X. Fig. 124A and Fig. 124D are photographs of a Grade 2 adenocarcinoma. Fig. 124B and Fig. 124E are photographs of a Grade 2 adenocarcinoma. Fig. 124C and Fig. 124F are photographs of a Grade 2 adenocarcinoma.

[00387] **Figure 125A-125C** shows photographs, array map and description of breast cancer tissue array 1141 stained with the anti-PSMGFR antibody 3C2B1 at 20ug/mL. Fig. 125A shows photographs of the tissue micro array. Fig. 125B shows map of the array with abbreviated tissue descriptors. Fig. 125C detailed description of the tissue micro array with non-identifying donor data.

[00388] **Figure 126A-126F** shows photographs of specific tissues from breast cancer tissue array 1141 stained with the anti-PSMGFR antibody 3C2B1 at 20ug/mL, magnified to 6X and 20X. Fig. 126A and Fig. 126D are photographs of a Grade 2 invasive ductal carcinoma. Fig. 126B and Fig. 126E are photographs of a Grade 2 invasive ductal carcinoma. Fig. 126C and Fig. 126F are photographs of a Grade 2 invasive carcinoma.

[00389] **Figure 127A-127C** shows photographs, array map and description of FDA normal tissue array 1021 stained with the anti-PSMGFR antibody 5C6F3 at 1ug/mL. Fig. 127A shows photographs of the tissue micro array. Fig. 127B shows map of the array with abbreviated tissue descriptors. Fig. 127C detailed description of the tissue micro array with non-identifying donor data.

[00390] **Figure 128A-128X** shows photographs of specific tissues from FDA normal tissue array 1021 stained with the anti-PSMGFR antibody 5C6F3 at 1ug/mL, magnified to 6X and 20X. Fig. 128A and Fig. 128E are adrenal gland. Fig. 128B and Fig. 128F are breast. Fig. 128C and Fig. 128G are fallopian tube. Fig. 128D and Fig. 128H are kidney. Fig. 128I and Fig. 128M are heart muscle. Fig. 128J and Fig. 128N are liver. Fig. 128K and Fig. 128O are lung. Fig. 128L and Fig. 128P are ureter. Fig. 128Q and Fig. 128U are eye. Fig. 128R and Fig. 128V are cerebral cortex. Fig. 128S and Fig. 128W are bone marrow. Fig. 128T and Fig. 128X are skeletal muscle.

[00391] **Figure 129A-129C** shows photographs, array map and description of pancreatic cancer tissue array PA1003 stained with the anti-PSMGFR antibody 5C6F3 at 1-20ug/mL. Fig. 129A shows photographs of the tissue micro array. Fig. 129B shows map of the array with abbreviated tissue descriptors. Fig. 129C detailed description of the tissue micro array with non-identifying donor data.

[00392] **Figure 130A-130F** shows photographs of specific tissues from pancreatic cancer tissue array PA1003 stained with the anti-PSMGFR antibody 5C6F3 at 1ug/mL, magnified to 6X and 20X. Fig. 130A and Fig. 130D are photographs of a Grade 2 adenocarcinoma. Fig. 130B and Fig. 130E are photographs of a Grade 2 adenocarcinoma. Fig. 130C and Fig. 130F are photographs of a Grade 2 adenocarcinoma.

[00393] **Figure 131A-131C** shows photographs, array map and description of breast cancer tissue array 1141 stained with the anti-PSMGFR antibody 5C6F3 at 1ug/mL. Fig. 131A shows photographs of the tissue micro array. Fig. 131B shows map of the array with abbreviated tissue descriptors. Fig. 131C detailed description of the tissue micro array with non-identifying donor data.

[00394] **Figure 132A-132F** shows photographs of specific tissues from breast cancer tissue array 1141 stained with the anti-PSMGFR antibody 5C6F3 at 1ug/mL, magnified to 6X and 20X. Fig. 132A and Fig. 132D are photographs of a Grade 2 invasive ductal carcinoma. Fig. 132B and Fig. 132E are photographs of a Grade 2 invasive ductal carcinoma. Fig. 132C and Fig. 132F are photographs of a Grade 2 invasive carcinoma.

[00395] **Figure 133A-133C** shows photographs, array map and description of FDA normal tissue array 1021 stained with the anti-PSMGFR antibody 18B4 at 10ug/mL. Fig. 133A shows photographs of the tissue micro array. Fig. 133B shows map of the array with abbreviated tissue descriptors. Fig. 133C detailed description of the tissue micro array with non-identifying donor data.

[00396] **Figure 134A-134X** shows photographs of specific tissues from FDA normal tissue array 1021 stained with the anti-PSMGFR antibody 18B4 at 10ug/mL, magnified to 6X and 20X. Fig. 134A and Fig. 134E are adrenal gland. Fig. 134B and Fig. 134F are breast. Fig. 134C and Fig. 134G are fallopian tube. Fig. 134D and Fig. 134H are kidney. Fig. 134I and Fig. 134M are heart muscle. Fig. 134J and Fig. 134N are liver. Fig. 134K and Fig. 134O are lung. Fig. 134L and Fig. 134P are ureter. Fig. 134Q and Fig. 134U are eye. Fig. 134R and Fig. 134V are cerebral cortex. Fig. 134S and Fig. 134W are bone marrow. Fig. 134T and Fig. 134X are skeletal muscle.

[00397] **Figure 135A-135C** shows photographs, array map and description of breast cancer tissue array 1141 stained with the anti-PSMGFR antibody 18B4 at 10ug/mL. Fig. 135A shows photographs of the tissue micro array. Fig. 135B shows map of the array with abbreviated tissue descriptors. Fig. 135C detailed description of the tissue micro array with non-identifying donor data.

[00398] **Figure 136A-136F** shows photographs of specific tissues from breast cancer tissue array 1141 stained with the anti-PSMGFR antibody 18B4 at 10ug/mL, magnified to 6X and 20X. Fig. 136A and Fig. 136D are photographs of a Grade 2 invasive ductal carcinoma. Fig. 136B and Fig. 136E are photographs of a Grade 2 invasive ductal carcinoma. Fig. 136C and Fig. 136F are photographs of a Grade 2 invasive ductal carcinoma.

[00399] **Figure 137A-137C** shows photographs, array map and description of esophageal cancer tissue array BC001113 stained with the anti-PSMGFR antibody 18B4 at 10ug/mL. Fig. 137A shows photographs of the tissue micro array. Fig. 137B shows map of the array with abbreviated tissue descriptors. Fig. 137C detailed description of the tissue micro array with non-identifying donor data.

[00400] **Figure 138A-138F** shows photographs of specific tissues from esophageal cancer tissue array BC001113 stained with the anti-PSMGFR antibody 18B4 at 10ug/mL, magnified to 6X and 20X. Fig. 138A and Fig. 138D are photographs of the specimen at position A1. Fig. 138B and Fig. 138E are photographs of the specimen at position A7. Fig. 138C and Fig. 138F are photographs of the specimen at position A8.

[00401] **Figure 139A-139C** shows photographs, array map and description of FDA normal tissue array 1021 stained with the anti-PSMGFR antibody 18G12 at 10ug/mL. Fig. 139A shows photographs of the tissue micro array. Fig. 139B shows map of the array with abbreviated tissue descriptors. Fig. 139C detailed description of the tissue micro array with non-identifying donor data.

[00402] **Figure 140A-140X** shows photographs of specific tissues from FDA normal tissue array 1021 stained with the anti-PSMGFR antibody 18G12 at 10ug/mL, magnified to 6X and 20X. Fig. 140A and Fig. 140E are adrenal gland. Fig. 140B and Fig. 140F are breast. Fig. 140C and Fig. 140G are fallopian tube. Fig. 140D and Fig. 140H are kidney. Fig. 140I and Fig. 140M are heart muscle. Fig. 140J and Fig. 140N are liver. Fig. 140K and Fig. 140O are lung. Fig. 140L and Fig. 140P are ureter. Fig. 140Q and Fig. 140U are eye. Fig. 140R and Fig. 140V are cerebral cortex. Fig. 140S and Fig. 140W are bone marrow. Fig. 140T and Fig. 140X are skeletal muscle.

[00403] **Figure 141A-141C** shows photographs, array map and description of breast cancer tissue array 1141 stained with the anti-PSMGFR antibody 18G12 at 15ug/mL. Fig. 141A shows photographs of the tissue micro array. Fig. 141B shows map of the array with abbreviated tissue descriptors. Fig. 141C detailed description of the tissue micro array with non-identifying donor data.

[00404] **Figure 142A-142F** shows photographs of specific tissues from breast cancer tissue array 1141 stained with the anti-PSMGFR antibody 18G12 at 15ug/mL, magnified to 6X and 20X. Fig. 142A and Fig. 142D are photographs of a Grade 2 invasive ductal carcinoma. Fig. 142B and Fig. 142E are photographs of a Grade 2 invasive ductal carcinoma. Fig. 142C and Fig. 142F are photographs of a Grade 2 invasive ductal carcinoma.

[00405] **Figure 143A-143C** shows photographs, array map and description of pancreatic cancer tissue array PA1003 stained with the anti-PSMGFR antibody 18G12 at 15ug/mL. Fig. 143A shows photographs of the tissue micro array. Fig. 143B shows map of the array with abbreviated tissue descriptors. Fig. 143C detailed description of the tissue micro array with non-identifying donor data.

[00406] **Figure 144A-144F** shows photographs of specific tissues from pancreatic cancer tissue array PA1003 stained with the anti-PSMGFR antibody 18G12 at 15ug/mL, magnified to 6X and 20X. Fig. 144A and Fig. 144D are photographs of a Grade 2 adenocarcinoma. Fig. 144B and Fig. 144E are photographs of a Grade 2 adenocarcinoma. Fig. 144C and Fig. 144F are photographs of a Grade 2-3 adenocarcinoma with lymph node involvement.

[00407] **Figure 145A-145C** shows photographs, array map and description of esophageal cancer tissue array BC001113 stained with the anti-PSMGFR antibody 18G12 at 30ug/mL. Fig. 145A shows photographs of the tissue micro array. Fig. 145B shows map of the array with abbreviated tissue descriptors. Fig. 145C detailed description of the tissue micro array with non-identifying donor data.

[00408] **Figure 146A-146F** shows photographs of specific tissues from esophageal cancer tissue array BC001113 stained with the anti-PSMGFR antibody 18G12 at 30ug/mL, magnified to 6X and 20X. Fig. 146A and Fig. 146D are photographs of the specimen at position A1. Fig.

146B and Fig. 146E are photographs of the specimen at position A7. Fig. 146C and Fig. 146F are photographs of the specimen at position A8.

[00409] **Figure 147A-147C** shows photographs, array map and description of FDA normal tissue array 1021 stained with the anti-PSMGFR antibody 25E6 at 5.0ug/mL. Fig. 147A shows photographs of the tissue micro array. Fig. 147B shows map of the array with abbreviated tissue descriptors. Fig. 147C detailed description of the tissue micro array with non-identifying donor data.

[00410] **Figure 148A-148X** shows photographs of specific tissues from FDA normal tissue array 1021 stained with the anti-PSMGFR antibody 25E6 at 5.0ug/mL, magnified to 6X and 20X. Fig. 148A and Fig. 148E are adrenal gland. Fig. 148B and Fig. 148F are breast. Fig. 148C and Fig. 148G are fallopian tube. Fig. 148D and Fig. 148H are kidney. Fig. 148I and Fig. 148M are heart muscle. Fig. 148J and Fig. 148N are liver. Fig. 148K and Fig. 148O are lung. Fig. 148L and Fig. 148P are ureter. Fig. 148Q and Fig. 148U are eye. Fig. 148R and Fig. 148V are cerebral cortex. Fig. 148S and Fig. 148W are bone marrow. Fig. 148T and Fig. 148X are skeletal muscle.

[00411] **Figure 149A-149C** shows photographs, array map and description of breast cancer tissue array 1141 stained with the anti-PSMGFR antibody 25E6 at 5.0ug/mL. Fig. 149A shows photographs of the tissue micro array. Fig. 149B shows map of the array with abbreviated tissue descriptors. Fig. 149C detailed description of the tissue micro array with non-identifying donor data.

[00412] **Figure 150A-150F** shows photographs of specific tissues from breast cancer tissue array 1141 stained with the anti-PSMGFR antibody 25E6 at 5.0ug/mL, magnified to 6X and 20X. Fig. 150A and Fig. 150D are photographs of a Grade 2 invasive ductal carcinoma. Fig. 150B and Fig. 150E are photographs of a Grade 2 invasive ductal carcinoma. Fig. 150C and Fig. 150F are photographs of a Grade 2 invasive ductal carcinoma.

[00413] **Figure 151A-151C** shows photographs, array map and description of pancreatic cancer tissue array PA1003 stained with the anti-PSMGFR antibody 25E6 at 5.0ug/mL. Fig. 151A shows photographs of the tissue micro array. Fig. 151B shows map of the array with abbreviated tissue descriptors. Fig. 151C detailed description of the tissue micro array with non-identifying donor data.

[00414] **Figure 152A-152F** shows photographs of specific tissues from pancreatic cancer tissue array PA1003 stained with the anti-PSMGFR antibody 25E6 at 5.0ug/mL, magnified to 6X and 20X. Fig. 152A and Fig. 152D are photographs of a Grade 2 adenocarcinoma. Fig. 152B and Fig. 152E are photographs of a Grade 1 adenocarcinoma. Fig. 152C and Fig. 152F are photographs of a Grade 1 adenocarcinoma.

[00415] **Figure 153A-153C** shows photographs, array map and description of FDA normal tissue array 1021 stained with the anti-PSMGFR antibody 28F9 at 15.0ug/mL. Fig. 153A shows photographs of the tissue micro array. Fig. 153B shows map of the array with abbreviated tissue descriptors. Fig. 153C detailed description of the tissue micro array with non-identifying donor data.

[00416] **Figure 154A-154X** shows photographs of specific tissues from FDA normal tissue array 1021 stained with the anti-PSMGFR antibody 28F9 at 15.0ug/mL, magnified to 6X and 20X. Fig. 154A and Fig. 154E are adrenal gland. Fig. 154B and Fig. 154F are breast. Fig. 154C and Fig. 154G are fallopian tube. Fig. 154D and Fig. 154H are kidney. Fig. 154I and Fig. 154M are heart muscle. Fig. 154J and Fig. 154N are liver. Fig. 154K and Fig. 154O are lung. Fig. 154L and Fig. 154P are ureter. Fig. 154Q and Fig. 154U are eye. Fig. 154R and Fig. 154V are cerebral cortex. Fig. 154S and Fig. 154W are bone marrow. Fig. 154T and Fig. 154X are skeletal muscle.

[00417] **Figure 155A-155C** shows photographs, array map and description of breast cancer tissue array 1141 stained with the anti-PSMGFR antibody 28F9 at 15.0ug/mL. Fig. 155A shows photographs of the tissue micro array. Fig. 155B shows map of the array with abbreviated tissue descriptors. Fig. 155C detailed description of the tissue micro array with non-identifying donor data.

[00418] **Figure 156A-156F** shows photographs of specific tissues from breast cancer tissue array 1141 stained with the anti-PSMGFR antibody 28F9 at 15.0ug/mL, magnified to 6X and 20X. Fig. 156A and Fig. 156D are photographs of a Grade 2 invasive ductal carcinoma. Fig. 156B and Fig. 156E are photographs of a Grade 2 invasive ductal carcinoma. Fig. 156C and Fig. 156F are photographs of a Grade 2 invasive ductal carcinoma.

[00419] **Figure 157A-157C** shows photographs, array map and description of FDA normal tissue array 1021 stained with the N+20/C-27 antibody 1E4 at 7.5ug/mL. Fig. 157A shows photographs of the tissue micro array. Fig. 157B shows map of the array with abbreviated tissue descriptors. Fig. 157C detailed description of the tissue micro array with non-identifying donor data.

[00420] **Figure 158A-158X** shows photographs of specific tissues from FDA normal tissue array 1021 stained with the N+20/C-27 antibody 1E4 at 7.5ug/mL, magnified to 6X and 20X. Fig. 158A and Fig. 158E are adrenal gland. Fig. 158B and Fig. 158F are breast. Fig. 158C and Fig. 158G are fallopian tube. Fig. 158D and Fig. 158H are kidney. Fig. 158I and Fig. 158M are heart muscle. Fig. 158J and Fig. 158N are liver. Fig. 158K and Fig. 158O are lung. Fig. 158L and Fig. 158P are ureter. Fig. 158Q and Fig. 158U are eye. Fig. 158R and Fig. 158V are cerebral cortex. Fig. 158S and Fig. 158W are bone marrow. Fig. 158T and Fig. 158X are skeletal muscle.

[00421] **Figure 159A-159C** shows photographs, array map and description of breast cancer tissue array BR1007 stained with the N+20/C-27 antibody 1E4 at 10.0ug/mL. Fig. 159A shows photographs of the tissue micro array. Fig. 159B shows map of the array with abbreviated tissue descriptors. Fig. 159C detailed description of the tissue micro array with non-identifying donor data.

[00422] **Figure 160A-160F** shows photographs of specific tissues from breast cancer tissue array BR1007 stained with the N+20/C-27 antibody 1E4 at 10.0ug/mL, magnified to 6X and 20X. Fig. 160A and Fig. 160D are photographs of a Grade 2 invasive ductal carcinoma with positive lymph nodes. Fig. 160B and Fig. 160E are photographs of a Grade 2 invasive ductal carcinoma. Fig. 160C and Fig. 160F are photographs of a Grade 2 invasive ductal carcinoma.

[00423] **Figure 161A-161C** shows photographs, array map and description of FDA normal tissue array 1021 stained with the N+20/C-27 antibody 29H1 at 0.5ug/mL. Fig. 161A shows photographs of the tissue micro array. Fig. 161B shows map of the array with abbreviated tissue descriptors. Fig. 161C detailed description of the tissue micro array with non-identifying donor data.

[00424] **Figure 162A-162X** shows photographs of specific tissues from FDA normal tissue array 1021 stained with the N+20/C-27 antibody 29H1 at 0.5ug/mL, magnified to 6X and 20X. Fig. 162A and Fig. 162E are adrenal gland. Fig. 162B and Fig. 162F are breast. Fig. 162C and Fig. 162G are fallopian tube. Fig. 162D and Fig. 162H are kidney. Fig. 162I and Fig. 162M are heart muscle. Fig. 162J and Fig. 162N are liver. Fig. 162K and Fig. 162O are lung. Fig. 162L and Fig. 162P are ureter. Fig. 162Q and Fig. 162U are eye. Fig. 162R and Fig. 162V are cerebral cortex. Fig. 162S and Fig. 162W are bone marrow. Fig. 162T and Fig. 162X are skeletal muscle.

[00425] **Figure 163A-163C** shows photographs, array map and description of breast cancer tissue array 1141 stained with the N+20/C-27 antibody 29H1 at 0.5ug/mL. Fig. 163A shows photographs of the tissue micro array. Fig. 163B shows map of the array with abbreviated tissue descriptors. Fig. 163C detailed description of the tissue micro array with non-identifying donor data.

[00426] **Figure 164A-164F** shows photographs of specific tissues from breast cancer tissue array 1141 stained with the N+20/C-27 antibody 29H1 at 0.5ug/mL, magnified to 6X and 20X. Fig. 164A and Fig. 164D are photographs of a Grade 2 invasive ductal carcinoma. Fig. 164B and Fig. 164E are photographs of a Grade 2 invasive ductal carcinoma. Fig. 164C and Fig. 164F are photographs of a Grade 2 invasive ductal carcinoma.

[00427] **Figure 165A-165C** shows photographs, array map and description of pancreatic cancer tissue array PA1003 stained with the N+20/C-27 antibody 29H1 at 0.5ug/mL. Fig. 165A shows photographs of the tissue micro array. Fig. 165B shows map of the array with abbreviated tissue descriptors. Fig. 165C detailed description of the tissue micro array with non-identifying donor data.

[00428] **Figure 166A-166F** shows photographs of specific tissues from pancreatic cancer tissue array PA1003 stained with the N+20/C-27 antibody 29H1 at 0.5ug/mL, magnified to 6X and 20X. Fig. 166A and Fig. 166D are photographs of a Grade 2 adenocarcinoma. Fig. 166B and Fig. 166E are photographs of a Grade 2 adenocarcinoma. Fig. 166C and Fig. 166F are photographs of a Grade 3 adenocarcinoma.

[00429] **Figure 167A-167C** shows photographs, array map and description of FDA normal tissue array 1021 stained with the N+20/C-27 antibody 31A1 at 0.5ug/mL. Fig. 167A shows photographs of the tissue micro array. Fig. 167B shows map of the array with abbreviated tissue descriptors. Fig. 167C detailed description of the tissue micro array with non-identifying donor data.

[00430] **Figure 168A-168X** shows photographs of specific tissues from FDA normal tissue array 1021 stained with the N+20/C-27 antibody 31A1 at 0.5ug/mL, magnified to 6X and 20X. Fig. 168A and Fig. 168E are adrenal gland. Fig. 168B and Fig. 168F are breast. Fig. 168C and Fig. 168G are fallopian tube. Fig. 168D and Fig. 168H are kidney. Fig. 168I and Fig. 168M

are heart muscle. Fig. 168J and Fig. 168N are liver. Fig. 168K and Fig. 168O are lung. Fig. 168L and Fig. 168P are ureter. Fig. 168Q and Fig. 168U are eye. Fig. 168R and Fig. 168V are cerebral cortex. Fig. 168S and Fig. 168W are bone marrow. Fig. 168T and Fig. 168X are skeletal muscle.

[00431] **Figure 169A-169C** shows photographs, array map and description of breast cancer tissue array 1141 stained with the N+20/C-27 antibody 31A1 at 0.5ug/mL. Fig. 169A shows photographs of the tissue micro array. Fig. 169B shows map of the array with abbreviated tissue descriptors. Fig. 169C detailed description of the tissue micro array with non-identifying donor data.

[00432] **Figure 170A-170F** shows photographs of specific tissues from breast cancer tissue array 1141 stained with the N+20/C-27 antibody 31A1 at 0.5ug/mL, magnified to 6X and 20X. Fig. 170A and Fig. 170D are photographs of a Grade 2 invasive ductal carcinoma. Fig. 170B and Fig. 170E are photographs of a Grade 2 invasive ductal carcinoma. Fig. 170C and Fig. 170F are photographs of a Grade 2 invasive ductal carcinoma.

[00433] **Figure 171A-171C** shows photographs, array map and description of pancreatic cancer tissue array PA1003 stained with the N+20/C-27 antibody 31A1 at 0.5ug/mL. Fig. 171A shows photographs of the tissue micro array. Fig. 171B shows map of the array with abbreviated tissue descriptors. Fig. 171C detailed description of the tissue micro array with non-identifying donor data.

[00434] **Figure 172A-172F** shows photographs of specific tissues from pancreatic cancer tissue array PA1003 stained with the N+20/C-27 antibody 31A1 at 0.5ug/mL, magnified to 6X and 20X. Fig. 172A and Fig. 172D are photographs of a Grade 1 adenocarcinoma. Fig. 172B and Fig. 172E are photographs of a Grade 2 adenocarcinoma. Fig. 172C and Fig. 172F are photographs of a Grade 3 adenocarcinoma.

[00435] **Figure 173A-173C** shows photographs, array map and description of FDA normal tissue array 1021 stained with the N+20/C-27 antibody 32C1 at 0.25ug/mL. Fig. 173A shows photographs of the tissue micro array. Fig. 173B shows map of the array with abbreviated tissue descriptors. Fig. 173C detailed description of the tissue micro array with non-identifying donor data.

[00436] **Figure 174A-174X** shows photographs of specific tissues from FDA normal tissue array 1021 stained with the N+20/C-27 antibody 32C1 at 0.25ug/mL, magnified to 6X and 20X.

Fig. 174A and Fig. 174E are adrenal gland. Fig. 174B and Fig. 174F are breast. Fig. 174C and Fig. 174G are fallopian tube. Fig. 174D and Fig. 174H are kidney. Fig. 174I and Fig. 174M are heart muscle. Fig. 174J and Fig. 174N are liver. Fig. 174K and Fig. 174O are lung. Fig. 174L and Fig. 174P are ureter. Fig. 174Q and Fig. 174U are eye. Fig. 174R and Fig. 174V are cerebral cortex. Fig. 174S and Fig. 174W are bone marrow. Fig. 174T and Fig. 174X are skeletal muscle.

[00437] **Figure 175A-175C** shows photographs, array map and description of breast cancer tissue array 1141 stained with the N+20/C-27 antibody 32C1 at 5.0ug/mL. Fig. 175A shows photographs of the tissue micro array. Fig. 175B shows map of the array with abbreviated tissue descriptors. Fig. 175C detailed description of the tissue micro array with non-identifying donor data.

[00438] **Figure 176A-176F** shows photographs of specific tissues from breast cancer tissue array 1141 stained with the N+20/C-27 antibody 32C1 at 5.0ug/mL, magnified to 6X and 20X. Fig. 176A and Fig. 176D are photographs of a Grade 2 invasive ductal carcinoma. Fig. 176B and Fig. 176E are photographs of a Grade 2 invasive ductal carcinoma. Fig. 176C and Fig. 176F are photographs of a Grade 2 invasive ductal carcinoma.

[00439] **Figure 177A-177C** shows photographs, array map and description of esophageal cancer tissue array ES1001 stained with the N+20/C-27 antibody 32C1 at 1.0ug/mL. Fig. 177A shows photographs of the tissue micro array. Fig. 177B shows map of the array with abbreviated tissue descriptors. Fig. 177C detailed description of the tissue micro array with non-identifying donor data.

[00440] **Figure 178A-178F** shows photographs of specific tissues from esophageal cancer tissue array BC001113 stained with the N+20/C-27 antibody 32C1 at 1.0ug/mL, magnified to 6X and 20X. Fig. 178A and Fig. 178D are photographs of a squamous cell carcinoma. Fig. 178B and Fig. 178E are photographs of an adenocarcinoma. Fig. 178C and Fig. 178F are photographs of a squamous cell carcinoma.

[00441] **Figure 179A-179C** shows photographs, array map and description of FDA normal tissue array 1021 stained with the N+20/C-27 antibody 45C11 at 12.5ug/mL. Fig. 179A shows photographs of the tissue micro array. Fig. 179B shows map of the array with abbreviated tissue descriptors. Fig. 179C detailed description of the tissue micro array with non-identifying donor data.

[00442] **Figure 180A-180X** shows photographs of specific tissues from FDA normal tissue array 1021 stained with the N+20/C-27 antibody 45C11 at 12.5ug/mL, magnified to 6X and 20X. Fig. 180A and Fig. 180E are adrenal gland. Fig. 180B and Fig. 180F are breast. Fig. 180C and Fig. 180G are fallopian tube. Fig. 180D and Fig. 180H are kidney. Fig. 180I and Fig. 180M are heart muscle. Fig. 180J and Fig. 180N are liver. Fig. 180K and Fig. 180O are lung. Fig. 180L and Fig. 180P are ureter. Fig. 180Q and Fig. 180U are eye. Fig. 180R and Fig. 180V are cerebral cortex. Fig. 180S and Fig. 180W are bone marrow. Fig. 180T and Fig. 180X are skeletal muscle.

[00443] **Figure 181A-181C** shows photographs, array map and description of breast cancer tissue array BR1007 stained with the N+20/C-27 antibody 45C11 at 10.0ug/mL. Fig. 181A shows photographs of the tissue micro array. Fig. 181B shows map of the array with abbreviated tissue descriptors. Fig. 181C detailed description of the tissue micro array with non-identifying donor data.

[00444] **Figure 182A-182F** shows photographs of specific tissues from breast cancer tissue array BR1007 stained with the N+20/C-27 antibody 45C11 at 10.0ug/mL, magnified to 6X and 20X. Fig. 182A and Fig. 182D are photographs of a Grade 2 invasive ductal carcinoma with positive lymph nodes. Fig. 182B and Fig. 182E are photographs of a Grade 2 invasive ductal carcinoma. Fig. 182C and Fig. 182F are photographs of a Grade 2 invasive ductal carcinoma.

[00445] **Figure 183A-183C** shows photographs, array map and description of pancreatic cancer tissue array PA805c stained with the N+20/C-27 antibody 45C11 at 12.5ug/mL. Fig. 183A shows photographs of the tissue micro array. Fig. 183B shows map of the array with abbreviated tissue descriptors. Fig. 183C detailed description of the tissue micro array with non-identifying donor data.

[00446] **Figure 184A-184F** shows photographs of specific tissues from pancreatic cancer tissue array PA805c stained with the N+20/C-27 antibody 45C11 at 12.5ug/mL, magnified to 6X and 20X. Fig. 184A and Fig. 184D are photographs of a Grade 2 papillary adenocarcinoma. Fig. 184B and Fig. 184E are photographs of a Grade 2-3 ductal carcinoma. Fig. 184C and Fig. 184F are photographs of a Grade 3 invasive adenocarcinoma.

[00447] **Figure 185A-185C** shows photographs, array map and description of FDA normal tissue array 1021 stained with the N+9/C-9 antibody 3C5 at 10.0ug/mL. Fig. 185A shows photographs of the tissue micro array. Fig. 185B shows map of the array with abbreviated tissue descriptors. Fig. 185C detailed description of the tissue micro array with non-identifying donor data.

[00448] **Figure 186A-186X** shows photographs of specific tissues from FDA normal tissue array 1021 stained with the N+9/C-9 antibody 3C5 at 10.0ug/mL, magnified to 6X and 20X. Fig. 186A and Fig. 186E are adrenal gland. Fig. 186B and Fig. 186F are breast. Fig. 186C and Fig. 186G are fallopian tube. Fig. 186D and Fig. 186H are kidney. Fig. 186I and Fig. 186M are heart muscle. Fig. 186J and Fig. 186N are liver. Fig. 186K and Fig. 186O are lung. Fig. 186L and Fig. 186P are ureter. Fig. 186Q and Fig. 186U are eye. Fig. 186R and Fig. 186V are cerebral cortex. Fig. 186S and Fig. 186W are bone marrow. Fig. 186T and Fig. 186X are skeletal muscle.

[00449] **Figure 187A-187C** shows photographs, array map and description of pancreatic cancer tissue array PA1003 stained with the N+9/C-9 antibody 3C5 at 10.0ug/mL. Fig. 187A shows photographs of the tissue micro array. Fig. 187B shows map of the array with abbreviated tissue descriptors. Fig. 187C detailed description of the tissue micro array with non-identifying donor data.

[00450] **Figure 188A-188F** shows photographs of specific tissues from pancreatic cancer tissue array PA1003 stained with the N+9/C-9 antibody 3C5 at 10.0ug/mL, magnified to 6X and 20X. Fig. 188A and Fig. 188D are photographs of a Grade 2 adenocarcinoma. Fig. 188B and Fig. 188E are photographs of a Grade 2 adenocarcinoma. Fig. 188C and Fig. 188F are photographs of a Grade 2-3 adenocarcinoma with lymph node involvement.

[00451] **Figure 189A-189C** shows photographs, array map and description of FDA normal tissue array 1021 stained with the N+9/C-9 antibody 8A9 at 15.0ug/mL. Fig. 189A shows photographs of the tissue micro array. Fig. 189B shows map of the array with abbreviated tissue descriptors. Fig. 189C detailed description of the tissue micro array with non-identifying donor data.

[00452] **Figure 190A-190X** shows photographs of specific tissues from FDA normal tissue array 1021 stained with the N+9/C-9 antibody 8A9 at 15.0ug/mL, magnified to 6X and 20X. Fig. 190A and Fig. 190E are adrenal gland. Fig. 190B and Fig. 190F are breast. Fig. 190C and Fig. 190G are fallopian tube. Fig. 190D and Fig. 190H are kidney. Fig. 190I and Fig. 190M are heart muscle. Fig. 190J and Fig. 190N are liver. Fig. 190K and Fig. 190O are lung. Fig. 190L and Fig. 190P are ureter. Fig. 190Q and Fig. 190U are eye. Fig. 190R and Fig. 190V are cerebral cortex. Fig. 190S and Fig. 190W are bone marrow. Fig. 190T and Fig. 190X are skeletal muscle.

[00453] **Figure 191A-191C** shows photographs, array map and description of pancreatic cancer tissue array PA1003 stained with the N+9/C-9 antibody 8A9 at 15.0ug/mL. Fig. 191A shows photographs of the tissue micro array. Fig. 191B shows map of the array with abbreviated tissue descriptors. Fig. 191C detailed description of the tissue micro array with non-identifying donor data.

[00454] **Figure 192A-192F** shows photographs of specific tissues from pancreatic cancer tissue array PA1003 stained with the N+9/C-9 antibody 8A9 at 15.0ug/mL, magnified to 6X and 20X. Fig. 192A and Fig. 192D are photographs of a Grade 2 adenocarcinoma. Fig. 192B and Fig. 192E are photographs of a Grade 2 adenocarcinoma. Fig. 192C and Fig. 192F are photographs of a Grade 2 adenocarcinoma.

[00455] **Figure 193A-193C** shows photographs, array map and description of FDA normal tissue array 1021 stained with the N+9/C-9 antibody 17H6 at 30.0ug/mL. Fig. 193A shows photographs of the tissue micro array. Fig. 193B shows map of the array with abbreviated tissue descriptors. Fig. 193C detailed description of the tissue micro array with non-identifying donor data.

[00456] **Figure 194A-194X** shows photographs of specific tissues from FDA normal tissue array 1021 stained with the N+9/C-9 antibody 17H6 at 30.0ug/mL, magnified to 6X and 20X. Fig. 194A and Fig. 194E are adrenal gland. Fig. 194B and Fig. 194F are breast. Fig. 194C and Fig. 194G are fallopian tube. Fig. 194D and Fig. 194H are kidney. Fig. 194I and Fig. 194M are heart muscle. Fig. 194J and Fig. 194N are liver. Fig. 194K and Fig. 194O are lung. Fig. 194L and Fig. 194P are ureter. Fig. 194Q and Fig. 194U are eye. Fig. 194R and Fig. 194V are cerebral cortex. Fig. 194S and Fig. 194W are bone marrow. Fig. 194T and Fig. 194X are skeletal muscle.

[00457] **Figure 195A-195C** shows photographs, array map and description of pancreatic cancer tissue array PA805c stained with the N+9/C-9 antibody 17H6 at 30.0ug/mL. Fig. 195A shows photographs of the tissue micro array. Fig. 195B shows map of the array with abbreviated tissue descriptors. Fig. 195C detailed description of the tissue micro array with non-identifying donor data.

[00458] **Figure 196A-196F** shows photographs of specific tissues from pancreatic cancer tissue array PA805c stained with the N+9/C-9 antibody 17H6 at 30.0ug/mL, magnified to 6X and 20X. Fig. 196A and Fig. 196D are photographs of a Grade 2 papillary adenocarcinoma. Fig.

196B and Fig. 196E are photographs of a Grade 2-3 ductal carcinoma with lymph node involvement. Fig. 196C and Fig. 196F are photographs of a Grade 3 invasive adenocarcinoma.

[00459] **Figure 197A-197C** shows photographs, array map and description of FDA normal tissue array 1021 stained with the N+9/C-9 antibody 39H5 at 5.0ug/mL. Fig. 197A shows photographs of the tissue micro array. Fig. 197B shows map of the array with abbreviated tissue descriptors. Fig. 197C detailed description of the tissue micro array with non-identifying donor data.

[00460] **Figure 198A-198X** shows photographs of specific tissues from FDA normal tissue array 1021 stained with the N+9/C-9 antibody 39H5 at 5.0ug/mL, magnified to 6X and 20X. Fig. 198A and Fig. 198E are adrenal gland. Fig. 198B and Fig. 198F are breast. Fig. 198C and Fig. 198G are fallopian tube. Fig. 198D and Fig. 198H are kidney. Fig. 198I and Fig. 198M are heart muscle. Fig. 198J and Fig. 198N are liver. Fig. 198K and Fig. 198O are lung. Fig. 198L and Fig. 198P are ureter. Fig. 198Q and Fig. 198U are eye. Fig. 198R and Fig. 198V are cerebral cortex. Fig. 198S and Fig. 198W are bone marrow. Fig. 198T and Fig. 198X are skeletal muscle.

[00461] **Figure 199A-199C** shows photographs, array map and description of pancreatic cancer tissue array PA1003 stained with the N+9/C-9 antibody 39H5 at 5.0ug/mL. Fig. 199A shows photographs of the tissue micro array. Fig. 199B shows map of the array with abbreviated tissue descriptors. Fig. 199C detailed description of the tissue micro array with non-identifying donor data.

[00462] **Figure 200A-200F** shows photographs of specific tissues from pancreatic cancer tissue array PA1003 stained with the N+9/C-9 antibody 39H5 at 5.0ug/mL, magnified to 6X and 20X. Fig. 200A and Fig. 200D are photographs of a Grade 2 adenocarcinoma. Fig. 200B and Fig. 200E are photographs of a Grade 2 adenocarcinoma. Fig. 200C and Fig. 200F are photographs of a Grade 2 adenocarcinoma.

[00463] **Figure 201A-201C** show graphs of ELISA assays to determine the binding of another set of antibodies generated by immunizing animals with the PSMGFR peptide. Fig. 201A shows binding to the PSMGFR peptide. Fig. 201B shows binding to the N-10 peptide. Fig. 201C shows binding to the C-10 peptide. As can be seen, none of the antibodies bound to the C-10 peptide. F3, B12, B2, B7, B9, 8C7F3 and H11 all bound to the PSMGFR peptide and to the N-10 peptide.

[00464] **Figure 202A-202C** shows photographs of pancreatic cancer tissue array PA1003 that has been stained with monoclonal antibody 1E4, monoclonal antibody 18B4 or the polyclonal anti-PSMGFR antibody SDIX. 18B4 binds to the GTINVHDVET epitope at the most N-terminal portion of the PSMGFR peptide, while the 1E4 antibody binds to the QFNQYKTEA epitope that is immediately adjacent and C-terminal to the 18B4 epitope.

[00465] **Figure 203A-203F** shows magnified images of the tissue specimen at position A2 of the pancreatic cancer array PA1003. Fig. 203A and Fig. 203B show the specimen stained with antibody 1E4. Fig. 203C and Fig. 203D show the specimen stained with antibody 18B4. Fig. 203E and Fig. 203F show the specimen stained with polyclonal antibody SDIX.

[00466] **Figure 204A-204D** shows magnified images of the tissue specimen at position D4 of the pancreatic array PA1003. Fig. 204A and Fig. 204B show the specimen stained with antibody 18B4. Fig. 204C and Fig. 204D show the specimen stained with polyclonal antibody SDIX.

[00467] **Figure 205A-205D** shows magnified images of the tissue specimen at position E1 of the pancreatic cancer array PA1003. Fig. 205A and Fig. 205B show the specimen stained with antibody 18B4. Fig. 205C and Fig. 205D show the specimen stained with polyclonal antibody SDIX.

[00468] **Figure 206A-206D** shows magnified images of the tissue specimen at position C3 of the pancreatic cancer array PA1003. Fig. 206A and Fig. 206B show the specimen stained with antibody 1E4. Fig. 206C and Fig. 206D show the specimen stained with polyclonal antibody SDIX.

[00469] **Figure 207A-207D** shows magnified images of the tissue specimen at position D1 of the pancreatic cancer array PA1003. Fig. 207A and Fig. 207B show the specimen stained with antibody 1E4. Fig. 207C and Fig. 207D show the specimen stained with polyclonal antibody SDIX.

[00470] **Figure 208A-208C** shows photographs of the pancreatic cancer array PA1003. Fig. 208A shows the specimen stained with polyclonal antibody SDIX. Fig. 208B shows the specimen stained with antibody 20A10. Fig. 208C shows the specimen stained with antibody 29H1.

[00471] **Figure 209A-209D** shows photographs of the esophageal cancer array ES1001 stained with various antibodies. Fig. 209A shows the array stained with polyclonal antibody SDIX. Fig. 209B shows the array stained with antibody 20A10. Fig. 209C shows the array stained with antibody 29H1. Fig. 209D shows the array stained with antibody 31A1.

[00472] **Figure 210A-210C** shows photographs of the pancreatic cancer array PA1003 stained with various antibodies. Fig. 210A shows the array stained with polyclonal antibody SDIX. Fig. 210B shows the array stained with antibody 20A10. Fig. 210C shows the array stained with antibody 29H1.

[00473] **Figure 211A- 211C** show graphs of an ELISA experiment measuring the amount of IL-18 secreted into the condition media of MUC1* positive cancer cells co-cultured with huMNC2-CAR44 T cells wherein the cells also bear an NFAT inducible IL-18. Fig. 211A shows the graph of IL-18 secreted into the supernatant of T47D breast cancer cells co-cultured with untransduced human T cells. Fig. 211B shows the graph of IL-18 secreted into the supernatant of T47D breast cancer cells co-cultured with huMNC2-CAR44 T cells that also bore an NFAT inducible IL-18 gene inserted into a portion of the Foxp3 enhancer. Fig. 211C shows the graph of IL-18 secreted into the supernatant of T47D breast cancer cells co-cultured with huMNC2-CAR44 T cells that also bore an NFAT inducible IL-18 gene inserted into a portion of the IL-2 enhancer.

[00474] **Figure 212A- 212X** shows photographs of T47D breast cancer cells (red) doped with varying percentages of T47D cells engineered to express more MUC1* (green). The target cancer cells have been co-cultured with huMNC2-CAR44 T cells with NFAT inducible IL-18 wherein the IL-18 gene has been inserted into either the Foxp3 enhancer/promoter or the IL-2 enhancer/promoter. Fig. 212A-212C, 212I-212K, and 212Q-212S show the cancer cells co-cultured with untranduced T cells. Fig. 212D-212F, 212L-212N, and 212T-212V show the cancer cells co-cultured with hiMNC2-CAR44 T cells with the NFAT inducible IL-18 gene inserted into the Foxp3 enhancer/promoter. Fig. 212G-212H, 212O-212P, and 212W-212X show the cancer cells co-cultured with hiMNC2-CAR44 T cells with the NFAT inducible IL-18 gene inserted into the IL-2 enhancer/promoter.

[00475] **Figure 213A- 213B** shows graphs of ELISA experiments in which levels of IL-18 secreted into the conditioned media are measured for huMNC1-CAR44 T cells with NFAT inducible IL-18 gene, inserted into the Foxp3 enhancer or promoter, co-cultured with either MUC1* positive cancer cells or MUC1 negative non-cancerous cells. Fig. 213A shows IL-18 secretion from huMNC2-CAR44 T cells with NFAT inducible IL-18 in co-culture with T47D breast cancer cells where the population has been doped with 5%, 10% or 30% T47D cells that had been transfected with even more MUC1*. Fig. **213**B shows IL-18 secretion from huMNC2-

CAR44 T cells with NFAT inducible IL-18 in co-culture with non-cancerous, MUC1 negaive HEK293 cells where the cell population has been doped with 5%, 10% or 30% T47D cells that had been transfected with more MUC1*.

[00476] **Figure 214A-214X** shows photographs of T47D breast cancer cells (red) or non-cancerous HEK293 cells (also red), where both cell types have been doped with varying percentages of T47D cells engineered to express more MUC1* (green). These target cancer cells have been co-cultured with huMNC2-CAR44 T cells with NFAT inducible IL-18 wherein the IL-18 gene has been inserted into the Foxp3 enhancer/promoter. Fig. 214A-214F shows either T47D cells or HEK293 cells that have not been doped with T47D cells engineered to express high MUC1* density. Fig. 214G-214L shows either T47D cells or HEK293 cells that have been doped with 5% T47D cells engineered to express high MUC1* density. Fig. 214M-214R shows either T47D cells or HEK293 cells that have been doped with 10% T47D cells engineered to express high MUC1* density. Fig. 214S-214X shows either T47D cells or HEK293 cells that have been doped with 30% T47D cells engineered to express high MUC1* density. Fig. 214A-B, G-H, M-N, and S-T show T47D breast cancer cells. Fig. 214C-F, I-L, O-R, and U-X show HEK293 cells. As can be seen in the figures, the induced secretion of IL-18 resulted in low MUC1* density T47D cells being killed but did not induce non-specific killing of the MUC1* negative HEK293 cells.

[00477] **Figure 215A-215C** shows the consensus sequences of the heavy chain CDRs wherein the consensus sequences were generated for each group of antibodies that bound to the same epitope in the PSMGFR and N-terminally extended PSMGFR peptide. Fig. 215A shows consensus sequences for heavy chain CDR1. Fig. 215B shows consensus sequences for heavy chain CDR2. Fig. 215C shows consensus sequences for heavy chain CDR3.

[00478] **Figure 216A-216C** shows the consensus sequences of the light chain CDRs wherein the consensus sequences were generated for each group of antibodies that bound to the same epitope in the PSMGFR and N-terminally extended PSMGFR peptide. Fig. 216A shows consensus sequences for light chain CDR1. Fig. 216B shows consensus sequences for light chain CDR2. Fig. 216C shows consensus sequences for light chain CDR3.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

[00479] In the present application, “a” and “an” are used to refer to both single and a plurality of objects.

[00480] As used herein, occasionally, in short hand, a polypeptide is indicated as being “transduced or transfected” into a cell. In these occurrences, it is understood that the nucleic acid encoding the polypeptide sequence is transduced or transfected into the cell, as it is an impossibility that a polypeptide could be transduced or transfected into a cell.

[00481] As used herein, occasionally when referring to number of cells injected into an animal or otherwise contextually wherein the number of cells is referred to, “M” refers to millions, and “K” refers to thousands.

[00482] As used herein, interchangeable designations for various monoclonal antibodies are used, such as, “MN-C2”, which is interchangeable with “C2”, “Min-C2” and “MNC2”; “MN-E6”, which is interchangeable with “E6”, “Min-E6” and “MNE6”; “MN-C3”, which is interchangeable with “C3”, “Min-C3” and “MNC3”; and “MN-C8”, which is interchangeable with “C8”, “Min-C8” and “MNC8”. The monoclonal antibodies provided herein follow the same convention.

[00483] As used herein, “h” or “hu” placed before an antibody construct is short-hand for humanized.

[00484] As used herein, the term “antibody-like” means a molecule that may be engineered such that it contains portions of antibodies but is not an antibody that would naturally occur in nature. Examples include but are not limited to CAR (chimeric antigen receptor) T cell technology and the Ylanthia® technology. The CAR technology uses an antibody epitope fused to a portion of a T cell so that the body’s immune system is directed to attack a specific target protein or cell. The Ylanthia® technology consists of an “antibody-like” library that is a collection of synthetic human Fabs that are then screened for binding to peptide epitopes from target proteins. The selected Fab regions can then be engineered into a scaffold or framework so that they resemble antibodies.

[00485] As used herein, “PSMGFR” is abbreviation for Primary Sequence of the MUC1 Growth Factor Receptor which is identified by SEQ ID NO:2, and thus is not to be confused with a six amino acid sequence. “PSMGFR peptide” or “PSMGFR region” refers to a peptide or region that incorporates the Primary Sequence of the MUC1 Growth Factor Receptor (SEQ ID NO:2).

[00486] As used herein, the “MUC1*” extra cellular domain is defined primarily by the PSMGFR sequence (GTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA (SEQ ID NO:2)). Because the exact site of MUC1 cleavage depends on the enzyme that clips it, and that the cleavage enzyme varies depending on cell type, tissue type or the time in the evolution of the cell, the exact sequence of the MUC1* extra cellular domain may vary at the N-terminus.

[00487] Other clipped amino acid sequences may include SNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTEAASRY (SEQ ID NO:620); or SVVVQLTLAFREGTINVHDVETQFNQYKTEAASRY (SEQ ID NO:621).

[00488] As used herein, the term “PSMGFR” is an acronym for Primary Sequence of MUC1 Growth Factor Receptor as set forth as GTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA (SEQ ID NO:2). In this regard, the “N-number” as in “N-10 PSMGFR” or simply “N-10”, “N-15 PSMGFR” or simply “N-15”, or “N-20 PSMGFR” or simply “N-20” refers to the number of amino acid residues that have been deleted at the N-terminal end of PSMGFR. Likewise “C-number” as in “C-10 PSMGFR” or simply “C-10”, “C-15 PSMGFR” or simply “C-15”, or “C-20 PSMGFR” or simply “C-20” refers to the number of amino acid residues that have been deleted at the C-terminal end of PSMGFR. A mixture of deletions and additions is also possible. For instance, N+20/C-27 refers to a peptide fragment of wild-type MUC1 in which 20 amino acids are added to the PSMGFR at the N-terminus and 27 amino acids are deleted from the C-terminus.

[00489] As used herein, the “extracellular domain of MUC1*” refers to the extracellular portion of a MUC1 protein that is devoid of the tandem repeat domain. In most cases, MUC1* is a cleavage product wherein the MUC1* portion consists of a short extracellular domain devoid of tandem repeats, a transmembrane domain and a cytoplasmic tail. The precise location of cleavage of MUC1 is not known perhaps because it appears that it can be cleaved by more than one enzyme. The extracellular domain of MUC1* will include most of the PSMGFR sequence but may have an additional 10-20 N-terminal amino acids.

[00490] As used herein “sequence identity” means homology in sequence of a particular polypeptide or nucleic acid to a reference sequence of nucleic acid or amino acid such that the function of the homologous peptide is the same as the reference peptide or nucleic acid. Such homology can be so close with the reference peptide such that at times the two sequences may be 90%, 95% or 98% identical yet possess the same function in binding or other biological activities.

[00491] As used herein, "MUC1 positive" cell refers to a cell that expresses a gene for MUC1, MUC1-Y or MUC1-Z or other MUC1 variant.

[00492] As used herein, "MUC1 negative" cell refers to a cell that does not express a gene for MUC1.

[00493] As used herein, "MUC1* positive" cell refers to a cell that expresses a gene for MUC1, wherein that gene's expressed protein is a transmembrane protein that is devoid of tandem repeats, which may be a consequence of post-translational modification, cleavage, alternative splicing, or transfecting or transducing a cell with a MUC1 protein that is devoid of tandem repeats.

[00494] As used herein, "MUC1* negative" cell refers to a cell that may or may not express a gene for MUC1 but does not express a MUC1 transmembrane protein that is devoid of tandem repeats.

[00495] As used herein, "MUC1 positive" cancer cell refers to a cancer cell that overexpresses the gene for MUC1, expresses MUC1 in an aberrant pattern, wherein its expression is not restricted to the apical border and/or expresses a MUC1 that is devoid of tandem repeats.

[00496] As used herein, "MUC1 negative" cancer cell refers to a cancer cell that may or may not express a gene for MUC1 but does not overexpress MUC1 or does not overexpress a MUC1 transmembrane protein that is devoid of tandem repeats.

[00497] As used herein, "MUC1* positive" cancer cell refers to a cancer cell that overexpresses a MUC1 transmembrane protein that is devoid of tandem repeats.

[00498] As used herein, "MUC1* negative" cancer cell refers to a cancer cell that may or may not express a gene for MUC1 but does not overexpress a MUC1 transmembrane protein that is devoid of tandem repeats.

[00499] As used herein "conformational epitope" refers to a peptide sequence that is required to be present in a specific three-dimensional structure or conformation for an antibody to bind. However the antibody binds when the peptide sequence is in the three-dimensional structure or conformation and is not bound when linear. A common technique for determining whether an antibody binds to a linear stretch or a conformational epitope is to use the antibody to probe a denaturing Western blot. Traveling through a denaturing gel linearizes proteins and peptides. Antibodies that do not work in a denaturing Western but do recognize the native target, for example expressed on an intact cell, are determined to recognize a conformational epitope. As used herein, the antibody may or may not actually bind to the "conformational epitope", however the presence of the "conformational epitope" sequence is required to render a three dimensional structure so that the MUC1* region on cancer cells is able to be bound by the antibody that is specific for cancer treatment. Thus, the conformational epitope is an amino acid sequence that induces the binding of the antibody to the MUC1* region on cancer cells. Thus, a term "conformational inducing peptide sequence" may be used, which indicates that a peptide sequence is present within a larger peptide not as a binding site but that induces binding of an antibody to the larger peptide by causing a three-dimensional structure to form that facilitates the binding of the antibody to the larger peptide.

[00500] MUC1* antibodies (anti-PSMGFR) for treatment or prevention of cancers

[00501] We discovered that a cleaved form of the MUC1 (SEQ ID NO:1) transmembrane protein is a growth factor receptor that drives the growth of over 75% of all human solid tumor cancers. The cleaved form of MUC1, which we called MUC1* (pronounced muk 1 star), is a powerful growth factor receptor. Enzymatic cleavage releases the bulk of the MUC1 extracellular domain. It is the remaining portion comprising a truncated extracellular domain, transmembrane domain and cytoplasmic tail that is called MUC1*. Cleavage and release of the bulk of the extracellular domain of MUC1 unmasks a binding site for activating ligands dimeric NME1, NME6, NME8, NME7$_{AB}$, NME7-X1 or NME7. Cell growth assays show that it is ligand-induced dimerization of the MUC1* extracellular domain that promotes growth (**Fig. 1A-1D**). MUC1* positive cells treated with either bivalent 'bv' anti-MUC1* antibody, monovalent 'mv' or Fab, NM23-H1 dimers or NME7-AB. Bivalent anti-MUC1* antibodies stimulate growth of cancer cells whereas the monovalent Fab inhibits growth. Classic bell-shaped curve indicates ligand induced dimerization stimulates growth. Dimeric NM23-H1, aka NME1, stimulates growth of MUC1* positive cancer cells but siRNA to suppress MUC1 expression eliminate its effect (**Fig. 1C**). NME7-AB also stimulates the growth of MUC1* positive cells (**Fig. 1D**).

[00502] MUC1* is an excellent target for cancer drugs as it is aberrantly expressed on over 75% of all cancers and is likely overexpressed on an even higher percentage of metastatic cancers. After MUC1 cleavage, most of its extracellular domain is shed from the cell surface. The remaining portion has a truncated extracellular domain that at least comprises the primary growth factor receptor sequence, PSMGFR (SEQ ID NO:2). Antibodies that bind to the PSMGFR sequence and especially those that competitively inhibit the binding of activating ligands such as NME proteins, including NME1, NME6, NME8, NME7$_{AB}$, NME7-X1 and NME7, are ideal therapeutics and can be used to treat or prevent MUC1 positive or MUC1* positive cancers, as stand-alone antibodies, antibody fragments or variable region fragments thereof incorporated into bispecific antibodies, or chimeric antigen receptors also called CARs, which are then transfected or transduced into immune cells, then administered to a patient.

[00503] Therapeutic anti-MUC1* antibodies can be monoclonal, polyclonal, antibody mimics, engineered antibody-like molecules, full antibodies or antibody fragments. Examples of antibody fragments include but are not limited to Fabs, scFv, and scFv-Fc. Human or humanized antibodies are preferred for use in the treatment or prevention of cancers. In any of these antibody-like molecules, mutations can be introduced to prevent or minimize dimer formation. Anti-MUC1* antibodies that are monovalent or bispecific are preferred because MUC1* function is activated by ligand induced dimerization. Typical binding assays show that NME1 and NME7$_{AB}$ bind to the PSMGFR peptide portion of MUC1* (**Fig. 2A, 2D**). Further, they show that these activating growth factors bind to the membrane proximal portion of MUC1*, as they do not bind to the PSMGFR peptide if the 10 C-terminal amino acids are missing. Similarly, anti-MUC1* antibodies MN-C2 and MN-E6 bind to the PSMGFR peptide if an only if the 10 C-terminal amino acids are present (**Fig. 2B, 2C**). Antibodies MN-C3 and MN-C8 bind to epitopes that are different from MN-C2 and MN-E6, as they do not depend on the presence of the 10 C-terminal amino acids of the PSMGFR peptide (**Fig. 2E, 2F**). Antibodies MN-C2, MN-E6, or fragments derived from them, can be administered to a patient for the treatment or prevention of cancers, as stand-alone antibodies or incorporated into bispecific antibodies, BiTEs or chimeric antigen receptors also called CARs that have been transduced into immune cells. MNC2 and MNE6 and other anti-MUC1* antibodies that competitively inhibit the binding of NME1 and NME7$_{AB}$ are preferred for use as stand alone antibody therapeutics.

[00504] Therapeutic anti-MUC1* antibodies for use as a stand alone antibody therapeutic or for integration into a BiTE or a CAR can be selected based on specific criteria. The parent antibody can be generated using typical methods for generating monoclonal antibodies in animals. Alternatively, they can be selected by screening antibody and antibody fragment libraries for their ability to bind to a MUC1* peptide, which can be:

[00505] (i) PSMGFR region of MUC1;

[00506] (ii) PSMGFR peptide;

[00507] (iii) a peptide having amino acid sequence of QFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA (N-10)

[00508] (iv) a peptide having amino acid sequence of

[00509] ASRYNLTISDVSVSDVPFPFSAQSGA (N-19)

[00510] (v) a peptide having amino acid sequence of

[00511] NLTISDVSVSDVPFPFSAQSGA (N-23)

[00512] (vi) a peptide having amino acid sequence of

[00513] ISDVSVSDVPFPFSAQSGA (N-26)

[00514] (vii) a peptide having amino acid sequence of

[00515] SVSDVPFPFSAQSGA (N-30)

[00516] (viii) a peptide having amino acid sequence of

[00517] QFNQYKTEAASRYNLTISDVSVSDVPFPFS (N-10/C-5)

[00518] (ix) a peptide having amino acid sequence of

[00519] ASRYNLTISDVSVSDVPFPFS (N-19/C-5) or

[00520] (x) a peptide having amino acid sequence of

[00521] FPFSAQSGA (N-36).

[00522] Resultant antibodies or antibody fragments generated or selected in this way can then be further selected by passing additional screens. For example, antibodies or antibody fragments become more preferred based on their ability to bind to MUC1* positive cancer cells or tissues but not to MUC1 negative cancer cells or to normal tissues. Further, anti-MUC1* antibodies or antibody fragments may be de-selected as anti-cancer therapeutics if they bind to stem or progenitor cells. Anti-MUC1* antibodies or antibody fragments become more preferred if they have the ability to competitively inhibit the binding of activating ligands to MUC1*. **Figs. 3A-3C** shows that MN-E6 and MN-C2 competitively inhibit the binding of activating ligands NME1 and NME7 to MUC1*.

[00523] A process for selecting anti-MUC1* antibodies for use in treating a patient diagnosed with a MUC1 positive cancer, at risk of developing a MUC1 positive cancer or suspected of having a MUC1 positive cancer comprises one or more of the following steps of selecting antibodies or antibody fragments that 1) bind to the PSMGFR peptide; 2) bind to the N-10 PSMGFR peptide; 3) bind to cancer cells; 4) do not bind to stem or progenitor cells; and 5) competitively inhibited the binding of dimeric NME1 or NME7-AB to the PSMGFR peptide. For example, **Figs. 3A-3C** show that monoclonals MN-E6 and MN-C2 satisfy all five criteria, while monoclonals MN-C3 and MN-C8 do not competitively inhibit the binding of activating ligands NME1 and NME7 (**Fig. 3C**). Recall that the MUC1* growth factor receptor is activated by ligand-induced dimerization of its extracellular domain. Therefore, the ideal antibody therapeutic should not dimerize the MUC1* extracellular domain. Preferably, suitable antibodies in this regard include monovalent antibodies such as those generated in lamas and camels, Fabs, scFv's, single domain antibodies (sdAb), scFv-Fc as long as the Fc portion is constructed such that it does not homo-dimerize.

[00524] FACS scans show that anti-MUC1* antibodies MN-C2 and MN-E6 specifically bind to MUC1* positive solid tumor cancer cells and MUC1* transfected cells but not MUC1* negative or MUC1 negative cells. In one example, a humanized MN-C2 scFv is shown to bind to ZR-75-1, aka 1500, MUC1* positive breast cancer cells (**Fig. 4A-4C**). MN-E6 was shown to bind to MUC1 negative HCT-116 colon cancer cells if an only if they were transfected with MUC1*. MN-E6 also bound to MUC1* positive cancer cells such as ZR-75-1, aka 1500, MUC1* positive breast cancer cells (**Fig. 4D-4F**). Binding assays such as ELISAs, immunofluorescence, and the like all confirm that MN-C2 and MN-E6 bind to the PSMGFR peptide and to live MUC1 positive cancer cells. Humanized anti-MUC1* antibodies are selected based on their ability to also bind to the PSMGFR peptide or to MUC1 positive cancer cells. Figure 5 shows that humanized MN-C2 scFv binds with high affinity to the MUC1* peptide PSMGFR with an EC-50 of about 333nM. Humanized MN-C2 scFv, like Fabs, potently inhibits the growth of MUC1* positive cancer cells as is shown in one example in **Figs. 6A, 6B**. Like the parent antibodies, humanized scFv's show the same binding pattern. huMNE6-scFv binds to the PSMGFR peptide, binds to the N-10 peptide but does not bind to the C-10 peptide (SEQ ID NO:825) (Fig. 8). Murine or humanized MNC3-scFv binds to the, PSMGFR peptide, binds to the N-10 peptide and binds to the C-10 peptide (Fig. 9).

[00525] The Fabs of MN-E6 and MN-C2 or the comparable single chain variable regions derived from them potently inhibit the growth of MUC1* positive cancers *in vitro* and in vivo. In several examples, the Fabs of Anti-MUC1* antibodies inhibited the growth of human MUC1* positive cancers in vivo. In one case, immune-compromised mice were implanted with human breast tumors then treated with MN-E6 Fab after tumor engraftment. **Fig. 7A** shows that MN-E6 Fab potently inhibited the growth of MUC1* positive breast cancers. Female nu/nu mice implanted with 90-day estrogen pellets were implanted with 6 million T47D human breast cancer cells that had been mixed 50/50 with Matrigel. Mice bearing tumors that were at least 150 mm^3 and had three successive increases in tumor volume were selected for treatment. Animals were injected sub-cutaneously twice per week with 80 mg/kg MN-E6 Fab and an equal number of mice fitting the same selection criteria were injected with vehicle alone (**Fig. 7A**).

[00526] In another aspect, MN-E6 was shown to halt the growth of prostate cancer. **Fig. 7B** shows that MN-E6 Fab potently inhibited the growth of MUC1* positive prostate cancers. Male NOD/SCID mice were implanted with 6 million DU-145 human prostate cancer cells that had been mixed 50/50 with Matrigel. Mice bearing tumors that were at least 150 mm^3 and had three successive increases in tumor volume were selected for treatment. Animals were injected sub-cutaneously every 48 hours with 160 mg/kg MN-E6 Fab and an equal number of mice fitting the same selection criteria were injected with vehicle alone (**Fig. 7B**). Tumors were measured independently by two researchers twice per week and recorded. Statistics were blindly calculated by independent statistician, giving a P value of 0.0001 for each. Anti-MUC1* Fab inhibited breast cancer growth and prostate cancer growth. Treatment had no effect on weight, bone marrow cell type or number. The MN-E6 Fab effectively inhibited the growth of the tumors, while the control group's tumors continued to grow until sacrifice. No adverse effects of treatment were observed or detected.

[00527] Recombinant forms of MN-E6 and MNC2 were constructed that like the Fab are monomeric. In this case, MN-E6 was humanized and MN-C2 was humanized. There are a number of methods known to those skilled in the art for humanizing antibodies. In addition to humanizing, libraries of human antibodies can be screened to identify other fully human antibodies that bind to the PSMGFR.

[00528] A single chain of the humanized MN-E6 variable region, called an scFv, was genetically engineered such that it was connected to the Fc portion of the antibody (SEQ ID NO:256 and 257). Fc regions impart certain benefits to antibody fragments for use as therapeutics. The Fc portion of an antibody recruits complement, which in general means it can recruit other aspects of the immune system and thus amplify the anti-tumor response beyond just inhibiting the target. The addition of the Fc portion also increases the half-life of the antibody fragment (Czajkowsky DM, Hu J, Shao Z and Pleass RJ. (2012) Fc-fusion proteins: new developments and future perspectives. EMBO Mol Med. 4(10):1015-1028). However, the Fc portion of an antibody homo-dimerizes, which in the case of anti-MUC1* antibody based therapeutics is not optimal since ligand-induced dimerization of the MUC1* receptor stimulates growth. Therefore, mutations in the Fc region that resist dimer formation are preferred for anti-MUC1* anti-cancer therapeutics. Deletion of the hinge region and other mutations in the Fc region that make the Fc-mutant resistant to dimerization were made and could be used as therapeutics.

[00529] A human or humanized MN-E6 antibody or antibody fragment, Fab, MN-E6 scFv or hu MN-E6 scFv-Fc_{mut} are effective anti-cancer agents that can be administered to a person diagnosed with a MUC1 or MUC1* positive cancer, suspected of having a MUC1 or MUC1* positive cancer or is at risk of developing a MUC1 or MUC1* positive cancer.

[00530] Humanizing

[00531] Humanized antibodies or antibody fragments or fully human antibodies that bind to the extracellular domain of -MUC1* are preferred for therapeutic use. The techniques described herein for humanizing antibodies are but a few of a variety of methods known to those skilled in the art. The invention is not meant to be limited by the technique used to humanize the antibody.

[00532] Humanization is the process of replacing the non-human regions of a therapeutic antibody (usually mouse monoclonal antibody) by human one without changing its binding specificity and affinity. The main goal of humanization is to reduce immunogenicity of the therapeutic monoclonal antibody when administered to human. Three distinct types of humanization are possible. First, a chimeric antibody is made by replacing the non-human constant region of the antibody by the human constant region. Such antibody will contain the mouse Fab region and will contain about 80-90% of human sequence. Second, a humanized antibody is made by grafting of the mouse CDR regions (responsible of the binding specificity) onto the variable region of a human antibody, replacing the human CDR (CDR-grafting method). Such antibody will contain about 90-95% of human sequence. Third and last, a full human antibody (100% human sequence) can be created by phage display, where a library of human antibodies is screened to select antigen specific human antibody or by immunizing transgenic mice expressing human antibody.

[00533] A general technique for humanizing an antibody is practiced approximately as follows. Monoclonal antibodies are generated in a host animal, typically in mice. Monoclonal antibodies are then screened for affinity and specificity of binding to the target. Once a monoclonal antibody that has the desired effect and desired characteristics is identified, it is sequenced. The sequence of the animal-generated antibody is then aligned with the sequences of many human antibodies in order to find human antibodies with sequences that are the most homologous to the animal antibody. Biochemistry techniques are employed to paste together the human antibody sequences and the animal antibody sequences. Typically, the non-human CDRs are grafted into the human antibodies that have the highest homology to the non-human antibody. This process can generate many candidate humanized antibodies that need to be tested to identify which antibody or antibodies has the desired affinity and specificity.

[00534] Once a human antibody or a humanized antibody has been generated it can be further modified for use as an Fab fragment, as a full antibody, or as an antibody-like entity such as a single chain molecule containing the variable regions, such as scFv or an scFv-Fc. In some cases it is desirable to have Fc region of the antibody or antibody-like molecule mutated such that it does not dimerize.

[00535] In addition to methods that introduce human sequences into antibodies generated in non-human species, fully human antibodies can be obtained by screening human antibody libraries with a peptide fragment of an antigen. A fully human antibody that functions like MN-E6 or MN-C2 is generated by screening a human antibody library with a peptide having the sequence of the PSMGFR N-10 peptide. Humanized anti-MUC1* antibodies were generated based on the sequences of the mouse monoclonal antibodies MN-E6 and MN-C2. In one aspect of the invention, a patient diagnosed with a MUC1* positive cancer is treated with an effective amount of a murine or camelid MNC2, MNE6, 20A10 (SEQ ID NOS:1574-1581), 3C2B1 (SEQ ID NOS:1572-1573), 5C6F3, 25E6 (SEQ ID NO:1598-1601), 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, or H11. In another aspect of the invention, a patient diagnosed with a MUC1* positive cancer is treated with an effective amount of humanized MN-E6 or MN-C2. In a preferred embodiment, a patient diagnosed with a MUC1* positive cancer is treated with an effective amount of humanized MNC2 , MNE6, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, or H11. In another aspect of the invention, a patient diagnosed with a MUC1* positive cancer is treated with an effective amount of humanized monovalent MNC2, MNE6, 20A10 (SEQ ID NOS:1574-1581) , 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, or H11, wherein monovalent means the corresponding Fab fragment, the corresponding scFv or the corresponding scFv-Fc fusion. In a preferred embodiment, a patient diagnosed with a MUC1* positive cancer is treated with an effective amount of a humanized scFv or monomeric humanized scFv-Fc of MNC2, MNE6, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, or H11. Since the MUC1* growth factor receptor is activated by ligand induced dimerization of its extracellular domain, and because the Fc portion of an antibody homo-dimerizes, it is preferable that a construct that includes an Fc portion uses a mutated Fc region that prevents or minimizes dimerization.

[00536] Antibodies that bind to PSMGFR (SEQ ID NO:2) peptide, and more specifically to the N-10 peptide, of the extracellular domain of the MUC1* receptor are potent anti-cancer therapeutics that are effective for the treatment or prevention of MUC1* positive cancers. They have been shown to inhibit the binding of activating ligands dimeric NME1 (SEQ ID NO:1781) and $\mathrm{NME7_{AB}}$ (SEQ ID NOS:827) to the extracellular domain of MUC1*. Anti-MUC1* antibodies that bind to the PSMGFR sequence inhibit the growth of MUC1*-positive cancer cells, specifically if they inhibit ligand-induced receptor dimerization. Fabs of anti-MUC1* antibodies have been demonstrated to block tumor growth in animals. Thus, antibodies or antibody fragments that bind to the extracellular domain of MUC1* would be beneficial for the treatment of cancers wherein the cancerous tissues express MUC1*.

[00537] Antibodies that bind to PSMGFR region of MUC1* or bind to a synthetic PSMGFR peptide are preferred. We have identified several monoclonal antibodies that bind to the extracellular domain of MUC1*. Among this group are mouse monoclonal antibodies MNC2 (SEQ ID NOS:118-131, 144-158, 163-164, 168-181, 194-209), MNE6 (SEQ ID NOS:12-25, 39-59, 65-78, 93-114), 20A10 (SEQ ID NOS:988-1019, 1574-1597, 1659-1666); 3C2B1 (SEQ ID NOS:1386-1413, 1572-1573), 5C6F3 (SEQ ID NOS:1356-1385), 25E6 (SEQ ID NOS:1020-1051, 1598-1617, 1667-1674), 18G12 (SEQ ID NOS:956-987), 28F9 (SEQ ID NOS:1052-1083), 1E4 (SEQ ID NOS:1116-1227), B12 (SEQ ID NOS:1414-1431, 1733-1742), B2 (SEQ ID NOS:1432-1459), B7 (SEQ ID NOS:1460-1487), B9 SEQ ID NOS:1544-1571), 8C7F3 (SEQ ID NOS:1488-1515), or H11 (SEQ ID NOS:1516-1543), the variable regions of which were sequenced and are given as for MN-E6 SEQ ID NOS: 12-13 and 65-66, for MN-C2 SEQ ID NOS: 118-119 and 168-169. The CDRs of these antibodies make up the recognition units of the antibodies and are the most important parts of the mouse antibody that should be retained when grafting into a human antibody. The sequences of the CDRs for each mouse monoclonal are as follows, heavy chain sequence followed by light chain: MN-E6 CDR1 (SEQ ID NO:16-17 and 69-70) CDR2 (SEQ ID NO:20-21 and 73-74) CDR3 (SEQ ID NO: 24-25 and 77-78), MN-C2 CDR1 (SEQ ID NO:122-123 and 172-173) CDR2 (SEQ ID NO:126-127 and 176-177) CDR3 (SEQ ID NO:130-131 and 180-181). In some cases, portions of the framework regions that by modeling are thought to be important for the 3-dimensional structure of the CDRs, are also imported from the mouse sequence.

[00538] Monoclonal antibodies MN-E6 and MN-C2 have greater affinity for MUC1* as it appears on cancer cells. Monoclonal antibodies MN-C3 and MN-C8 have greater affinity for MUC1* as it appears on stem cells.

[00539] All four antibodies have been humanized, which process has resulted in several humanized forms of each antibody. CDRs derived from the variable regions of the mouse antibodies were biochemically grafted into a homologous human antibody variable region sequence. Humanized variable regions of MN-E6 (SEQ ID NOS: 38-39 and 93-94), MN-C2 (SEQ ID NOS: 144-145 and 194-195), MN-C3 (SEQ ID NOS: 439-440 and 486-487) and MN-C8 (SEQ ID NOS: 525-526 and 543-544) were generated by grafting the mouse CDRs into the variable region of a homologous human antibody. The humanized heavy chain variable constructs were then fused into constant regions of either human IgG1 heavy chain constant region (SEQ ID NOS:58-59) or human IgG2 heavy chain constant region (SEQ ID NO:54-55), which are then paired with either humanized light chain variable constructs fused to a human kappa chain (SEQ ID NO: 109-110) or human lambda chain (SEQ ID NO: 113-114) constant region. Other IgG isotypes could be used as constant region including IgG3 or IgG4.

[00540] Examples of humanized MN-E6 variable region into an IgG2 heavy chain (SEQ ID NOS:52-53) and into an IgG1 heavy chain (SEQ ID NOS:56-57), humanized MN-C2 variable into an IgG1 heavy chain (SEQ ID NOS: 157-158) or into an IgG2 heavy chain (SEQ ID NOS: 163-164) paired with either Lambda light chain (SEQ ID NO: 111-112 and 216-219) or Kappa chain (SEQ ID NO:107-108 and 210-213) and , humanized MN-C3 (SEQ ID NOS: 455-456, 453-454 and 500-501, 502-503) and MN-C8 (SEQ ID NOS: 541-542, 539-540 and 579-580, 581-582) antibodies were generated. Which IgG constant region is fused to the humanized variable region depends on the desired effect since each isotype has its own characteristic activity. The isotype of the human constant region is selected on the basis of things such as whether antibody dependent cell cytotoxicity (ADCC) or complement dependent cytotoxicity (CDC) is desired but can also depend on the yield of antibody that is generated in cell-based protein expression systems. In a preferred embodiment, humanized anti-MUC1* antibodies or antibody fragments are administered to a person diagnosed with or at risk of developing a MUC1-positive cancer.

[00541] One method for testing and selecting the humanized anti-MUC1* antibodies that would be most useful for the treatment of persons with cancer or at risk of developing cancers is to test them for their ability to inhibit the binding of activating ligands to the MUC1* extracellular domain. Dimeric NME1 can bind to and dimerize the MUC1* extracellular domain and in so doing stimulates cancer cell growth. Antibodies and antibody fragments that compete with NME1 for binding to the MUC1* extracellular domain are therefore anti-cancer agents. $NME7_{AB}$ is another activating ligand of MUC1*. In some cases, it is preferable to identify antibodies that block the binding of NME7, or an $NME7_{AB}$ truncation or cleavage product of NME7-X1, to the MUC1* extracellular domain. Antibodies and antibody fragments that compete with NME7 and NME7 variants for binding to the MUC1* extracellular domain are effective as anti-cancer therapeutics. These antibodies include but are not limited to MNC2, MNE6, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, or H11 as well as single chain versions, such as scFv, of these antibodies and humanized version thereof. Other NME proteins also bind to MUC1 or MUC1* including NME6 and NME8. Antibodies that compete with these proteins for binding to MUC1* may also be useful as therapeutics. In a preferred embodiment, murine, camelid, human or humanized anti-MUC1* antibodies or antibody fragments are administered to a person diagnosed with or at risk of developing a MUC1-positive cancer. In a more preferred embodiment, single chain antibody fragments, or monomeric scFv-Fc fusions, derived from humanized sequences of MNC2, MNE6, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, or H11 are administered to a person diagnosed with or at risk of developing a MUC1-positive cancer.

[00542] Single chain variable fragments, scFv, or other forms that result in a monovalent antibody or antibody-like protein are also useful. In some cases it is desired to prevent dimerization of the MUC1* extracellular domain. Single chain variable fragments, Fabs and other monovalent antibody-like proteins have been shown to be effective in binding to the extracellular domain of MUC1* and blocking MUC1* dimerization. These single chain variable fragments, Fabs and other monovalent antibody-like molecules effectively blocked cancer growth *in vitro* and in animals xenografted with human MUC1-positive cancer cells. Thus, humanized single chain variable fragments or monovalent anti-MUC1* antibodies or antibody-like molecules would be very effective as an anti-cancer therapeutic. Such humanized single chain antibodies, Fabs and other monovalent antibody-like molecules that bind to the MUC1* extracellular domain or to a PSMGFR peptide are therefore useful as anti-cancer therapeutics. Anti-MUC1* single chain variable fragments are generated by grafting non-human CDRs of antibodies, which bind to extracellular domain of MUC1* or bind to PSMGFR peptide, into a framework of a homologous variable region human antibody. The resultant humanized heavy and light chain variable regions are then connected to each other via a suitable linker, wherein the linker should be flexible and of length that it allows heavy chain binding to light chain but discourages heavy chain of one molecule binding to the light chain of another. For example a linker of about 10-15 residues. Preferably, the linker includes $[(\text{Glycine})_4\ (\text{Serine})_1]_3$ (SEQ ID NOS: 401-402), but is not limited to this sequence as other sequences are possible.

[00543] In one aspect, the humanized variable regions of MN-E6 (SEQ ID NOS: 38-39 and 93-94), MN-C2 (SEQ ID NOS: 144-145 and 194-195), or other antibodies of the invention are biochemically grafted into a construct that connects heavy and light chains via a linker. Examples of humanized single chain anti-MUC1* antibodies comprising humanized sequences from the variable regions of MN-E6 and MN-C2, were generated. Several humanized MN-E6 single chain proteins were generated (SEQ ID NOS: 232-237). Several humanized MN-C2 single chain proteins were generated (SEQ ID NOS: 238-243). In a preferred embodiment, humanized anti-MUC1* antibody fragments, including variable fragments, scFv antibody fragments MN-E6 scFv, MN-C2 scFv, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, or H11 scFv are administered to a person diagnosed with or at risk of developing a MUC1-positive cancer.

[00544] One aspect of the invention is a method for treating a patient diagnosed with, suspected of having, or at risk of developing a MUC1 positive or MUC1* positive cancer, wherein the patient is administered an effective amount of a monomeric MN-E6 scFv, MN-C2 scFv, or MN-E6 scFv-Fc, MN-C2 scFv-Fc, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, or H11, wherein the antibody variable fragment portions are human or have been humanized and wherein the Fc portion of the antibody-like protein has been mutated such that it resists dimer formation.

[00545] CAR T and cancer immunotherapy techniques

[00546] In another aspect of the invention, some or all of the single chain portions of anti-MUC1* antibody fragments are biochemically fused onto immune system molecules, using several different chimeric antigen receptor, 'CAR' strategies. The idea is to fuse the recognition portion of an antibody, typically as a single chain variable fragment, to an immune system molecule that has a transmembrane domain and a cytoplasmic tail that is able to transmit signals that activate the immune system. The recognition unit can be an antibody fragment, a single chain variable fragment, scFv, or a peptide. In one aspect, the recognition portion of the extracellular domain of the CAR is comprised of sequences from the humanized variable region of MN-E6 (SEQ ID NOS:38-39 and 93-94), MN-C2 (SEQ ID NOS:144-145 and 194-195), 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, or H11. Examples of murine or humanized antibodies of the invention, or their single chain fragments, scFv's, which can be incorporated into CARs, BiTEs or ADCs are given as: 3C2B1 (SEQ ID NOS: 1572-1573), 20A10 (SEQ ID NOS: 1574-1581), 25E6 (SEQ ID NOS:1598-1601). In another aspect, it is comprised of sequences from a single chain variable fragment. Examples of single chain constructs are given. Several humanized MN-E6 single chain proteins, scFv, were generated (SEQ ID NOS: 232-237). Several humanized MN-C2 single chain proteins, scFv, were generated (SEQ ID NOS: 238-243). The transmembrane region of the CAR can be derived from CD8, CD4, antibody domains or other transmembrane region, including the transmembrane region of the proximal cytoplasmic co-stimulatory domain, such as CD28, 4-1BB or other. The cytoplasmic tail of the CAR can be comprised of one or more motifs that signal immune system activation. This group of cytoplasmic signaling motifs, sometimes referred to as, co-stimulatory cytoplasmic domains, includes but is not limited to CD3-zeta, CD27, CD28, 4-1BB, OX40, CD30, CD40, ICAm-1, LFA-1, ICOS, CD2, CD5, CD7 and Fc receptor gamma domain. A minimal CAR may have the CD3-zeta or an Fc receptor gamma domain then one or two of the above domains in tandem on the cytoplasmic tail. In one aspect, the cytoplasmic tail comprises CD3-zeta, CD28, 4-1BB and/or OX40.

[00547] The extracellular domain recognition unit of a MUC1* targeting CAR can comprise variable regions of any non-human, humanized or human antibody that is able to bind to at least 12 contiguous amino acids of the PSMGFR peptide (SEQ ID NO:2) or the N-10 peptide. In one aspect, the MUC1* targeting portion of the CAR comprises variable regions from non-human, humanized or human MNC2, MNE6, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, or H11. Examples of a few antibodies of the invention, incorporated into CARs as either murine or humanized are given as 20A10 (SEQ ID NOS:1582-1597) and 25E6 (SEQ ID NOS:1602-1617). In the humanization process, the antibody CDRs can be inserted into a number of different framework regions; as a demonstration we generated three versions of a humanized 20A10 which differ only in the framework regions. These have been incorporated into CARs (SEQ ID NOS:1675, 1678, 1685) that when transduced into human T cells are able to recognize target MUC1* expressing cells and kill them. In one aspect, the extracellular domain recognition unit of a CAR is comprised essentially of a humanized MNC2, MNE6, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, or H11 single chain variable fragment scFv. The transmembrane region of the CAR can be derived from CD8 (SEQ ID NOS:363-364), or can be the transmembrane domain of CD3-zeta, CD28, 41bb, OX40 or other transmembrane region (SEQ ID NOS:361-372) and the cytoplasmic domain of a CAR with antibody fragment targeting MUC1* extracellular domain can be comprised of one or more selected from the group comprising an immune system co-stimulatory cytoplasmic domain. The group of immune system co-stimulatory domains includes but is not limited to CD3-zeta, CD27, CD28, 4-1BB, OX40, CD30, CD40, ICAm-1, LFA-1, ICOS, CD2, CD5, CD7 and Fc receptor gamma domain (SEQ ID NOS:373-382).

[00548] The CARs described can be transfected or transduced into a cell of the immune system. In a preferred embodiment, a MUC1* targeting CAR is transfected or transduced into a T cell. In one aspect, the T cell is a CD3+/CD28+ T cell. In another case it is a dendritic cell. In another case it is a B cell. In another case it is a mast cell. In yet another case it is a Natural Killer, NK, cell. The recipient cell can be from a patient or from a donor. If from a donor, it can be engineered to remove molecules that would trigger rejection. Cells transfected or transduced with a CAR of the invention can be expanded ex vivo or *in vitro* then administered to a patient. Administrative routes are chosen from a group containing but not limited to bone marrow transplant, intravenous injection, in situ injection or transplant. In a preferred embodiment, the

MUC1* targeting CAR is administered to a person diagnosed with or at risk of developing a MUC1-positive cancer.

[00549] There are many possible anti-MUC1* CAR constructs that can be transduced into T cells or other immune cells for the treatment or prevention of MUC1* positive cancers. CARs are made up of modules and the identity of some of the modules is relatively unimportant, while the identity of other modules is critically important.

[00550] We and others have shown that intracellular signaling modules, such as CD3-zeta (SEQ ID NOS: 373-376), CD28 (SEQ ID NOS: 377-378) and 41BB (SEQ ID NOS: 379-380), alone or in combinations stimulate immune cell expansion, cytokine secretion and immune cell mediated killing of the targeted tumor cells (Pulè MA, Straathof KC, Dotti G, Heslop HE, Rooney CM and Brenner MK (2005) A chimeric T cell antigen receptor that augments cytokine release and supports clonal expansion of primary human T cells. Mol Ther. 12(5):933-941; Hombach AA, Heiders J, Foppe M, Chmielewski M and Abken H. (2012) OX40 costimulation by a chimeric antigen receptor abrogates CD28 and IL-2 induced IL-10 secretion by redirected CD4(+) T cells. Oncoimmunology. 1(4):458-466; Kowolik CM, Topp MS, Gonzalez S, Pfeiffer T, Olivares S, Gonzalez N, Smith DD, Forman SJ, Jensen MC and Cooper LJ. (2006) CD28 costimulation provided through a CD19-specific chimeric antigen receptor enhances in vivo persistence and antitumor efficacy of adoptively transferred T cells. Cancer Res. 66(22):10995-11004; Loskog A, Giandomenico V, Rossig C, Pule M, Dotti G and Brenner MK. (2006) Addition of the CD28 signaling domain to chimeric T-cell receptors enhances chimeric T-cell resistance to T regulatory cells. Leukemia. 20(10):1819-1828; Milone MC, Fish JD, Carpenito C, Carroll RG, Binder GK, Teachey D, Samanta M, Lakhal M, Gloss B, Danet-Desnoyers G, Campana D, Riley JL, Grupp SA and June CH. (2009) Chimeric receptors containing CD137 signal transduction domains mediate enhanced survival of T cells and increased antileukemic efficacy in vivo. Mol Ther. 17(8):1453-1464; Song DG, Ye Q, Carpenito C, Poussin M, Wang LP, Ji C, Figini M, June CH, Coukos G, Powell DJ Jr. (2011) In vivo persistence, tumor localization, and antitumor activity of CAR-engineered T cells is enhanced by costimulatory signaling through CD137 (4-1BB). Cancer Res. 71(13):4617-4627). Antibodies of the invention including but not limited to fragments of MNC2, MNE6, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, or H11 can also be incorporated into CARs that have mutated cytoplasmic tails, such as mutated tyrosines or ITAMs. In any of the CARs described above, the cytoplasmic tails may include mutations that dampen signaling. Such mutations include but are not limited to Tyrosines that are mutated to inhibit phosphorylation and signaling (Salter et al, 2018;). In any of the CARs described above, the ITAMs of CD3-zeta may be mutated to inhibit or dampen signaling (Feucht et al 2019). In any of the CARs described above, the CD3 of the cytoplasmic tail may comprise mutations in the ITAMs including those referred to as 1XX**.** Examples of antibodies of the invention incorporated into CARs with 1XX mutations in ITAMs of CD3-zeta are given in the following sequences: MNC2 (SEQ ID NOS: 1618-1625), MNE6 (SEQ ID NOS:1626-1633), 20A10 (SEQ ID NOS:1590-1595), 25E6 (SEQ ID NOS:1610-1617). We note that the CDRs of antibodies can be inserted into a background of a number of different framework regions. As an example, 20A10 CDRs were inserted into three different sets of framework regions (SEQ ID NOS:1692, 1699 and 1706) and all were able to function when transduced into T cells. In any of the CARs described above, the T cell may be engineered to overexpress c-Jun as a method to inhibit T cell exhaustion (Lynn et al 2019). A variety of promoters can be used upstream of the genes for CARs and other compositions of the invention, including insertion into a naturally occurring promoter in the cell, such as the TRAC locus, using CRISPR, Sleeping Beauty or similar technology for site directed insertion of a gene. Among the promoters commonly used are the CMV promoter, or a mini CMV (SEQ ID NO: 1634), a minimal IL-2 promoter (SEQ ID NO: 1635), or Minimal Promoter minip (SEQ ID NO: 1636).

[00551] Single chain antibody fragments that included the variable domain of the monoclonal anti-MUC1* antibodies called MN-E6 or MN-C2 were engineered into a panel of CARs. The MUC1* targeting CARs were then transduced, separately or in combinations, into immune cells. When challenged with surfaces presenting a MUC1* peptide, an antigen presenting cell transfected with MUC1*, or MUC1* positive cancer cells, the immune cells that were transduced with MUC1* targeting CARs elicited immune responses, including cytokine release, killing of the targeted cells and expansion of the immune cells.

[00552] For example, the gene encoding the CARs and activated T cell induced genes described herein can be virally transduced into an immune cell using viruses, or inserted into a region downstream of one of the cell's promoters or enhancers, such as the TRAC (T cell receptor alpha chain) locus. Virus delivery systems and viral vectors including but not limited to retroviruses, including gamma-retroviruses, lentivirus, adenoviruses, adeno-associated viruses, baculoviruses, poxvirus, herpes simplex viruses, oncolytic viruses, HF10, T-Vec and the like can be used. In addition to viral transduction, CARs and activated T cell induced genes described herein can be directly spliced into the genome of the recipient cell using methods such as CRISPR technology, CRISPR-Cas9 and -CPF1, TALEN, Sleeping Beauty transposon system, and SB 100X.

[00553] Similarly, the identity of molecules that make up the non-targeting portions of the CAR such as the extracellular domain, transmembrane domain and membrane proximal portion of the cytoplasmic domain, are not essential to the function of a MUC1*-targeting CAR. For example, the extracellular domain, transmembrane domain and membrane proximal portion of the cytoplasmic domain can be comprised of portions of CD8, CD4, CD28, or generic antibody domains such as Fc, CH2CH3, or CH3. Further, the non-targeting portions of a CAR can be a composite of portions of one or more of these molecules or other family members.

[00554] One aspect of the invention is a method for treating a patient diagnosed with, suspected of having, or at risk of developing a MUC1 positive or MUC1* positive cancer, wherein the patient is administered an effective amount of immune cells that have been transduced with a MUC1* targeting CAR. In another aspect of the invention, the immune cells are T cells isolated from a patient, which are then transduced with CARs wherein the targeting head of the CAR binds to MUC1*, and after expansion of transduced T cells, the CAR T cells are administered in an effective amount to the patient. In yet another aspect of the invention, the immune cells are T cells isolated from a patient, which are then transduced with CARs wherein the targeting head of the CAR comprises portions of MNC2, MNE6, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, or H11, and after optional expansion of transduced T cells, the CAR T cells are administered in an effective amount to the patient.

[00555] **Specificity of anti-MUC1* targeting antibodies**

[00556] As these experiments demonstrate, the critical portion of a CAR is the antibody fragment that directs the immune cell to the tumor cell. As we will show in the following section, MN-E6 and MN-C2 are specific for the form of MUC1* that is expressed on tumor cells. The next most important part of a CAR is the cytoplasmic tail bearing immune system co-stimulatory domains. The identity of these domains modulates the degree of immune response but does not affect the specificity. As shown, the identity of the transmembrane portion of a CAR is the least important. It appears that as long as the transmembrane portion has some flexibility and is long enough to allow the antibody fragment to reach its cognate receptor on the tumor cell, it will suffice. CARs comprising the MN-E6 targeting antibody fragment, and intracellular co-stimulatory domains 41BB and CD3-zeta but having a variety of different extracellular, transmembrane and short cytoplasmic tail all worked in that they specifically killed the targeted cells while stimulating the expansion of the host T cells.

[00557] The most accurate way of demonstrating antibody specificity is testing the antibody on normal human tissue specimens compared to cancerous tissue specimens. MN-C2 and MN-E6 were shown to specifically bind to MUC1 or MUC1* positive cancer cells. Several breast tumor arrays were assayed using several anti-MUC1 or MUC1* antibodies. Essentially the studies involving serial sections of breast cancer tissue specimens from over 1,200 different breast cancer patients showed that very little full-length MUC1 remains on breast cancer tissues. The vast majority of the MUC1 expressed is MUC1* and is stained by MN-C2. The analysis was performed by Clarient Diagnostics and tissue staining was scored using the Allred method. For example, **Fig. 10** shows serial sections of breast cancer tissue arrays that were stained with either VU4H5, a commercially available anti-MUC1 antibody that binds to the tandem repeats, or MN-C2 that binds to MUC1*. **Figs. 10** and **11** are photographs of breast cancer tissue arrays stained with either VU4H5 which recognizes MUC1-FL (full length) or MN-C2 which recognizes cancerous MUC1*. Tissue staining was scored using Allred scoring method which combines an intensity score and a distribution score. Below the photographs of the tissue arrays are color-coded graphs displaying the results. As can be seen, the arrays stained with VU4H5 are very light and many tissues do not stain at all despite the published reports that MUC1 is aberrantly expressed on over 96% of all breast cancers as evidenced by nucleic acid based diagnostics. In contrast, the arrays stained with MN-C2 are very dark (red versus yellow or white in graph). Additionally, many tissues did not stain at all with anti-full-length MUC1 but stained very dark with MN-C2, (see green boxes in graph). Similarly, we stained normal or cancerous breast tissues with humanized MN-E6 scFv-Fc. The antibody fragment was biotinylated so it could be visualized by a secondary streptavidin based secondary. As can be seen in **Fig. 12**, hMN-E6 scFv-Fc does not stain normal breast tissue but stains cancerous breast tissue. Further, the intensity and homogeneity of staining increases with tumor grade and/or metastatic grade of the patient (**Fig. 12-13**). Similarly, hMN-E6 scFv-Fc did not stain normal lung tissue but did stain lung cancer tissue (**Fig. 14-18**) and the intensity and distribution of staining increased as tumor grade or metastatic grade increased. **Fig. 19** shows photographs of normal small intestine and cancerous small intestine tissues stained with humanized MN-E6-scFv-Fc biotinylated anti-MUC1* antibody at 5 ug/mL, then stained with a secondary streptavidin HRP antibody. A) is a normal small intestine tissue. B) is small intestine cancer from patient as denoted in the figure. C,D are photographs of the corresponding serial sections that were stained with the secondary antibody alone. **Fig. 20** shows photographs of normal small intestine tissues stained with humanized MN-E6-scFv-Fc anti-MUC1* antibody at 50 ug/mL, then stained with a secondary goat-anti-human HRP antibody. A-D are normal small intestine tissue. E-H are photographs of the corresponding serial sections that were stained with the secondary antibody alone. **Fig. 21** shows photographs of cancerous small intestine tissues stained with humanized MN-E6-scFv-Fc anti-MUC1* antibody at 50 ug/mL, then stained with a secondary goat-anti-human HRP antibody. A-D are cancerous small intestine tissue from a patient as denoted in figure. E-H are photographs of the corresponding serial sections that were stained with the secondary antibody alone. **Fig. 22** shows photographs of cancerous small intestine tissues stained with humanized MN-E6-scFv-Fc anti-MUC1* antibody at 50 ug/mL, then stained with a secondary goat-anti-human HRP antibody. A-D are cancerous small intestine tissue from a patient as denoted in figure. E-H are photographs of the corresponding serial sections that were stained with the secondary antibody alone. **Fig. 23** shows photographs of normal colon tissues stained with humanized MN-E6-scFv-Fc anti-MUC1* antibody at 50 ug/mL, then stained with a secondary goat-anti-human HRP antibody. A-D are normal colon. E-H are photographs of the corresponding serial sections that were stained with the secondary antibody alone. **Fig. 24** shows photographs of colon cancer tissues stained with humanized MN-E6-scFv-Fc anti-MUC1* antibody at 50 ug/mL, then stained with a secondary goat-anti-human HRP antibody. A-D are colon cancer tissue from a metastatic patient as denoted in figure. E-H are photographs of the corresponding serial sections that were stained with the secondary antibody alone. **Fig. 25** shows photographs of colon cancer tissues stained with humanized MN-E6-scFv-Fc anti-MUC1* antibody at 50 ug/mL, then stained with a secondary goat-anti-human HRP antibody. A-D are colon cancer tissue from a Grade 2 patient as denoted in figure. E-H are photographs of the corresponding serial sections that were stained with the secondary antibody alone. **Fig. 26** shows photographs of colon cancer tissues stained with humanized MN-E6-scFv-Fc anti-MUC1* antibody at 50 ug/mL, then stained with a secondary goat-anti-human HRP antibody. A-D are colon cancer tissue from a metastatic patient as denoted in figure. E-H are photographs of the corresponding serial sections that were stained with the secondary antibody alone. **Fig. 27** shows photographs of prostate cancer tissues stained with humanized MN-E6-scFv-Fc anti-MUC1* antibody at 50 ug/mL, then stained with a secondary goat-anti-human HRP antibody. A-D are prostate cancer tissue from a patient as denoted in figure. E-H are photographs of the corresponding serial sections that were stained with the secondary antibody alone. **Fig. 28** shows photographs of prostate cancer tissues stained with humanized MN-E6-scFv-Fc anti-MUC1* antibody at 50 ug/mL, then stained with a secondary goat-anti-human HRP antibody. A-D are prostate cancer tissue from a patient as denoted in figure. E-H are photographs of the corresponding serial sections that were stained with the secondary antibody alone. **Fig. 29** shows photographs of prostate cancer tissues stained with humanized MN-E6-scFv-Fc anti-MUC1* antibody at 50 ug/mL, then stained with a secondary goat-anti-human HRP antibody. A-D are prostate cancer tissue from a patient as denoted in figure. E-H are photographs of the corresponding serial sections that were stained with the secondary antibody alone.

[00558] One aspect of the invention is a method for treating a patient diagnosed with, suspected of having, or at risk of developing a MUC1 positive or MUC1* positive cancer, wherein a specimen is obtained from the patient's cancer and is tested for reactivity with an antibody that binds to PSMGFR SEQ ID NO:2, or more specifically to the N-10 peptide. The patient is then treated with an scFv, scFv-Fc or CAR T that comprises antibody variable fragments from the antibody that reacted with their cancer specimen or can be chosen from among MNC2, MNE6, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, or H11. Another aspect of the invention is a method for treating a patient diagnosed with, suspected of having, or at risk of developing a MUC1 positive or MUC1* positive cancer, wherein a specimen is obtained from the patient's cancer and is tested for reactivity with MNC2, MNE6, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, or H11; the patient is then treated with the antibody, antibody fragment, scFv, scFv-Fc-mut, BiTE or CAR T that comprises portions of the antibody that reacted with their cancer specimen.

[00559] As we previously reported, it is MUC1*, the transmembrane cleavage product, not full-length MUC1, the is a growth factor receptor that drives tumor growth. The growth factors that activate MUC1* bind to ectopic sites that are only exposed after cleavage and release of the tandem repeat portion of MUC1. Antibodies of the invention, like the activating growth factors, cannot bind to full-length MUC1. FACS analysis clearly shows that anti-MUC1* antibody MNC2 is unable to bind to HCT-116, MUC1 negative cells (Fig. 35A), binds robustly to those cells if they are transfected with MUC1* (Fig. 35B), but will not bind to HCT cells transfected with full-length MUC1 (Fig. 35C). A commercially available anti-tandem repeat antibody VU4H5 clearly recognizes full-length MUC1 (Fig. 35D).

[00560] We discovered that MUC1 can be cleaved to MUC1* by more than one cleavage enzyme and that the site of cleavage affects its fold and consequently affects which monoclonal antibody is able to recognize that form of MUC1*. Different cancer cells or cancerous tissues express different cleavage enzymes. We tested various cleavage enzyme inhibitors on different cancer cell lines and found that an inhibitor that inhibits cleavage of MUC1 in one cancer cell line did not inhibit its cleavage in another cancer cell line. Similarly, PCR experiments showed that cleavage enzymes are expressed at different levels in different cells or cell lines. For example, hematopoietic stem cells of the bone marrow express a MUC1* that is recognized by monoclonal antibody MNC3 but not MNE6 or MNC2 (**Fig. 39**). The growth of DU145 prostate cancer cells and T47D breast cancer cells is inhibited by the Fabs of MNC2 and MNE6 but not by the Fabs of MNC3 or MNC8, indicating that the cancer cell lines express a MUC1* that is recognized by MNE6 and MNC2 but not by MNC3 or MNC8 (**Fig. 42**). PCR experiments show that CD34 positive cells of the bone marrow express about 2,500-times more MMP2 and about 350-times more ADAM28 than T47D breast cancer cells, while DU145 prostate cancer cells express about 2,000-times more ADAM TS16, about 400-times more MMP14 and about 100-times more MMP1 than T47D breast cancer cells (**Fig. 43 and Fig. 44**). Conversely, T47D breast cancer cells express about 80-times more MMP9 than the bone marrow cells and about twice as much as DU145 prostate cancer cells. Various cleavage enzyme inhibitors were tested for their ability to inhibit cleavage in different kinds of cancer cells.

[00561] General strategy for using antibodies, antibody fragments and CARs that target the extracellular domain of MUC1*

[00562] In one aspect of the invention, a second factor, which may be a cleavage enzyme, an antibody, a cytokine, or a second CAR, and a CAR are transduced into the same T cell. In another aspect of the invention, the second factor is on an inducible promoter such that its expression is activated when the CAR engages the targeted cancer cells. In some cases, the expression of the second factor is controlled by an inducible promoter. In one aspect of the invention, expression of the second factor is induced when the immune cell is activated, for example when it recognizes or engages its target. In one example, a T cell is transfected or transduced with a second factor whose expression is induced when the T cell recognizes a target cancer cell. One way to do this is to induce expression of the second factor when, or shortly after, an NFAT protein is expressed or translocated to the nucleus. For example, a sequence derived from an NFAT promoter region is put upstream of the gene for the second factor. In this way, when the transcription factors that bind to the promoter of the NFAT protein are present in sufficient concentration to bind to and induce transcription of the NFAT protein, they will also bind to that same promoter that is engineered in front of the sequence for transcription of the second factor. The NFAT protein may be NFAT1 also known as NFATc2, NFAT2 also known as NFATc or NFATc1, NFAT3 also known as NFATc4, NFAT4 also known as NFATc3, or NFAT5. In one aspect of the invention, the NFAT is NFATc1, NFATc3 or NFATc2. In one aspect of the invention, the NFAT is NFAT2 also known as NFATc1. SEQ ID NO:646 shows nucleic acid sequence of the upstream transcriptional regulatory region for NFAT2. The promoter sequence for NFAT gene may include the nucleic acid sequence of SEQ ID NO:781-783 or SEQ ID NO:815 as examples, but it can be seen that the optimal sequence or minimal sequence for expression of the second factor may be obtained by making fragments, extensions or mutations of the promoter and testing for the strength of the promoter with respect to expression of the second factor. In one aspect of the invention, the transcriptional regulatory region for NFAT2 is engineered upstream of the gene encoding the second factor, which if for cleavage enzyme MMP9 (SEQ ID NO:647) or the catalytic sub-unit of MMP9 (SEQ ID NO:648). In one aspect of the invention, the NFAT is NFATc3 and the promoter sequence of NFATc3 includes nucleic acid sequences from SEQ ID NO:816. In one aspect of the invention, the transcriptional regulatory region for NFATc3 is engineered upstream of the gene encoding the second factor, here as an example is MMP9. In another aspect of the invention, the NFAT is NFATc2. SEQ ID NO:817-818 shows nucleic acid sequence of the upstream transcriptional regulatory region for NFATc2. In one aspect of the invention, the transcriptional regulatory region for NFATc2 is engineered upstream of the gene encoding the second factor, which may be cleavage enzyme MMP9 (SEQ ID NO:647) or the catalytic sub-unit of MMP9 (SEQ ID NO:648).

[00563] Another method for having the expression of the second factor induced when the T cell or CAR T cell is activated is to have the gene for the second factor on an inducible promoter where the NFAT protein itself binds to and induces transcription of the second factor. In this case, an NFAT response element (NFAT RE) may be positioned upstream of the gene for the second factor or fragment of the second factor. The NFAT may bind to its responsive element upstream of the second factor alone or as part of a complex. The NFAT protein may be NFATc1, NFATc2, NFATc3, NFATc4, or NFAT5. In a preferred embodiment, the NFAT protein is NFAT2 aka NFATc1, aka NFATc. The gene of the second factor or fragment thereof is cloned downstream of an NFAT-response element (SEQ ID NO:649), which may be repeats of the response element (SEQ ID NO:650) and CMV minimal promoter (mCMV) (SEQ ID NO:651) to induce expression of second factor by NFAT protein. The NFAT response element may include nucleic acid sequence of NFAT consensus sequence (SEQ ID NO:804). The NFAT response element may include the nucleic acid sequence of SEQ ID NOS:805-814 as examples, but it can be seen that the optimal sequence or minimal sequence for expression of the second factor may be obtained by making fragments, extensions or mutations of the responsive element nucleic acid and testing for the strength of the responsive element with respect to expression of the second factor. The enhancer region of Foxp3 also contains NFAT response elements within the 120-bp from 2079 to 2098 (SEQ ID NO:821). The NFAT response element may include nucleic acid NFAT consensus sequence of (5'-cattttttccat-3') (SEQ ID NO:819) or (5'-tttttcca-3') (SEQ ID NO:820), which NFATc1 specifically binds to (Xu et al., Closely related T-memory stem cells correlate with in vivo expansion of CAR. CD19-T cells and are preserved by IL-7 and IL-15, Blood 2014 123:3750-3759), or repeats thereof. The NFAT response elements may also be separated by nucleic acid spacer sequences. Other NFAT responsive elements may exist and may further be discovered, and a skilled artisan in the art when directed to determine NFAT responsive element may do so by carrying out molecular biological assays to obtain it given the guidance of at least the responsive elements as set forth as SEQ ID NOS: 804-814 albeit as only mere examples. In one aspect of the invention, the cleavage enzyme that is downstream of the NFAT-response element and CMV minimal promoter is MMP9 (SEQ ID NO:652). In another aspect of the invention, the cleavage enzyme is a catalytic sub-unit of MMP9 (SEQ ID NO:653).

[00564] Because NFATs 1-4 are regulated by the calcineurin pathway, potential toxicities that may arise in a patient can be stopped by treatment with an immunosuppressive agent such as

FK506, Cyclosporin, Cyclosporin A, or Tacrolimus that block calcineurin activity and inhibit NFAT translocation to the nucleus. The T cell transduced or transfected with a cleavage enzyme on an inducible promoter may also be transfected or transduced with a CAR that recognizes a protein or molecule on the cancer cell. In a specific example, the cleavage enzyme is one that is able to cleave MUC1 full-length and the CAR bears an antibody fragment that directs it to MUC1* on the surface of cancer cells.

[00565] To determine which cleavage enzymes cleave MUC1 on cancer cells, we tested a series of MMP and ADAM enzyme inhibitors. These experiments pointed to MMP9 as being an important cleavage enzyme in cancer cells. To confirm that MMP9 cleaves MUC1 on cancer cells, we transfected HCT-116 MUC1 negative colon cancer cells with a mimic of full-length MUC1 having 41 tandem repeat domains: HCT-MUC1-41TR. Through single cell cloning we were able to establish this cell line wherein MUC1 only minimally gets cleaved to MUC1*. **Figs. 36A-36D** show Western blots and FACS analysis showing that HCT-MUC1-41TR is 95% positive for full-length MUC1 and only 5-10% positive for the cleaved form, MUC1*. HCT-MUC1-41TR cells were incubated with MMP9 at varying concentrations and then assayed by immunofluorescence to measure binding of MNC2 monoclonal antibody to the resultant cells. As can be seen in **Figs. 37A-37C** binding of MNC2 increased as the concentration of MMP9 added to the cells increased. These experiments show that MMP9 cleaves MUC1 to a form that is recognized by MNC2. The human cancer tissue array studies we performed (Fig. 30A-30F, Fig. 31A-31F, Fig. 32A-32F, Fig. 33A-33F) show that MNC2 recognizes the form of cleaved MUC1 that is present on cancerous tissue but not on healthy cells or tissues (Fig. 34A-34I). Importantly, MNC2 does not recognize the form of cleaved MUC1 that is expressed on healthy hematopoietic stem cells of the bone marrow (Figs. 39-41).

[00566] In one aspect of the invention, an immune cell is transduced with both a CAR to target the immune cell to the tumor, and a cleavage enzyme. The CAR and the cleavage enzyme can be encoded on the same plasmid or on two different plasmids. In one aspect, the cleavage enzyme is on an inducible promoter. In another aspect, expression of the cleavage enzyme is induced by a protein that is expressed when the immune cell is activated. In one case, expression of the cleavage enzyme is induced by an NFAT protein. In another aspect, expression of the cleavage enzyme is induced by NFATc1. In another aspect, expression of the cleavage enzyme is induced when one of the NFAT proteins binds to an NFAT response element that is inserted upstream of the gene for the cleavage enzyme or a catalytically active fragment thereof. In one aspect, the cleavage enzyme is MMP9 or a fragment of MMP9 that is catalytically active.

[00567] In one aspect of the invention, the cleavage enzyme is MMP9 (SEQ ID NO:643). Some cleavage enzymes are naturally expressed as pro-enzymes that need to be activated. This can be accomplished by biochemical means, by expressing a co-enzyme that activates a cleavage enzyme or by engineering the enzyme in an activated form. The invention anticipates overcoming this problem by co-expressing the cleavage enzyme with its activator. In one aspect of the invention, the cleavage enzyme is MMP9 and the co-activator is MMP3. In another aspect of the invention, the cleavage enzyme is expressed in a form that is already active, for example by expressing a fragment of the cleavage enzyme that still has catalytic function. In one case, the cleavage enzyme is an MMP9 fragment that is catalytically active. One example of an MMP9 catalytic fragment is given as SEQ ID NO:645.

[00568] MMP9, which must be activated by MMP3, is overexpressed in a large percentage of solid tumors. Further, it is known that MNC2 anti-MUC1* monoclonal antibody recognizes MUC1 after it is cleaved by MMP9. The various breast, ovarian, pancreatic and lung cancer tissue arrays that were shown in **Figs. 30-33** were probed with MNC2-scFv, further indicating that MUC1 in these cancers is being cleaved by MMP9. To see if cleavage of tumors by MMP9 would increase T cell access to the tumor, we did a series of experiments using a cell line that expresses full-length MUC1, HCT-MUC1-41TR, a breast cancer cell line that is a high expresser of both full-length MUC1 and MUC1* and a MUC1 negative cell line that we transfect with MUC1*$_{45}$. We transfected cells with MMP9 and MMP3, which activates MMP9. We took the supernatant of those cells, which contained activated MMP9, and added it to the various cells, which were then co-cultured with T cells transduced with an anti-MUC1* CAR: huMNC2-CAR44. The result was greatly increased CAR T cell killing of the targeted MUC1/MUC1* positive cancer cells, compared to the control cells that were not incubated with a MUC1 cleavage enzyme.

[00569] APMA is a biochemical that activates MMPs. We used APMA along with the conditioned media of cells that we transfected with either MMP9 or ADAM17 to see if any of these cleavage enzymes would cleave MUC1 on the HCT-MUC1-41TR cell line that only expresses full-length MUC1. As controls, we also tested the enzymes on HCT-MUC1* cells. The MUC1 and MUC1* expressing cells were stained with a red dye, CMTMR. Human T cells that were transduced with an anti-MUC1* CARs, CAR44 or CAR50 were co-cultured with the cancer cells. Untransduced T cells were used as a control (Fig. 45A-45P). As can be seen in **Fig. 45B**, **Fig. 45C**, and **Fig. 45D**, the anti-MUC1* CAR T cells effectively recognized and clustered the HCT-MUC1* cancer cells, which is a sign of T cell activation and killing. However, no CAR T cell induced clustering is visible in the wells containing HCT-MUC1-41TR, the full-length MUC1 expressing cells (**Fig. 45F**, **Fig. 45G**, and **Fig. 45H**). However, the cells that were incubated with activated MMP9 show dramatic increase in CAR T cell induced clustering (**Fig. 45J**, **Fig. 45K**, and **Fig. 45L**), indicating that MMP9 cleaved the full-length MUC1 to a form of MUC1* that is recognized by MNC2 monoclonal antibody and more specifically by huMNC2-scFv. ADAM17 had no apparent effect. ADAM17 either did not cleave MUC1 or cleaved it at a position that is not recognized by MNC2, which is more likely (Fig. 45N-45P).

[00570] We performed the same experiment, this time using T47D breast cancer cells that were hard to kill using anti-MUC1* CAR T cells presumably because they express high levels of full-length MUC1 as well as MUC1* (Fig. 46A-46T). As can be seen in **Figs. 46B**, **46C**, and **46D**, anti-MUC1* CAR44 and CAR50 have little effect on the T47D cancer cells. Only in **Fig. 46D**, which is CAR44 at the highest level of CAR expression in the T cells, do we see a small amount of CAR T cell induced clustering. However, the presence of activated MMP2 (**Fig. 46J**, **46K**, **46L**) or activated MMP9 (**Fig. 46R**, **46S**, **46T**) shows a dramatic increase in CAR T cell recognition, clustering and killing, showing that cleavage of full-length MUC1 increases T cell access to the cancer cells. To ensure that the addition of the APMA was not inducing cleavage or anti-MUC1* CAR T recognition by some other mechanism, we made a catalytically active form of MMP9 and added it to T47D cells that were then co-cultured with MNC2-CAR44 T cells (Fig. 47A-47I). As can be seen in the figure, MNC2-CAR T cells recognize and cluster cells transfected with MUC1* (Fig. 47B-47C), poorly cluster T47D breast cancer cells that express both full-length MUC1 and MUC1* (Fig. 47E-47F), but robustly bind to and cluster the T47D cells after the addition of the catalytically active MMP9 (Fig. 47H-47I). This results supports the claim that MNC2 does not recognize full-length MUC1 but does recognize the growth factor receptor MUC1*. Note that the full-length MUC1 expressed on this cell line may sterically hinder the binding of CAR T cells near the cell membrane.

[00571] In another example, T47D MUC1 positive tumor cells were incubated with a recombinant catalytic domain of MMP9 (Enzo Life Sciences, Inc., Farmingdale, NY) at either

100ng/mL or 500ng/mL. Western blot analysis showed that the MUC1/MUC1* positive cancer cells underwent extensive cleavage of MUC1 to MUC1*. In another example, T47D breast cancer cells were pre-incubated with a human recombinant MMP9 catalytic domain protein then co-cultured with anti-MUC1* CAR44 T cells. The specific killing of the T47D cells by CAR44 T cells was monitored in real-time on an xCelligence instrument that measures impedance as a function of time. This analysis uses electrode arrays upon which cancer cells are plated. The adherent cancer cells insulate the electrode and cause an increase in impedance as they grow. Conversely, T cells are not adherent and remain in suspension so do not increase or decrease impedance. However, if the T cells or CAR T cells kill the cancer cells on the electrode plate, the cancer cells ball up and float as they die, which causes the impedance to decrease. The addition of MMP9 catalytic domain dramatically increased the killing of T47D cancer cells. **Fig. 48** shows an xCelligence graph of T47D breast cancer cells in co-culture with either untransduced T cells, as a control, or huMNC2-CAR44 T cells over a 45 hour period. After 18 hours of cancer cell growth, a catalytic sub-unit MMP9 was added to some of the cells. At 25 hours, T cells were added. As can be seen, huMNC2-CAR44 T cell killing is greatly improved when the T47D cells are pre-incubated with cleavage enzyme MMP9. In the xCelligence system, target cancer cells, which are adherent, are plated onto electrode array plates. Adherent cells insulate the electrode and increase the impedance. The number of adherent cancer cells is directly proportional to impedance. T cells are not adherent and do not contribute to impedance. Therefore, increasing impedance reflects growth of cancer cells and decreasing impedance reflects killing of cancer cells. Prostate cancer cell line DU145 expresses both MUC1 and MUC1* but at a much lower level of expression than T47D cells. DU145 cells are efficiently killed by anti-MUC1* CAR T cells in the presence or absence of a cleavage enzyme.

[00572] **Fig. 49** shows an xCelligence graph of DU145 prostate cancer cells in co-culture with either untransduced T cells, as a control, or huMNC2-CAR44 T cells over a 45 hour period. After 18 hours of cancer cell growth, a catalytic sub-unit MMP9 was added to some of the cells. At 25 hours, T cells were added. As can be seen, huMNC2-CAR44 T cell killing of low density MUC1/MUC1* positive cancer cells is not affected by pre-incubation with cleavage enzyme MMP9. DU145 cancer cells express a significantly lower amount of MUC1 which includes the full-length form as well as MUC1*. The lower density of full-length MUC1 does not sterically hinder T cell access to the membrane proximal MUC1*. DU145 cells represent an early stage cancer that expresses both full length and cleaved MUC1 but at lower levels so that T cell access is not sterically hindered. T47D cells represent mid-stage cancers that express high levels of both MUC1 and MUC1*, wherein the density of MUC1 full-length sterically hinders access of T cells to the tumor. HCT-MUC1* cells are a MUC1 negative cell line that has been stably transfected with MUC1*$_{45}$, and they represent late stage cancer cells. It is significant that MUC1 cleaved to MUC1* by MMP9 is recognized by the anti-MUC1* antibody MNC2, which is the targeting head of the CAR. Immune cell access to tumor antigens on the cancer cell surface can be sterically hindered by the presence of bulky extra cellular domain proteins or other obstructing elements also known as the tumor micro-environment. The aforementioned serve as an example that can be extended to improve the efficacy of CAR T therapies that target other tumor antigens. In one aspect of the invention, an immune cell is transfected or transduced with both a CAR comprising an antibody fragment that targets a tumor antigen and a cleavage enzyme. In another aspect of the invention, an immune cell is transfected or transduced with both a CAR comprising an antibody fragment that targets a tumor antigen and a cleavage enzyme that cleaves a tumor antigen to a form recognized by the antibody fragment of the CAR. In one aspect, an immune cell is transfected or transduced with both a CAR comprising an antibody fragment that targets a tumor antigen and a cleavage enzyme that cleaves a tumor antigen to a form recognized by the antibody fragment of the CAR, wherein the antibody fragment of the CAR recognizes MUC1* extra cellular domain and the cleavage enzyme cleaves MUC1 to MUC1*. In one aspect, an immune cell, which may be a T cell or an NK cell, is transfected or transduced with a CAR comprising an antibody fragment derived from MNC2, MNE6, MNC3 or MNC8 and a cleavage enzyme chosen from the group comprising MMP1, MMP2, MMP3, MMP7, MMP8, MMP9, MMP11, MMP12, MMP13, MMP14, MMP16, ADAM9, ADAM10, ADAM17, ADAM 19, ADAMTS16, ADAM28 or a catalytically active fragment thereof.

[00573] In one aspect of the invention, a person diagnosed with cancer or at risk of developing cancer is administered a sufficient amount of an immune cell transduced with both a CAR and a cleavage enzyme. In another aspect of the invention, a person diagnosed with cancer or at risk of developing cancer is administered a sufficient amount of an immune cell transduced with both a CAR and a cleavage enzyme, wherein the cleavage enzyme is on an inducible promoter that is activated by proteins that are expressed when the immune cell becomes activated. In another aspect of the invention, a person diagnosed with cancer or at risk of developing cancer is administered a sufficient amount of an immune cell transduced with both a CAR and a cleavage enzyme, wherein the cleavage enzyme is on an inducible promoter that is activated by one or more NFAT. In one case the NFAT is NFATc1. In another aspect, the NFAT is NFATc3. In another aspect, the NFAT is NFATc2. In any of the instances above, the extra cellular domain of the CAR comprises a fragment of an anti-MUC1* antibody. In one aspect, the anti-MUC1* antibody is MNC2scFv or a humanized form of MNC2scFv. In another aspect, the anti-MUC1* antibody is MNE6scFv or a humanized form of MNE6scFv. In any of the instances above, the immune cell can be a T cell, an NK cell, a mast cell, or a dendritic cell.

[00574] It is not intended that the present invention be limited to one or two specific methods of having expression of a cleavage enzyme induced by an activated T cell. We have demonstrated specific expression of a cleavage enzyme only upon T cell activation by constructing a plasmid with the cleavage enzyme gene downstream of an NFAT promoter sequence or downstream of one or more repeats of NFAT response elements. In another aspect of the invention, expression of the cleavage enzyme is induced by constructing a plasmid where the cleavage enzyme gene is inserted downstream of an IL-2 promoter sequence or downstream of an IL-2 response element, then inserting the plasmid into an immune cell. In another aspect of the invention, expression of the cleavage enzyme is induced by constructing a plasmid where the cleavage enzyme gene is inserted downstream of a Calcineurin promoter sequence or downstream of a Calcineurin response element, then inserting the plasmid into an immune cell and then administering to a patient for the treatment or prevention of cancers. There are also drug-inducible plasmids that can be used to induce expression of the cleavage enzyme or used to stop expression induced by an element of an activated T cell. These drug inducible systems may include tetracycline-inducible systems, Tet-on, Tet-off, tetracycline response elements, doxycycline, tamoxifen inducible systems, ecdysone inducible systems and the like.

[00575] It is not intended that the present invention be limited to one or two specific promoters used in the plasmids encoding the CARs or inducible cleavage enzymes. As is known by those skilled in the art, many promoters can be interchanged including SV40, PGK1, Ubc, CAG, TRE, UAS, Ac5, polyhedron, CaMKIIa, GAL1, GAL10, TEF1, GDS, ADH1, CaMV35S, Ubi, H1 and U6.Another solution to the problem of steric hindrance of CAR T cell access, caused by bulky cell surface proteins such as MUC1-FL, is to increase the length of the linker region of the CAR that is expressed by the T cell. In standard design CARs, the length of the extracellular linker region between the transmembrane portion and the antibody fragment is about 45-50 amino acids in length. We made long-arm CARs where the length of the extracellular linker is extended from about 50 amino acids to 217 – 290 amino acids. Co-culture assays show that CARs with longer extracellular linkers have improved access to the tumor-associated antigen on the target cancer cells.

[00576] BiTEs

[00577] Divalent (or bivalent) single-chain variable fragments (di-scFvs, bi-scFvs) can be engineered by linking two scFvs. This can be done by producing a single peptide chain with two V_H and two V_L regions, yielding tandem scFvs. Another possibility is the creation of scFvs with linker peptides that are too short for the two variable regions to fold together (about five amino acids), forcing scFvs to dimerize. This type is known as diabodies. Diabodies have been shown to have dissociation constants up to 40-fold lower than corresponding scFvs, meaning that they have a much higher affinity to their target. Consequently, diabody drugs could be dosed much lower than other therapeutic antibodies and are capable of highly specific targeting of tumors *in vivo*. Still shorter linkers (one or two amino acids) lead to the formation of trimers, so-called triabodies or tribodies. Tetrabodies have also been produced. They exhibit an even higher affinity to their targets than diabodies.

[00578] All of these formats can be composed from variable fragments with specificity for two different antigens, in which case they are types of bispecific antibodies. The furthest developed of these are bispecific tandem di-scFvs, known as bi-specific T-cell engagers (BiTE antibody constructs). BiTEs are fusion proteins consisting of two scFvs of different antibodies, on a single peptide chain of about 55 kilodaltons. One of the scFvs may bind to T cells such as via the CD3 receptor, and the other to a tumor cell via a tumor specific molecule, such aberrantly expressed MUC1*.

[00579] Another aspect of the invention is a method for treating a patient diagnosed with, suspected of having, or at risk of developing a MUC1 positive or MUC1* positive cancer, wherein the patient is administered an effective amount of a BiTE wherein one antibody variable fragment of the BiTE binds to a T cell surface antigen and the other antibody variable fragment of the BiTE binds to PSMGFR (SEQ ID NO:2), or more specifically to N-10 peptide. In one case, the antibody variable fragment of the BiTE that binds to MUC1* comprises portions of

MNC2, MNE6, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, or H11.

[00580] In another aspect of the invention, MUC1* peptides including PSMGFR (SEQ ID NO:2), or most or all of N-10 peptide are used in adoptive T cell approaches. In this case, a patient's T cells are exposed to the MUC1* peptides and through various rounds of maturation, the T cells develop MUC1* specific receptors. The adapted T cells are then expanded and administered to the donor patient who is diagnosed with, suspected of having, or is at risk of developing a MUC1* positive cancer.

[00581] A series of CARs were also made that had MNC2 and humanized MNC2 as the extra cellular, targeting head of the CAR. The constructs for these CARs were inserted into a plasmid that was then inserted into a Lenti viral vector. Human T cells were then transduced with the lenti viral vector carrying the MNC2 CARs and huMNC2 CARs. MNC2-scFv-CARs that were mouse sequence or humanized were generated. In one aspect of the invention, the CAR comprised huMNC2-scFv-short hinge region-transmembrane domain derived from CD8-short intracellular piece-4-1BB-3zeta. In another aspect, the transmembrane domain was derived from CD4 transmembrane sequence. In another aspect, the intracellular co-stimulatory domain was CD28-3zeta. In yet another aspect, the intracellular co-stimulatory domain was CD28-4-1BB-3zeta.

[00582] There are a variety of methods for assessing whether or not T cells recognize a target cell and are in the process of mounting an immune response. T cells cluster when they recognize a target or foreign cell. This can be readily seen with the naked eye or at low magnification. The appearance of CAR T cell clustering when co-cultured with target cancer cells is one measure of: a) whether or not they recognize the cells as target cells; and b) whether or not they are getting activated to attack the targeted cells, which in this case are cancer cells. Figures 45-47 show photographs of MUC1* positive T47D breast cancer cells that were either stably transfected with mCherry or dyed with CMTMR, so are red, which were co-cultured with either human T cells without a CAR or human T cells transduced with huMNC2-scFv-CAR44, or with huMNC2-scFv-CAR50. The CAR T cells are clear. As can be seen, there is no T cell induced clustering of the cancer cells when the T cell does not carry a CAR. However, when T cells carrying a MUC1* targeting CAR, there is dramatic clustering of the MUC1* positive cancer cells.

[00583] After T cells recognize and cluster target cells, they overexpress perforin and granzyme B. Together these two molecules activate a cell death pathway in the targeted cell. It is thought that the perforin makes a hole in the target cell into which the T cell injects granzyme B which then activates apoptotic proteases, causing the target cell to lyse. **Figs. 55 and Fig. 56** show huMNC2-scFV-CAR44 T cells binding to target MUC1* positive prostate cancer and pancreatic cancer cells and injecting granzyme B.

[00584] Another measure of whether or not a T cell has recognized a target cell and is activated to kill that cell, is the upregulation and secretion of cytokines, interferon gamma (IFN-g) and interleukin-2 (IL-2), by the T cell. Activation of CAR T cells, as evidenced by IFN-g and IL-2 secretion, can be readily measured *in vitro*. CAR T cells are co-cultured with target cells and after an incubation period, the conditioned media is assayed by ELISA to detect secreted IFN-g and IL-2. In order to determine the cancer-specificity of CAR T cells wherein the targeting head of the CAR was either huMNC2 or huMNE6, these experiments were performed with huMNC2-CAR44 T cells and huMNE6-CAR44 T cells in co-culture with MUC1* positive cancer cells and normal cells. Table 1 details the MUC1 positive normal or primary cells that were tested.

[00585] **Table 1: Normal Cell Lines and Primary Cells**

[00586]

Cell Line	ATCC Designation	Tissue	Origin
Hep.G2		Liver	
THLE-3	CRL-11233	Liver	The THLE-2 (ATCC CRL-10149 and the THLE-3 (ATCC CRL-11233) cell lines were derived from primary normal liver cells by infection with SV40 large T antigen. THLE-2 and THLE-3 cells express phenotypic characteristics of normal adult liver epithelial cells. They are nontumorigenic when injected into athymic nude mice, have near-diploid karyotypes, and do not express alpha-fetoprotein.

Cell Line	**ATCC Designation**	**Tissue**	**Origin**
Lonza Primary Hepatocytes	HUM181141	Liver	Male, Caucasian 2.0 months old Induction Fold CYP1A2 (a) 14.0 Induction Fold CYP2B6 (b) 13.0 Induction Fold CYP3A4 (c) 44.0 Basal Activity CYP1A2 2.6 Basal Activity CYP2B6 0.7 Basal Activity CYP3A4 14.0 Additional Information: Inducer / Marker Metabolite (a) 0.05 mM Omeprazole / Acetaminophen (b) 1 mM Phenobarbital / Hydroxybupropion (c) 0.01 mM Rifampicin / 6-Beta-Hydroxytestosterone Basal activity is expressed as: pmol/million cells/minute
T/G HA-VSMC	CRL-1999	Aortic Smooth Muscle	11 months Female, Caucasian
CCD-18Lu	CCL-205	Lung	This fibroblast-like cell line was derived from the lung tissue of a **2 month, 17-day-old Black female.** The donor had cerebral anoxia, cardiac anomaly, sepsis, endocardial cushion defect and fetal alcoholic syndrome. Female, Black 2.5 months
HBEC-5i	CRL-3245	Brain endothelium	Derived from small fragments of human cerebral cortex obtained from patients who had died of various causes.
Hs 738.St/Int	CRL-7869	Stomach/Intestine	**18 weeks gestation fetus** Male, Caucasian Part of the NBL Cell Line Collection. This cell line is neither produced nor fully characterized by ATCC. We do not guarantee that it will maintain a specific morphology, purity, or any other property upon passage.
MCF-12A	CRL-10782	Breast	The MCF-12A cell line is a non-tumorigenic epithelial cell line established from tissue taken at reduction mammoplasty from a nulliparous patient with fibrocystic breast disease that contained focal areas of intraductal hyperplasia. The line was produced by long term culture in serum free medium with low Ca++ concentration. MCF-12A was

Cell Line	ATCC Designation	Tissue	Origin
			derived from adherent cells in the population.
Hs 1.Tes	CRL-7002	Testis	Male, Caucasian **second trimester** Part of the NBL Cell Line Collection. This cell line is neither produced nor fully characterized by ATCC. We do not guarantee that it will maintain a specific morphology, purity, or any other property upon passage.
HRCE	Lonza: catalogue # CC-2554 Lot # 0000542104	Kidney	Human Renal Cortical Cells (HRCE) are from proximal and distal tubules. Donor info: 49 year old female, passage 2, 95% viability, doubling time (hours) 24 hrs

[00587]

[00588] Figure 50 is a graph of PCR measurement of the various cell lines tested, wherein mRNA levels of MUC1 are measured. The cancer cell lines that were tested in these assays were HCT-MUC1* and T47D breast cancer cells. These cells were co-cultured with huMNC2-CAR44 human T cells. Co-culture of huMNC2-CAR44 T cells with the cancer cells induced the CAR T cells to secrete large amounts of IFN-g and IL-2 into the surrounding media, yet co-culture with the MUC1 positive normal cells induced no secretion of the cytokines (Fig. 51 and Fig. 52). In addition to testing for IFN-g and IL-2 secretion by the CAR T cells, the normal cells were assayed for signs of cell death, which could have been induced by the CAR T cells if the antibody targeting head were not extremely cancer-specific. After co-culture with huMNC2-CAR44 T cells, the cells were incubated with a cell death marker, then assayed by FACS. huMNC2-CAR44 T cells induced no cell death in the normal cells (Fig. 53A-53J).

[00589] In addition to FACS analysis, many researchers now use an xCELLigence instrument to measure CAR T killing of cancer cells. FACS is not the best method for tracking T cell induced cell killing because the T cells lyse the target cell. By FACS it is difficult to measure dead cells because they are excluded as cell debris, so one must infer an amount of cell killing and by various methods determine if the missing cells are T cells or cancer cells.

[00590] The xCELLigence instrument uses electrode arrays upon which cancer cells are plated. The adherent cancer cells insulate the electrode and so cause an increase in impedance as they grow. Conversely, T cells are not adherent and remain in suspension so do not contribute to insulation of the electrode which would increase impedance. However, if the T cells or CAR T cells kill the cancer cells on the electrode plate, the cancer cells ball up and float off as they die, which causes the impedance to decrease. The xCELLigence instrument measures impedance as a function of time, which is correlated to cancer cell killing. In addition, the electrode plates also have a viewing window. When CAR T cells effectively kill the adsorbed target cancer cells, there is a decrease in impedance but also one can see that there are no cancer cells left on the plate surface.

[00591] **Figs. 55A-55H** show the cytotoxic effect of huMNC2-CAR44 T cells on MUC1* positive DU145 prostate cancer cells as measured by a variety of assays. **Fig. 55A** is a fluorescent photograph of untransduced T cells co-cultured with the prostate cancer cells, wherein granzyme B is stained with a red fluorophore. **Fig. 55C** is a fluorescent photograph of huMNC2-CAR44 T cells co-cultured with the prostate cancer cells, wherein granzyme B is stained with a red fluorophore. **Fig. 55D** is the DAPI and granzyme B merge. **Fig. 55E** is a FACS scan for fluorescently labeled granzyme B for untransduced T cells incubated with the cancer cells. **Fig. 55F** is a FACS scan showing a positive increase in fluorescently labeled granzyme B for huMNC2-CAR44 T cells incubated with the cancer cells. **Fig. 55G** is a graph of the mean fluorescent intensity. **Fig. 55H** is an xCELLigence scan tracking the real-time killing of DU145 cancer cells by huMNC2-CAR44 T cells (blue trace) but not by untransduced T cells (green). **Figs. 56A-56H** show the cytotoxic effect of huMNC2-CAR44 T cells on MUC1* positive CAPAN-2 pancreatic cancer cells as measured by a variety of assays. **Fig. 56A** is a fluorescent photograph of untransduced T cells co-cultured with the pancreatic cancer cells, wherein granzyme B is stained with a red fluorophore. **Fig. 56B** is the DAPI and granzyme B merge. **Fig. 56C** is a fluorescent photograph of huMNC2-CAR44 T cells co-cultured with the pancreatic cancer cells, wherein granzyme B is stained with a red fluorophore. **Fig. 56D** is the DAPI and granzyme B merge. **Fig. 56E** is a FACS scan for fluorescently labeled granzyme B for untransduced T cells incubated with the cancer cells. **Fig. 56F** is a FACS scan showing a positive increase in fluorescently labeled granzyme B for huMNC2-CAR44 T cells incubated with the cancer cells. **Fig. 56G** is a graph of the mean fluorescent intensity. **Fig. 56H** is an xCELLigence scan tracking the real-time killing of CAPAN-2 cancer cells by huMNC2-CAR44 T cells (blue trace) but not by untransduced T cells (green). **Figs. 57A-57C** show xCELLigence scans tracking the real-time killing of MUC1* positive cancer cells, but not MUC1* negative cells, by huMNC2-CAR44 T cells. **Fig. 57A** shows that huMNC2-CAR44 T cells effectively kill HCT colon cancer cells that have been stably transfected with MUC1*. **Fig. 57B** shows that huMNC2-CAR44 T cells have almost no effect on HCT-MUC1-41TR, which is a MUC1 negative cancer cell that has been stably transfected with a MUC1 full-length. In this cell line only about 10% of the cell have MUC1 cleaved to MUC1*. **Fig. 57C** shows that huMNC2-CAR44 T cells have no effect on HCT-116 cells, which is a MUC1 negative colon cancer cell line.

[00592] These data demonstrate that T cells transduced with a CAR wherein the antibody fragment targeting head is MNC2, effectively kill MUC1* positive cancer cells. These data specifically show that huMNC2-scFV-CAR44 transduced into human T cells effectively kill MUC1* positive cancer cells. Because we and others have now demonstrated that the most important aspect of CAR T function is the targeting antibody fragment, it follows that an immune cell or a T cell transduced with any CAR having the antibody fragment MNC2-scFV or huMNC2-scFV would have similar efficacy against MUC1 or MUC1* positive tumors. For example, the hinge region that connects the scFv to the transmembrane portion could be any flexible linker. The intracellular co-stimulatory domains could be CD28-3zeta, CD28-4-1BB-3zeta or any combination of immune cell co-stimulatory domains.

[00593] Figure 61 shows an experiment in which huMNC2-scFv-CAR44 transduced human T cell that were bead stimulated (Protocol 1) or cancer cell stimulated (Protocol 2) were tested for their ability to inhibit tumor growth in animals. Human cancer cells that had been stably transfected with Luciferase were injected into female NOD/SCID/GAMMA (NSG) mice between 11 and 15 weeks of age. 500,000 BT-20 breast cancer cells were injected sub-cutaneously into a rear flank. Tumor engraftment was verified by injecting the animals with Luciferin and then imaging the fluorescent cancer cells using an IVIS instrument. IVIS images taken Day 5 post implantation showed the presence of tumor cells. On Day 6 after IVIS measurement, animals were given a one-time injection of 10 million of either human T cells transduced with huMNC2-scFv-CAR44 or untransduced T cells. 5 million T cells were injected intra-tumor and 5 million were injected into the tail vein. 10 minutes prior to IVIS photographs, mice were IP injected with Luciferin, which fluoresces after cleavage by Luciferase, thus making tumor cells fluoresce. Figs. 61A, 61D, 61G show photographs of mice that were treated with huMNC2-scFv-CAR44 T cells that had been pre-stimulated by co-culturing for 24 hours with 4μm beads to which was attached a synthetic MUC1*, PSMGFR peptide 24 hours prior to administration, "Protocol 1". Figs. 61B, 61E, 61H show photographs of mice that were treated with huMNC2-scFv-CAR44 T cells that had been pre-stimulated by twice co-culturing for 24 hours with MUC1* positive cancer cells 24 hours prior to administration, "Protocol 2". As can be seen in **Figure 61,** huMNC2-CAR44 T cells that were peptide-bead stimulated inhibited tumor growth better than cells pre-stimulated by incubation with live cancer cells, which likely contaminated the target cells and increased the tumor volume.

[00594] huMNC2-scFv-CAR44 transduced human T cell that were bead stimulated (Protocol 1) or cancer cell stimulated (Protocol 2) were also tested for their ability to inhibit tumor growth in animals. Human cancer cells that had been stably transfected with Luciferase were injected into female NOD/SCID/GAMMA (NSG) mice between 11 and 15 weeks of age. In another experiment, 500,000 BT-20 MUC1* positive triple negative breast cancer cells were injected sub-cutaneously into a rear flank. Tumor engraftment was verified by injecting the animals with Luciferin and then imaging the fluorescent cancer cells using an IVIS instrument. IVIS images taken Day 6 post implantation showed the presence of tumor cells. On Day 6, after IVIS imaging, 10M huMNC2-scFv-CAR44 T cells were administered to the animals. 5M of the CAR T cells were administered by intratumor injection and the other 5M were administered by tail vein injection. Control group was injected by same administration routes with the same number of untransduced T cells. IVIS measurements of tumor burden were taken on Days 6, 8, and 12. As can be seen in **Figs. 61A-61J**, both groups of mice treated with huMNC2-CAR44 T cells showed a decrease in tumor burden compared to the control group.

[00595] huMNC2-scFv-CAR44 transduced human T cell that were bead stimulated (Protocol 1) were also tested for their ability to inhibit ovarian cancer growth in animals. Human SKOV-3 MUC1* positive ovarian cancer cells that had been stably transfected with Luciferase were injected into female NOD/SCID/GAMMA (NSG) mice between 11 and 15 weeks of age. In one experiment, 500,000 SKOV-3 cancer cells were injected into the intraperitoneal cavity to mimic metastatic ovarian cancer in humans. Tumor engraftment was verified by injecting the animals with Luciferin and then imaging the fluorescent cancer cells using an IVIS instrument. IVIS images taken Day 3 post implantation showed the presence of tumor cells. On Day 4 and Day 11, post tumor implantation, 10M huMNC2-scFv-CAR44 T cells were IP administered to the animals. On Day 4, CAR T cells were IP injected. On Day 11 half the CAR T cells were injected into the intraperitoneal space and the other half was injected into the tail vein. Control groups were injected by same administration routes with either the same number of untransduced T cells or same volume of PBS. Subsequent IVIS measurements of tumor burden were taken on Day 7, Day 10 and Day 15. As can be seen in **Figs. 62A-62L**, control mice have tumors that are growing at a much faster rate than the huMNC2-CAR44 T cell treated mice. **Fig. 62M** shows the IVIS color bar correlating photons/second to color.

[00596] One aspect of the invention is a method for treating a patient diagnosed with, suspected of having, or at risk of developing a MUC1 positive or MUC1* positive cancer, wherein the patient is administered an effective amount of immune cells that have been transduced with a MUC1* targeting CAR, wherein the CAR is chosen from among the group consisting of MN-E6-CD8-CD28-3z (SEQ ID NOS:297-298); MN-E6-CD4-CD28-3z (SEQ ID NOS:748-749); MN-E6-CD8-41BB-3z (SEQ ID NOS:300-301); MN-E6-CD4-41BB-3z (SEQ ID NOS:750-751); MN-E6-CD8-CD28-41BB-3z (SEQ ID NOS:303-304); MN-E6-CD4-CD28-41BB-3z (SEQ ID NOS:754-755); MN-E6scFv-Fc-8-41BB-CD3z (SEQ ID NOS:310-311); MN-E6scFv-IgD-Fc-8-41BB-CD3z (SEQ ID NOS:770-771); MN-E6scFv-FcH-8-41BB-CD3z (SEQ ID NOS:315-316); MN-E6scFv-IgD-FcH-8-41BB-CD3z (SEQ ID NOS:772-773); MN-E6scFv-Fc-4-41BB-CD3z (SEQ ID NOS:318-319); MN-E6scFv-FcH-4-41BB-CD3z (SEQ ID NOS:321-322); MN-E6scFv-IgD-8-41BB-CD3z (SEQ ID NOS:323-324); MN-E6scFv-IgD-4-41BB-CD3z (SEQ ID NOS:327-328); MN-E6scFv-X4-8-41BB-CD3z (SEQ ID NOS:330-331); MN-E6scFv-X4-4-41BB-CD3z (SEQ ID NOS:333-334); MN-E6scFv-8-4-41BB-CD3z (SEQ ID NOS:336-337), or any of the aforementioned CARs wherein the MN-E6 is replaced by fragment derived from MNC2, MNE6, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, or H11. Another aspect of the invention is a method for treating a patient diagnosed with, suspected of having, or at risk of developing a cancer, wherein the patient is administered an effective amount of immune cells that have been transduced with one of the aforementioned CARs wherein the MN-E6 is replaced by a peptide comprising antibody variable domain fragments that are specific for a cancer antigen. In any of the above methods, the immune cell may be a T cell and may further be isolated from the patient to be treated.

[00597] Other MUC1 cleavage sites

[00598] It is known that MUC1 is cleaved to the growth factor receptor form, MUC1*, on some healthy cells in addition to cancer cells. For example, MUC1 is cleaved to MUC1* on healthy stem and progenitor cells. A large percentage of bone marrow cells are MUC1* positive. Portions of the intestine are MUC1* positive.

[00599] The inventors have discovered that MUC1 can be cleaved at different positions that are relatively close to each other but the location of cleavage changes the fold of the remaining portion of the extracellular domain. As a result, monoclonal antibodies can be identified that bind to MUC1* cleaved at a first position but do not bind to MUC1* that has been cleaved at a second position. This discovery is disclosed in WO2014/028668, filed August 14, 2013, the contents of which are incorporated by reference herein its entirety. We identified a set of anti-MUC1* monoclonal antibodies that bind to MUC1* as it appears on cancer cells but do not bind to MUC1* as it appears on stem and progenitor cells. Conversely, we identified a second set of monoclonal antibodies that bind to stem and progenitor cells but do not bind to cancer cells. One method used to identify stem specific antibodies is as follows: supernatants from monoclonal hybridomas were separately adsorbed onto 2 multi-well plates. Stem cells, which are non-adherent cells, were put into one plate and cancer cells which are adherent were put into an identical plate. After an incubation period, the plates were rinsed and inverted. If the non-adherent stem cells stuck to the plate, then the monoclonal antibody in that particular well recognizes stem cells and will not recognize cancer cells. Antibodies that did not capture stem cells or antibodies that captured cancer cells were identified as cancer specific antibodies. FACS analysis has confirmed this method works.

[00600] Antibodies MN-E6 and MN-C2 are examples of cancer-specific antibodies. Antibodies MN-C3 and MN-C8 are examples of stem-specific antibodies. Although both sets of antibodies are able to bind to a peptide having the PSMGFR sequence, FACS analysis shows that the anti-MUC1* polyclonal antibody and MN-C3 bind to MUC1* positive bone marrow cells but MN-E6 does not. The MUC1* polyclonal antibody was generated by immunizing a rabbit with the PSMGFR peptide. Similarly, MN-C3 binds to stem cells of the intestinal crypts but MN-E6 does not. Conversely, MN-E6 antibody binds to cancerous tissue while the stem-specific MN-C3 does not. Competition ELISA experiments indicate that the C-terminal 10 amino acids of the PSMGFR peptide are required for MN-E6 and MN-C2 binding, but not for MN-C3 and MN-C8. Therefore, another method for identifying antibodies that are cancer specific is to immunize with a peptide having the sequence of the PSMGFR peptide minus the 10 N-terminal amino acids or use that peptide to screen for antibodies or antibody fragments that will be cancer specific. Antibodies that bind to a peptide with a sequence of PSMGFR peptide minus the N-terminal 10 amino acids, referred to herein as N-10 peptide, but do not bind to a peptide with a sequence of PSMGFR peptide minus the C-terminal 10 amino acids, C-10 peptide, are cancer specific antibodies for use in the treatment or prevention of cancers.

[00601] The extracellular domain of MUC1 is also cleaved on stem cells and some progenitor cells, where activation of cleaved MUC1 by ligands NME1 in dimer form or NME7 promotes growth and pluripotency and inhibits differentiation. The transmembrane portion of MUC1 that remains after cleavage is called MUC1* and the extracellular domain is comprised essentially of the Primary Sequence of MUC1 Growth Factor Receptor (PSMGFR) sequence. However, the exact site of cleavage can vary depending on cell type, tissue type, or which cleavage enzyme a particular person expresses or overexpresses. In addition to the cleavage site that we previously identified which leaves the transmembrane portion of MUC1* comprising most or all of the PSMGFR (SEQ ID NO:2), other cleavage sites could possibly result in an extended MUC1* comprised of most or all of SNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTEAASRY (SEQ ID NO:620); or

[00602] SVVVQLTLAFREGTINVHDVETQFNQYKTEAASRY (SEQ ID NO:621).

[00603] To test this hypothesis, and to determine if antibodies to an N-terminally extended PSMGFR, would generated more cancer-specific antibodies than antibodies that bind to the PSMGFR, we generated monoclonal antibodies by immunization with peptides:

[00604] (PSMGFR) GTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA (SEQ ID NO:2),

[00605] (N+20/C-27) SNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTE (SEQ ID NO:822), or

[00606] (N+9/C-9) VQLTLAFREGTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVP (SEQ ID NO:824)

[00607] Monoclonal antibodies generated from immunization with the same peptide can also show differences in reactivity to the same cancerous tissue specimen. These results indicate that the monoclonal antibodies recognize different conformations of the truncated MUC1 extra cellular domain produced by immunizing with different length peptides, mimicking different cleavage sites, or from cleavage at different sites in the host animal. Antibodies that recognize different cleavage site conformations may be cancer sub-type specific or patient specific, depending on which cleavage enzyme their tumor expresses. In one aspect of the invention, a patient diagnosed with a certain type of cancer is treated with an antibody of the invention that recognizes a cleaved MUC1 wherein the antibody is specific for cleavage by a specific enzyme that is known to be typically expressed by that sub-type of cancer. In another aspect, a patient tumor is analyzed to determine which enzyme his or her tumor expresses and an antibody that recognizes a MUC1 cleaved by that enzyme is then administered to the patient for the treatment of their cancer. The antibody may be in the form of a CAR, a BiTE, an ADC, or a bispecific antibody.

[00608] We previously reported that it is the MUC1 transmembrane cleavage product, called MUC1* (muk1 star), that mediates tumor growth and not full-length MUC1 (Mahanta et al 2008). MUC1* is a growth factor receptor that is activated by ligand induced dimerization of its short extra cellular domain (Fig. 1A). Dimerization of the MUC1* extra cellular domain activates the MAP kinase signaling cascade and stimulates growth and survival of cancer cells (Fessler et al 2009). Bivalent antibodies that dimerize the MUC1* extra cellular domain stimulate cancer cell growth while the monovalent Fab of the same antibody, which cannot dimerize, inhibits cancer cell growth. We demonstrated this in vitro (Fig. 1B) and in vivo (Fig. 7A-7B).

[00609] We then identified the natural ligands that dimerize and activate MUC1* growth factor receptor function. Dimers of NME1 bind to and dimerize the MUC1* extra cellular domain and stimulate growth (Fig. 1C and Smagghe et al 2013). NME1 can turn its growth factor properties off. NME1 is secreted by MUC1* positive cells. Dimeric NME1 binds to MUC1* to stimulate growth. However, as the cell population grows, more and more NME1 is secreted from the cells. At high concentrations, the NME1 dimers multimerize and form hexamers, which do not bind to MUC1*, but likely bind to some unknown receptor, as the addition of NME1 hexamers turns off growth. NME1 is an adult form. The embryonic form is

$NME7_{AB}$ (Carter et al 2016). Each $NME7_{AB}$ monomer has two binding sites for MUC1* so as a monomer it dimerizes MUC1* (Fig. 1D), stimulates growth and cannot turn itself off. In the developing embryo, BRD4 turns off NME7 and its co-factor JMJD6 turns on the self-regulating form, NME1. However, in cancers, NME7, which should be silenced in adult life, is aberrantly expressed again, where is renders the MUC1* growth factor receptor constitutively active.

[00610] *In vitro*, NME1 (SEQ ID NO:4) and $NME7_{AB}$ (SEQ ID NO:827) bind to the PSMGFR portion of the MUC1* extra cellular domain. Both growth factors can bind to the PSMGFR peptide (SEQ ID NO:2) even if the 10 N-terminal amino acids are deleted, referred to herein as N-10 (SEQ ID NO:3). However, neither NME1 nor $NME7_{AB}$ can bind to the PSMGFR peptide if the 10 membrane proximal amino acids are deleted (Fig. 2A-2D), referred to herein as C-10 (SEQ ID NO:825). In summary, the epitope to which NME1 and $NME7_{AB}$ bind includes all or part of the 10 membrane proximal amino acids: PFPFSAQSGA (SEQ ID NO:1743). We tested various antibodies that were generated in animals by immunizing with the PSMGFR peptide for their ability to recognize cancer cells but not healthy cells. Among the most cancer selective were the MNC2 and MNE6 monoclonal anti-MUC1* antibodies. Two other monoclonal antibodies that were generated from immunizing animals with the PSMGFR peptide are MNC3 and MNC8. Although MNC2, MNE6, MNC3 and MNC8 all bind to the PSMGFR peptide, like NME1 and $NME7_{AB}$, MNC2 and MNE6 bind strongly to the N-10 peptide but not to the C-10 peptide (Fig. 2B-2C). In fact, MNC2 and MNE6 competitively inhibit the binding of NME1 and $NME7_{AB}$ to PSMGFR (Fig. 3A-3C). Conversely, MNC3 and MNC8 bind to the C-10 peptide, bind less well to the N-10 peptide and do not compete with NME1 nor $NME7_{AB}$ for binding to MUC1* peptides, including PSMGFR (Fig. 2E-2F). MNC3 and MNC8 are far less cancer specific than MNC2 and MNE6. MNC3 and MNC8 recognize stem and progenitor cells, such as hematopoietic stem cells, whereas MNC2 and MNE6 do not (Fig. 39-41). Because hematopoietic stem cells are the progenitor cells for the blood cells, it would be problematic to have a cancer therapeutic that would also target such an important normal cell type.

[00611] Because MUC1* is generated by enzymatic cleavage of MUC1, we researched which cleavage enzymes cleave MUC1 to a MUC1* and whether or not we could identify antibodies that would recognize a MUC1* generated by a first cleavage enzyme but not MUC1* generated by a second cleavage enzyme. We found that MNC2 and MNE6 recognized a MUC1* generated by cleavage of MUC1 by MMP9 but not by cleavage by other enzymes such as MMP2 (Fig. 37

and Fig. 75). We note that MMP9 is overexpressed in cancers and is a predictor of poor prognosis (vant Veer et al 2002; Dufour et al 2011) and has been implicated in metastasis (Owyong et al, 2019), whereas MMP2 is expressed in bone marrow. One antibody binding to a MUC1* generated by cleavage by a first enzyme but not by cleavage by a second enzyme implies that the antibody recognizes a conformational epitope rather than a linear epitope.

[00612] We reasoned that the most cancer specific antibodies would be those antibodies that are characterized by some combination of most or all of the following:

[00613] Antibody binds to PSMGFR peptide;

[00614] Antibody does not bind to full-length MUC1;

[00615] Antibody binds to N-10;

[00616] Antibody does not bind to C-10;

[00617] Antibody competitively inhibits binding of NME1 or $NME7_{AB}$ to MUC1* extra cellular domain or a PSMGFR peptide;

[00618] Antibody recognizes a MUC1* generated by cleavage by MMP9;

[00619] Antibody recognizes a conformational epitope not a linear epitope.

[00620] **MNC2 and MNE6 are cancer specific.**

[00621] Our experiments show that both MNC2 and MNE6: a) Bind to tumor cells; b) monovalent forms block tumor growth in vitro and in vivo; c) have minimal to no binding of normal tissue while having robust binding to a wide panel of tumor tissues; d) when incorporated into CAR T cells, MNC2 and MNE6 directed CAR T cells do not recognize full-length MUC1 and do not kill cells that only express full-length MUC1; e) MNC2 and MNE6 directed CAR T cells cluster then kill tumor cells expressing MUC1*; and f) MNC2 and MNE6 recognize a MUC1 cleavage product when it is cleaved by MMP9.

[00622] MNC2 directed CAR T cells do not recognize normal, healthy cells that are MUC1* positive. A panel of normal cell lines, as well as primary cells, were co-cultured with huMNC2-CAR44 T cells. The normal cell populations were analyzed to determine whether or not the MNC2 directed CAR T cells killed them. The CAR T cells were analyzed to see if co-culture with the MUC1 positive normal cells activated the killing function of the CAR T cells, as measured by secretion of IL-2 or interferon gamma. As **Figures 50-52** show, the MNC2 directed CAR T cells did not kill the normal cells, nor was there cytokine secretion, indicative of T cell activation. In addition, over 2,000 human tissue specimens were analyzed. The results showed that neither MNC2 nor MNE6 showed any significant binding to normal tissues but showed robust staining of a wide panel of cancerous tissues. For example, MNC2 stained 93% breast cancer specimens, 83% ovarian, 78% pancreatic and 71% lung cancer specimens. In addition, patient-matched primary tumors (Fig. 54) and subsequent metastases showed that the amount of MNC2-reactive MUC1* increased with tumor progression and metastases. In summary, MNC2 is a highly cancer specific antibody.

[00623] Characterization of MNC2 and MNE6

[00624] Our gold standard, cancer-specific antibodies MNC2 and MNE6: 1) bind to N-10 peptide but not to the C-10 peptide; 2) compete with $NME7_{AB}$ and dimeric NME1 for the same binding site near the C-terminus of the PSMGFR peptide, which is the membrane proximal portion of MUC1* on cells; 3) do not work in a Western blot assay indicating that they recognize a conformational rather than linear epitope; 4) recognize a MUC1* generated when MUC1 is cleaved by MMP9; 5) do not bind to full-length MUC1 but only to the cleaved form, MUC1*, in model cell lines as well as cancer cell lines; 6) show little to no binding to normal tissues but robustly stain a wide variety of tumor tissues; and 7) share some consensus sequences in their Complementarity Determining Regions, CDRs.

[00625] In an effort to identify other antibodies that are highly cancer-specific, like MNC2 and MNE6, we subjected new antibodies to a set of seven (7) characterization experiments: 1) epitope binding assays; 2) functional assays such as the ability to displace activating growth factor $NME7_{AB}$ or dimeric NME1 from binding to MUC1* peptides PSMGFR or N-10; 3) Western blots to determine whether or not the antibodies recognized a linear epitope versus a conformational epitope, in which case the antibodies would not work in a Western; 4) binding assays to see if the antibodies recognized a cleaved MUC1 that was dependent on cleavage by MMP9; 5) FACS analysis to measure the ability of the antibodies to recognize MUC1* positive cells but not full-length MUC1; and FACS analysis to measure the ability of the antibodies to recognize MUC1/MUC1* positive cancer cells; 6) immunohistochemistry, IHC, assays of normal tissues versus cancerous tissues to determine true cancer specificity; and 7) aligning antibody sequences to determine if subsets of antibodies shared consensus sequences that could predict their cancer specificity or lack thereof.

[00626] Monoclonal antibodies were produced by immunizing animals with peptides derived from a MUC1 that is devoid of tandem repeats. These antibodies included PSMGFR and peptides that were extended at the N-terminus of PSMGFR. Immunizing peptides were:

[00627] PSMGFR (SEQ ID NO:2))

[00628] N+9/C-9 (9 amino acids added onto the N-terminus and 9 amino acids deleted from the C-terminus) (SEQ ID NO:824)

[00629] N+20/C-27 (20 amino acids added onto the N-terminus and 27 amino acids deleted from the C-terminus) (SEQ ID NO:823)

[00630] These monoclonal antibodies were then tested to determine which satisfied the seven (7) characterization criteria cited above, which we reasoned would identify the most cancer specific antibodies.

[00631] Epitope binding assays

[00632] ELISA assays were performed to determine if, in addition to recognizing their immunizing peptide, they recognized PSMGFR, N-10 or C-10. In addition, they were tested for their ability to bind to N+20/C-27, N+9/C-9. We first did the ELISA assay on our set of reference antibodies, MNC2, MNE6, which we know are cancer-specific plus MNC3, which we know recognizes stem cells and progenitor cells (Fig. 63A-63B). None of the reference antibodies bound to the N+20/C-27 peptide. MNC2 and MNE6 cannot bind to PSMGFR peptides with 27, 10 or 9 C-terminal deletions, however, MNC3 binds to C-10 and to N+9/C-9 peptides.

[00633] This same ELISA assay was performed on the antibodies of the invention (Fig. 64-66 and Fig. 201). The binding patterns of the antibodies that were generated by immunizing with the PSMGFR peptide are shown in Fig. 64A-64B. Note that only 20A10 exactly matches the binding profile of MNC2 and MNE6. 25E6, 28F9 and 18G12 are all able to bind to the N-10 peptide. 18B4 is the only antibody raised against the PSMGFR peptide that requires the 10 most N-terminal amino acids of the peptide. The color of the bars for each antibody in the ELISA graph are color coded to match the deductive cognate sequence, or a portion thereof, of that antibody. In addition, another set of antibodies was assayed by ELISA (Fig. 201). Of this set, B12, B2, B7, B9, 8C7F3, and H11 bound to the PSMGFR peptide, bound to the N-10 peptide, but not to the C-10 peptide (Fig. 201). The binding patterns of the antibodies that were generated by immunizing with the N+20/C-27 peptide are shown in **Fig. 65A-65B**. Although these antibodies were raised against the N+20/C-27 peptide, all but one, 45C11, still bind to the PSMGFR peptide, albeit at the N-terminal portion of PSMGFR. The binding of 45C11 is weak but deductive reasoning shows that all or some of the cognate epitope must lie within SNIKFRPGSVV (SEQ ID NO:1744).

[00634] Of the antibodies generated by immunizing with the N+9/C-9 peptide, 8A9 and 17H6 do not bind to the PSMGFR peptide, so must bind to the 9 additional N-terminal amino acids. Antibodies 3C5 and 39H5 appear to bind to the 10 most N-terminal amino acids of the PSMGFR peptide.

[00635] In order to further refine the epitopes to which each antibody binds, a series of smaller peptides derived from the PSMGFR sequence were synthesized: N-30 (SEQ ID NO:7), N-26 (SEQ ID NO:6), N-19 (SEQ ID NO:4), N-10/C-5 (SEQ ID NO:8), N-19/C-5 (SEQ ID NO:9). Each of the antibodies was tested in an ELISA assay for their ability to bind to this refined set of peptides, plus PSMGFR, N-10 and C-10 peptides (Fig. 67-69).

[00636] In **Fig. 67A-67D**, antibodies generated by immunization with the PSMGFR peptide were assayed. As can be seen in the figure, amino acids ASRYNLT (SEQ ID NO:1745), which are essentially in the middle of the PSMGFR peptide, are important or essential for the binding of 28F9, 18G12, 25E6, and MNC3 antibodies. Amino acids GTINVHDVET (SEQ ID NO:1746), which comprise the most N-terminal part of the PSMGFR peptide are important or essential for the binding of the 18B4 antibody. Amino acids FPFS (SEQ ID NO:1747) are important or essential for the binding of 20A10, MNC2 and MNE6. We note that these three antibodies recognize a conformational epitope, not a linear epitope. Because the proline in the FPFS sequence significantly alters the conformation of nearby portions of the PSMGFR peptide, it is also possible that the antibodies do not bind directly to these four amino acids, but that the absence of the proline alters the fold of the remaining peptide such that the conformation to which20A10, MNC2 and MNE6 bind, is no longer present.

[00637] In **Fig. 68A-68D**, antibodies generated by immunization with the N+20/C-27 peptide were assayed. As can be seen in the figure, amino acids GTINVHDVET, which comprise the most N-terminal part of the PSMGFR peptide are important or essential for the binding of the 29H1, 32C1, and 31A1 antibodies. Amino acids SNIKFRPGSVVVQLTLAFRE (SEQ ID NO:1748), which is 20 additional amino acids N-terminal to the PSMGFR peptide and outside of the PSMGFR peptide, are important or essential for the binding of antibody 45C11. However, referring back to **Fig. 65**, antibody 45C11 was not able to bind to the N+9/C-9 peptide, therefore we conclude that amino acids within the SNIKFRPGSVV sequence are essential for the binding of 45C11. Amino acids QFNQYKTEA (SEQ ID NO:1749), which are still within the sequence of PSMGFR, are important or essential for the binding of antibody 1E4.

[00638] In **Fig. 69A-69D**, antibodies generated by immunization with the N+9/C-9 peptide were assayed. As can be seen in the figure, amino acids GTINVHDVET, which comprise the most N-terminal part of the PSMGFR peptide are important or essential for the binding of the 39H5 and 3C5 antibodies. As can be seen in the figure, amino acids VQLTLAFRE (SEQ ID NO:1750), which is 9 additional amino acids N-terminal to the PSMGFR peptide and outside of the PSMGFR peptide, are important or essential for the binding of antibodies 17H6 and 8A9. Because the 17H6 and 8A9 antibodies do not bind to any of the smaller peptides shown in this figure, refer to **Figure 66A-66C**, which shows that these two antibodies only bind to the peptide that has 9 additional amino acids N-terminal to the PSMGFR peptide.

[00639] Table 2 below lists antibodies of the invention and their cognate epitopes.

Table 2		
Immunizing Peptide	**Antibody Name**	**Cognate Sequence**
PSMGFR	MNC2	FPFS or PFPFSAQSGA
	MNE6	FPFS or PFPFSAQSGA
	20A10	FPFS or PFPFSAQSGA
	3C2B1	FPFS or PFPFSAQSGA
	5C6F3	SVSDV
	MNC3	ASRYNLT
	25E6	ASRYNLT
	28F9	ASRYNLT
	18G12	ASRYNLT
	18B4	GTINVHDVET
N+20/C-27		
	45C11	SNIKFRPGSVV
	29H1	GTINVHDVET
	32C1	GTINVHDVET
	31A1	GTINVHDVET
	1E4	QFNQYKTEA
N+9/C-9		
	17H6	VQLTLAFRE
	8A9	VQLTLAFRE
	39H5	GTINVHDVET

	3C5	GTINVHDVET

[00640] Ability to displace NME7$_{AB}$ binding to the MUC1* extra cellular domain peptide PSMGFR

[00641] We previously reported that dimeric NME1 dimerizes MUC1* extra cellular domain and stimulates growth. Monomeric NME7$_{AB}$ has two binding sites for MUC1* so that as a monomer it dimerizes MUC1* and mediates cancer cell growth. We showed that NME1 and NME7$_{AB}$ can bind to the MUC1* extra cellular domain. In vitro, NME1 and NME7$_{AB}$ bind to the PSMGFR peptide even if the 10 N-terminal amino acids are deleted, referred to herein as N-10 (SEQ ID NO:3). However, neither NME1 nor NME7$_{AB}$ can bind to the PSMGFR peptide if the 10 membrane proximal amino acids are deleted, referred to herein as C-10 (SEQ ID NO:825). In summary, the epitope to which NME1 and NME7$_{AB}$ bind includes all or part of the 10 membrane proximal amino acids: PFPFSAQSGA (SEQ ID NO:1743). We tested various antibodies that were generated in animals by immunizing with the PSMGFR peptide for their ability to recognize cancer cells but not healthy cells. Among the most cancer selective were the MNC2 and MNE6 monoclonal anti-MUC1* antibodies. Two other monoclonal antibodies that were generated from immunizing animals with the PSMGFR peptide are MNC3 and MNC8. Although MNC2, MNE6, MNC3 and MNC8 all bind to the PSMGFR peptide, like NME1 and NME7$_{AB}$, MNC2 and MNE6 bind strongly to the N-10 peptide but not to the C-10 peptide. In fact, MNC2 and MNE6 competitively inhibit the binding of NME1 and NME7$_{AB}$ to PSMGFR. Conversely, MNC3 and MNC8 are able to bind to the C-10 peptide, bind less well to the N-10 peptide and do not compete with NME1 nor NME7$_{AB}$ for binding to MUC1* peptides, including PSMGFR (Fig. 70). MNC3 and MNC8 are less cancer specific than MNC2 and MNE6. MNC3 and MNC8 recognize stem and progenitor cells, such as hematopoietic stem cells, whereas MNC2 and MNE6 do not. Because hematopoietic stem cells are the progenitor cells for the blood cells, it would be problematic to have a cancer therapeutic that would also target such an important normal cell type.

[00642] In this experiment, antibodies of the invention were tested for their ability to displace NME7$_{AB}$ from binding to the PSMGFR peptide. In this experiment, a multi-well plate was coated with the PSMGFR peptide. Recombinant NME7$_{AB}$ was allowed to bind to the surface-immobilized PSMGFR peptide. Wash steps followed. Various antibodies were added, followed by wash steps. The amount of $NME7_{AB}$ that remained attached to the PSMGFR coated plate, after antibody competition, was measured by detecting a tag on the $NME7_{AB}$. As a control, anti-$NME7_{AB}$ antibodies were also tested for their ability to displace $NME7_{AB}$ from the PSMGFR. Figure 70 shows a graph of an ELISA displacement assay. The bar graph is color coded to indicate the cognate epitope to which each antibody binds. As can be seen in the figure, the antibodies that bind to the more C-terminal portions of PSMGFR are the most potent at disrupting the binding of onco-embryonic growth factor $NME7_{AB}$ to the MUC1* extra cellular domain or the PSMGFR peptide. The rank order of potency for disrupting binding of NME7AB to PSMGFR according to their cognate epitope is as follows: FPFS> ASRYNLT> QFNQYKTEA>GTINVHDVET. Antibodies that bind to epitopes outside of the PSMGFR peptide, such as 45C11, 8A9 and 17H6 did not compete with $NME7_{AB}$ for binding.

[00643] Western blot assay to determine linear versus conformational cognate epitope

[00644] Antibodies were tested to determine whether they recognize a linear or a conformational epitope. Only antibodies that recognize a linear epitope work in Western blots when using denaturing gels. For comparison, known antibodies were tested for their ability to bind to HCT-116, a MUC1 negative cancer cell line, HCT-MUC1-18, which is a cleavage resistant clone of HCTs transfected with full-length MUC1, and HCTs transfected with MUC1*, wherein the extra cellular domain comprises only the PSMGFR sequence. The antibodies tested for comparison are MNC2 and MNE6, which were known to only recognize a conformational epitope, SDIX which is a polyclonal antibody raised against PSMGFR and VU4H5, which is a commercially available monoclonal antibody that recognizes the tandem repeats of full-length MUC1 **(Fig. 71A-71D)**. As can be seen, neither MNC2 nor MNE6 recognize a MUC1 or MUC1* specific linear epitope. The SDIX polyclonal antibody recognizes HCT-MUC1* but not full-length MUC1 and VU4H5 only recognizes full-length MUC1. These same antibodies were also tested for their ability to work in Western blots of two breast cancer cell lines 1500, aka Zr-75-1, and T47D cells and show the same binding pattern **(Fig. 71E-71H)**.

[00645] Antibodies that were raised against the PSMGFR peptide were tested the same way in Western blots (**Fig. 72A-72P**). As can be seen, antibodies 25E6 and 18B4 recognize linear epitopes but 20A10, 3C2B1, 5C6F3, 18G12 and 28F9 do not, indicating that they bind to a conformational epitope. Antibodies that were raised against the N+20/C-27 peptide were tested the same way in Western blots (**Fig. 73A-73J**). As can be seen, antibodies 31A1 and 32C1 recognize linear epitopes. Antibodies 1E4 and 45C11 may recognize a conformational epitope. Antibodies that were raised against the N+9/C-9 peptide were tested the same way in Western blots (**Fig. 74A-74H**). As can be seen, none of these antibodies recognize linear MUC1 or MUC1* specific epitopes. These antibodies may recognize a conformational epitope. However, an alternative interpretation is that the lack of binding in a Western blot means that they do not specifically recognize MUC1 or a MUC1 cleavage product or that the concentration used in this assay was insufficient.

[00646] Recognition of a MUC1 cleavage product after cleavage by MMP9

[00647] We previously demonstrated that MNC2 recognizes a MUC1* that is generated when full-length MUC1 is cleaved by matrix metalloprotease 9, MMP9 (**Fig. 37**). MMP9 is expressed by tumor tissues and is a predictor of poor prognosis for breast cancers (vant Veer et al 2002; Dufour et al 2011). MMP9 has also been implicated in metastasis (Owyong et al 2019). Recall also that MNC2 competitively inhibits the binding of onco-embryonic growth factor $NME7_{AB}$ to the MUC1* extra cellular domain (Fig. 3). Therefore, it follows that onco-embryonic growth factor, which activates growth and survival functions of MUC1*, also recognizes a MUC1* generated by cleavage by MMP9. It then follows that the most cancer specific antibodies are those that recognize a conformational epitope formed when MUC1 is cleaved to MUC1* by MMP9.

[00648] Antibodies generated by immunization with PSMGFR, N+20/C-27, or N+9/C-9 were tested for their ability to recognize MUC1 after it is cleaved by MMP9. To do this, we transfected HCT-116, a MUC1 negative colon cancer cell line, with full-length MUC1 and isolated a single cell clone that is cleavage resistant; this cleavage resistant cell line is called HCT-MUC1-18. To HCT-MUC1-18 cells was added either a catalytically active MMP9 or MMP2. The enzymes, added over a range of concentrations, were incubated with the cells for 24 hours. The resultant cells were then incubated with the various antibodies and analyzed by FACS to determine which bound to a MUC1 cleavage product produced by cleavage by MMP9 (**Fig. 75A-75N**). Note that the first bar of each graph shows that none of the antibodies binds to full-length MUC1 in the absence of cleavage. Each bar graph is labeled with both the name of the antibody used in that assay and its cognate epitope. The order of the graphs from right to left corresponds to the distance from the cell surface of the antibody's cognate epitope. The antibodies that bind to the more C-terminal epitopes within PSMGFR peptide, such as 20A10 and 25E6, showed the most increased binding to a MUC1 cleavage product after cleavage by MMP9 but not MMP2. Antibody 45C11, which binds to the SNIKFRPGSVV epitope, which is outside of the PSMGFR portion of MUC1, does not recognize a MUC1 cleavage product after cleavage by MMP9 or MMP2 (Fig. 75K). Similarly, antibodies 8A9 and 17H6 bind to the VQLTLAFRE epitope, which is also outside of the PSMGFR sequence, and they do not bind to a MUC1 cleaved by MMP9 or MMP2. This result is consistent with the idea that MMP9 cleaves MUC1 such that the extra cellular domain of the remaining transmembrane cleavage product comprises essentially the amino acids of the PSMGFR peptide. For the greatest degree of cancer specificity, the antibody should recognize a conformational epitope of a MUC1 cleavage product created when MUC1 is cleaved by MMP9. Of the antibodies shown in Fig. 75A-75N, only 20A10 recognizes the MUC1 cleavage product produced by cleavage by MMP9 and also does not work in a Western blot, indicating it recognizes a conformational epitope, as do MNC2 and MNE6. Cleavage and release of the massive tandem repeat domain of MUC1 unmasks the ectopic binding site on MUC1*; linear epitopes will be unmasked in addition to conformational epitopes.

[00649] FACS analysis of binding to a panel of cancer cell lines

[00650] Fluorescence Activated Cell Sorting, FACS, was performed on reference antibodies as well as new antibodies of the invention. FACS analyses of reference antibodies MNC2, “C2”, and VU4H5 binding to either the MUC1-negative cell line HCT-116, HCTs transfected with MUC1*, “HCT-MUC1*”, a cleavage resistant single cell clone of HCTs transfected with MUC1 full-length, “HCT-MUC1-18”, and MNC2 binding to breast cancer cells line T47D or breast cancer cell line 1500 also known as ZR-75-1, was performed (Fig. 76A-76J). This analysis shows that MNC2 binds to an ectopic binding site on the extra cellular domain of MUC1*, which is only available after cleavage and release of the bulk of the extra cellular domain comprising the tandem repeat domain. VU4H5 binds to hundreds of repeating epitopes in the tandem repeat domain of full-length MUC1 and does not bind to MUC1*. Although we know that cancer cell lines express both full-length MUC1 and MUC1*, antibodies against full-length MUC1 have, as yet, been shown to have no therapeutic value. Stimuvax, ImMucin, IMGN242, SAR566658, PankoMab and AS1402 were all antibodies that bound to full-length MUC1 and all failed to show efficacy in clinical trials. MUC1*, and not full-length MUC1, is a potent growth factor receptor that mediates the growth of cancer cells (Mahanta et al 2008) and their resistance to chemotherapy agents (Fessler et al 2009). These studies showed that full-length MUC1 had no tumor promoting activity. Further, IHC studies show that as tumor stage increases, the amount of MUC1* increases as the amount of full-length MUC1 decreases (Fig. 54). In fact, studies with tissue micro arrays of breast cancers show that nearly 30% of breast cancer specimens had no detectable full-length MUC1, compared to only 5% that were negative for MUC1* (Fig. 10-11). A point to consider for therapeutics that target full-length MUC1 is that if cells expressing full-length MUC1 are eliminated, that would simply enrich the tumor population for the more virulent MUC1* growth factor receptor expressing cells, which would make the cancers worse.

[00651] Reference antibody MNC2, “C2”, was analyzed by FACS for its ability to bind to a panel of cancer cell lines that are all MUC1* positive, with the exception of MDA-MB-231, which expresses MUC1 and MUC1* at a level that is so low that it is often used as a negative control (Fig. 77A-77N). The panel of cancer cells that was probed with MNC2 included T47D and 1500 breast cancer cells, NCI-H292 and NCI-H1975 lung cancer cells, SKOV-3 ovarian cancer cells, HPAF-II and Capan-1 pancreatic cancer cells, DU145 prostate cancer cells, and MDA-MB-231, breast cancer cells, which are nearly MUC1 and MUC1* negative. MNC2 robustly recognized a wide range of cancer cell lines. We note that although MNC2 recognized HPAF-II pancreatic cells, it did not recognize another pancreatic cell line, Capan-1, as well. Similarly, MNC2 did not recognize prostate cancer cell line DU145 very well. In IHC tissue studies, we found that MNC2 recognized about 57% of prostate cancer tissues and 78% of pancreatic tissues, albeit with significant tumor heterogeneity.

[00652] **Figure 78A-78C** shows a color coded schematic of the PSMGFR sequence that has been extended or deleted at both the N- and C-termini. Antibodies of the invention were tested against this subset of peptides to further refine the epitopes to which each antibody binds or the critical amino acids within the epitope to which each antibody binds. Fig. 78A is an aligned schematic of the various subsets of peptides. Fig. 78B lists the antibodies that bind to each of the color coded sequences. Fig. 78C lists the cancer cell lines that each antibody recognizes.

[00653] Figures 80-87 show graphs of FACS analyses wherein antibodies of the invention are compared for their ability to specifically recognize different types of cancer cells. Percent cells recognized as well as the Mean Fluorescence Intensity, MFI, was measured. Considering only these FACS experiments, they show that only antibodies that recognize the PSMGFR peptide are able to recognize cancer cell lines. Antibodies that bind to epitopes outside of the PSMGFR sequence do not specifically recognize these cancer cell lines.

[00654] IHC tissue studies of normal versus cancerous tissues to determine true cancer specificity

[00655] Immunohistochemistry, IHC, tissue studies of tissue micro arrays, "TMAs", are a more stringent test of the cancer specificity of antibodies than FACS analysis of a single cancer cell line. Cancer cell lines are a single cell from a single patient that have been expanded in a lab for decades. Cell lines are limited in that they are not representative of a cross section of the human population. Further, after culturing the cell line in vitro for decades it may no longer look like the original cell. Also, there are no real normal cell lines for comparison, as they have to be made immortal. Tissue studies are more informative because each tissue micro array comprises tissues from multiple donors and the cells are in their natural environment, without years of culturing under non-physiologic conditions. Additionally, tissues provide information regarding tumor heterogeneity as well as information regarding normal patterns of expression. Each antibody of the invention was used to probe a normal tissue micro array, FDA Normal Array 1021. In addition the antibody was also used to probe a panel of cancerous tissue arrays. In some cases, antibodies that showed strong staining of normal tissues, especially of critical organs such as heart or lung, were tested on a limited number of cancerous tissue arrays, since their cross reactivity to normal tissues eliminated them from consideration as anti-cancer therapeutics.

[00656] **Figures 113-200** show photographs of the IHC staining of normal TMAs versus cancerous TMAs for each antibody of the invention.

[00657] **Figure 113-120** show photographs of tissues studies probed with antibody 20A10. Recall that 20A10 binds to the PSMGFR peptide, binds to the N-10 peptide, but does not bind to the C-10 peptide. Refined epitope mapping shows that like MNC2 and MNE6, the binding of 20A10 depends on amino acids FPFS being present in the PSMGFR peptide. 20A10 binds to the most membrane proximal part of the MUC1* extra cellular domain. An overview of FDA Normal Tissue Array 1021 is shown in Figure 113. Figure 114A-114X show that there is little to no cross reactivity of 20A10 for normal tissues. We note that MNC2, MNE6 and 20A10 all react with the MUC1* that is expressed on the luminal edge of the terminal breast ducts, luminal edge of the fallopian tubes, luminal edge of about 10% of the distal collecting ducts of normal kidney, and luminal edge of ureter. Because the staining is strictly limited to the luminal edge of a subset of ducts and glands, these antibodies are considered to be safe as therapeutics as the inside of ducts and glands are protected from large entities carried by blood, such as antibodies or CAR T cells. Importantly, MNC2, MNE6 and 20A10 show no staining of critical organs, such as heart, lung and brain. In stark contrast, 20A10, like MNC2 and MNE6, robustly binds to cancerous tissues. 20A10 stains nearly all specimens of the BR1141 breast cancer array (Fig. 115-116). In addition to robust staining of the breast cancer tissue, the staining is membrane staining, indicating that 20A10 recognizes an extra cellular portion of MUC1*, which is critical for an effective antibody-based anti-cancer therapeutic. 20A10 also showed robust and membranous staining of pancreatic cancer tissues (Fig. 117-118) and esophageal cancer tissues (Fig. 119-120). In summary, 20A10 shows great cancer specificity and as an anti-cancer therapeutic offers a large therapeutic window because of the vast difference between staining of normal tissues and cancerous tissues, in terms of the location and intensity of staining.

[00658] Anti-MUC1* antibody 3C2B1 is an antibody that like MNC2, MNE6 and 20A10, binds to N-10 but not to C-10. More refined epitope mapping shows that like these three other highly cancer-specific antibodies, 3C2B1 requires the FPFS sequence for binding to a MUC1* extra cellular domain peptide. **Figure 121** shows the photograph of the FDA normal array 1021. **Figure 122A-122X** shows photographs of specific tissues from FDA normal tissue array 1021 stained with the anti-PSMGFR antibody 3C2B1 at 20ug/mL. As can be seen, there is no binding of 3C2B1 to any critical normal organs. **Figure 123** shows photograph of pancreatic cancer tissue array PA1003 stained with the anti-PSMGFR antibody 3C2B1 at 1-20ug/mL. **Figure 124** shows photographs of specific tissues from pancreatic cancer tissue array PA1003 stained with the anti-PSMGFR antibody 3C2B1 at 20ug/mL. **Figure 125** shows photograph of breast cancer tissue array 1141 stained with the anti-PSMGFR antibody 3C2B1 at 20ug/mL. **Figure 126A-126F** shows magnified photographs of specific tissues from breast cancer tissue array 1141 stained with the anti-PSMGFR antibody 3C2B1 at 20ug/mL. As can be seen in the figure, 3C2B1 robustly stains breast cancer tissues.

[00659] Anti-MUC1* antibody 5C6F3 binds to the N-10 peptide, does bind to the C-10 peptide, although binding is reduced somewhat. Its cognate epitope comprises all or some of the sequence SVSDV (SEQ ID NO:1751). **Figure 127** shows photograph of FDA normal tissue array 1021 stained with the anti-PSMGFR antibody 5C6F3 at 1ug/mL. **Figure 128** shows photographs of specific tissues from FDA normal tissue array 1021 stained with the anti-

PSMGFR antibody 5C6F3 at 1ug/mL. **Figure 129** shows photograph of pancreatic cancer tissue array PA1003 stained with the anti-PSMGFR antibody 5C6F3 at 1-20ug/mL. **Figure 130** shows photographs of specific tissues from pancreatic cancer tissue array PA1003 stained with the anti-PSMGFR antibody 5C6F3 at 1ug/mL. **Figure 131** shows photograph of breast cancer tissue array 1141 stained with the anti-PSMGFR antibody 5C6F3 at 1ug/mL. **Figure 132** shows photographs of specific tissues from breast cancer tissue array 1141 stained with the anti-PSMGFR antibody 5C6F3 at 1ug/mL. As can be seen in the figure 5C6F3 is a high affinity antibody that has great cancer-specificity and with the exception of adrenal, which may be an artefact of that tissue, did not show binding to normal tissues.

[00660] In contrast to 20A10, which binds to the most membrane proximal part of the MUC1* extra cellular domain, **18B4** binds within the GTINVHDVET sequence, which is the most distal part of the PSMGFR sequence. Unlike antibodies MNC2, MNE6 or 20A10, 18B4 cannot bind to the N-10 peptide but does bind to the C-10 peptide. Figure 133-134 show the binding of antibody 18B4 to normal tissues. In contrast to 20A10, antibody 18B4 shows strong binding to a wide range of normal tissues (Fig. 134), including lung (Fig. 134K). Figure 135-138 show 18B4 staining of breast cancer tissues and esophageal cancer tissues. Because of the strong binding of 18B4 to normal tissues, there is less cancer specificity to this antibody.

[00661] **Figure 139-144** show the binding of PSMGFR antibody **18G12** to normal tissues, breast cancer tissues and esophageal cancer tissues. 18G12 is able to bind to the N-10 peptide, but is also able to bind to the C-10 peptide. 18G12 binds to the ASRYNLT epitope within the PSMGFR peptide. Antibody 18G12 binds to the luminal edge of many of the collecting ducts of normal kidney (Fig. 140D), binds to normal heart muscle (Fig. 140I) as well as to normal skeletal muscle (Fig. 140X). However, there is a clear cancer specificity in that 18G12 binds much more strongly to cancerous tissues than to the few normal tissues. In addition, 18G12 stains the entire cancerous tissues rather than just a luminal edge here or there. Figure 141-146 show 18G12 staining of breast cancer tissues, pancreatic cancer tissues and esophageal cancerous tissues. The contrast between the staining of the normal tissues and the cancer tissues clearly demonstrates cancer specificity.

[00662] **Figure 147-148** show the binding of PSMGFR antibody 25E6 to normal tissues. 25E6 is able to bind to the N-10 peptide, but is also able to bind to the C-10 peptide. 25E6 binds to the ASRYNLT epitope within the PSMGFR peptide. Like MNC2, MNE6 and 20A10, antibody 25E6 binds to the luminal edge of terminal breast ducts, luminal edge of fallopian tubes, to the luminal edge of a subset of the distal collecting ducts of normal kidney and to the luminal edge of ureter. Unlike MNC2, MNE6 and 20A10, 25E6 binds, albeit very weakly, to normal heart muscle (Fig. 148I) as well as to normal skeletal muscle (Fig. 148X). However, there is a clear cancer specificity in that 25E6 binds much more strongly to cancerous tissues than to the few normal tissues. In addition, 25E6 stains the entire cancerous tissues rather than just a luminal edge here or there. Figure 149-152 show 25E6 staining of breast cancer tissues and pancreatic cancerous tissues. The contrast between the staining of the normal tissues and the cancer tissues clearly demonstrates cancer specificity.

[00663] **Figure 153-156** show the binding of PSMGFR antibody **28F9** to normal tissues and breast cancer tissues. 28F9 is able to bind to the N-10 peptide, but is also able to bind to the C-10 peptide. 28F9 binds to the ASRYNLT epitope within the PSMGFR peptide. Like MNC2, MNE6 and 20A10, antibody 25E6 binds to the luminal edge of terminal breast ducts, luminal edge of fallopian tubes, to the luminal edge of a subset of the distal collecting ducts of normal kidney and to the luminal edge of ureter. Figure 155-156 show 28F9 staining of breast cancer tissues..

[00664] Figure 157-158 show the binding of the N+20/C-27 antibody **1E4** to normal tissues. 1E4 is able to bind to the N-10 peptide but also is able to bind to the C-10 peptide. 1E4 binds to the QFNQYKTEA sequence which is within the PSMGFR sequence. Examination of the entire normal tissue micro array (Fig. 157A) shows that antibody 1E4 binds to many normal tissues, including brain, cerebellum, all 3 liver specimens, pancreas, parathyroid, spinal cord and skeletal muscle. Magnified images show that 1E4 stains heart (Fig. 158I) as well. 1E4 staining of a breast cancer array (Fig. 159-160) shows that there is some cancer specificity.

[00665] Figure 161-162 show the binding of the N+20/C-27 antibody **29H1** to normal tissues. **29H1** binds within the GTINVHDVET sequence, which is the most distal part of the PSMGFR sequence. Unlike antibodies MNC2, MNE6 or 20A10, 29H1 cannot bind to the N-10 peptide but does bind to the C-10 peptide. Examination of the entire normal tissue micro array (Fig. 157A) shows that even at concentration as low as 0.5 ug/mL, antibody 29H1 strongly stains a wide range of normal tissues, including brain, heart, liver and lung. 29H1 staining of a breast cancer array (Fig. 163-164) and staining of a pancreatic cancer tissue array (Fig. 165-166) shows that there is no cancer specificity.

[00666] Antibody 31A1 is similar to 29H1 in that they are both N+20/C-27 antibodies that bind within the GTINVHDVET (SEQ ID NO:1746) sequence, which is the most distal part of the PSMGFR sequence. Unlike antibodies MNC2, MNE6 or 20A10, neither 31A1 nor 29H1 can bind to the N-10 peptide but do bind to the C-10 peptide. Examination of the entire normal tissue micro array and the magnified images (Fig. 167-168) shows that even at concentration as low as 0.5 ug/mL, antibody 31A1 strongly stains a wide range of normal tissues, including brain, heart, lung, spleen, bone marrow, and skeletal muscle. 31A1 was used to stain a breast cancer array, (Fig. 169-170). 31A1 was used over a range of concentrations to stain a pancreatic cancer tissue array (Fig. 171-172). These figure shows that 31A1 has insufficient cancer specificity.

[00667] Antibody **32C1** is similar to 29H1 and 31A1 in that they are all N+20/C-27 antibodies that bind within the GTINVHDVET sequence, which is the most distal part of the PSMGFR sequence. Unlike antibodies MNC2, MNE6 or 20A10, none of 32C1, 31A1 or 29H1 can bind to the N-10 peptide but all do bind to the C-10 peptide. Examination of the entire normal tissue micro array and the magnified images (Fig. 173-174) shows that even at concentration as low as 0.25 ug/mL, antibody 32C1 strongly stains a wide range of normal tissues, including brain, heart, lung, liver, spleen and bone marrow. 32C1 was also used to probe a breast cancer array (Fig. 175-176). 32C1 was used over a range of concentrations to stain an esophageal cancer tissue array (Fig. 177-178). Taken together, these figures show that 32C1 has insufficient cancer specificity.

[00668] Antibody **45C11** is an N+20/C-27 antibody that binds to epitope SNIKFRPGSVV (SEQ ID NO:1744) that is 20 amino acids outside of the PSMGFR sequence at the N-terminal end. 45C11 does not bind to the N-10 peptide. Normal tissue array FDA 1021 was stained with 45C11 at 12.5ug/mL (Fig. 179-180). As can be seen in the figures, 45C11 shows strong binding to many normal tissues, including brain, heart, lung, liver, spleen, skeletal muscle and bone marrow. 45C11 was used over a range of concentrations to stain a breast cancer tissue array (Fig. 181-182). 45C11 was also used to stain a pancreatic cancer tissue array (Fig. 183-184). Taken together, these figures show that 45C11 has no cancer specificity.

[00669] Antibody **3C5** is an N+9/C-9 antibody that binds to epitope GTINVHDVET. Like the other antibodies that bind to this epitope such as 32C1**,** 29H1 and 31A1, they bind to the most distal, that is to say the most N-terminal, part of the PSMGFR sequence. Unlike antibodies MNC2, MNE6 or 20A10, none of 3C5, 32C1, 31A1 or 29H1 can bind to the N-10 peptide but all do bind to the C-10 peptide. Examination of the entire normal tissue micro array, where 3C5 was used at 10ug/mL, and the magnified images (Fig. 185-186) shows that antibody 3C5 strongly stains some normal tissues, including brain, heart, adrenal gland and bone marrow. 3C5 was also used to probe a pancreatic cancer array at 10ug/mL, (Fig. 187-188). Taken together, these figures show that 3C5 has no cancer specificity.

[00670] Antibody **8A9** is an N+9/C-9 antibody that binds to epitope VQLTLAFRE which is outside of the PSMGFR sequence. Antibody 8A9 cannot bind to the N-10 peptide. Normal tissue array FDA 1021 was stained with 8A9 (Fig. 189-190). As can be seen in the figures, like antibody 45C11, which also binds an epitope that is N-terminal beyond the PSMGFR sequence, antibody 8A9 shows strong binding to many normal tissues, including adrenal, brain, heart, lung, liver, spleen, skeletal muscle and bone marrow. A pancreatic cancer array stained with antibody 8A9 showed weak binding to a subset of pancreatic cancer tissues (Fig. 191-192). Taken together, these figures show that 8A9 has no cancer specificity.

[00671] Antibody **17H6** is an N+9/C-9 antibody that binds to epitope VQLTLAFRE, which is outside of the PSMGFR sequence. 17H6 was used to stain normal tissue array 1021. Examination of the entire normal tissue micro array and the magnified images (Fig. 193-194) shows that antibody 17H6 stains some normal tissues, including brain, heart, adrenal gland, bone marrow and skeletal muscle. 17H6 was used to probe a pancreatic cancer array and showed weak binding to most pancreatic cancer tissues (Fig. 195-196). However, the binding of 17H6 to several normal tissues of critical organs shows that 17H6 has little cancer specificity.

[00672] Antibody **39H5** is an N+9/C-9 antibody that binds weakly to the intact PSMGFR peptide but not significantly to any of the subset peptides. 39H5 may bind to the GTINVHDVET, which is the most distal part of the PSMGFR sequence. Examination of the entire normal tissue micro array and the magnified images (Fig. 197-198) shows that antibody 39H5 stains some normal tissues, including brain, heart, liver and bone marrow. 39H5 was used to probe a pancreatic cancer array, (Fig. 199-200). Although 39H5 stained a good percentage of the pancreatic cancer specimens, considering the normal tissues that 39H5 stained, 39H5 has little cancer specificity.

[00673] Summary of FACS analysis

[00674] Determining the cancer specificity of antibodies using cell lines is difficult, as these cells were obtained from a single patient's tumor decades ago, and then propagated in culture for decades. Even if the patient's tumor was at one point heterogeneous, the decades of in vitro culture have essentially made the cell line a single cell clone. Antibodies of the invention were assayed by FACS to determine if they bound to MUC1 or MUC1* positive cancer cells but not MUC1 negative cells. The results of these experiments are shown in Figures 76-87. What is very clear is that antibodies that bind to epitopes of the MUC1 sequence that are outside of and N-terminal to PSMGFR sequence show no cancer specificity. Referring now to the readings of Mean Fluorescence Intensity (MFI) it appears that antibodies with cognate epitopes at the very N-terminus of the PSMGFR sequence, such as those that bind to an epitope within GTINVHDVET, show far less cancer specificity than the antibodies that recognize more C-terminal epitopes. For example, antibody MNC2 that will not bind to the C-10 peptide binds strongly to nearly every MUC1* positive cell line (Fig. 76-77). However, closer examination reveals that MNC2 binds lung cancer line NCI-H1975 much more strongly than NCI-H292. Similarly, MNC2 binds pancreatic cell line HPAF-II much better than Capan-1 or prostate cancer line DU145. PCR measurements show that the expression levels of cleavage enzymes varies greatly across a panel of cancer cell lines (Fig. 43 and Fig. 44). The fold of the MUC1* extra cellular domain can vary greatly depending on which cleavage enzyme clips it, which likely accounts for differences between cancer cell lines that a single antibody recognizes. This variation in antibody recognition of various cell lines, even within a cancer sub-type is apparent in the figures.

[00675] Summary of IHC data

[00676] IHC analysis of real tissues, including both normal and cancerous tissues, is more informative than the study of cultured cell lines, as is necessary in FACS analysis. Each antibody was first tested over a range of concentrations to determine optimal concentration. Antibody concentration was increased until the stroma also picked up stain, which indicates non-specific background binding. The optimal concentration for that particular antibody was then deemed to be just below the concentration at which the antibody stained the stroma.

[00677] An overview of the IHC tissue studies is shown in Figure 88-112. Here, we focused on the binding of antibodies to critical organ tissues, since binding to certain normal tissues would likely eliminate therapeutic use of that antibody. In these figures, the antibodies were grouped according to their cognate epitope. What is evident from the tissue studies is that the further the epitope is from the cell membrane, the more it binds to normal MUC1 on normal tissues. For example, binding to normal heart tissue by representative antibodies that recognize a specific epitope are shown in Figure 88A-88L. As the figure illustrates, antibodies that bind to epitopes that are N-terminal to the PSMGFR peptide such as epitope within SNIKFRPGSVV or VQLTLAFRE show such strong binding to normal heart that they could not be used in therapeutics. In addition, antibodies that bind to the more N-terminal portion of PSMGFR, such as 29H1, also show binding to normal heart. The antibodies with the least binding to normal tissues and the strongest binding to cancerous tissues bind to epitopes within the FPFS or PFPFSAQSGA. Some antibodies that bind to epitopes within the ASRYNLT portion may also be suitable as therapeutics. These antibodies and others that recognize the same epitopes are desirable as anti-cancer therapeutics because they have a large therapeutic window, meaning that because of the low binding to normal tissues, and low side effects, patients can be dosed with antibody levels high enough to effectively kill the tumor cells. More detailed photographs of antibodies of the invention binding, or not binding, to other critical tissues are also shown. Figures 89-94 show magnified photographs of each antibody binding to normal heart tissue, where the antibodies have been categorized according to which epitope they bind. Figures 95-100 show magnified photographs of each antibody binding to normal liver tissue, where the antibodies have been categorized according to which epitope they bind. Figures 101-106 show magnified photographs of each antibody binding to normal lung tissue, where the antibodies have been categorized according to which epitope they bind. Figures 107-112 show magnified photographs of each antibody binding to normal bone marrow, where the antibodies have been categorized according to which epitope they bind.

[00678] The results of the IHC studies (Fig. 88-Fig. 200) are summarized in **Table 3**.

Table 3: Summary of Antibody Cross-Reactivity to Normal Tissues

Antibody Name	HEART	BRAIN	LUNG	LIVER	SPLEEN	BONE MARROW	KIDNEY	SKELETAL MUSCLE	ADRENAL
PSMGFR									
MNC2									
MNE6									
20A10									
25E6	~+							~+	

18B4			+++			+			
18G12	++						+++	+++	
28F9								~+	
3C2B1									
5C6F3			+			~+	++		++++
N+20/C-27									
1E4	++	++		+++		~+		+++	
31A1	++	+++	++		++++	++++		+	
32C1	+++	+++	+++	++	+++	++++			++
29H1	+	++++	++++	++++	++				++++
45C11	+++++	++++	++	+++++	++	+++	+	+++++	+
N+9/C-9									
8A9	+++++	+++++	+++	+++++	++++	++++	+	++++	+++
17H6	+++	++++				+			++
3C5	+++	++++		+		++++			+++
39H5	++++	+++++	+	+++	+++	++++			++++

[00679] As can be clearly seen in the table, the further away from the cell membrane that the antibody binds, the more non-specific binding there is. Although these antibodies were generated by immunizing with the PSMGFR peptide, N+20/C-27 peptide or the C+9/C-9 peptide, some of the antibodies generated by immunizing with an extended peptide still bind within the PSMGFR sequence, see Figures 63-69 for the details of epitope binding for each antibody. Some binding to normal tissues can be tolerated if the antibody is incorporated into an appropriate therapeutic format. For example, cellular therapies, such as CAR T, are carried by the blood and meet with physiological barriers including lamina propia and blood-brain barrier that limits the cell's access to luminal edge of ducts and glands. Other antibodies that bind much more strongly to cancerous tissues but do show some binding to normal tissues could also be safe and useful therapeutics if administered locally or if cancer-specificity is enhanced by incorporating into a bi-specific antibody. However, widespread antibody binding to many normal organs or to essential organs for which there is no physical barrier could be lethal to the patient.

[00680] The most cancer-specific antibodies with little to no binding to normal tissues are MNC2, MNE6, 20A10, 3C2B1 and 25E6. An ideal antibody therapeutic is one that stains no normal tissues but robustly stains cancer cells. Unfortunately, cancer antigens are also expressed on normal tissues, so zero staining of normal tissue is not possible. The aim is to identify an antibody that binds much more strongly to tumor tissue than normal tissue and that either binds to non-critical normal tissues or binds to them in a way that would not be physiologically possible in an intact organ. For example, CAR T cells are carried by the blood and the lamina propia is a barrier to their getting to the luminal edge of a duct or gland. Similarly, the blood brain barrier prevents the passage of large molecules like antibodies from the blood into the brain. The usefulness of an antibody as a therapeutic also depends on the format of the therapeutic. As mentioned, cell based therapies have natural barriers that prevent the CAR T cells from getting to some normal tissues. Antibody Drug Conjugate (ADC) based therapies sometimes depend on a local, cancer-specific molecule to activate the toxin attached to the antibody, minimizing the importance of whether or not a naked antibody binds to some normal tissue. In another example, antibodies and antibody-based therapeutics can be administered locally, including intraperitoneally, to maximize the effect on tumor cells while minimizing their effect on normal tissues. In yet another example, an antibody that is not purely cancer-specific can be made more cancer-specific if it is incorporated into a bi-specific antibody where a first side of the molecule binds to a first cancer antigen and the second side of the molecule binds to a second antigen that may be a tissue specific antigen, another cancer specific antigen or even an antigen on a cell such as a T cell, which are called BiTES, bispecific T cell engagers. In yet another example, the less cancer-specific antibody can be incorporated into a cell-based therapy where its expression is induced only after the cell recognizes a tumor. In one aspect, a CAR T cell can express a first CAR that recognizes a first antigen which recognition induces expression of a second antibody, or CAR incorporating the second antibody. In one aspect the cell expresses a CAR directed by an antibody fragment that is cancer-specific and a second antibody or CAR expressing the second antibody is induced to be expressed in an NFAT inducible system. In one aspect the nucleic acids encoding the second antibody or second CAR are down stream of NFAT response elements. The NFAT inducible gene may be inserted into a Foxp3 enhancer or promoter.

[00681] Figure 202 shows photographs of pancreatic cancer tissues, each from a different patient. As can be seen, the staining pattern of 1E4 is very different from that of 18B4 and the polyclonal antibody SDIX. 18B4 and SDIX antibodies were generated by immunizing animals with the same peptide (PSMGFR), while the 1E4 antibody was generated from immunization with a different peptide (N+20). Figures 203-207 show magnified images of selected tissues from this array to highlight the differences between these antibodies. Figure 208 compares the staining of polyclonal antibody SDIX to monoclonal antibody 20A10, which were both generated from immunization with the PSMGFR peptide. Also shown is the difference in staining pattern for antibody 29H1 which was generated by immunization with an N+20 peptide. Although the antibody staining is lighter, antibody 29H1 recognizes more pancreatic cancer tissue specimens than the SDIX polyclonal or 20A10. Figure 209 shows that esophageal cancers are better recognized by antibodies that bind to a MUC1* peptide with an extended N-terminus, such as antibody 29H1 and antibody 31A1. Similarly, Figure 210 shows that prostate cancers are better recognized by antibodies that bind to a MUC1* peptide with an extended N-terminus, such as antibody 29H1.

[00682] Below Table 4 shows a summary of the test criteria to determine the cancer-specificity of the various monoclonal antibodies.

Table 4: Cancer-Specificity Test Criteria

		1	2	3	4	5	6	7
mAb Name	**Binds PSMGFR**	**Binds N-10**	**Does not bind C-10**	**Displaces NME7$_{AB}$ from MUC1***	**Does not recognize linear epitope**	**Recognizes MUC1 after cleavage by MMP9**	**Cancer selective by FACS**	**Cancer selective by IHC**
	VQLTLAFREGTINVHDVET**QFNQYKTEA**ASRYNLT**ISDV**SVSDV**P**FPFS**AQSGA**							
FPFS								
MNC2	☑	☑	☑	☑	☑	☑	☑	☑☑☑
MNE6	☑	☑	☑	☑	☑	☑	☑	☑☑☑
20A10	☑	☑	☑	☑	☑	☑	☑	☑☑☑
3C2B1	☑	☑	☑	☑	☑	☑	☑	☑☑☑
SVSDV								
5C6F3	☑	☑	~▨	☑	☑	☑	☑	☑☑
ASRYNLT								
25E6	☑	☑	▨	☑	▨	☑	☑	☑☑
MNC3	☑	~√	▨	▨	☑	▨	ND	☑
18G12	☑	☑	▨	☑	☑	▨	~√	☑
28F9	☑	☑	▨	☑	☑	▨	~√	☑
QFNQYKTEA								
1E4	☑	☑	▨	☑	▨	☑	~√	☑
GTINVHDVET								
18B4	☑	▨	▨	~√	▨	☑	☑	☑

29H1	☑	☒	☒	~√	☒	☑	☒	☒
31A1	☑	☒	☒	☑	☒	☑	☒	☒
32C1	☑	☒	☒	~√	☒	☑	☒	☒
39H5	☑	☒	☑	~√	☒	☒	☒	☒
3C5	☑	☒	☑	☒	☒	☒	☒	☒☒
VQLTLAFRE								
8A9	☒	☒	☑	☒	☒	☒	☒	☒☒
17H6	☒	☒	☑	☒	☒	☒	☒	☒
SNIKFRPGSVV								
45C11	☒	☒	☑	☒	☑	☒	☒	☒☒☒

[00683] To summarize, we found that antibodies that bound to sequences that are N-terminal to the PSMGFR sequence had no cancer-specificity. Further, the closer to the cell membrane that the antibody binds, the more cancer-specific is the antibody. More importantly, test criteria 1-4 or even 1-5 provide a set of rapid, multiplexed and inexpensive tests that can be performed on hundreds or thousands of impure hybridoma clone supernatants to identify antibodies that are highly selective for cancer-specific forms of MUC1*.

[00684] Satisfies test criteria

[00685] In a preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on satisfying four (4) of the seven (7) criteria set out in Table 4. In a more preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on satisfying five (5) of the seven (7) criteria set out in Table 4. In a yet more preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on satisfying six (6) of the seven (7) criteria set out in Table 4. In a more preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on satisfying all seven (7) of the criteria set out in Table 4.

[00686] Bind to N-10

[00687] We have demonstrated that a MUC1 transmembrane protein, devoid of tandem repeats and having an extra cellular domain of 45 amino acids of PSMGFR sequence, is sufficient to function as a growth factor receptor and confers oncogenic characteristics to the cell (Mahanta et al 2008). Antibodies that bind to the PSMGFR peptide or portion of a transmembrane MUC1 cleavage product can be cancer specific but may also bind to stem or progenitor cells. Antibodies that bind to the N-10 peptide are more cancer-specific. In a preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on the ability of the antibody to bind to the N-10 peptide.

[00688] Do not bind to C-10

[00689] We have demonstrated that the MUC1 extra cellular domain contains an ectopic binding site that is only exposed if the tandem repeat domain is missing, which can occur as a consequence of alternative splice variant or cleavage and release of the extra cellular domain. Cancer-specific antibodies MNC2 and MNE6 will not bind to full-length MUC1, but do bind to the remaining portion when MUC1 is cleaved and the tandem repeat domain is shed. MNC2 and MNE6 will bind to a MUC1*-like protein if it is devoid of tandem repeats, for example if a MUC1 negative cell is transfected or transduced with an engineered MUC1 that is devoid of tandem repeats, especially if extra cellular domain comprises the PSMGFR. Thus, the ectopic site to which MNC2 and MNE6 bind is unmasked when tandem repeat domain is missing or removed. Both MNC2 and MNE6 require the 10 membrane proximal amino acids of a MUC1* extra cellular domain for binding; they do not bind to the C-10 peptide. That means that the ectopic binding site for MNC2 and MNE6 is within or contains all or part of the 10 C-terminal amino acids of the PSMGFR: PFPFSAQSGA. In a preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on the inability of the antibody to bind to the C-10 peptide. In a preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on the ability of the antibody to bind to the N-10 peptide and the inability of the antibody to bind to the C-10 peptide.

[00690] Compete with NME7$_{AB}$ or NME7-X1 for binding to MUC1* positive cell, PSMGFR peptide or N-10 peptide

We have demonstrated that cancer-specific antibodies MNC2 and MNE6 bind to an ectopic epitope that comprises all or part of the 10 C-terminal amino acids of the PSMGFR peptide: PFPFSAQSGA. We have shown that growth factors, dimeric NME1 and NME7$_{AB}$, also bind to an ectopic epitope that comprises all or part of the 10 C-terminal amino acids of the PSMGFR peptide. MNC2 and MNE6 compete with dimeric NME1 or NME7$_{AB}$ for binding to the PSMGFR peptide and the N-10 peptide. In a preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on the ability of the antibody to disrupt the binding of NME1, NME7$_{AB}$, or NME7-X1 to the PSMGFR peptide, the N-10 peptide, or to the surface of a MUC1* positive cancer cell.

[00691] Recognize a conformational epitope rather than a linear epitope

[00692] Antibodies that are cancer-specific will be chosen based on their ability to bind to a MUC1 that is devoid of tandem repeats and for their inability to bind to full-length MUC1. Most often, MUC1* is generated when MUC1 is cleaved by a cleavage enzyme and the tandem repeat domain is released from the cell surface. Cleavage and release of the tandem repeat domain may also unmask portions of MUC1*-like cleavage products that exist on normal tissues. However, antibodies that recognize a conformation, rather than a linear epitope, are more selective. Antibodies that recognize a conformational epitope rather than a linear epitope can be identified by a variety of means. In particular, antibodies that recognize a conformational epitope will not work in a denaturing Western blot assay. In a preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on the ability of the antibody to recognize a conformational epitope.

[00693] Recognize a MUC1* generated by cleavage by MMP9 or other tumor-associated cleavage enzyme

[00694] The fold, or conformation, of the MUC1* truncated extra cellular domain differs depending on which enzyme cleaves MUC1. Cleaved MUC1* or MUC1*-like cleavage products can function as growth factor receptors on normal healthy tissues. More than one cleavage enzyme is able to cleave MUC1 to a MUC1*-like form. Cleavage by first enzyme may produce a conformation or a fold that is not the same as that produced by cleavage by a second enzyme. Support for this can be found in this application and is illustrated in Figures 39-41. These figures show that although a polyclonal antibody that binds to PSMGFR recognizes a cleaved MUC1 on hematopoietic stem cells, some monoclonal antibodies that bind to the PSMGFR peptide can bind to this MUC1*-like form on hematopoietic stem cells while others cannot. For example, MNC3 readily recognizes this cleaved form of MUC1 on hematopoietic stem cells, but MNC2 and MNE6 do not. We know that MNC2 and MNE6 recognize a MUC1* that is produced by cleavage by MMP9 but not when it is cleaved by MMP2. MNC2 and MNE6 are cancer-specific while MNC3 is not, as it recognizes stem and progenitor cells. We also know that MMP9 is overexpressed in cancers. Bone marrow, where hematopoietic stem cells are made expresses nearly 2,500-times more MMP2 than MMP9 (Fig. 65). MMP14 is another enzyme that cleaves MUC1 to a MUC1* growth factor receptor form (Fig. 38). In one aspect of the invention, an antibody is chosen for the treatment, prevention or diagnosis of cancer based on the ability of the antibody to recognize a MUC1 cleavage product generated when MUC1 is cleaved by MMP14. In a preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on the ability of the antibody to recognize a MUC1 cleavage product generated when MUC1 is cleaved by MMP9. In a preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on the ability of the antibody to recognize a MUC1 cleavage product generated when MUC1 is cleaved by MMP9 and also recognizes a conformational epitope.

[00695] Binds to cancer cells more than normal cells

[00696] A traditional approach to identifying antibodies that are cancer-specific involves testing a panel of antibodies against a panel of different cancer cell lines and determining, by FACS, IF, immunoprecipitation or other method, if the antibody binds to cancer cells. Although this approach is traditional, it is sequential and time-consuming, and thus limits the analysis of large numbers of monoclonal antibody clones, which is required to find an ideal antibody suitable for cancer therapeutic or diagnostic. In addition, there are no real normal cell lines and the selection of normal primary cells is limited. The selection criteria presented above provide a rapid, multiplexed method for identifying monoclonal antibody clones that are specific for MUC1* positive cancers. For many of the selection criteria, hybridoma supernatants can be used. This provides a huge advantage over state of the art methods for identifying antibodies that are specific for MUC1* positive cancers. The ability to select antibodies from assay performed using the impure hybridoma supernatants means that much of the selection can be done on hundreds or thousands of clones rapidly and at very little cost. Methods such as FACS analysis ans IHC tissue studies require the use of purified antibodies which limits the number of clones that can be tested to tens, not even hundreds.

[00697] However, selecting an antibody based on its ability to bind to cancer cells, or a cancer cell type or to a cell engineered to express a certain antigen is important for antibody selection. In a preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on the ability of the antibody to bind to MUC1* positive cancer cells.

[00698] Binds to tumor tissue more than normal tissue

[00699] Immunohistochemistry, IHC, tissue studies of cancerous versus normal tissues is a more stringent test of the cancer specificity of antibodies than FACS analysis. Cancer cell lines are a single cell from a single patient that have been expanded in a lab for decades and are not representative of a cross section of the human population. Further, analysis of cell lines is blind to the heterogeneity of actual tumors. Tissue studies require purified antibody, are very expensive, time-consuming and require a skilled pathologist to analyze each stained tissue specimen. However, antibody staining of tissues from normal tissues versus cancerous tissues can reveal which antibodies cannot be used as therapeutics or diagnostics because of their cross-reactivity with normal tissues. Our systematic studies of numerous antibodies with thousands of human normal tissues or cancerous tissues, across several cancer sub-types showed that antibodies that bind to N-10, not C-10, disrupt the binding of NME1 or NME7$_{AB}$, or NME7-X1 to the PSMGFR peptide, the N-10 peptide, or to the surface of a MUC1* positive cancer cell, recognize a conformational epitope, and recognize a conformational epitope created by cleavage by MMP9 are the most cancer-specific.

[00700] In a preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on the ability of the antibody to bind to MUC1* positive tumor tissue at least 2-times more than it binds to normal tissues. In a preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on the ability of the antibody to bind to MUC1* positive tumor tissue at least 5-times more than it binds to normal tissues. In a preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on the ability of the antibody to bind to MUC1* positive tumor tissue at least 10-times more than it binds to normal tissues.

[00701] Antibodies that bind to refined epitopes

[00702] In a preferred embodiment, an antibody, or fragments thereof, that binds to a peptide comprising the sequence QFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA are incorporated into anti-cancer therapeutics or diagnostics.

[00703] In a more preferred embodiment, an antibody, or fragments thereof, that binds to a peptide comprising the sequence ASRYNLTISDVSVSDVPFPFSAQSGA are incorporated into anti-cancer therapeutics or diagnostics.

[00704] In a yet more preferred embodiment, an antibody, or fragments thereof, that binds to a peptide comprising the sequence SDVSVSDVPFPFSAQSGA are incorporated into anti-cancer therapeutics or diagnostics.

[00705] In a still more preferred embodiment, an antibody, or fragments thereof, that binds to a peptide comprising the sequence SVSDV are incorporated into anti-cancer therapeutics or diagnostics.

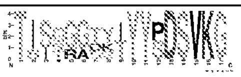
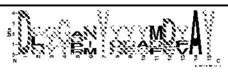
[00706] In a yet still more preferred embodiment, an antibody, or fragments thereof, that binds to a peptide comprising some or all of the sequence PFPFSAQSGA are incorporated into anti-cancer therapeutics or diagnostics.

[00707] Consensus Sequences

[00708] Antibodies of the invention were categorized according to cognate epitope. Sequences of their respective heavy chain CDRs are shown in **Table 5**. Sequences of their respective light chain CDRs are shown in **Table 6**. Consensus sequences for CDR1, CDR2 and CDR3 for each epitope-specific set of antibodies were computer generated. Figure 215 and Figure 216 show how the CDR consensus sequences change as the position of the antibodies' cognate epitope moves from the membrane-proximal portion of PSMGFR toward the more distal portions.

[00709] As can be seen in Table 5 and Table 6, the sequences for CDR1 and CDR2 for antibodies that bind to epitopes within the 10 membrane-proximal (C-terminal) portion of PSMGFR peptide closely adhere to the consensus sequence.

[00710] Table 5: HEAVY CHAIN CDRs

GTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA				
Epitope	**Name**	**CDR1**	**CDR2**	**CDR3**
FPFS	MNC2	FTFSGYAMS	TISSGGTYIYYPDSVKG	-LGGDNYYEYFDV--
FPFS	MNE6	FTFSRYGMS	TISGGGTYIYYPDSVKG	DNYGRNYDYGMDY--
FPFS	20A10	FTFSTYAMS	-SIGRAGSTYYSDSVKG	---GPIYNDYDEFAY
FPFS	3C2B1	ITFSTYTMS	TISTGGDKTYYSDSVKG	-GTTAMYYYAMDY—
Consensus Sequence				
SVSDV	5C6F3	FTFSTYAMS	AISNGGGYTYYPDSLKG	RYYDHYFDY
ASRYNLT	25E6	FTFSSYGMS	TISNGGRHTFYPDSVKG	QTGTEGWFAY
ASRYNLT	MNC3	YRFTDYAMN	VISTFSGNTNFNQKFKG	SDYYGPYFDY
ASRYNLT	18G12	YTFTGYFLY	GINPDNGGIDFNEKFRN	--LIGNY---
ASRYNLT	28F9	YTFTGYFLY	GIHPSNGDTDFNEKFKN	--LIGVY---
Consensus Sequence				
QFNQYKTEA	1E4	YAFSTYWMN	QIYPGDSDTNYNGKFKG	GNHASMDY

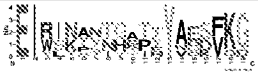
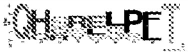
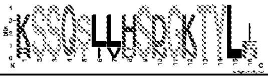
GTINVHDVET	18B4	FTFNDAWMD	EIRSTANIHTTYYAESVQG	-----LLYGFAY
GTINVHDVET	29H1	FTFSDAWMD	EIRSKATNHATYYAESVKG	-----LLYGFAY
GTINVHDVET	31A1	YTFTSYWMH	--YINPSTGYTEYNQKFKD	-----AYIDY--
GTINVHDVET	32C1	FTFSNYWMN	EIRLKSNNYAIHYAESVKG	VPGLDAY-----
GTINVHDVET	39H5	YTFTNYGMN	--WINTYTGEPTYVGDFKG	--GIHGYVDY--
GTINVHDVET	3C5	YTFTNYGMN	--WINTYTGKPTYADDFKG	-GGLDGYYGY–
Consensus Sequence				

Table 6: LIGHT CHAIN CDRs

GTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA				
Epitope	**Name**	**CDR1**	**CDR2**	**CDR3**
FPFS	MNC2	RASKS--VSTSGYSYMH	LASNLES	QHSRELPFT
FPFS	MNE6	-------SATSSVSYIH	STSNLAS	QQRSSSPFT
FPFS	20A10	KSSQSVLYSSNQKNYLA	WASTRES	-HQYLSSLT
FPFS	3C2B1	RASKS---ISTSDYNYIH	LASNLES	QHSRELPLT
Consensus Sequence				
SVSDV	5C6F3	RSSQTIVHSNGNTYLE	KVSNRFS	FQDSHVPLT
ASRYNLT	25E6	KSSQSLLDSDGKTYLN	LVSKLDS	WQGTHFPQT
ASRYNLT	MNC3	RSSQTIVHSNGNTYLE	KVSNRFS	FQGSHVPFT
ASRYNLT	18G12	KSSQSLLHSDGKTYLI	LVSKLDS	CQGTHFPWT
ASRYNLT	28F9	KSSQSLLHSDGKTYLI	LVSKLDS	CQGTHFPWT
Consensus Sequence				
QFNQYKTEA	1E4	RSSQSLVHSNGNTYLH	KVSNRFS	SQKTHVPWT
GTINVHDVET	18B4	RTSQSLVHSNGNTYLH	KVSSRFS	SQNTHVPYT
GTINVHDVET	29H1	RSGQSLVHSNGHTYLH	KVSNRFS	SQTTHVPWT
GTINVHDVET	31A1	RSSQSIVHSNGNTYLE	KVSNRFS	FQVSHFPWT
GTINVHDVET	32C1	RSSQSLVHSNGNTYLH	KVSNRFS	SQITHVPYT
GTINVHDVET	39H5	RSSQSIVHRNGNTYL–	KVSNRFS	FQGSHLPWT
GTINVHDVET	3C5	KSSQSLLHSKGKTYLN	LVSKLES	LQTTHFPWT
Consensus Sequence				

[00711] Whereas Heavy Chain CDR1 for MNC2 is FTFSGYAMS, with the amino acids numbered from left to right 1 through 9, the consensus of other antibodies that bind to that portion of PSMGFR is: F or I at position 1, T at position 2, F at position 3, S at position 4, T, G, or R at position 5, Y at position 6, A, G or T at position 7, M at position 8 and S at position 9.

[00712] In a preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on having a heavy chain CDR1 that is at least 90% identical to a CDR1 comprising the following amino acids at the specified positions: F or I at position 1, T at position 2, F at position 3, S at position 4, T, G, or R at position 5, Y at position 6, A, G or T at position 7, M at position 8 and S at position 9.

[00713] Whereas Heavy Chain CDR2 for MNC2 is TISSGGTYIYYPDSVKG, with the amino acids numbered from left to right 1 through 17, the consensus of other antibodies that bind to that portion of PSMGFR is: T at position 1, I or S at position 2, I or S at position 3, G or R at position 5, G or A at position 6, T or I at position 9, Y at position 10, Y at position 11, P or S at position12 and DSVKG for positions 13-17.

[00714] In a preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on having a heavy chain CDR2 that is at least 90% identical to a CDR2 comprising the following amino acids at the specified positions: T at position 1, I or S at position 2, I or S at position 3, G or R at position 5, G or A at position 6, T or I at position 9, Y at position 10, Y at position 11, P or S at position12 and DSVKG for positions 13-17.

[00715] Whereas Heavy Chain CDR3 for MNC2 is –LGGDNYYEYFDV--, with the amino acids numbered from left to right 1 through 15, the consensus of other antibodies that bind to that portion of PSMGFR is: G, L, or N at position 2, G or T at position 4, Y at position 7, D or E at position 12, A at position 14, and Y at position 15.

[00716] In a preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on having a heavy chain CDR3 that is at least 90% identical to a CDR3 comprising the following amino acids at the specified positions: G, L, or N at position 2, G or T at position 4, Y at position 7, D or E at position 12, A at position 14, and Y at position 15.

[00717] Whereas Light Chain CDR1 for MNC2 is RASKS--VSTSGYSYMH, with the amino acids numbered from left to right 1 through 17, the consensus of other antibodies that bind to that portion of PSMGFR is: K or R at position 1, A or S at position 2, S at position 3, K or Q at position 4, S at position 5, V at position 6, L at position 7, T or S at position 10, Y at position 15, and I, L or M at position 16.

[00718] In a preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on having a light chain CDR1 that is at least 90% identical to a CDR1 comprising the following amino acids at the specified positions: K or R at position 1, A or S at position 2, S at position 3, K or Q at position 4, S at position 5, L or V at position 6, L at position 7, T or S at position 10, Y at position 15, and I, L or M at position 16.

[00719] Whereas Light Chain CDR2 for MNC2 is LASNLES, with the amino acids numbered from left to right 1 through 7, the consensus of other antibodies that bind to that portion of PSMGFR is: L or W, or S at position 1, A or T at position 2, S at position 3, N or T at position 4, L or R at position 5, E or A at position 6, and S at position 7.

[00720] In a preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on having a light chain CDR2 that is at least 90% identical to a CDR2 comprising the following amino acids at the specified positions: L or W, or S at position 1, A or T at position 2, S at position 3, N or T at position 4, L or R at position 5, E or A at position 6, and S at position 7.

[00721] Whereas Light Chain CDR3 for MNC2 is QHSRELPFT, with the amino acids numbered from left to right 1 through 9, the consensus of other antibodies that bind to that portion of PSMGFR is: Q at position 1, H or Q at position 2, S, Q or R at position 3, R, S or Y at position 4, E, L, or S at position 5, L or S at position 6, P or S at position 7, F or L at position 8 and T at position 9.

[00722] In a preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on having a light chain CDR3 that is at least 90% identical to a CDR3 comprising the following amino acids at the specified positions: Q at position 1, H or Q at position 2, S, Q or R at position 3, R, S or Y at position 4, E, L, or S at position 5, L or S at position 6, P or S at position 7, F or L at position 8 and T at position 9.

[00723] Another set of antibodies was generated and resultant clones were tested for their ability to bind to PSMGFR, N-10 and C-10 peptides. Antibody clones that bound to PSMGFR and N-10 peptides, but not to the C-10 peptide were selected. These antibodies were sequenced. Table 7 shows the sequences of the heavy chain CDRs for cancer-specific antibodies MNC2, MNE6, 20A10, 3C2B1, plus new antibodies B2, B7, 8C7F3, H11 and B9. Table 8 shows the sequences of the light chain CDRs for cancer-specific antibodies MNC2, MNE6, 20A10, 3C2B1, plus new antibodies B2, B7, 8C7F3, H11 and B9. Consensus sequences for the heavy and light chain CRDs were generated and are shown in Table 7 and Table 8. Although antibodies 5C6F3 and 25E6 showed great cancer specificity in IHC tissue studies and they both bound to the PSMGFR and N-10 peptides, but not to the C-10 peptide, epitope mapping showed that they bound to epitopes that were a bit N-terminal to the epitopes to which MNC2, MNE6, 20A10 and 3C2B1 bound. For this reason, consensus sequences were generated for MNC2, MNE6, 20A10, 3C2B1 and the new antibodies plus consensus sequences were generated for all the antibodies that bound to N-10 but not to C-10.

[00724] As can be seen in Table 7 and Table 8, the sequences for CDR1, CDR2 and CDR3 for antibodies that require for binding the 10 membrane-proximal (C-terminal) amino acids of PSMGFR peptide closely adhere to a common consensus sequence.

[00725] Table 7: HEAVY CHAIN CDRs for antibodies that share broader epitope in that they cannot bind to the C-10 peptide

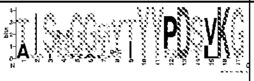
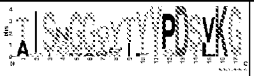
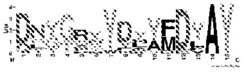
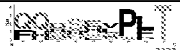
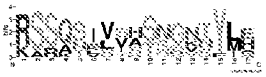
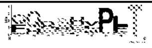
GTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA				
Epitope	**Name**	**CDR1**	**CDR2**	**CDR3**
FPFS	MNC2	FTFSGYAMS	TISSGGTYIYYPDSVKG	-LGGDNYYEYFDV--
FPFS	MNE6	FTFSRYGMS	TISGGGTYIYYPDSVKG	DNYGRNYDYGMDY--
FPFS	20A10	FTFSTYAMS	-SIGRAGSTYYSDSVKG	---GPIYNDYDEFAY
FPFS	3C2B1	ITFSTYTMS	TISTGGDKTYYSDSVKG	-GTTAMYYYAMDY--
PFPFSAQSGA	B2	FAFSTFAMS	AISNGGGYTYYPDTLKG	----RYYDLYFDL--
PFPFSAQSGA	B7	FTFSRYGMS	TISSGGTYIYYPDSVKG	DNYGSSYDYAMDY--
PFPFSAQSGA	8C7F3	FTFSTYAMS	AISNGGGYTYYPDSLKG	----RYYDHYFDY--
PFPFSAQSGA	H11	FAFSTFAMS	AISNGGGYTYYPDTLKG	----RYYDLYFDL--
PFPFSAQSGA	B9	FTFSRYGMS	TISSGGTYIYYPDSVKG	DNYGSSYDYAMDY--
Consensus Sequence - all of antibodies above				
SVSDV	5C6F3	FTFSTYAMS	AISNGGGYTYYPDSLKG	RYYDHYFDY
ASRYNLT	25E6	FTFSSYGMS	TISNGGRHTFYPDSVKG	QTGTEGWFAY
Consensus Sequence - all antibodies				

Table 8: LIGHT CHAIN CDRs for antibodies that share broader epitope in that they cannot bind to the C-10 peptide

GTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA				
Epitope	**Name**	**CDR1**	**CDR2**	**CDR3**
FPFS	MNC2	RASKS--VSTSGYSYMH	LASNLES	QHSRELPFT
FPFS	MNE6	-------SATSSVSYIH	STSNLAS	QQRSSSPFT

FPFS	20A10	KSSQSVLYSSNQKNYLA	WASTRES	-HQYLSSLT
FPFS	3C2B1	RASKS---ISTSDYNYIH	LASNLES	QHSRELPLT
PFPFSAQSGA	B2	RSSQNIV-HSNGNTYLE	KVSNRFS	FQDSHVPLT
PFPFSAQSGA	B7	RSSQTIV-HSNGNTYLE	KVSNRFS	FQDSHVPLT
PFPFSAQSGA	8C7F3	--RASESVATYGNNFMQ	LASTLDS	QQNNEDPPT
PFPFSAQSGA	H11	RSSQNIV-HSNGNTYLE	KVSNRFS	FQDSHVPLT
PFPFSAQSGA	B9	-------SASSSVSYMH	TTSNLAS	QQRSSYPF-
Consensus Sequence - all of antibodies above				
SVSDV	5C6F3	RSSQTIVHSNGNTYLE	KVSNRFS	FQDSHVPLT
ASRYNLT	25E6	KSSQSLLDSDGKTYLN	LVSKLDS	WQGTHFPQT
Consensus Sequence - all antibodies				

[00726] Whereas Heavy Chain CDR1 for MNC2 is FTFSGYAMS, with the amino acids numbered from left to right 1 through 9, the consensus sequence of MNC2, MNE6, 20A10, 3C2B1 and new antibodies B2, B7, 8C7F3, H11 and B9 is: F or I at position 1, T or A at position 2, F at position 3, S at position 4, T, G, or R at position 5, Y or F at position 6, A, G or T at position 7, M at position 8 and S at position 9. The underlined amino acids at positions 2 and 6 are the only additional variants to the consensus sequence generated for cancer-specific antibodies MNC2, MNE6, 20A10, 3C2B1 alone.

[00727] As can be seen in Table 7, the inclusion of antibodies 5C6F3 and 25E6 into the generation of consensus sequence did not change in any way the consensus sequence for heavy chain CDR1 that describes a cancer-specific anti-MUC1* antibody.

[00728] In a preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on having a heavy chain CDR1 that is at least 90% identical to a CDR1 comprising the following amino acids at the specified positions: F or I at position 1, T or A at position 2, F at position 3, S at position 4, T, G, or R at position 5, Y or F at position 6, A, G or T at position 7, M at position 8 and S at position 9.

[00729] Whereas Heavy Chain CDR2 for MNC2 is TISSGGTYIYYPDSVKG, with the amino acids numbered from left to right 1 through 17, the consensus sequence of MNC2, MNE6, 20A10, 3C2B1 and new antibodies B2, B7, 8C7F3, H11 and B9 is:

[00730] T or A at position 1, I or S at position 2, I or S at position 3, N, S, T or G at position 4, G or R at position 5, G or A at position 6, G, T, or D at position 7, Y, K or S at position 8, T or I at position 9, Y at position 10, Y at position 11, P or S at position12 and D at position 13, S or T at position 14, V or L at position 15 and KG for positions 16-17. The underlined amino acids indicate how this more inclusive consensus sequence differs from the consensus sequence generated for MNC2, MNE6, 20A10 and 3C2B1 alone. Of the 17 amino acids in heavy chain CDR2, the consensus sequence for all nine antibodies differs from the consensus sequence for the original cancer-specific four by only 4 amino acids. Note that 2 of the 4 variants are homologous changes, T for S and L for V, which generally do not significantly impact the structure or specificity of a protein.

[00731] As can be seen in Table 7, the inclusion of antibodies 5C6F3 and 25E6 into the generation of consensus sequence for heavy chain CDR2 only changed the consensus sequence by the addition of two other possible amino acids: a possible H at position 8, and a possible F at position 10, for a heavy chain CDR2 that describes a cancer-specific anti-MUC1* antibody. We note that the change of Y to F at position 10 is a homologous change, which generally does not significantly impact the structure or specificity of a protein.

[00732] In a preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on having a heavy chain CDR2 that is at least 90% identical to a CDR2 comprising the following amino acids at the specified positions: T or A at position 1, I or S at position 2, I or S at position 3, N, S, T or G at position 4, G or R at position 5, G or A at position 6, G, T, or D at position 7, Y, K, H or S at position 8, T or I at position 9, Y or F at position 10, Y at position 11, P or S at position12 and D at position 13, S or T at position 14, V or L at position 15 and KG for positions 16-17.

[00733] Whereas Heavy Chain CDR3 for MNC2 is LGGDNYYEYFDV, with the amino acids numbered from left to right 2 through 13, the consensus sequence of MNC2, MNE6, 20A10, 3C2B1 and new antibodies B2, B7, 8C7F3, H11 and B9 is:

[00734] G, L, or N at position 2, G, T, or Y at position 3, G or T at position 4, A, D, P, R, or S at position 5, Y, M, I or S at position 6, Y at position 7, D, Y, or N at position 8, E, D, Y, L or

H at position 9, Y, A, or G at position 10, M, D or F at position 11, D or E at position 12, V, F, Y or L at position 13, and AY at position 14-15. The underlined amino acids indicate how this more inclusive consensus sequence differs from the consensus sequence generated for MNC2, MNE6, 20A10 and 3C2B1 alone. Of the 15 amino acids in heavy chain CDR3, the consensus sequence for all nine antibodies differs from the consensus sequence for the original cancer-specific four by 7 amino acids, with 3 of the 7 substitutions at position 6. For this reason, we conclude that the amino acid at position 6 can be varied without altering the specificity of the antibody.

[00735] Analysis of the consensus sequence generated with the inclusion of antibodies 5C6F3 and 25E6 highlighted which amino acids were conserved among all eleven antibodies. For this reason, our preferred consensus sequence for heavy chain CDR3 defines amino acids at positions 2, 3, 4, 7, 10, 11, 12, 14 and 15, where for 11 antibodies, there were 3 or less variants at these positions.

[00736] In a preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on having a heavy chain CDR3 that is at least 90% identical to a CDR3 comprising the following amino acids at the specified positions: G, L, or N at position 2, G, T, or Y at position 3, G or T at position 4, Y at position 7, Y, A, or G at position 10, M, D or F at position 11, D or E at position 12 and AY at position 14-15.

[00737] Whereas Light Chain CDR1 for MNC2 is RASKS--VSTSGYSYMH, with the amino acids numbered from left to right 1 through 17, the consensus sequence of MNC2, MNE6, 20A10, 3C2B1 and new antibodies B2, B7, 8C7F3, H11 and B9 is:

[00738] K or R at position 1, A or S at position 2, S or R at position 3, K, Q or A at position 4, S, N or T at position 5, V, I, E, or K at position 6, L, V or S at position 7, S, Y, I or V at position 8, A, S, or H at position 9, T or S at position 10, N, S, or Y at position 11, G, S, D, or Q at position 12, V, Y, K or N at position 13, N, S, or T at position 14, Y or F at position 15, and I, L or M at position 16, and H, A, E or Q at position 17. The underlined amino acids indicate how this more inclusive consensus sequence differs from the consensus sequence generated for MNC2, MNE6, 20A10 and 3C2B1 alone. Of the 17 amino acids in light chain CDR1, the consensus sequence for all nine antibodies differs from the consensus sequence for the original cancer-specific four by 13 amino acids. 4 of the 13 are homologous substitutions, which in general do not significantly alter the structure or specificity of the protein. Of the remaining 9 substitutions, 1 is at position 4, 1 is at position 5, 3 are at position 6, 1 is at position 7, 1 is at position 11, and 2 are at is at position 17. The inclusion of the 5 new antibodies did not alter the amino acids, excluding homologous substitutions, at positions 1, 2, 3, 8, 9, 10, 12, 13, 14, 15 or 16. For this reason, we conclude that the conserved consensus sequence for light chain CDR1 that defines a MUC1* cancer-specific antibody comprises the amino acids given above for positions 1, 2, 3, 8, 10, 12, 13, 14, 15 and 16.

[00739] Analysis of the consensus sequence generated with all the antibodies, including 5C6F3 and 25E6 further altered the consensus sequence for light chain CDR1 with amino acid substitutions as follows: L at position 6; D at position 9; D at position 11 and N at position 17. We note that none of these substitutions were at positions that were invariant for the original four cancer-specific antibodies plus the five new antibodies. Thus, we conclude that a conserved consensus sequence for light chain CDR1 that defines at least 90% identity of a cancer-specific antibody comprises amino acids defined above at positions 1, 2, 3, 8, 10, 12, 13, 14, 15 and 16.

[00740] In a preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on having a light chain CDR1 that is at least 90% identical to a CDR1 comprising K or R at position 1, A or S at position 2, S or R at position 3, S, Y, I or V at position 8, T or S at position 10, G, S, D, or Q at position 12, V, Y, K or N at position 13, N, S, or T at position 14, Y or F at position 15, and I, L or M at position 16.

[00741] Whereas Light Chain CDR2 for MNC2 is LASNLES, with the amino acids numbered from left to right 1 through 7, the consensus sequence of MNC2, MNE6, 20A10, 3C2B1 and new antibodies B2, B7, 8C7F3, H11 and B9 is: L, W, S, T or K at position 1, A, T or V at position 2, S at position 3, N or T at position 4, L or R at position 5, E, A, F or D at position 6, and S at position 7. The underlined amino acids indicate how this more inclusive consensus sequence differs from the consensus sequence generated for MNC2, MNE6, 20A10 and 3C2B1 alone.

[00742] In a preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on having a light chain CDR2 that is at least 90% identical to a CDR2 comprising the following amino acids at the specified positions: L, W, S, T or K at position 1, A, T or V at position 2, S at position 3, N or T at position 4, L or R at position 5, E, A, F or D at position 6, and S at position 7. Of the 7 positions, the inclusion of the five new antibodies introduced 5 substitutions of which only 2 were not homologous substitutions.

[00743] Analysis of the consensus sequence generated with all the antibodies, including 5C6F3 and 25E6 further altered the consensus sequence for light chain CDR2 with amino acid substitutions as follows: K at position 4, which is a substitution that is homologous to N.

[00744] In a preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on having a light chain CDR2 that is at least 90% identical to a CDR2 comprising: A, T or V at position 2, S at position 3, N, T, or K at position 4, L or R at position 5, E, A, F or D at position 6, and S at position 7.

[00745] Whereas Light Chain CDR3 for MNC2 is QHSRELPFT, with the amino acids numbered from left to right 1 through 9, t the consensus sequence of MNC2, MNE6, 20A10, 3C2B1 and new antibodies B2, B7, 8C7F3, H11 and B9 is: Q or F at position 1, H or Q at position 2, S, Q, R, D or N at position 3, R, S, Y or N at position 4, E, L, S or H at position 5, L, S, V, D or Y at position 6, P or S at position 7, F, L or P at position 8 and T at position 9. The underlined amino acids indicate how this more inclusive consensus sequence differs from the consensus sequence generated for MNC2, MNE6, 20A10 and 3C2B1 alone.

[00746] Analysis of the consensus sequence generated with all the antibodies, including 5C6F3 and 25E6 further altered the consensus sequence for light chain CDR2 with amino acid substitutions as follows: W at position 1; G at position 3; T at position 4; F at position 5; Q at position 8.

[00747] In a preferred embodiment an antibody is chosen for the treatment, prevention or diagnosis of cancer based on having a light chain CDR3 that is at least 90% identical to a CDR2 comprising: Q, F or W at position 1, H or Q at position 2, R, S, T, Y or N at position 4, E, L, S or H at position 5, L, S, V, D or Y at position 6, P or S at position 7, and T at position 9.

[00748] **Other general strategy for using antibodies, antibody fragments and CARs that target the extracellular domain of MUC1***

[00749] In another aspect, the invention is directed to a composition that includes at least two different plasmids transfected into the same immune cell, wherein the first encodes a CAR comprising an antibody fragment, scFv, or peptide that binds to a tumor antigen and the other encodes a gene that is not a CAR, wherein the gene that is not a CAR is expressed from an inducible promoter that is activated by elements of an activated immune cell. In one aspect, the immune cell is a T cell or an NK cell. In one aspect the CAR comprises an antibody fragment, scFv or peptide that binds to the extra cellular domain of MUC1*. In one aspect the CAR comprises an scFv derived from MNC2, MNE6, 20A10, 3C2B1, 5C6F3, 25E6, 18G12, 28F9, 1E4, B12, B2, B7, B9, 8C7F3, or H11. In one aspect the non-CAR species is a cleavage enzyme. In one aspect the cleavage enzyme is MMP2, MMP3, MMP9, MMP13, MMP14, MMP16, ADAM10, ADAM17, ADAM28 or catalytically active fragments thereof. In another aspect the non-CAR species is a cytokine. In one aspect, the Cytokine is IL-7. In one aspect the cytokine is IL-15. In one aspect the cytokine is IL-12. In one aspect the cytokine is IL-18. The sequence of an activated IL-18 is given (SEQ ID NOS:1637-1638). Two examples of NFAT-inducible IL-18 embedded in the Foxp3 enhancer region are given (SEQ ID NOS:1639-1640). Two examples of NFAT-inducible IL-18 embedded in the IL-2 enhancer region are given (SEQ ID NOS:1641-1642). In one case, there are three (3) NFAT response elements and in the other acse there are six (6) NFAT response elements. The number of NFAT response elements can be varied in order to get the desired amount of IL-18 expressed upon CAR T cell recognition of the target. Examples of antibodies of the invention incorporated into CARS with inducible IL-18 are shown as: murine or human MNC2 in a CAR with a 4-1BB or CD28 co-stimulatory domain plus inducible IL-18 (SEQ ID NOS:1643-1646), or also with a 1XX mutated CD3-zeta (SEQ ID NOS:1647-1650); murine or human MNE6 in a CAR with a 4-1BB or CD28 co-stimulatory domain plus inducible IL-18 (SEQ ID NOS:1651-1654), or also with a 1XX mutated CD3-zeta (SEQ ID NOS:1655-1658); murine or human 20A10 in a CAR with a 4-1BB or CD28 co-stimulatory domain plus inducible IL-18 (SEQ ID NOS:1659-1662), or also with a 1XX mutated CD3-zeta (SEQ ID NOS:1663-1666); murine or human 25E6 in a CAR with a 4-1BB or CD28 co-stimulatory domain plus inducible IL-18 (SEQ ID NOS:1667-1670), or also with a 1XX mutated CD3-zeta (SEQ ID NOS:1671-1674). In another aspect the cytokine is IL-7 and IL-15. In one case expression of the non-CAR species is induced by elements of an activated immune cell. In one aspect the element of an activated immune cell is an NFAT. In one aspect the NFAT is NFATc1, NFATc3 or NFATc2. Cytokines IL-7, IL-15, IL-12 and IL-18 are known to promote T cell persistence. In one aspect of the invention an immune cell described above is administered to a patient for the treatment or prevention of cancer. In one aspect of the invention, the cancer is a MUC1 positive cancer or a MUC1* positive cancer.

[00750] In addition to making CAR T cells that also induce expression of a cleavage enzyme, we made CAR T cells that also induce local and transient expression of IL-18. Many of the T cell based inducible systems reported insert the gene to be inducibly expressed into an IL-2 promoter or enhancer. We compared inducible expression off an IL-2 promoter/enhancer to inducible expression off of a portion of the Foxp3 enhancer. In this particular example, human T cells were transduced with both huMNC2-CAR44 and an NFAT inducible IL-18, wherein the Il-18 gene was either inserted into an IL-2 promoter or the Foxp3 enhancer region. It is known in the field that a major problem with CAR Ts with inducible second factors is that the second factor is leaky, meaning that significant expression of the second factor occurs without activation of the CAR T cell. The other problem with existing inducible systems is the length of time that goes by between when the CAR T cell is activated and the second factor is induced is typically very long so that the cell secreting the second factor may be far away from the tumor by the time the second factor is expressed.

[00751] **Figure 211A- 211C** show graphs of an ELISA experiment measuring the amount of IL-18 secreted into the condition media of huMNC2-CAR44 T cells, which also bear an NFAT inducible IL-18, co-cultured with MUC1* positive cancer cells. As a method of inducing varying levels of IL-18 expression, we co-cultured the CAR T cells with cancer cells doped with increasing amounts of cells that were engineered to express even more MUC1*. In these figures we show T47D cancer cells that are either wild-type, or doped with 5%, 10% or 30% of the T47D cells expressing more MUC1*. Fig. 211A shows the graph of IL-18 secreted into the supernatant of T47D breast cancer cells co-cultured with untransduced human T cells. Fig. 211B shows the graph of IL-18 secreted into the supernatant of T47D breast cancer cells co-cultured with huMNC2-CAR44 T cells that also bore an NFAT inducible IL-18 gene inserted into a portion of the Foxp3 enhancer. Fig. 211C shows the graph of IL-18 secreted into the supernatant of T47D breast cancer cells co-cultured with huMNC2-CAR44 T cells that also bore an NFAT inducible IL-18 gene inserted into a portion of the IL-2 enhancer. As can be seen in the figure, the Foxp3 system induces rapid and robust expression of IL-18, which is significantly faster and higher than that of the same construct in an IL-2 promoter. In this example, the IL-18 gene is inserted downstream of six (6) NFAT response elements, however one can attenuate the amount of the second factor by using a lesser number of response elements or enhance the amount by increasing the number of NFAT response elements.

[00752] It has been reported that IL-18 increases persistence of CAR T cells in vivo. However, we observed an unexpected result. In a dose-dependent manner, secretion of IL-18 increased the killing of low antigen density cells by the CAR T cells. We differentially labeled the T47D-wt cells (red: mCherry) and those T47Ds that were transduced to express more MUC1* (green: GFP). **Figure 212A- 212X** shows photographs of T47D breast cancer cells (red) doped with varying percentages of T47D cells engineered to express more MUC1* (green). The target cancer cells have been co-cultured with huMNC2-CAR44 T cells with NFAT inducible IL-18 wherein the IL-18 gene has been inserted into either the Foxp3 enhancer/promoter or the IL-2 enhancer/promoter. Fig. 212A-212C, 212I-212K, and 212Q-212S show the cancer cells co-cultured with untransduced T cells. Fig. 212D-212F, 212L-212N, and 212T-212V show the cancer cells co-cultured with hiMNC2-CAR44 T cells with the NFAT inducible IL-18 gene inserted into the Foxp3 enhancer/promoter. Fig. 212G-212H, 212O-212P, and 212W-212X show the cancer cells co-cultured with hiMNC2-CAR44 T cells with the NFAT inducible IL-18 gene inserted into the IL-2 enhancer/promoter. As can be seen in the figure, the low antigen density T47D-wt type cells (red) are being killed when doped with higher percentages of cells that express more MUC1* and thus secrete more IL-18. The experiment shows that this is not just a bystander effect, because the cells expressing IL-18 off of the IL-2 promoter, which expresses much lower levels of IL-18, do not kill the low antigen density cells even when they are doped with 30% cells expressing more MUC1*.

[00753] We then showed that the CAR T mediated killing is specific for the CAR T specific antigen. We performed a similar experiment, wherein control, MUC1/MUC1* negative cells were doped with 5%, 10% or 30% of the T47D cells expressing more MUC1*, and co-cultured with MUC1* specific CAR T cells. **Figure 213A- 213B** shows graphs of ELISA experiments in which levels of IL-18 secreted into the conditioned media are measured for huMNC1-CAR44 T cells with NFAT inducible IL-18 gene, inserted into the Foxp3 enhancer or promoter, co-cultured with either MUC1* positive cancer cells or MUC1 negative non-cancerous cells. Fig. 213A shows IL-18 secretion from huMNC2-CAR44 T cells with NFAT inducible IL-18 in co-culture with T47D breast cancer cells where the population has been doped with 5%, 10% or 30% T47D cells that had been transfected with even more MUC1*. Fig. **213**B shows IL-18 secretion from huMNC2-CAR44 T cells with NFAT inducible IL-18 in co-culture with non-cancerous, MUC1 negative HEK293 cells where the cell population has been doped with 5%, 10% or 30% T47D cells that had been transfected with more MUC1*. As can be seen in the figure, the amount of IL-18 secreted into the media can be attributed to the MUC1* positive cells that the population was doped with. Time course fluorescent photographs of the experiment show that even when doped with significant percentages of high antigen density MUC1* positive cells, the MUC1 negative cells are not killed by the MUC1* targeting CAR T cells. **Figure 214A-214X** shows photographs of T47D breast cancer cells (red) or non-cancerous HEK293 cells (also red), where both cell types have been doped with varying percentages of T47D cells engineered to express more MUC1* (green). These target cancer cells have been co-cultured with huMNC2-CAR44 T cells with NFAT inducible IL-18 wherein the IL-18 gene has been inserted into the Foxp3 enhancer/promoter. Fig. 214A-214F shows either T47D cells or HEK293 cells that have not been doped with T47D cells engineered to express high MUC1* density. Fig. 214G-214L shows either T47D cells or HEK293 cells that have been doped with 5% T47D cells engineered to express high MUC1* density. Fig. 214M-214R shows either T47D cells or HEK293 cells that have been doped with 10% T47D cells engineered to express high MUC1* density. Fig. 214S-214X shows either T47D cells or HEK293 cells that have been doped with 30% T47D cells engineered to express high MUC1* density. Fig. 214A-B, G-H, M-N, and S-T show T47D breast cancer cells. Fig. 214C-F, I-L, O-R, and U-X show HEK293 cells. As can be seen in the figures, the induced secretion of IL-18 resulted in low MUC1* density T47D cells being killed but did not induce non-specific killing of the MUC1* negative HEK293 cells. Taken together these results show that the Foxp3 system is a superior system for the inducible expression of a second factor and especially useful in CAR T systems. Further we have demonstrated the unexpected result that IL-18 increases the killing of low antigen density cells without the unwanted effect of killing nearby MUC1/MUC1* negative cells.

[00754] In another aspect, the invention is directed to a composition that includes at least two different plasmids transfected into the same immune cell, wherein the first encodes a CAR comprising an antibody fragment, scFv or peptide that binds to the extra cellular domain of an antigen on the surface of a B cell and the other encodes a gene that is not a CAR, wherein the gene that is not a CAR is expressed from an inducible promoter that is activated by elements of an activated immune cell. In one aspect, the immune cell is a T cell or an NK cell. In one aspect the CAR comprises an antibody fragment, scFv or peptide that binds to CD19. In another aspect the antibody fragment, scFv or peptide binds to a surface antigen of a B cell or a B cell precursor, or binds to CD19, CD20, CD22, BCMA, CD30, CD138, CD123, CD33 or LeY antigen. In one aspect the non-CAR species is a cleavage enzyme. In another aspect the non-CAR species is a cytokine. In one aspect, the Cytokine is IL-7. In one aspect the cytokine is IL-

15. In another aspect the cytokine is IL-7 and IL-15. In one case expression of the non-CAR species is induced by elements of an activated immune cell. In one aspect the element of an activated immune cell is an NFAT. In one aspect the NFAT is NFATc1, NFATc3 or NFATc2. that is not a CAR, wherein the gene that is not a CAR is expressed from an inducible promoter wherein expression is induced by elements of an activated immune cell. In one aspect the immune cell transfected or transduced with the composition is administered to a patient for the treatment or prevention of cancer. In one case the cancer is a leukemia, lymphoma or blood cancer.

[00755] It is not intended for the invention to be limited by a specific method or technology for inserting the gene or plasmid comprising a sequence encoding a CAR or activated T cell inducible protein or peptide there encoded. For example, the gene encoding the CARs and activated T cell induced genes described herein can be virally transduced into an immune cell using viruses, which may or may not result in the CAR gene being integrated into the genome of the recipient cell. Virus delivery systems and viral vectors include but are not limited to retroviruses, including gamma-retroviruses, lentivirus, adenoviruses, adeno-associated viruses, baculoviruses, poxvirus, herpes simplex viruses, oncolytic viruses, HF10, T-Vec and the like. In addition to viral transduction, CARs and activated T cell induced genes decribed herein can be directly spliced into the genome of the recipient cell using methods such as CRISPR technology, CRISPR-Cas9 and -CPF1, TALEN, Sleeping Beauty transposon system, and SB 100X.

[00756] Bulky cell surface proteins such as MUC1-FL can also cause a steric hindrance problem for BiTEs. A BiTE is a two-headed bi-specific antibody wherein one head binds to a T cell and the other head binds to a tumor-associated antigen. In this way, the BiTE links together the T cell and the tumor cells. The antibody that binds to the T cell should be an antibody that activates the T cell, such as an antibody against CD3 or CD28. To solve the steric hindrance problem, the linker between the T cell specific antibody and the tumor specific antibody is lengthened.

[00757] In another aspect of the invention, an anti-MUC1* single chain molecule is fused to a cleavage enzyme or a catalytically active fragment of a cleavage enzyme. In one aspect of the invention, the cleavage enzyme is MMP9 (SEQ ID NO:643). In another aspect of the invention, the enzyme is a catalytically active fragment of MMP9 (SEQ ID NO:645). In some cases, the antibody fragment of the CAR is chosen for its ability to recognize MUC1* when cleaved by that specific cleavage enzyme. In one embodiment, the cleavage enzyme is MMP9, MMP3, MMP14, MMP2, ADAM17, ADAM TS16, and/or ADAM28. In one embodiment, the antibody or antibody fragment binds to a peptide having the sequence of (PSMGFR) GTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA, PSMGFR N-10, QFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA, or PSMGFR N+20 SNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFS AQSGA. In another embodiment, cleavage enzymes MMP9 and MMP3 are transduced into a T cell that is also transduced with a CAR with an antibody fragment that is a fragment of MNC2.

[00758] In many cases it is desirable to have the cleavage enzyme expressed only after an immune cell recognizes the tumor-associated target on a solid tumor. In this way, the cleavage enzyme will not freely move throughout the body, cleaving MUC1, MUC16 or other proteins, wherein their cleavage could actually promote cancer. However, there are cancers that are physically accessible to direct application of chemotherapy agents, CAR T cells and other anti-cancer agents. For example, types of brain cancers, prostate cancer and ovarian cancers have all shown the benefit of direct application of anti-cancer agents into the local vicinity of the cancer. CAR T cells have been injected directly into the brain and/or cerebral spinal fluid of glioblastoma patients. Radiation has been directed to the prostate area for the treatment of prostate cancers, including those that have metastasized. Hot chemo therapy agents have been directly injected into the intraperitoneal cavity for the treatment of ovarian cancers. In these and other cases, where the cancers that are physically accessible to direct application of chemotherapy agents, a cleavage enzyme is administered in the presence or absence of another anti-cancer agent, which could be a CAR T cell, an immune cell engineered to recognize a tumor-associated antigen, a BiTE, an ADC, a biological or a standard chemotherapy agent. Although ovarian cancer can metastasize to anywhere in the body, it usually stays in the abdomen as it spreads to adjacent organs, such as the intestines, liver and stomach. This makes ovarian cancer an ideal test case for improving the effect of anti-cancer agents by administering a cleavage enzyme in combination with other anti-cancer agents, including a platinum-based drug such as carboplatin (Paraplatin) or cisplatin, and/or a taxane such as paclitaxel (Taxol) or docetaxel (Taxotere). Alkeran (Melphalan), Avastin (Bevacizumab), Carboplatin, Clafen (Cyclophosphamide), and Cytoxan have all been approved for the treatment of ovarian cancer. Other treatments that are being tested for the treatment of ovarian cancers include agents that target MUC1, MUC16 and as described herein, MUC1*.

[00759] Other cleavage enzymes can be used in addition to or in place of MMP9. MMP14 for example, has been shown to efficiently cleave MUC1 to MUC1* (Fig. 38). In one aspect of the invention, MMP14 is expressed in an immune cell that is also engineered to express a CAR. In one case the CAR is an anti-MUC1* CAR. For example, it can be an MNC2-CAR44 transduced T cell. In another aspect of the invention, the MMP14 is directly administered to the patient either in the location of the tumor or by i.v.

[00760] In yet another aspect of the invention, the cancer is an ovarian cancer and either MMP9 or MMP14 is directly injected into the abdominal area along with an anti-cancer agent, which can be a chemotherapy agent, a biological, an anti-MUC1* CAR T or an anti-MUC16 CAR T.

[00761] In addition to local administration of the cleavage enzyme, + iv administration alone or secreted from an immune cell, which may be a CAR T cell, which further may be expressed off of an inducible promoter is contemplated.

[00762] Methods used in carrying out experimentation in relation to the present invention

[00763] 1. *Lentivirus production* and viral transduction of immune cells

[00764] HEK293 or HEK293T cells (ATCC) were used to produce lentivirus. The day prior transfection plates (6well plate) were coated with poly-D-lysine and cells seeded so that cell density reaches 90-95% at the time of transfection and cultures in a 5% CO_2 atmosphere. The next day cells were transfected with Lipofectamine 3000 (life technologies) and Opti-MEM® I Reduced Serum Medium according to the manufacturer instructions (0.75ug of lentiviral expression vector and 2.25ug of pPACKH1 packaging mix was used). After 6h incubation, the media was changed and media containing lentivirus was harvested after 24 and 48 hours. Lentivirus was concentrated with Lenti-X concentrator (Clontech) and titer was calculated using the Lenti-X p@4 Rapid Titer Kit (Clontech). Lentivirus was store at -80C in single-use aliquots.

[00765] Transduction of immune cells with constructs including CARs

[00766] Human T cells, if frozen, were thawed and pre-warmed in 100-200 units IL-2 and TexMACS medium, 20 ml, and pelleted by centrifugation. Cells were resuspended in 10 ml of

medium and cultured at 37°C, 5% CO_2 at $1x10^6$ cells/ml in complete medium with anti-CD3/anti-CD28 beads (TransAct kit).

[00767] After 4 days in culture, cells were counted and 450 ul of cell suspension was placed in single well of a 24-well plate at a density of approximately $1x10^6$ cells/ml. Cells were allowed to settle. 150 ul was carefully removed from the top of each well. To each well was added an appropriate dilution of lentiviral vector, diluted in plain TexMACS medium, along with protamine sulfate to a final concentration of 10 ug/ml, in a 150 ul volume, for a final total volume of 450 ul per well and incubated for 24 hrs. Transduced cells were removed, pelleted by centrifugation, and resuspended in fresh medium, adjusting cell density, not to exceed 1.0×10^6 cells/ml. Transduced T cells can be expanded and frozen or used directly. Typically transduced T cells are used or frozen between Day 7 and Day 20 post activation with IL-2 and TransAct media.

[00768] **2. Comparing anti-MUC1* CAR T cell activity in the presence or absence of exogenous cleavage enzymes**

[00769] Human T cells (ALLCELLS) were transduced with huMNC2-CAR44 or huMNC2-CAR50. CAR44 is huMNC2-scFv-CD8-CD8 (transmembrane-41BB-3z). CAR50 is the same as CAR44 except that CAR50 has a murine MNC2-scFv and a CD4 transmembrane domain. The CAR T cells were incubated for 18 hours with target and non-target cells that have been dyed red using CMTMR. When T cells recognize a target cell, they cluster the target cells and begin to kill them. As can be seen in **Figures 45-47** the CAR T cells effectively cluster and kill the target MUC1* positive cancer cells. Figure 45 shows huMNC2-CAR44 or huMNC2-CAR50 T cells being co-cultured with HCT-116 cells transduced to express MUC1*, "HCT-MUC1*" or with HCT-116 cells transduced with a full-length MUC1, "HCT-MUC1-41TR". Recall that MNC2 recognizes an ectopic epitope that is only revealed after cleavage and release of the MUC1 tandem repeat domain. Neither huMNC2-CAR44 nor huMNC2-CAR50 T cells recognize the cells expressing full-length MUC1 (Fig. 45F-45H). However, when MMP9 plus activator APMA is added, the CAR T cells recognize the cells, cluster and kill them (Fig. 45J-45L). The addition of cleavage enzyme ADAM-17 did not affect the recognition of either CAR T cell for full-length MUC1 (Fig. 45N-45P). The reason could be that ADAM-17 doesn't cleave MUC1 or the cleavage product is not recognized by MNC2. A similar experiment was performed (Fig. 46) that showed that MMP2 was only weakly effective at either cleavage MUC1 or that the MMP2 cleavage product was only weakly recognized by MNC2. Figure 47 shows the contrast between huMNC2-CAR44 recognition of HCT-MUC1* cells, T47D-wt breast cancer cells, and T47D cells with added MMP9 which presumably cleaves the full-length MUC1 to an MNC2 recognizable MUC1*.

[00770] 3. Confocal imaging of CAR T cells giving the "kiss of death" to MUC1* positive cancer cells.

[00771] Confocal images of Human T cells that were transduced with huMNC2-CAR44, co-cultured for 24 hours with MUC1* positive DU145 prostate cancer cells showed the CAR T cells inserting Granzyme B into the target cancer cells. Figure 55 shows fluorescent images of the huMNC2-CAR44 T cells secreting Granzyme B when co-cultured with the prostate cancer cells, FACS analysis showing increased expression of Granzyme B by the CAR T cells and an xCELLigence experiment showing that the target prostate cancer cells were in fact killed.

[00772] 5. Analysis of CAR T cell induced killing of MUC1* positive cancer cells by FACS analysis

[00773] We have demonstrated the killing effect of huMNC2-CAR44 T cells on T47D MUC1* positive breast cancer cells, wherein the breast cancer cells have been transfected with increasing amounts of additional MUC1*. The killing effect of the huMNC2-CAR44 T cells increases as the amount of target MUC1* expressed on the cells increases.

[00774] IFN-γ secretion in media was measured using a human IFN-γ ELISA kit (Biolegend). Plates were coated with an anti- IFN-γ antibody (capture antibody, 1X in coating buffer). After overnight incubation at 4°C, the plate was washed 4 times with PBS-T and blocking solution was added to block remaining binding site on the well. After 1h at RT (shaking at 500rpm) the plate was washed 4 times with PBS-T and conditioned media (CM) and IFN-γ standard, was added. After 2h at RT with shaking, the plate was washed 4 times with PBS-T and detection antibody (1x), was added. After 1h at RT with shaking, the plate was washed 4 times with PBS-T and Avidin-HRP (1x) was added. After 30min at RT with shaking, the plate was washed 5 times with PBS-T (soak 1min each wash) and TMB substrate solution was added. The reaction was stopped after 20min by adding the stop solution and absorbance was read at 450nm (minus absorbance at 570nm) within 15 min of stopping.

[00775] 6. Analysis of CAR T cell induced killing of MUC1* positive cancer cells by xCELLigence

[00776] In addition to FACS analysis, many researchers now use an xCELLigence instrument to measure CAR T killing of cancer cells. The xCELLigence instrument uses electrode arrays upon which cancer cells are plated. The adherent cancer cells insulate the electrode and so cause an increase in impedance as they grow. Conversely, T cells are not adherent and remain in suspension so do not contribute to insulation of the electrode which would increase impedance. However, if the T cells or CAR T cells kill the cancer cells on the electrode plate, the cancer cells ball up and float off as they die, which causes the impedance to decrease. The xCELLigence instrument measures impedance as a function of time, which is correlated to cancer cell killing. In addition, the electrode plates also have a viewing window. When CAR T cells effectively kill the adsorbed target cancer cells, there is a decrease in impedance but also one can see that there are no cancer cells left on the plate surface.

[00777] In most of the XCELLigence experiments, 5,000 cancer cells were plated per well of a 96-well electrode array plate. Cells were allowed to adhere and grow for 24 hours. CAR T cells were then added at an Effector to Target ratio (E:T) of 0.5:1, 1:1, 2:1, 5:1, 10:1 and sometimes 20:1. The E:T ratio assumes 100% transduction of the CAR into the T cells, when the actual transduction efficiency is 40%.

[00778] The xCELLigence instrument records impedance as a function of time and experiments can go on for up to 7 days.

[00779] **Fig. 48**, **Fig. 49**, **Fig. 55H**, **Fig. 56H**, **Figs. 57A-57C**, all show results of CAR T and cancer cell experiments performed on an xCELLigence instrument.

[00780] **7. Anti-MUC1* CAR T cell therapy in mice bearing human tumors**

[00781] Female NOD/SCID/GAMMA (NSG) mice between 8-12 weeks of age were implanted with 500,000 human cancer cells, wherein the cancer cells had previously been stably transfected with Luciferase. Mice bearing Luciferase positive cells can be injected with the enzyme's substrate Luciferin just prior to imaging, which makes the cancer cells fluoresce. The cancer cells are imaged in live mice within 10-15 minutes after injection with Luciferin on an IVIS instrument. The readout is flux or photons per second. Tumors were allowed to engraft until tumors were clearly visible by IVIS.

[00782] **Figures 58A-58F** show fluorescent photographs of mice taken on an IVIS instrument. 10 minutes prior to IVIS photographs, mice were injected intraperitoneally (IP) with Luciferin, which fluoresces after cleavage by Luciferase, thus making tumor cells fluoresce. NSG

(NOD/SCID/GAMMA) immune compromised mice that on Day 0 were subcutaneously implanted on the flank with 500,000 human MUC1* positive cancer cells that had been stably transfected with Luciferase. Tumors were allowed to engraft. On Day 7 after IVIS measurement, animals were tail vein injected with either PBS, 10 million untransduced human T cells or 8.5M huMNC2-scFv-CAR44 T cells. As can be seen in the figure, control mice had to be sacrificed on Day 20 due to excess tumor burden (Fig. 58A-58B). huMNC2-CAR44 T cell treated mice were tumor free after a single CAR T cell injection until Day 100 when they were sacrificed (Fig. 58C). Figure 58E shows Kaplan-Meier survival curves that demonstrate the efficacy of T cell therapy guided by anti-MUC1* antibody. Figure 58F shows a table summarizing the characteristics of the human T cells that were collected from the test mice upon sacrifice. The starting Car T cell population was 50% CD4 positive helper T cells and 50% CD8 positive killer T cells. As can be seen in the table, the percent of CD8 positive cells has increased in the CAR T treated group, indicating in vivo expansion of that group of cells, which is an indicator of efficacy. We also note that in the treated group, the CAR T cells express higher levels of PD1 which is a marker of T cell exhaustion.

[00783] In another animal experiment, NSG mice were sub-cutaneously implanted into the flank with 500,000 tumor cells then injected on Day 7 and again on Day 14 with either saline solution, PBS, or 10M huMNC2-CAR44 T cells (Fig. 59A-59C). In this experiment the amount of MUC1* expressed on the tumor cells was varied. In one case, the tumor cells that were implanted were T47D-wildtype (Fig. 59B). In another case, the T47D cells were doped with 95% T47D cells that had been transfected to express even more MUC1* (Fig. 59C). As can be seen, the tumors comprised of cells expressing more MUC1* were eliminated more quickly and did not recur. In a similar experiment, the tumor cells were doped with a relatively small amount of cells that expressed more MUC1*. Figure 60A-60C shows NSG mice implanted with T47D-wt breast cancer cells that have been doped with 30% of T47D cells transfected to express more MUC1*. As can be seen, even a small percentage of cells expressing high levels of MUC1* is sufficient to trigger CAR T cell mediated killing of the entire tumor. Naturally occurring tumors are heterogeneous and are comprised of both high and low antigen expressing cells. This experiment indicates that huMNC2-CAR44 T cells would be effective in eradicating naturally occurring tumors.

[00784] **Figures 61A-61J** show fluorescent photographs of mice taken on an IVIS instrument. NSG (NOD/SCID/GAMMA) immune compromised mice that on Day 0 were subcutaneously injected into the flank with 500K human BT-20 cells which are a MUC1* positive triple negative breast cancer cell line. The cancer cells had been stably transfected with Luciferase. Tumors were allowed to engraft. On Day 6 after IVIS measurement, animals were given a one-time injection of 10 million of either human T cells transduced with huMNC2-scFv-CAR44 or untransduced T cells. 5 million T cells were injected intra-tumor and 5 million were injected into the tail vein. 10 minutes prior to IVIS photographs, mice were IP injected with Luciferin. In one case the huMNC2-CAR44 T cells were first incubated with beads to which was attached the PSMGFR peptide to pre-stimulate the T cells and in the figure is marked Protocol 1. In Protocol 2, the huMNC2-CAR44 T cells were pre-stimulated with live tumor cells, which likely injected more tumor cells into the animals' circulation.

[00785] **Figures 62A-62M** show fluorescent photographs of mice taken on an IVIS instrument. NSG (NOD/SCID/GAMMA) immune compromised mice that on Day 0 were injected into the intraperitoneal cavity (IP) with 500K human SKOV-3 cells which are a MUC1* positive ovarian cancer cell line. The cancer cells had been stably transfected with Luciferase. Tumors were allowed to engraft. On Day 3 after IVIS measurement, animals were IP injected with 10M either human T cells transduced with huMNC2-CAR44 T cells, untransduced T cells or PBS. Animals were IVIS imaged again on Day 7. 10 minutes prior to IVIS photographs, mice were IP injected with Luciferin. As can be seen in the figure the anti-MUC1* CAR T cells effectively reduced ovarian tumor volume by Day 15.

[00786] **9. NFAT-induced IL-18 sequences and cloning**

[00787] Cloning of IL18 in pGL4-14 3xNFAT:

[00788] An activated IL18 (SEQ ID NO:1644) was synthesized with the CD8 leader sequence. The pGL4-14 3xIL2 NFAT and pGL4-14 3xFoxP3 NFAT were digested with XhoI and HindIII restriction enzymes (New England Biolabs). The purified plasmids and the synthesized IL18 sequences were assembled using the Gibson assembly cloning kit (New England Biolab). The resulting constructs (pGL4-14 3xIL2NFAT-IL18 and pGL4-14 3xFoxP3NFAT-IL18) contains 3 repeats of NFAT response element (IL2 or FoxP3) followed by a minimum promoter (mCMV: SEQ ID NO:1634) and IL18 (SEQ ID NOS:1752-1753) with CD8 leader sequence.

[00789] Cloning of MNC2 CAR with IL18 in pCDNA vector:

[00790] MNC2 CAR sequence was amplified from previously made vector by polymerase chain reaction (PCR) using the following primers: 5’-agggagacccaagctggctagttaagcttggatggccttaccagtgaccgccttgc-3’ (SEQ ID NO:1754) and 5’-taggccagagaaatgttctggcattatcagcgagggggcagggcctgc-3’ (SEQ ID NO:1755).

[00791] IL18 sequence including NFAT response element was amplify from pGL4-14 3xNFAT-IL18 by polymerase chain reaction (PCR) using the following primers: 5’-tgccagaacatttctctgg-3’ (SEQ ID NO:1756) and 5’-acagtcgaggctgatcagcgggtttaaacttatcagtcctcgttctgcacgg-3’ (SEQ ID NO: 1757). The purified PCR fragments and digested pCDNA 3.1 V5 (ThermoFisher scientific) were assembled using the Gibson assembly cloning kit (New England Biolab) to create the construct pCDNA MNC2CAR-3xIL2NFAT-IL18 and pCDNA MNC2CAR-3xFoxP3NFAT-IL18.

[00792] Cloning of MNC2 CAR-NFAT-IL18 in lentivector:

[00793] MNC2 CAR-NFAT-IL18 sequence was amplified from pCDNA MNC2CAR-3xIL2NFAT-IL18 and pCDNA MNC2CAR-3xFoxP3NFAT-IL18.by polymerase chain reaction (PCR) using the following primers: 5’-atgcaggccctgccccctcgctgataagtttaaactgccagaacatttctctggcctaac-3’ (SEQ ID NO:1758) and 5’-accggagcgatcgcagatccttcgcggccgcttatcagtcctcgttctgcacggtgaac-3’ (SEQ ID NO:1759). The purified PCR fragments and digested pCDH Dual Hygro (System Biosciences, CA) were assembled using the Gibson assembly cloning kit (New England Biolab) to create the construct pCDH MNC2CAR-3xIL2NFAT-IL18 and pCDH MNC2CAR-3xFoxP3NFAT-IL18.

[00794] Creation of lentivector with MSCV promoter

[00795] MSCV promoter sequence was amplified from pCDH-MSCV-MCS-EF1a-GFP (System Biosciences).by polymerase chain reaction (PCR) using the following primers: 5’-attgcactagttgaaagaccccacctgtagg-3’ (SED ID NO:1760) and 5’- aatgctctagaatacgggtatccagg-3’ (SEQ ID NO:1761). After digestion with SpeI and XbaI restriction enzymes (New England Biolabs), the purified fragment was cloned into pCDH CMV MCS (System Bioscience) digested with the same restriction enzymes to create the construct pCDH MSCV MCS.

[00796] Cloning of MNC2 CAR-NFAT-IL18 in pCDH MSCV MCS:

[00797] MNC2 CAR-IL2NFAT-IL18 sequence was amplified from pCDNA MNC2CAR-3xIL2NFAT-IL18 by polymerase chain reaction (PCR) using the following primers: 5’ atagcgaattcgtaccgagggccaccatgg-3’ (SEQ ID NO:1762) and 5’-taggcctcccaccgtacacgcctaggtaccacgccttctgtatg-3’ (SEQ ID NO:1763) MNC2 CAR-IL2NFAT-IL18 sequence was amplified from pCDNA MNC2CAR-3xFoxP3NFAT-IL18 by polymerase chain reaction (PCR) using the following primers: 5’ atagcgaattcgtaccgagggccaccatgg -3’ (SEQ ID NO:1762) and 5’- taggcctcccaccgtacacgcctaggtacctctgcagtaaatgg-3’ (SEQ ID NO:1764). After digestion with EcoRI and KpnI restriction enzymes (New England Biolabs), the purified fragment was cloned into pCDH MSCV MCS digested with the same restriction enzymes to create the construct pCDH MSCV MNC2CAR-3xIL2NFAT-IL18 and pCDH MSCV MNC2CAR-3xFoxP3NFAT-IL18.

[00798] Cloning of 6xNFAT response elements:

[00799] 6xNFAT (IL2 and FoxP3) response element were synthesized followed by different minimal promoter: mCMV (SEQ ID NO:1634), mIL2P (SEQ ID NO:1635) and miniP (SEQ ID NO:1636). A total of six 6 sequences were synthesized: SEQ ID NOS: 1768-1779.

[00800] 6xNFAT sequences were amplified by polymerase chain reaction (PCR) using the following primers: 5’-tgccagaacatttctctgg-3’ (SEQ ID NO:1756) and 5’- taaggccatggtggctagc-3’ (SEQ ID NO:1765). The purified PCR fragments and digested (KpnI and XhoI) pCDNA MNC2CAR 3XNFAT IL18 were assembled using the Gibson assembly cloning kit (New England Biolab) to create constructs with 6x NFAT response elements in place of the 3x NFAT response elements.

[00801] 6xNFAT sequences were amplified, from the pCDNA vector created above, by polymerase chain reaction (PCR) using the following primers: 5’-aataagtttaaactgccagaacatttctctgg-3’ (SEQ ID NO:1766) and 5’-atatagcggccgcttatcagtcctcgttctgcacgg-3’ (SEQ ID NO:1767). After digestion with PmeI and NotI restriction enzymes (New England Biolabs), the purified fragments were cloned into pCDH MSCV MNC2CAR digested with the same restriction enzymes to create the construct pCDH MSCV MNC2CAR-6xIL2NFAT-IL18 and pCDH MSCV MNC2CAR-6xFoxP3NFAT-IL18. For each construct 3 minimal promoter were tested.

[00802] **Sequence Listing Free Text**

[00803] As regards the use of nucleotide symbols other than a, g, c, t, they follow the convention set forth in WIPO Standard ST.25, Appendix 2, Table 1, wherein k represents t or g; n represents a, c, t or g; m represents a or c;

r represents a or g; s represents c or g; w represents a or t and y represents c or t.

MUC1 Receptor

(Mucin 1 precursor, Genbank Accession number: P15941)
MTPGTQSPFFLLLLLTVLTVVTGSGHASSTPGGEKETSATQRSSVPSSTEKNAVSMTSSVLSSHSPGSGSSTTQGQDV
TLAPATEPASGSAATWGQDVTSVPVTRPALGSTTPPAHDVTSAPDNKPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAH
GVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPP
AHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTA
PPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGS
TAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAP
GSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRP
APGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDT
RPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAP
DTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTS
APDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGV
TSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAH
GVTSAPDNRPALGSTAPPVHNVTSASGSASGSASTLVHNGTSARATTTPASKSTPFSIPSHHSDTPTTLASHSTKTDA
SSTHHSSVPPLTSSNHSTSPQLSTGVSFFFLSFHISNLQFNSSLEDPSTDYYQELQRDISEMFLQIYKQGGFLGLSNI
KFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGAGVPGWGIALLVLVCVL
VALAIVYLIALAVCQCRRKNYGQLDIFPARDTYHPMSEYPTYHTHGRYVPPSSTDRSPYEKVSAGNGGSSLSYTNPAV
AAASANL (SEQ ID NO:1)

PSMGFR

GTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA (SEQ ID NO: 2)

[00804] **N-10 peptide**

[00805] QFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA (SEQ ID NO:3)

[00806] N-19

[00807] ASRYNLTISDVSVSDVPFPFSAQSGA (SEQ ID NO:4)

[00808] N-23

[00809] NLTISDVSVSDVPFPFSAQSGA (SEQ ID NO:5)

[00810] N-26

[00811] ISDVSVSDVPFPFSAQSGA (SEQ ID NO:6)

[00812] N-30

[00813] SVSDVPFPFSAQSGA (SEQ ID NO:7)

[00814] N-10/C-5

[00815] QFNQYKTEAASRYNLTISDVSVSDVPFPFS (SEQ ID NO:8)

[00816] N-19/C-5

[00817] ASRYNLTISDVSVSDVPFPFS (SEQ ID NO:9)

[00818] N-36

[00819] FPFSAQSGA (SEQ ID NO:10)

Mouse E6 Heavy chain variable region sequence:

(DNA)

gaggtgaaggtggtggagtctgggggagacttagtgaagcctggagggtccctgaaactctcctgtgtagtctctgga
ttcactttcagtagatatggcatgtcttgggttcgccagactccaggcaagaggctggagtgggtcgcaaccattagt
ggtggcggtacttacatctactatccagacagtgtgaaggggcgattcaccatctccagagacaatgccaagaacacc
ctgtacctgcaaatgagcagtctgaagtctgaggacacagccatgtatcactgtacaagggataactacggtaggaac
tacgactacggtatggactactggggtcaaggaacctcagtcaccgtctcctca (SEQ ID NO:12)

(amino acids)
EVKVVESGGDLVKPGGSLKLSCVVSGFTFSRYGMSWVRQTPGKRLEWVATISGGGTYIYYPDSVKGRFTISRDNAKNT
LYLQMSSLKSEDTAMYHCTRDNYGRNYDYGMDYWGQGTSVTVSS (SEQ ID NO:13)

Mouse E6 heavy chain variable framework region 1 (FWR1) sequence:
(DNA)
gaggtgaaggtggtggagtctgggggagacttagtgaagcctggagggtccctgaaactctcctgtgtagtctct
(SEQ ID NO:14)

(amino acids)
EVKVVESGGDLVKPGGSLKLSCVVSGFTFS (SEQ ID NO:15)

Mouse E6 heavy chain variable complementarity determining regions 1 (CDR1) sequence:
(DNA)
ggattcactttcagtagatatggcatgtct (SEQ ID NO:16)

(amino acids)
RYGMS (SEQ ID NO:17)

Mouse E6 heavy chain variable framework region 2 (FWR2) sequence:
(DNA)
tgggttcgccagactccaggcaagaggctggagtgggtcgca (SEQ ID NO:18)

(amino acids)
WVRQTPGKRLEWVA (SEQ ID NO:19)

Mouse E6 heavy chain variable complementarity determining regions 2 (CDR2) sequence:
(DNA)
accattagtggtggcggtacttacatctactatccagacagtgtgaagggg (SEQ ID NO:20)

(amino acids)
TISGGGTYIYYPDSVKG(SEQ ID NO:21)

Mouse E6 heavy chain variable framework region 3 (FWR3) acid sequence:
(DNA)
cgattcaccatctccagagacaatgccaagaacaccctgtacctgcaaatgagcagtctgaagtctgaggacacagc
catgtatcactgtacaagg (SEQ ID NO:22)

(amino acids)
RFTISRDNAKNTLYLQMSSLKSEDTAMYHCTR (SEQ ID NO:23)

Mouse E6 heavy chain variable complementarity determining regions 3 (CDR3) sequence:
(DNA)
gataactacggtaggaactacgactacggtatggactac (SEQ ID NO:24)

(amino acids)
DNYGRNYDYGMDY (SEQ ID NO:25)

Humanized E6 heavy chain variable region sequence from IGHV3-21*03:
(DNA)
gaggtgcagctggtggagtctgggggaggcctggtcaagcctggggggtccctgagactctcctgtgcagcctctgg
attcaccttcagtaggtatggcatgagctgggtccgccaggctccagggaagaggctggagtgggtctcaaccatta
gtggcggaggcacctacatatactacccagactcagtgaagggccgattcaccatctccagagacaacgccaagaac
accctgtatctgcaaatgaacagcctgagagccgaggacacggctgtgtattactgtaccagagataactatggccg
caactatgattatggcatggattattggggccagggcaccctggtgaccgtgagcagc (SEQ ID NO:38)

(amino acids)
EVQLVESGGGLVKPGGSLRLSCAASGFTFSRYGMSWVRQAPGKRLEWVSTISGGGTYIYYPDSVKGRFTISRDNAKN
TLYLQMNSLRAEDTAVYYCTRDNYGRNYDYGMDYWGQGTLVTVSS (SEQ ID NO:39)

Humanized E6 heavy chain variable framework region 1 (FWR1) acid sequence:
(DNA)
gaggtgcagctggtggagtctgggggaggcctggtcaagcctggggggtccctgagactctcctgtgcagcctctgg
attcaccttcagt (SEQ ID NO:40)

(amino acids)
EVQLVESGGGLVKPGGSLRLSCAASGFTFS (SEQ ID NO:41)
Humanized E6 heavy chain variable complementarity determining regions 1 (CDR1) sequence:
(DNA)
aggtatggcatgagc (SEQ ID NO:42)

(amino acids)
RYGMS (SEQ ID NO:43)

Humanized E6 heavy chain variable framework region 2 (FWR2) acid sequence:
(DNA)
tgggtccgccaggctccagggaagaggctggagtgggtctca (SEQ ID NO:44)

(amino acids)
WVRQAPGKRLEWVS (SEQ ID NO:45)

Humanized E6 heavy chain variable complementarity determining regions 2 (CDR2) sequence:
(DNA)
accattagtggcggaggcacctacatatactacccagactcagtgaagggc (SEQ ID NO:46)

(amino acids)
TISGGGTYIYYPDSVKG (SEQ ID NO:47)

Humanized E6 heavy chain variable framework region 3 (FWR3) acid sequence:
(DNA)
cgattcaccatctccagagacaacgccaagaacaccctgtatctgcaaatgaacagcctgagagccgaggacacggct
gtgtattactgtaccaga (SEQ ID NO:48)

(amino acids)
RFTISRDNAKNTLYLQMNSLRAEDTAVYYCTR (SEQ ID NO:49)

Humanized E6 heavy chain variable complementarity determining regions 3 (CDR3) sequence:
(DNA)
gataactatggccgcaactatgattatggcatggattat (SEQ ID NO:50)

(amino acids)
DNYGRNYDYGMDY (SEQ ID NO:51)

Humanized E6 IgG2 heavy chain synthesized by Genescript:
(DNA)
gaattctaagcttgggccaccatggaactggggctccgctgggttttccttgttgctattttagaaggtgtccagtgt
gaggtgcagctggtggagtctgggggaggcctggtcaagcctggggggtccctgagactctcctgtgcagcctctgga
ttcaccttcagtaggtatggcatgagctgggtccgccaggctccagggaagaggctggagtgggtctcaaccattagt
ggcggaggcacctacatatactacccagactcagtgaagggccgattcaccatctccagagacaacgccaagaacacc
ctgtatctgcaaatgaacagcctgagagccgaggacacggctgtgtattactgtaccagagataactatggccgcaac
tatgattatggcatggattattggggccagggcaccctggtgaccgtgagcagcgcctccaccaagggcccatcggtc
ttccccctggcgccctgctccaggagcacctccgagagcacagccgccctgggctgcctggtcaaggactacttcccc
gaaccggtgacggtgtcgtggaactcaggcgctctgaccagcggcgtgcacaccttcccagctgtcctacagtcctca
ggactctactccctcagcagcgtggtgaccgtgccctccagcaacttcggcacccagacctacacctgcaacgtagat
cacaagcccagcaacaccaaggtggacaagacagttgagcgcaaatgttgtgtcgagtgcccaccgtgcccagcacca
cctgtggcaggaccgtcagtcttcctcttccccccaaaacccaaggacaccctcatgatctcccggacccctgaggtc
acgtgcgtggtggtggacgtgagccacgaagaccccgaggtccagttcaactggtacgtggacggcgtggaggtgcat
aatgccaagacaaagccacgggaggagcagttcaacagcacgttccgtgtggtcagcgtcctcaccgttgtgcaccag
gactggctgaacggcaaggagtacaagtgcaaggtctccaacaaaggcctcccagcccccatcgagaaaaccatctcc
aaaaccaaagggcagccccgagaaccacaggtgtacaccctgcccccatcccgggaggagatgaccaagaaccaggtc
agcctgacctgcctggtcaaaggcttctaccccagcgacatcgccgtggagtgggagagcaatgggcagccggagaac
aactacaagaccacacctcccatgctggactccgacggctccttcttcctctacagcaagctcaccgtggacaagagc
aggtggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcctc
tccctgtctccgggtaaatagtaagtttaaactctaga (SEQ ID NO:52)

(amino acids)
EF*AWATMELGLRWVFLVAILEGVQCEVQLVESGGGLVKPGGSLRLSCAASGFTFSRYGMSWVRQAPGKRLEWVSTIS
GGGTYIYYPDSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCTRDNYGRNYDYGMDYWGQGTLVTVSSASTKGPSV
FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVD
HKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVH
NAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQV
SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK**V*TLX (SEQ ID NO:53)

Human IgG2 heavy chain constant region sequence:
(DNA)
gcctccaccaagggcccatcggtcttccccctggcgccctgctccaggagcacctccgagagcacagccgccctgggc
tgcctggtcaaggactacttccccgaaccggtgacggtgtcgtggaactcaggcgctctgaccagcggcgtgcacacc
ttcccagctgtcctacagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagcaacttcggcacc
cagacctacacctgcaacgtagatcacaagcccagcaacaccaaggtggacaagacagttgagcgcaaatgttgtgtc
gagtgcccaccgtgcccagcaccacctgtggcaggaccgtcagtcttcctcttccccccaaaacccaaggacaccctc
atgatctcccggacccctgaggtcacgtgcgtggtggtggacgtgagccacgaagaccccgaggtccagttcaactgg
tacgtggacggcgtggaggtgcataatgccaagacaaagccacgggaggagcagttcaacagcacgttccgtgtggtc
agcgtcctcaccgttgtgcaccaggactggctgaacggcaaggagtacaagtgcaaggtctccaacaaaggcctccca
gcccccatcgagaaaaccatctccaaaaccaaagggcagccccgagaaccacaggtgtacaccctgcccccatcccgg
gaggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctaccccagcgacatcgccgtggagtgg
gagagcaatgggcagccggagaacaactacaagaccacacctcccatgctggactccgacggctccttcttcctctac
agcaagctcaccgtggacaagagcaggtggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctctgcac
aaccactacacgcagaagagcctctccctgtctccgggtaaatag (SEQ ID NO:54)

(amino acids)
ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGT
QTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNW
YVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSR
EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH
NHYTQKSLSLSPGK (SEQ ID NO:55)

Humanized E6 IgG1 heavy chain sequence:
(DNA)

gaggtgcagctggtggagtctgggggaggcctggtcaagcctggggggtccctgagactctcctgtgcagcctctgga
ttcaccttcagtaggtatggcatgagctgggtccgccaggctccagggaagaggctggagtgggtctcaaccattagt
ggcggaggcacctacatatactacccagactcagtgaagggccgattcaccatctccagagacaacgccaagaaccca
ctgtatctgcaaatgaacagcctgagagccgaggacacggctgtgtattactgtcccagagataactatggccgcaac
tatgattatggcatggattattggggccagggcaccctggtgaccgtgagcagcgctagcaccaagggcccatcggtc
ttccccctggcaccctcctccaagagcacctctgggggcacagcggccctgggctgcctggtcaaggactacttcccc
gaaccggtgacggtgtcgtggaactcaggcgccctgaccagcggcgtgcacaccttcccggctgtcctacagtcctca
ggactctactccctcagcagcgtggtgacagtgccctccagcagcttgggcacccagacctacatctgcaacgtgaat
cacaagcccagcaacaccaaggtggacaagaaagttgagcccaaatcttgtgacaaaactcacacatgcccaccgtgc
ccagcacctgaactcctggggggaccgtcagtcttcctcttccccccaaaacccaaggacaccctcatgatctcccgg
acccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggc
gtggaggtgcataatgccaagacaaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcacc
gtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgag
aaaaccatctccaaagccaaagggcagccccgagaaccacaggtgtacaccctgcccccatcccgggaggagatgacc
aagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggagtgggagagcaatggg
cagccggagaacaactacaagaccacgcctcccgtgctggactccgacggctccttcttcctctacagcaagctcacc
gtggacaagagcaggtggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacg
cagaagagcctctccctgtctccgggtaaatgataa (SEQ ID NO:56)

(amino acids)
EVQLVESGGGLVKPGGSLRLSCAASGFTFSRYGMSWVRQAPGKRLEWVSTISGGGTYIYYPDSVKGRFTISRDNAKNP
LYLQMNSLRAEDTAVYYCPRDNYGRNYDYGMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC
PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK** (SEQ ID NO:57)

Human IgG1 heavy chain constant region sequence:
(DNA)
gctagcaccaagggcccatcggtcttccccctggcaccctcctccaagagcacctctgggggcacagcggccctgggc
tgcctggtcaaggactacttccccgaaccggtgacggtgtcgtggaactcaggcgccctgaccagcggcgtgcacacc
ttcccggctgtcctacagtcctcaggactctactccctcagcagcgtggtgacagtgccctccagcagcttgggcacc
cagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagaaagttgagcccaaatcttgtgac
aaaactcacacatgcccaccgtgcccagcacctgaactcctggggggaccgtcagtcttcctcttccccccaaaaccc
aaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtc
aagttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccgcgggaggagcagtacaacagcacg
taccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaac
aaagccctcccagcccccatcgagaaaaccatctccaaagccaaagggcagccccgagaaccacaggtgtacaccctg
cccccatcccgggaggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatc
gccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactccgacggctcc
ttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcaggggaacgtcttctcatgctccgtgatgcat
gaggctctgcacaaccactacacgcagaagagcctctccctgtctccgggtaaatgataa (SEQ ID NO:58)

(amino acids)
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT
QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPGK** (SEQ ID NO:59)

Mouse E6 Light Chain variable region sequence:
(DNA)
caaattgttctcacccagtctccagcaatcatgtctgcatctccaggggaggaggtcaccctaacctgcagtgccacc
tcaagtgtaagttacatacactggttccagcagaggccaggcacttctcccaaactctggatttatagcacatccaac
ctggcttctggagtccctgttcgcttcagtggcagtggatatgggacctcttactctctcacaatcagccgaatggag

gctgaagatgctgccacttattactgccagcaaaggagtagttccccattcacgttcggctcggggacaaagttggaa
ataaaa (SEQ ID NO:65)
(amino acids)
QIVLTQSPAIMSASPGEEVTLTCSATSSVSYIHWFQQRPGTSPKLWIYSTSNLASGVPVRFSGSGYGTSYSLTISRME
AEDAATYYCQQRSSSPFTFGSGTKLEIK (SEQ ID NO:66)

Mouse E6 light chain variable framework region 1 (FWR1) sequence:
(DNA)
caaattgttctcacccagtctccagcaatcatgtctgcatctccaggggaggaggtcaccctaacctgc (SEQ ID NO:67)

(amino acids)
QIVLTQSPAIMSASPGEEVTLTC (SEQ ID NO:68)

Mouse E6 light chain variable complementarity determining regions 1 (CDR1) sequence:
(DNA)
AGTGCCACCTCAAGTGTAAGTTACATACAC (SEQ ID NO:69)

(amino acids)
SATSSVSYIH (SEQ ID NO:70)

Mouse E6 light chain variable framework region 2 (FWR2) sequence:
(DNA)
tggttccagcagaggccaggcacttctcccaaactctggatttat (SEQ ID NO:71)

(amino acids)
WFQQRPGTSPKLWIY (SEQ ID NO:72)
Mouse E6 light chain variable complementarity determining regions 2 (CDR2) sequence:
(DNA)
agcacatccaacctggcttct (SEQ ID NO:73)

(amino acids)
STSNLAS (SEQ ID NO:74)

Mouse E6 light chain variable framework region 3 (FWR3) sequence:
(DNA)
ggagtccctgttcgcttcagtggcagtggatatgggacctcttactctctcacaatcagccgaatggaggctgaaga
tgctgccacttattactgc (SEQ ID NO:75)

(amino acids)
GVPVRFSGSGYGTSYSLTISRMEAEDAATYYC (SEQ ID NO:76)

Mouse E6 light chain variable complementarity determining regions 3 (CDR3) sequence:
(DNA)
cagcaaaggagtagttccccattcacg (SEQ ID NO:77)

(amino acids)
QQRSSSPFT (SEQ ID NO:78)

Humanized E6 light chain variable region sequence from IGKV3-11*02:
(DNA)
gaaattgtgttgacacagtctccagccaccctgtctttgtctccaggggaaagagccaccctcacctgcagcgccacc
agcagtgttagctacatccactggtaccaacagaggcctggccagagccccaggctcctcatctatagcacctccaac

ctggccagcggcatcccagccaggttcagtggcagtgggtctgggagcgactacactctcaccatcagcagcctagag
cctgaagattttgcagtttattactgtcagcagcgtagcagctcccctttcacctttggcagcggcaccaaagtggaa
attaaa (SEQ ID NO:93)

(amino acids)
EIVLTQSPATLSLSPGERATLTCSATSSVSYIHWYQQRPGQSPRLLIYSTSNLASGIPARFSGSGSGSDYTLTISSLE
PEDFAVYYCQQRSSSPFTFGSGTKVEIK (SEQ ID NO:94)

Humanized E6 light chain variable framework region 1 (FWR1) acid sequence:
(DNA)
gaaattgtgttgacacagtctccagccaccctgtctttgtctccaggggaaagagccaccctcacctgc (SEQ ID NO:95)

(amino acids)
EIVLTQSPATLSLSPGERATLTC (SEQ ID NO:96)

Humanized E6 light chain variable complementarity determining regions 1 (CDR1) sequence:
(DNA)
agcgccaccagcagtgttagctacatccac (SEQ ID NO:97)

(amino acids)
SATSSVSYIH (SEQ ID NO:98)

Humanized E6 heavy light variable framework region 2 (FWR2) acid sequence:
(DNA)
tggtaccaacagaggcctggccagagccccaggctcctcatctat (SEQ ID NO:99)

(amino acids)
WYQQRPGQSPRLLIY (SEQ ID NO:100)

Humanized E6 light chain variable complementarity determining regions 2 (CDR2) sequence:
(DNA)
agcacctccaacctggccagc (SEQ ID NO:101)

(amino acids)
STSNLAS (SEQ ID NO:102)

Humanized E6 light chain variable framework region 3 (FWR3) acid sequence:
(DNA)
ggcatcccagccaggttcagtggcagtgggtctgggagcgactacactctcaccatcagcagcctagagcctgaagat
tttgcagtttattactgt (SEQ ID NO:103)

(amino acids)
GIPARFSGSGSGSDYTLTISSLEPEDFAVYYC (SEQ ID NO:104)

Humanized E6 light chain variable complementarity determining regions 3 (CDR3) sequence:
(DNA)
cagcagcgtagcagctcccctttcacc (SEQ ID NO:105)

(amino acids)
QQRSSSPFT (SEQ ID NO:106)

Humanized E6 Kappa light chain synthesized by Genescript:
(DNA)
gaattctaagcttgggccaccatggaagccccagcgcagcttctcttcctcctgctactctggctcccagataccact
ggagaaattgtgttgacacagtctccagccaccctgtctttgtctccaggggaaagagccaccctcacctgcagcgcc

accagcagtgttagctacatccactggtaccaacagaggcctggccagagccccaggctcctcatctatagcacctcc
aacctggccagcggcatcccagccaggttcagtggcagtgggtctgggagcgactacactctcaccatcagcagccta
gagcctgaagattttgcagtttattactgtcagcagcgtagcagctcccctttcacctttggcagcggcaccaaagtg
gaaattaaaaggacggtggctgcaccatctgtcttcatcttcccgccatctgatgagcagttgaaatctggaactgcc
tctgttgtgtgcctgctgaataacttctatcccagagaggccaaagtacagtggaaggtggataacgccctccaatcg
ggtaactcccaggagagtgtcacagagcaggacagcaaggacagcacctacagcctcagcagcaccctgacgctgagc
aaagcagactacgagaaacacaaagtctacgcctgcgaagtcacccatcagggcctgagctcgcccgtcacaaagagc
ttcaacaggggagagtgttagtaagtttaaactctaga (SEQ ID NO:107)

(amino acids)
EF*AWATMEAPAQLLFLLLLWLPDTTGEIVLTQSPATLSLSPGERATLTCSATSSVSYIHWYQQRPGQSPRLLIYSTS
NLASGIPARFSGSGSGSDYTLTISSLEPEDFAVYYCQQRSSSPFTFGSGTKVEIKRTVAAPSVFIFPPSDEQLKSGTA
SVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKS
FNRGEC**V*TLX (SEQ ID NO:108)

Human Kappa light chain constant region sequence:
(DNA)
aggacggtggctgcaccatctgtcttcatcttcccgccatctgatgagcagttgaaatctggaactgcctctgttgtg
tgcctgctgaataacttctatcccagagaggccaaagtacagtggaaggtggataacgccctccaatcgggtaactcc
caggagagtgtcacagagcaggacagcaaggacagcacctacagcctcagcagcaccctgacgctgagcaaagcagac
tacgagaaacacaaagtctacgcctgcgaagtcacccatcagggcctgagctcgcccgtcacaaagagcttcaacagg
ggagagtgttag (SEQ ID NO:109)

(amino acids)
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKAD
YEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:110)

Humanized E6 lambda light chain sequence:
(DNA)
gaaattgtgttgacacagtctccagccaccctgtctttgtctccaggggaaagagccaccctcacctgcagcgccacc
agcagtgttagctacatccactggtaccaacagaggcctggccagagccccaggctcctcatctatagcacctccaac
ctggccagcggcatcccagccaggttcagtggcagtgggtctgggagcgactacactctcaccatcagcagcctagag
cctgaagattttgcagtttattactgtcagcagcgtagcagctcccctttcacctttggcagcggcaccaaagtggaa
attaaaggtcagcccaaggctgccccctcggtcactctgttcccgccctcctctgaggagcttcaagccaacaaggcc
acactggtgtgtctcataagtgacttctacccgggagccgtgacagtggcctggaaggcagatagcagccccgtcaag
gcgggagtggagaccaccacaccctccaaacaaagcaacaacaagtacgcggccagcagctatctgagcctgacgcct
gagcagtggaagtcccacagaagctacagctgccaggtcacgcatgaagggagcaccgtggagaagacagtggcccct
acagaatgttcatagtaa (SEQ ID NO:111)

(amino acids)
EIVLTQSPATLSLSPGERATLTCSATSSVSYIHWYQQRPGQSPRLLIYSTSNLASGIPARFSGSGSGSDYTLTISSLE
PEDFAVYYCQQRSSSPFTFGSGTKVEIKGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK
AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS** (SEQ ID NO:112)

Humanized lambda light chain constant region sequence:
(DNA)
ggtcagcccaaggctgccccctcggtcactctgttcccgccctcctctgaggagcttcaagccaacaaggccacactg
gtgtgtctcataagtgacttctacccgggagccgtgacagtggcctggaaggcagatagcagccccgtcaaggcggga
gtggagaccaccacaccctccaaacaaagcaacaacaagtacgcggccagcagctatctgagcctgacgcctgagcag
tggaagtcccacagaagctacagctgccaggtcacgcatgaagggagcaccgtggagaagacagtggcccctacagaa
tgttcatagtaa (SEQ ID NO:113)

(amino acids)
GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQ
WKSHRSYSCQVTHEGSTVEKTVAPTECS** (SEQ ID NO:114)

Mouse C2 heavy chain variable region sequence:

(DNA)
gaggtccagctggaggagtcaggggggaggcttagtgaagcctggagggtccctgaaactctcctgtgcagcctctgg
attcactttcagtggctatgccatgtcttgggttcgccagactccggagaagaggctggagtgggtcgcaaccatta
gtagtggtggtacttatatctactatccagacagtgtgaaggggcgattcaccatctccagagacaatgccaagaac
accctgtacctgcaaatgagcagtctgaggtctgaggacacggccatgtattactgtgcaagacttgggggggataa
ttactacgaatacttcgatgtctggggcgcagggaccacggtcaccgtctcctccgccaaaacgacacccccatctg
tctat (SEQ ID NO:118)

(amino acids)
EVQLEESGGGLVKPGGSLKLSCAASGFTFSGYAMSWVRQTPEKRLEWVATISSGGTYIYYPDSVKGRFTISRDNAKN
TLYLQMSSLRSEDTAMYYCARLGGDNYYEYFDVWGAGTTVTVSSAKTTPPSVY (SEQ ID NO:119)

Mouse C2 heavy chain variable framework region 1 (FWR1) sequence:

(DNA)
gaggtccagctggaggagtcaggggggaggcttagtgaagcctggagggtccctgaaactctcctgtgcagcctctgg
attcactttcagt (SEQ ID NO:120)

(amino acids)
EVQLEESGGGLVKPGGSLKLSCAASGFTFS (SEQ ID NO:121)

Mouse C2 heavy chain variable complementarity determining regions 1 (CDR1) sequence:

(DNA)
ggctatgccatgtct (SEQ ID NO:122)

(amino acids)
GYAMS (SEQ ID NO:123)

Mouse C2 heavy chain variable framework region 2 (FWR2) sequence:

(DNA)
tgggttcgccagactccggagaagaggctggagtgggtcgca (SEQ ID NO:124)

(amino acids)
WVRQTPEKRLEWVA (SEQ ID NO:125)

Mouse C2 heavy chain variable complementarity determining regions 2 (CDR2) sequence:

(DNA)
accattagtagtggtggtacttatatctactatccagacagtgtgaagggg (SEQ ID NO:126)

(amino acids)
TISSGGTYIYYPDSVKG (SEQ ID NO:127)

Mouse C2 heavy chain variable framework region 3 (FWR3) sequence:

(DNA)
cgattcaccatctccagagacaatgccaagaacaccctgtacctgcaaatgagcagtctgaggtctgaggacacggcc
atgtattactgtgcaaga (SEQ ID NO:128)

(amino acids)
RFTISRDNAKNTLYLQMSSLRSEDTAMYYCAR (SEQ ID NO:129)

Mouse C2 heavy chain variable complementarity determining regions 3 (CDR3) sequence:

(DNA)
cttgggggggataattactacgaatacttcgatgtc (SEQ ID NO:130)

(amino acids)

LGGDNYYEYFDV (SEQ ID NO:131)

Humanized derived from **IGHV3-21*04:**
Humanized C2 heavy chain variable region sequence:
(DNA)
gaggtgcagctggtggagtctgggggaggcctggtcaagcctggggggtccctgagactctcctgtgcagcctctgga
ttcaccttcagtggctatgccatgagctgggtccgccaggctccagggaaggggctggagtgggtctcaaccattagt
agtggcggaacctacatatactaccccgactcagtgaagggccgattcaccatctccagagacaacgccaagaactca
ctgtatctgcaaatgaacagcctgagagccgaggacacggccgtgtattactgtgcgagacttgggggggataattac
tacgaatacttcgatgtctggggcaaagggaccacggtcaccgtctcctcc (SEQ ID NO:144)

(amino acids)
EVQLVESGGGLVKPGGSLRLSCAASGFTFSGYAMSWVRQAPGKGLEWVSTISSGGTYIYYPDSVKGRFTISRDNAKNS
LYLQMNSLRAEDTAVYYCARLGGDNYYEYFDVWGKGTTVTVSS (SEQ ID NO:145)

Humanized C2 heavy chain variable framework region 1 (FWR1) sequence:
(DNA)
gaggtgcagctggtggagtctgggggaggcctggtcaagcctggggggtccctgagactctcctgtgcagcctctgga
ttcaccttcagt (SEQ ID NO:146)

(amino acids)
EVQLVESGGGLVKPGGSLRLSCAASGFTFS (SEQ ID NO:147)
Humanized C2 heavy chain variable complementarity determining regions 1 (CDR1) sequence:
(DNA)
ggctatgccatgagc (SEQ ID NO:148)

(amino acids)
GYAMS (SEQ ID NO:149)

Humanized C2 heavy chain variable framework region 2 (FWR2) sequence:
(DNA)
tgggtccgccaggctccagggaaggggctggagtgggtctcaa (SEQ ID NO:150)

(amino acids)
WVRQAPGKGLEWVS (SEQ ID NO:151)

Humanized C2 heavy chain variable complementarity determining regions 2 (CDR2) sequence:
(DNA)
accattagtagtggcggaacctacatatactaccccgactcagtgaagggc (SEQ ID NO:152)

(amino acids)
TISSGGTYIYYPDSVKG (SEQ ID NO:153)

Humanized C2 heavy chain variable framework region 3 (FWR3) sequence:
(DNA)
cgattcaccatctccagagacaacgccaagaactcactgtatctgcaaatgaacagcctgagagccgaggacacggcc
gtgtattactgtgcgaga (SEQ ID NO:154)

(amino acids)
RFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR (SEQ ID NO:155)

Humanized C2 heavy chain variable complementarity determining regions 3 (CDR3) sequence:
(DNA)
cttgggggggataattactacgaatacttcgatgtc (SEQ ID NO:156)

(amino acids)
LGGDNYYEYFDV (SEQ ID NO:157)

Humanized C2 IgG1 heavy chain sequence

(DNA)
gaggtgcagctggtggagtctgggggaggcctggtcaagcctggggggtccctgagactctcctgtgcagcctctgga
ttcaccttcagtggctatgccatgagctgggtccgccaggctccagggaaggggctggagtgggtctcaaccattagt
agtggcggaacctacatatactaccccgactcagtgaagggccgattcaccatctccagagacaacgccaagaactca
ctgtatctgcaaatgaacagcctgagagccgaggacacggccgtgtattactgtgcgagacttgggggggataattac
tacgaatacttcgatgtctggggcaaagggaccacggtcaccgtctcctccgctagcaccaagggcccatcggtcttc
cccctggcaccctcctccaagagcacctctgggggcacagcggccctgggctgcctggtcaaggactacttccccgaa
ccggtgacggtgtcgtggaactcaggcgccctgaccagcggcgtgcacaccttcccggctgtcctacagtcctcagga
ctctactccctcagcagcgtggtgacagtgccctccagcagcttgggcacccagacctacatctgcaacgtgaatcac
aagcccagcaacaccaaggtggacaagaaagttgagcccaaatcttgtgacaaaactcacacatgcccaccgtgccca
gcacctgaactcctggggggaccgtcagtcttcctcttccccccaaaacccaaggacaccctcatgatctcccggacc
cctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtg
gaggtgcataatgccaagacaaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtc
ctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaa
accatctccaaagccaaagggcagccccgagaaccacaggtgtacaccctgcccccatcccgggaggagatgaccaag
aaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggagtgggagagcaatgggcag
ccggagaacaactacaagaccacgcctcccgtgctggactccgacggctccttcttcctctacagcaagctcaccgtg
gacaagagcaggtggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcag
aagagcctctccctgtctccgggtaaatgataa (SEQ ID NO:157)

(amino acids)
EVQLVESGGGLVKPGGSLRLSCAASGFTFSGYAMSWVRQAPGKGLEWVSTISSGGTYIYYPDSVKGRFTISRDNAKNS
LYLQMNSLRAEDTAVYYCARLGGDNYYEYFDVWGKGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP
APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ
PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK** (SEQ ID NO:158)

Humanized C2 IgG2 heavy chain sequence

(DNA)
gaggtgcagctggtggagtctgggggaggcctggtcaagcctggggggtccctgagactctcctgtgcagcctctgga
ttcaccttcagtggctatgccatgagctgggtccgccaggctccagggaaggggctggagtgggtctcaaccattagt
agtggcggaacctacatatactaccccgactcagtgaagggccgattcaccatctccagagacaacgccaagaactca
ctgtatctgcaaatgaacagcctgagagccgaggacacggccgtgtattactgtgcgagacttgggggggataattac
tacgaatacttcgatgtctggggcaaagggaccacggtcaccgtctcctccgcctccaccaagggcccatcggtcttc
cccctggcgccctgctccaggagcacctccgagagcacagccgccctgggctgcctggtcaaggactacttccccgaa
ccggtgacggtgtcgtggaactcaggcgctctgaccagcggcgtgcacaccttcccagctgtcctacagtcctcagga
ctctactccctcagcagcgtggtgaccgtgccctccagcaacttcggcacccagacctacacctgcaacgtagatcac
aagcccagcaacaccaaggtggacaagacagttgagcgcaaatgttgtgtcgagtgcccaccgtgcccagcaccacct
gtggcaggaccgtcagtcttcctcttccccccaaaacccaaggacaccctcatgatctcccggacccctgaggtcacg
tgcgtggtggtggacgtgagccacgaagaccccgaggtccagttcaactggtacgtggacggcgtggaggtgcataat
gccaagacaaagccacgggaggagcagttcaacagcacgttccgtgtggtcagcgtcctcaccgttgtgcaccaggac
tggctgaacggcaaggagtacaagtgcaaggtctccaacaaaggcctcccagcccccatcgagaaaaccatctccaaa
accaaagggcagccccgagaaccacaggtgtacaccctgcccccatcccgggaggagatgaccaagaaccaggtcagc
ctgacctgcctggtcaaaggcttctaccccagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaac
tacaagaccacacctcccatgctggactccgacggctccttcttcctctacagcaagctcaccgtggacaagagcagg
tggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcctctcc
ctgtctccgggtaaatagtaa (SEQ ID NO:163)

(amino acids)

EVQLVESGGGLVKPGGSLRLSCAASGFTFSGYAMSWVRQAPGKGLEWVSTISSGGTYIYYPDSVKGRFTISRDNAKNS
LYLQMNSLRAEDTAVYYCARLGGDNYYEYFDVWGKGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPE
PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPP
VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQD
WLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN
YKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK** (SEQ ID NO:164)

Mouse C2 light chain variable region sequence:
(DNA)
gacattgtgatcacacagtctacagcttccttaggtgtatctctggggcagagggccaccatctcatgcagggccagc
aaaagtgtcagtacatctggctatagttatatgcactggtaccaacagagaccaggacagccacccaaactcctcatc
tatcttgcatccaacctagaatctggggtccctgccaggttcagtggcagtgggtctgggacagacttcaccctcaac
atccatcctgtggaggaggaggatgctgcaacctattactgtcagcacagtagggagcttccgttcacgttcggaggg
gggaccaagctggagataaaacgggctgatgctgcaccaactgtatcc (SEQ ID NO:168)

(amino acids)
DIVITQSTASLGVSLGQRATISCRASKSVSTSGYSYMHWYQQRPGQPPKLLIYLASNLESGVPARFSGSGSGTDFTLN
IHPVEEEDAATYYCQHSRELPFTFGGGTKLEIKRADAAPTVS (SEQ ID NO:169)

Mouse C2 light chain variable framework region 1 (FWR1) sequence:
(DNA)
gacattgtgatcacacagtctacagcttccttaggtgtatctctggggcagagggccaccatctcatgc (SEQ ID NO:170)

(amino acids)
DIVITQSTASLGVSLGQRATISC (SEQ ID NO:171)

Mouse C2 light chain variable complementarity determining regions 1 (CDR1) sequence:
(DNA)
agggccagcaaaagtgtcagtacatctggctatagttatatgcac (SEQ ID NO:172)

(amino acids)
RASKSVSTSGYSYMH (SEQ ID NO:173)

Mouse C2 light chain variable framework region 2 (FWR2) sequence:
(DNA)
tggtaccaacagagaccaggacagccacccaaactcctcatctat (SEQ ID NO:174)

(amino acids)
WYQQRPGQPPKLLIY (SEQ ID NO:175)

Mouse C2 light chain variable complementarity determining regions 2 (CDR2) sequence:
(DNA)
cttgcatccaacctagaatc (SEQ ID NO:176)

(amino acids)
LASNLES (SEQ ID NO:177)

Mouse C2 light chain variable framework region 3 (FWR3) sequence:
(DNA)
tggggtccctgccaggttcagtggcagtgggtctgggacagacttcaccctcaacatccatcctgtggaggaggagga
tgctgcaacctattactgt (SEQ ID NO:178)

(amino acids)
GVPARFSGSGSGTDFTLNIHPVEEEDAATYYC (SEQ ID NO:179)

Mouse C2 light chain variable complementarity determining regions 3 (CDR3) sequence:
(DNA)
cagcacagtagggagcttccgttcacg (SEQ ID NO:180)

(amino acids)
QHSRELPFT (SEQ ID NO:181)

Humanized derived from **IGKV7-3*01**
Humanized C2 light chain variable region sequence:
(DNA)
gacattgtgctgacccagtctccagcctccttggccgtgtctccaggacagagggccaccatcacctgcagagccagtaagagtgtcagtaccagcggatactcctacatgcactggtatcagcagaaaccaggacaacctcctaaactcctgatttacctggcatccaatctggagagcggggtcccagccaggttcagcggcagtgggtctgggaccgatttcaccctcacaattaatcctgtggaagctaatgatactgcaaattattactgtcagcacagtagggagctgcctttcacattcggcggagggaccaaggtggagatcaaacgaact (SEQ ID NO:194)

(amino acids)
DIVLTQSPASLAVSPGQRATITCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLASNLESGVPARFSGSGSGTDFTLTINPVEANDTANYYCQHSRELPFTFGGGTKVEIKRT (SEQ ID NO:195)
Humanized C2 light chain variable framework region 1 (FWR1) acid sequence:
(DNA)
gacattgtgctgacccagtctccagcctccttggccgtgtctccaggacagagggccaccatcacctgc (SEQ ID NO:196)

(amino acids)
DIVLTQSPASLAVSPGQRATITC (SEQ ID NO:197)
Humanized C2 light chain variable complementarity determining regions 1 (CDR1) sequence:
(DNA)
agagccagtaagagtgtcagtaccagcggatactcctacatgcac (SEQ ID NO:198)

(amino acids)
RASKSVSTSGYSYMH (SEQ ID NO:199)

Humanized C2 heavy light variable framework region 2 (FWR2) acid sequence:
(DNA)
tggtatcagcagaaaccaggacaacctcctaaactcctgatttac (SEQ ID NO:200)

(amino acids)
WYQQKPGQPPKLLIY (SEQ ID NO:201)

Humanized C2 light chain variable complementarity determining regions 2 (CDR2) sequence:
(DNA)
ctggcatccaatctggagagc (SEQ ID NO:202)

(amino acids)
LASNLES (SEQ ID NO:203)

Humanized C2 light chain variable framework region 3 (FWR3) acid sequence:
(DNA)
ggggtcccagccaggttcagcggcagtgggtctgggaccgatttcaccctcacaattaatcctgtggaagctaatgatactgcaaattattactgt (SEQ ID NO:204)

(amino acids)

GVPARFSGSGSGTDFTLTINPVEANDTANYYC (SEQ ID NO:205)

Humanized C2 light chain variable complementarity determining regions 3 (CDR3) sequence:
(DNA)
cagcacagtagggagctgcctttcaca (SEQ ID NO:206)

(amino acids)
QHSRELPFT (SEQ ID NO:207)

Humanized C2 light chain variable complementarity determining regions 3 (CDR3) sequence:
(DNA)
ctgcagagtaagaattttcctcccaca (SEQ ID NO:208)

(amino acids)
LQSKNFPPT (SEQ ID NO:209)

Murine Ig kappa chain leader sequence
(DNA)
atggagacagacacactcctgctatgggtactgctgctctgggttccaggttccactggtgac (SEQ ID NO:222)

(amino acids)
METDTLLLWVLLLWVPGSTGD (SEQ ID NO:223)

Interleukin-2 (IL-2) leader sequence
(DNA)
atgtacaggatgcaactcctgtcttgcattgcactaagtcttgcacttgtcacaaacagt (SEQ ID NO:224)

(amino acids)
MYRMQLLSCIALSLALVTNS (SEQ ID NO:225)

CD33 leader sequence
(DNA)
atgcctcttctgcttctgcttcctctgctttgggctggagctcttgct (SEQ ID NO:226)

(amino acids)
MPLLLLLPLLWAGALA (SEQ ID NO:227)

IGHV3-21*03 leader sequence
(DNA)
atggaactggggctccgctgggttttccttgttgctattttagaaggtgtccagtgt (SEQ ID NO:228)

(amino acids)
MELGLRWVFLVAILEGVQC (SEQ ID NO:229)

IGHV3-11*02 leader sequence
(DNA)
atggaagccccagcgcagcttctcttcctcctgctactctggctcccagataccactgga (SEQ ID NO:230)

(amino acids)
MEAPAQLLFLLLLWLPDTTG (SEQ ID NO:231)
Humanized E6 single chain GS3
(DNA)
gaggtgcagctggtggagtctgggggaggcctggtcaagcctggggggtccctgagactctcctgtgcagcctctgga
ttcaccttcagtaggtatggcatgagctgggtccgccaggctccagggaagaggctggagtgggtctcaaccattagt

ggcggaggcacctacatatactacccagactcagtgaagggccgattcaccatctccagagacaacgccaagaacacc
ctgtatctgcaaatgaacagcctgagagccgaggacacggctgtgtattactgtaccagagataactatggccgcaac
tatgattatggcatggattattggggccagggcaccctggtgaccgtgagcagcggcggtggcggatccggcggtggc
ggatccggcggtggcggatccgaaattgtgttgacacagtctccagccaccctgtctttgtctccaggggaaagagcc
accctcacctgcagcgccaccagcagtgttagctacatccactggtaccaacagaggcctggccagagccccaggctc
ctcatctatagcacctccaacctggccagcggcatcccagccaggttcagtggcagtgggtctgggagcgactacact
ctcaccatcagcagcctagagcctgaagattttgcagtttattactgtcagcagcgtagcagctcccctttcaccttt
ggcagcggcaccaaagtggaaattaaa (SEQ ID NO:232)
(amino acids)
EVQLVESGGGLVKPGGSLRLSCAASGFTFSRYGMSWVRQAPGKRLEWVSTISGGGTYIYYPDSVKGRFTISRDNAKN
TLYLQMNSLRAEDTAVYYCTRDNYGRNYDYGMDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPATLSLSPGE
RATLTCSATSSVSYIHWYQQRPGQSPRLLIYSTSNLASGIPARFSGSGSGSDYTLTISSLEPEDFAVYYCQQRSSSP
FTFGSGTKVEIK (SEQ ID NO:233)

Humanized E6 single chain IgG1noC
(DNA)
gaggtgcagctggtggagtctgggggaggcctggtcaagcctggggggtccctgagactctcctgtgcagcctctgga
ttcaccttcagtaggtatggcatgagctgggtccgccaggctccagggaagaggctggagtgggtctcaaccattagt
ggcggaggcacctacatatactacccagactcagtgaagggccgattcaccatctccagagacaacgccaagaacacc
ctgtatctgcaaatgaacagcctgagagccgaggacacggctgtgtattactgtaccagagataactatggccgcaac
tatgattatggcatggattattggggccagggcaccctggtgaccgtgagcagcgataaaacccatactaaaccgcca
aaaccggcgccggaactgctgggtggtcctggtaccggtgaaattgtgttgacacagtctccagccaccctgtctttg
tctccaggggaaagagccaccctcacctgcagcgccaccagcagtgttagctacatccactggtaccaacagaggcct
ggccagagccccaggctcctcatctatagcacctccaacctggccagcggcatcccagccaggttcagtggcagtggg
tctgggagcgactacactctcaccatcagcagcctagagcctgaagattttgcagtttattactgtcagcagcgtagc
agctcccctttcacctttggcagcggcaccaaagtggaaattaaa (SEQ ID NO:234)

(amino acids)
EVQLVESGGGLVKPGGSLRLSCAASGFTFSRYGMSWVRQAPGKRLEWVSTISGGGTYIYYPDSVKGRFTISRDNAKN
TLYLQMNSLRAEDTAVYYCTRDNYGRNYDYGMDYWGQGTLVTVSSDKTHTKPPKPAPELLGGPGTGEIVLTQSPATL
SLSPGERATLTCSATSSVSYIHWYQQRPGQSPRLLIYSTSNLASGIPARFSGSGSGSDYTLTISSLEPEDFAVYYCQ
QRSSSPFTFGSGTKVEIK (SEQ ID NO:235)
Humanized E6 single chain X4 (linker is IgG1 and IgG2 modified hinge region)
(DNA)
gaggtgcagctggtggagtctgggggaggcctggtcaagcctggggggtccctgagactctcctgtgcagcctctgga
ttcaccttcagtaggtatggcatgagctgggtccgccaggctccagggaagaggctggagtgggtctcaaccattagt
ggcggaggcacctacatatactacccagactcagtgaagggccgattcaccatctccagagacaacgccaagaacacc
ctgtatctgcaaatgaacagcctgagagccgaggacacggctgtgtattactgtaccagagataactatggccgcaac
tatgattatggcatggattattggggccagggcaccctggtgaccgtgagcagcgataaaacccatactaaaccgcca
aaaccggcgccggaactgctgggtggtcctggtaccggtactggtggtccgactattaaacctccgaaacctccgaaa
cctgctccgaacctgctgggtggtccggaaattgtgttgacacagtctccagccaccctgtctttgtctccaggggaa
agagccaccctcacctgcagcgccaccagcagtgttagctacatccactggtaccaacagaggcctggccagagcccc
aggctcctcatctatagcacctccaacctggccagcggcatcccagccaggttcagtggcagtgggtctgggagcgac
tacactctcaccatcagcagcctagagcctgaagattttgcagtttattactgtcagcagcgtagcagctcccctttc
acctttggcagcggcaccaaagtggaaattaaa (SEQ ID NO:236)

(amino acids)
EVQLVESGGGLVKPGGSLRLSCAASGFTFSRYGMSWVRQAPGKRLEWVSTISGGGTYIYYPDSVKGRFTISRDNAKN
TLYLQMNSLRAEDTAVYYCTRDNYGRNYDYGMDYWGQGTLVTVSSDKTHTKPPKPAPELLGGPGTGTGGPTIKPPKP
PKPAPNLLGGPEIVLTQSPATLSLSPGERATLTCSATSSVSYIHWYQQRPGQSPRLLIYSTSNLASGIPARFSGSGS
GSDYTLTISSLEPEDFAVYYCQQRSSSPFTFGSGTKVEIK (SEQ ID NO:237)

Humanized C2 single chain GS3
(DNA)
gaggtgcagctggtggagtctgggggaggcctggtcaagcctggggggtccctgagactctcctgtgcagcctctgga
ttcaccttcagtggctatgccatgagctgggtccgccaggctccagggaaggggctggagtgggtctcaaccattagt
agtggcggaacctacatatactaccccgactcagtgaagggccgattcaccatctccagagacaacgccaagaactca

ctgtatctgcaaatgaacagcctgagagccgaggacacggccgtgtattactgtgcgagacttgggggggataattac
tacgaatacttcgatgtctggggcaaagggaccacggtcaccgtctcctccggcggtggcggatccggcggtggcgga
tccggcggtggcggatccgacattgtgctgacccagtctccagcctccttggccgtgtctccaggacagagggccacc
atcacctgcagagccagtaagagtgtcagtaccagcggatactcctacatgcactggtatcagcagaaaccaggacaa
cctcctaaactcctgatttacctggcatccaatctggagagcggggtcccagccaggttcagcggcagtgggtctggg
accgatttcaccctcacaattaatcctgtggaagctaatgatactgcaaattattactgtcagcacagtagggagctg
cctttcacattcggcggagggaccaaggtggagatcaaacgaact (SEQ ID NO:238)

(amino acids)
EVQLVESGGGLVKPGGSLRLSCAASGFTFSGYAMSWVRQAPGKGLEWVSTISSGGTYIYYPDSVKGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARLGGDNYYEYFDVWGKGTTVTVSSGGGGSGGGGSGGGGSDIVLTQSPASLAVSPGQR
ATITCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLASNLESGVPARFSGSGSGTDFTLTINPVEANDTANYYCQHS
RELPFTFGGGTKVEIKRT (SEQ ID NO:239)

Humanized C2 single chain X4 (linker is IgG1 and IgG2 modified hinge region)
(DNA)
gaggtgcagctggtggagtctgggggaggcctggtcaagcctggggggtccctgagactctcctgtgcagcctctgga
ttcaccttcagtggctatgccatgagctgggtccgccaggctccagggaaggggctggagtgggtctcaaccattagt
agtggcggaacctacatatactaccccgactcagtgaagggccgattcaccatctccagagacaacgccaagaactca
ctgtatctgcaaatgaacagcctgagagccgaggacacggccgtgtattactgtgcgagacttgggggggataattac
tacgaatacttcgatgtctggggcaaagggaccacggtcaccgtctcctccgataaaacccatactaaaccgccaaaa
ccggcgccggaactgctgggtggtcctggtaccggtactggtggtccgactattaaacctccgaaacctccgaaacct
gctccgaacctgctgggtggtccggacattgtgctgacccagtctccagcctccttggccgtgtctccaggacagagg
gccaccatcacctgcagagccagtaagagtgtcagtaccagcggatactcctacatgcactggtatcagcagaaacca
ggacaacctcctaaactcctgatttacctggcatccaatctggagagcggggtcccagccaggttcagcggcagtggg
tctgggaccgatttcaccctcacaattaatcctgtggaagctaatgatactgcaaattattactgtcagcacagtagg
gagctgcctttcacattcggcggagggaccaaggtggagatcaaacgaact (SEQ ID NO:242)

(amino acids)
EVQLVESGGGLVKPGGSLRLSCAASGFTFSGYAMSWVRQAPGKGLEWVSTISSGGTYIYYPDSVKGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARLGGDNYYEYFDVWGKGTTVTVSSDKTHTKPPKPAPELLGGPGTGTGGPTIKPPKPP
KPAPNLLGGPDIVLTQSPASLAVSPGQRATITCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLASNLESGVPARFS
GSGSGTDFTLTINPVEANDTANYYCQHSRELPFTFGGGTKVEIKRT (SEQ ID NO:243)

Humanized C3 single chain GS3
(DNA)
caggttcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggt
tacacctttaccgactacgccatgaactgggtgcgacaggcccctggacaagggcttgagtggatgggagtgatcagc
accttcagcggtaacacaaacttcaaccagaagttcaagggcagagtcaccatgaccacagacacatccacgagcaca
gcctacatggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgagaagcgactactacggccca
tacttcgactactggggccagggcaccaccctgaccgtgtccagcggcggtggcggatccggcggtggcggatccggc
ggtggcggatccgatattgtgatgacccagactccactctctctgtccgtcacccctggacagccggcctccatctcc
tgcaggtctagtcagaccattgtccatagtaatggaaacacctatttggagtggtacctgcagaagccaggccagtct
ccacagctcctgatctataaggtttccaaccggttctctggagtgccagataggttcagtggcagcgggtcagggaca
gatttcacactgaaaatcagccgggtggaggctgaggatgttggggtttattactgcttccaaggtagccacgtgcct
ttcaccttcggcggagggaccaaggtggagatcaaacgaact (SEQ ID NO:244)

(amino acids)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYAMNWVRQAPGQGLEWMGVISTFSGNTNFNQKFKGRVTMTTDTSTST
AYMELRSLRSDDTAVYYCARSDYYGPYFDYWGQGTTLTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASI
SCRSSQTIVHSNGNTYLEWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSH
VPFTFGGGTKVEIKRT (SEQ ID NO:245)

Humanized C3 single chain X4 (linker is IgG1 and IgG2 modified hinge region)
(DNA)

caggttcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggt
tacacctttaccgactacgccatgaactgggtgcgacaggcccctggacaagggcttgagtggatgggagtgatcagc
accttcagcggtaacacaaacttcaaccagaagttcaagggcagagtcaccatgaccacagacacatccacgagcaca
gcctacatggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgagaagcgactactacggccca
tacttcgactactggggccagggcaccaccctgaccgtgtccagcgataaaacccatactaaaccgccaaaaccggcg
ccggaactgctgggtggtcctggtaccggtactggtggtccgactattaaacctccgaaacctccgaaacctgctccg
aacctgctgggtggtccggatattgtgatgacccagactccactctctctgtccgtcacccctggacagccggcctcc
atctcctgcaggtctagtcagaccattgtccatagtaatggaaacacctatttggagtggtacctgcagaagccaggc
cagtctccacagctcctgatctataaggtttccaaccggttctctggagtgccagataggttcagtggcagcgggtca
gggacagatttcacactgaaaatcagccgggtggaggctgaggatgttggggtttattactgcttccaaggtagccac
gtgcctttcaccttcggcggagggaccaaggtggagatcaaacgaact (SEQ ID NO:248)

(amino acids)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYAMNWVRQAPGQGLEWMGVISTFSGNTNFNQKFKGRVTMTTDTSTST
AYMELRSLRSDDTAVYYCARSDYYGPYFDYWGQGTTLTVSSDKTHTKPPKPAPELLGGPGTGTGGPTIKPPKPPKPA
PNLLGGPDIVMTQTPLSLSVTPGQPASISCRSSQTIVHSNGNTYLEWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGS
GSGTDFTLKISRVEAEDVGVYYCFQGSHVPFTFGGGTKVEIKRT (SEQ ID NO:249)

Humanized C8 single chain GS3 (linker is [Gly$_4$Ser$_1$]$_3$)
(DNA)
gaggtgcagctggtggagtctgggggaggcctggtcaagcctggggggtccctgagactctcctgtgcagcctctgga
ttcaccttcagtggctatgccatgagctgggtccgccaggctccagggaaggggctggagtgggtctcaaccattagt
agtggcggaacctacatatactaccctgactcagtgaagggccgattcaccatctccagagacaacgccaagaactca
ctgtatctgcaaatgaacagcctgagagccgaggacacggccgtgtattactgtgcgagactgggcggcgataactat
tatgaatattggggcaaagggaccacggtcaccgtctcctccggcggtggcggatccggcggtggcggatccggcggt
ggcggatccgacatcgtgatgacccagtctccagactccctggctgtgtctctgggcgagagggccaccatcaactgc
agggccagcaagagtgttagcaccagcggctacagctacatgcactggtaccagcagaaaccaggacagcctcctaag
ctgctcatttacctggtgtctaacctggaatccggggtccctgaccgattcagtggcagcgggtctgggacagatttc
actctcaccatcagcagcctgcaggctgaagatgtggcagtttattactgtcaacacattcgggaactgaccaggagt
gaattcggcggagggaccaaggtggagatcaaacgaact (SEQ ID NO:250)

(amino acids)
EVQLVESGGGLVKPGGSLRLSCAASGFTFSGYAMSWVRQAPGKGLEWVSTISSGGTYIYYPDSVKGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARLGGDNYYEYWGKGTTVTVSSGGGGSGGGGSGGGGSDIVMTQSPDSLAVSLGERATI
NCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLVSNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQHIREL
TRSEFGGGTKVEIKRT (SEQ ID NO:251)

pSECTag2 E6 scFV-FC
(DNA)
atggagacagacacactcctgctatgggtactgctgctctgggttccaggttccactggtgacgcggcccagccggcc
gaggtgcagctggtggagtctgggggaggcctggtcaagcctggggggtccctgagactctcctgtgcagcctctgga
ttcaccttcagtaggtatggcatgagctgggtccgccaggctccagggaagaggctggagtgggtctcaaccattagt
ggcggaggcacctacatatactacccagactcagtgaagggccgattcaccatctccagagacaacgccaagaacacc
ctgtatctgcaaatgaacagcctgagagccgaggacacggctgtgtattactgtaccagagataactatggccgcaac
tatgattatggcatggattattggggccagggcaccctggtgaccgtgagcagcggcggtggcggatccggcggtggc
ggatccggcggtggcggatccgaaattgtgttgacacagtctccagccaccctgtctttgtctccaggggaaagagcc
accctcacctgcagcgccaccagcagtgttagctacatccactggtaccaacagaggcctggccagagccccaggctc
ctcatctatagcacctccaacctggccagcggcatcccagccaggttcagtggcagtgggtctgggagcgactacact
ctcaccatcagcagcctagagcctgaagattttgcagtttattactgtcagcagcgtagcagctcccctttcaccttt
ggcagcggcaccaaagtggaaattaaagagcccaaatcttgtgacaaaactcacacatgcccaccgtgcccagcacct
gaactcctggggggaccgtcagtcttcctcttccccccaaaacccaaggacaccctcatgatctcccggacccctgag
gtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtg
cataatgccaagacaaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcac
caggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaaccatc
tccaaagccaaagggcagccccgagaaccacaggtgtacaccctgcccccatcccgggaggagatgaccaagaaccag
gtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggagtgggagagcaatgggcagccggag

aacaactacaagaccacgcctcccgtgctggactccgacggctccttcttcctctacagcaagctcaccgtggacaag
agcaggtggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagc
ctctccctgtctccgggtaaatgataa (SEQ ID NO:256)

(amino acids)
METDTLLLWVLLLWVPGSTGDAAQPAEVQLVESGGGLVKPGGSLRLSCAASGFTFSRYGMSWVRQAPGKRLEWVSTI
SGGGTYIYYPDSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCTRDNYGRNYDYGMDYWGQGTLVTVSSGGGGSG
GGGSGGGGSEIVLTQSPATLSLSPGERATLTCSATSSVSYIHWYQQRPGQSPRLLIYSTSNLASGIPARFSGSGSGS
DYTLTISSLEPEDFAVYYCQQRSSSPFTFGSGTKVEIKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS
RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
IEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK** (SEQ ID NO:257)

Human IgG1 Fc sequence:
(DNA)
gagcccaaatcttgtgacaaaactcacacatgcccaccgtgcccagcacctgaactcctggggggaccgtcagtcttc
ctcttccccccaaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagc
cacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccgcgggag
gagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtac
aagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaaccatctccaaagccaaagggcagccccgagaa
ccacaggtgtacaccctgcccccatcccgggaggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggc
ttctatcccagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtg
ctggactccgacggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcaggggaacgtcttc
tcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtctccgggtaaatgataa
(SEQ ID NO:272)

(amino acids)
EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
K** (SEQ ID NO:273)

Human IgG1 CH2-CH3 domain sequence:
(DNA)
ccgtgcccagcacctgaactcctggggggaccgtcagtcttcctcttccccccaaaacccaaggacaccctcatgatc
tcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtg
gacggcgtggaggtgcataatgccaagacaaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtc
ctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagccccc
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atgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggagtgggagagc
aatgggcagccggagaacaactacaagaccacgcctcccgtgctggactccgacggctccttcttcctctacagcaag
ctcaccgtggacaagagcaggtggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaaccac
tacacgcagaagagcctctccctgtctccgggtaaatgataa (SEQ ID NO:274)

(amino acids)
PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK** (SEQ ID
NO:275)

Human IgG1 CH3 domain sequence:
(DNA)
gggcagccccgagaaccacaggtgtacaccctgcccccatcccgggaggagatgaccaagaaccaggtcagcctgacc
tgcctggtcaaaggcttctatcccagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaag
accacgcctcccgtgctggactccgacggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcag

caggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtct
ccgggtaaatgataa (SEQ ID NO:276)

(amino acids)
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK** (SEQ ID NO:277)

CAR-T E6 CD8/CD8/CD28/CD3z sequence:
N-CD8ls-huMNE6scFv-CD8ecd fragment- CD8 transmembrane- CD28- CD3zeta-C
(DNA)
atggccctgcccgtgaccgctttgctgctccccctggcgctgctgctgcacgccgccaggccagaggtccagctggtt
gagagtggcggtgggctggttaagcctggcggctccctgcggctgagctgcgccgcgagtggatttactttcagccga
tatgggatgagttgggtgcggcaagctcccgggaagaggctggaatgggtctcaacaatctccgggggggcacttac
atctattaccccgactcagtcaaggggagatttaccatttcacgagacaacgctaagaataccctgtatttgcagatg
aattctctgagagcagaggacacagctgtttactattgtacccgcgacaactatggcaggaactacgactacggtatg
gactattggggacaagggacattggttacagtgagcagtggcggcgggggcagcggaggaggaggcagcggtgggggg
ggcagcgagatagtgctcacgcagtcacccgcgactctcagtctctcacctggggaacgagctaccctgacgtgctct
gctacctcctcagtgtcatatattcactggtatcagcaacggcccgggcagtcccctagattgctcatttatagtacc
tctaatctggcctcaggtatccctgcacgatttctggatctggttcaggttctgattacaccctcactatctctagc
ctggagcctgaagactttgccgtttattactgccagcagaggtctagctccccattcacctttgggagtgggaccaag
gttgaaattaaaacgacaaccccggcccccagaccaccaacgccagcccccaccatcgccagccaacccctgtctctg
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cggctcctgcattctgattacatgaacatgaccccaagaagaccaggccccaccaggaaacattaccagccctacgct
ccgccacgcgacttcgctgcctaccggtcccgcgttaagttctcccgatcagccgacgcgcctgcttacaagcagggc
cagaaccaactgtacaacgagctgaatctcggtagacgggaagagtacgacgtgttggacaaacggagaggccgcgac
ccagaaatgggcggcaagcctcgcaggaaaaacccccaggagggactgtacaatgagttgcagaaagataagatggca
gaagcttatagcgagatcggaatgaagggggaaaggagacgagggaaaggacacgacggcctttatcagggcctgtcc
acagcaacaaaagatacgtatgacgccctccatatgcaggcacttccaccacggtgataa
(SEQ ID NO:297)

(amino acids)
MALPVTALLLPLALLLHAARPEVQLVESGGGLVKPGGSLRLSCAASGFTFSRYGMSWVRQAPGKRLEWVSTISGGGT
YIYYPDSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCTRDNYGRNYDYGMDYWGQGTLVTVSSGGGGSGGGGSG
GGGSEIVLTQSPATLSLSPGERATLTCSATSSVSYIHWYQQRPGQSPRLLIYSTSNLASGIPARFSGSGSGSDYTLT
ISSLEPEDFAVYYCQQRSSSPFTFGSGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFAC
DIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAP
AYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDG
LYQGLSTATKDTYDALHMQALPPR** (SEQ ID NO:298)

CAR-T E6 CD8/CD8/4-1BB/CD3z sequence:
N-CD8ls-huMNE6scFv-CD8ecd fragment- CD8 transmembrane- 4-1BB- CD3zeta-C
(DNA)
atggccctgcccgtgaccgctttgctgctccccctggcgctgctgctgcacgccgccaggccagaggtccagctggtt
gagagtggcggtgggctggttaagcctggcggctccctgcggctgagctgcgccgcgagtggatttactttcagccga
tatgggatgagttgggtgcggcaagctcccgggaagaggctggaatgggtctcaacaatctccgggggggcacttac
atctattaccccgactcagtcaaggggagatttaccatttcacgagacaacgctaagaataccctgtatttgcagatg
aattctctgagagcagaggacacagctgtttactattgtacccgcgacaactatggcaggaactacgactacggtatg
gactattggggacaagggacattggttacagtgagcagtggcggcgggggcagcggaggaggaggcagcggtgggggg
ggcagcgagatagtgctcacgcagtcacccgcgactctcagtctctcacctggggaacgagctaccctgacgtgctct
gctacctcctcagtgtcatatattcactggtatcagcaacggcccgggcagtcccctagattgctcatttatagtacc
tctaatctggcctcaggtatccctgcacgatttctggatctggttcaggttctgattacaccctcactatctctagc
ctggagcctgaagactttgccgtttattactgccagcagaggtctagctccccattcacctttgggagtgggaccaag
gttgaaattaaaacgacaaccccggcccccagaccaccaacgccagcccccaccatcgccagccaacccctgtctctg
agaccagaagcctgtaggcctgccgccggtggagctgtgcacacaagaggactggatttcgcctgtgatatctacatt

tgggccccgctcgcaggcacatgtggagtgctcctcctctccctggtgattaccctgtactgcaaaaggggccgcaaa
aaactcctttacattttaagcagccttttatgaggccagtacagacgactcaagaggaagacgggtgctcatgccgc
tttcctgaggaggaggaaggagggtgcgaactgcgcgttaagttctcccgatcagccgacgcgcctgcttacaagcag
ggccagaaccaactgtacaacgagctgaatctcggtagacgggaagagtacgacgtgttggacaaacggagaggccgc
gacccagaaatgggcggcaagcctcgcaggaaaaacccccaggagggactgtacaatgagttgcagaaagataagatg
gcagaagcttatagcgagatcggaatgaaggggaaaggagacgagggaaaggacacgacggcctttatcagggcctg
tccacagcaacaaaagatacgtatgacgccctccatatgcaggcacttccaccacggtgataa
(SEQ ID NO:300)

(amino acids)
MALPVTALLLPLALLLHAARPEVQLVESGGGLVKPGGSLRLSCAASGFTFSRYGMSWVRQAPGKRLEWVSTISGGGT
YIYYPDSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCTRDNYGRNYDYGMDYWGQGTLVTVSSGGGGSGGGGSG
GGGSEIVLTQSPATLSLSPGERATLTCSATSSVSYIHWYQQRPGQSPRLLIYSTSNLASGIPARFSGSGSGSDYTLT
ISSLEPEDFAVYYCQQRSSSPFTFGSGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFAC
DIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADA
PAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHD
GLYQGLSTATKDTYDALHMQALPPR**
(SEQ ID NO:301)

CAR-T E6 CD8/CD8/CD28/4-1BB/CD3z sequence:
N-CD8ls-huMNE6scFv-CD8ecd fragment- CD8 transmembrane- CD28- 4-1BB- CD3zeta-C
(DNA)
atggccctgcccgtgaccgctttgctgctccccctggcgctgctgctgcacgccgccaggccagaggtccagctggtt
gagagtggcggtgggctggttaagcctggcggctccctgcggctgagctgcgccgcgagtggatttactttcagccga
tatgggatgagttgggtgcggcaagctcccgggaagaggctggaatgggtctcaacaatctccgggggggcacttac
atctattaccccgactcagtcaaggggagatttaccatttcacgagacaacgctaagaataccctgtatttgcagatg
aattctctgagagcagaggacacagctgtttactattgtacccgcgacaactatggcaggaactacgactacggtatg
gactattggggacaagggacattggttacagtgagcagtggcggcgggggcagcggaggaggaggcagcggtgggggg
ggcagcgagatagtgctcacgcagtcacccgcgactctcagtctctcacctggggaacgagctaccctgacgtgctct
gctacctcctcagtgtcatatattcactggtatcagcaacggcccgggcagtcccctagattgctcatttatagtacc
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tgggccccgctcgcaggcacatgtggagtgctcctcctctccctggtgattaccctgtactgcagaagcaagcggtct
cggctcctgcattctgattacatgaacatgaccccaagaagaccaggccccaccaggaaacattaccagccctacgct
ccgccacgcgacttcgctgcctaccggtccaaaaggggccgcaaaaaactcctttacattttaagcagccttttatg
aggccagtacagacgactcaagaggaagacgggtgctcatgccgctttcctgaggaggaggaaggagggtgcgaactg
cgcgttaagttctcccgatcagccgacgcgcctgcttacaagcagggccagaaccaactgtacaacgagctgaatctc
ggtagacgggaagagtacgacgtgttggacaaacggagaggccgcgacccagaaatgggcggcaagcctcgcaggaaa
aacccccaggagggactgtacaatgagttgcagaaagataagatggcagaagcttatagcgagatcggaatgaagggg
gaaaggagacgagggaaaggacacgacggcctttatcagggcctgtccacagcaacaaaagatacgtatgacgccctc
catatgcaggcacttccaccacggtgataa
(SEQ ID NO:303)

(amino acids)
MALPVTALLLPLALLLHAARPEVQLVESGGGLVKPGGSLRLSCAASGFTFSRYGMSWVRQAPGKRLEWVSTISGGGT
YIYYPDSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCTRDNYGRNYDYGMDYWGQGTLVTVSSGGGGSGGGGSG
GGGSEIVLTQSPATLSLSPGERATLTCSATSSVSYIHWYQQRPGQSPRLLIYSTSNLASGIPARFSGSGSGSDYTLT
ISSLEPEDFAVYYCQQRSSSPFTFGSGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFAC
DIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSKRGRKKLLYIF
KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG
GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR** (SEQ ID
NO:304)

CAR-T C2 CD8/CD8/CD28/4-1BB/CD3z sequence:
N-CD8ls-huMNC2scFv-CD8ecd fragment- CD8 transmembrane- CD28- 4-1BB- CD3zeta-C
(DNA)
atggccttgccagtgacggccctgctgctgccattggctcttctgttgcacgctgccaggcctgaagtgcagctcgta
gagagtggcgggggactggtgaagcccggtggaagcctcagactcagttgcgccgcctcaggtttcactttttcaggt
tacgccatgtcctgggtaagacaggcaccggggaaaggactcgagtgggtgtctactatcagctcaggaggcacttat
atatattatcctgactctgtaaaaggccgatttacgatttctcgcgacaatgcaaagaactccctctacctccaaatg
aacagtcttagggcagaagacactgctgtatactattgtgcacgcctcggcggcgacaactactacgagtactttgac
gtgtggggggaaagggactaccgtgacagtttcaagcggaggaggtggctcaggtggaggcgggtcagggggggggagga
agtgatattgtgctcacacaatccccagcctccctggctgtgtctcccggccaacgcgctacaattacatgtcgggcc
tccaaaagcgtgagcaccagcggctacagctacatgcactggtatcaacagaaaccaggacaacccccaaactgttg
atttatctcgcttcaaacttggagtccggcgtgcctgcgcgcttttcagggagtgggagcggcacagatttacgctg
actatcaaccccgtagaagcaaacgatacagcgaattattattgtcaacattcccgggaactcccctttacgttcggc
gggggcacaaaggtcgaaattaagagaaccacgacaaccccggcccccagaccaccaacgccagcccccaccatcgcc
agccaacccctgtctctgagaccagaagcctgtaggcctgccgccggtggagctgtgcacacaagaggactggatttc
gcctgtgatatctacatttgggccccgctcgcaggcacatgtggagtgctcctcctctccctggtgattaccctgtac
tgcagaagcaagcggtctcggctcctgcattctgattacatgaacatgaccccaagaagaccaggccccaccaggaaa
cattaccagccctacgctccgccacgcgacttcgctgcctaccggtccaaaagggggccgcaaaaaactcctttacatt
tttaagcagccttttatgaggccagtacagacgactcaagaggaagacgggtgctcatgccgctttcctgaggaggag
gaaggagggtgcgaactgcgcgttaagttctcccgatcagccgacgcgcctgcttacaagcagggccagaaccaactg
tacaacgagctgaatctcggtagacgggaagagtacgacgtgttggacaaacggagaggccgcgacccagaaatgggc
ggcaagcctcgcaggaaaaacccccaggagggactgtacaatgagttgcagaaagataagatggcagaagcttatagc
gagatcggaatgaaggggggaaaggagacgagggaaaggacacgacggcctttatcagggcctgtccacagcaacaaaa
gatacgtatgacgccctccatatgcaggcacttccaccacggtgataa (SEQ ID NO:306)

(amino acids)
EVQLVESGGGLVKPGGSLRLSCAASGFTFSGYAMSWVRQAPGKGLEWVSTISSGGTYIYYPDSVKGRFTISRDNAKNS
LYLQMNSLRAEDTAVYYCARLGGDNYYEYFDVWGKGTTVTVSSGGGGSGGGGSGGGGSDIVLTQSPASLAVSPGQRAT
ITCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLASNLESGVPARFSGSGSGTDFTLTINPVEANDTANYYCQHSREL
PFTFGGGTKVEIKRTTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSL
VITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCR
FPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM
AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR** (SEQ ID NO:307)

Humanized E6 scFV sequence in CAR:
(DNA)
gaggtccagctggttgagagtggcggtgggctggttaagcctggcggctccctgcggctgagctgcgccgcgagtgga
tttactttcagccgatatgggatgagttgggtgcggcaagctcccgggaagaggctggaatgggtctcaacaatctcc
gggggggcacttacatctattaccccgactcagtcaaggggagatttaccatttcacgagacaacgctaagaatacc
ctgtatttgcagatgaattctctgagagcagaggacacagctgtttactattgtacccgcgacaactatggcaggaac
tacgactacggtatggactattggggacaagggacattggttacagtgagcagtggcggcgggggcagcggaggagga
ggcagcggtgggggggcagcgagatagtgctcacgcagtcacccgcgactctcagtctctcacctggggaacgagct
accctgacgtgctctgctacctcctcagtgtcatatattcactggtatcagcaacggcccgggcagtcccctagattg
ctcatttatagtacctctaatctggcctcaggtatccctgcacgattttctggatctggttcaggttctgattacacc
ctcactatctctagcctggagcctgaagactttgccgtttattactgccagcagaggtctagctccccattcaccttt
gggagtgggaccaaggttgaaattaaa (SEQ ID NO:341)

(amino acids)
EVQLVESGGGLVKPGGSLRLSCAASGFTFSRYGMSWVRQAPGKRLEWVSTISGGGTYIYYPDSVKGRFTISRDNAKN
TLYLQMNSLRAEDTAVYYCTRDNYGRNYDYGMDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPATLSLSPGE
RATLTCSATSSVSYIHWYQQRPGQSPRLLIYSTSNLASGIPARFSGSGSGSDYTLTISSLEPEDFAVYYCQQRSSSP
FTFGSGTKVEIK (SEQ ID NO:342)

CD8 leader sequence:
(DNA)
atggccctgcccgtgaccgctttgctgctcccccctggcgctgctgctgcacgccgccaggcca (SEQ ID NO:343)

(amino acids)
MALPVTALLLPLALLLHAARP (SEQ ID NO:344)

CD8 hinge domain sequence:
(DNA)
acgacaaccccggcccccagaccaccaacgccagcccccaccatcgccagccaacccctgtctctgagaccagaagcc
tgtaggcctgccgccggtggagctgtgcacacaagaggactggatttcgcctgtgat (SEQ ID NO:345)

(amino acids)
TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACD (SEQ ID NO:346)

CD4 hinge domain sequence:
(DNA)
tcgggacaggtcctgctggaatccaacatcaaggttctgcccacatggtccaccccggtgcagcca (SEQ ID
NO:347)

(amino acids)
SGQVLLESNIKVLPTWSTPVQP (SEQ ID NO:348)

CD28 hinge domain sequence:
(DNA)
aaacacctttgtccaagtcccctatttcccggaccttctaagccc (SEQ ID NO:349)

(amino acids)
KHLCPSPLFPGPSKP (SEQ ID NO:350)

CD3 zeta transmembrane domain sequence:
(DNA)
ctctgctacctgctggatggaatcctcttcatctatggtgtcattctcactgccttgttcctg (SEQ ID
NO:361)

(amino acids)
LCYLLDGILFIYGVILTALFL (SEQ ID NO:362)

CD8 transmembrane domain sequence:
(DNA)
atctacatttgggccccgctcgcaggcacatgtggagtgctcctcctctccctggtgattaccctgtactgc (SEQ
ID NO:363)

(amino acids)
IYIWAPLAGTCGVLLLSLVITLYC (SEQ ID NO:364)

CD4 transmembrane domain sequence:
(DNA)
atggccctgattgtgctgggggcgtcgccggcctcctgcttttcattgggctaggcatcttcttc (SEQ ID
NO:365)

(amino acids)
MALIVLGGVAGLLLFIGLGIFF (SEQ ID NO:366)

CD28 transmembrane domain sequence:
(DNA)
ttttgggtgctggtggtggttggtggagtcctggcttgctatagcttgctagtaacagtggcctttattattttctg
ggtg (SEQ ID NO:367)

(amino acids)

FWVLVVVGGVLACYSLLVTVAFIIFWV (SEQ ID NO:368)

4-1BB transmembrane domain sequence:
(DNA)
atcatctccttctttcttgcgctgacgtcgactgcgttgctcttcctgctgttcttcctcacgctccgtttctctgt
tgtt (SEQ ID NO:369)

(amino acids)
IISFFLALTSTALLFLLFFLTLRFSVV (SEQ ID NO:370)

OX40 transmembrane domain sequence:
(DNA)
gttgccgccatcctgggcctgggcctggtgctggggctgctgggcccctggccatcctgctggccctgtacctgctc
(SEQ ID NO:371)

(amino acids)
VAAILGLGLVLGLLGPLAILLALYLL (SEQ ID NO:372)

CD3 zeta domain sequence:
(DNA)
cgcgttaagttctcccgatcagccgacgcgcctgcttacaagcagggccagaaccaactgtacaacgagctgaatctc
ggtagacgggaagagtacgacgtgttggacaaacggagaggccgcgacccagaaatgggcggcaagcctcgcaggaaa
aacccccaggagggactgtacaatgagttgcagaaagataagatggcagaagcttatagcgagatcggaatgaagggg
gaaaggagacgagggaaaggacacgacggcctttatcagggcctgtccacagcaacaaaagatacgtatgacgccctc
catatgcaggcacttccaccacgg (SEQ ID NO:373)

(amino acids)
RVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKG
ERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO:374)

CD3 zeta domain variant sequence:
(DNA)
agagtgaagttcagcaggagcgcagacgcccccgcgtaccagcagggccagaaccagctctataacgagctcaatct
aggacgaagagaggagtacgatgttttggacaagagacgtggccgggaccctgagatggggggaaagccgagaagga
agaaccctcaggaaggcctgtacaatgaactgcagaaagataagatggcggaggcctacagtgagattgggatgaaa
ggcgagcgccggaggggcaaggggcacgatggcctttaccagggtctcagtacagccaccaaggacacctacgacgc
ccttcacatgcaggccctgccccctcgc (SEQ ID NO:375)

(amino acids)
RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMK
GERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO:376)

CD28 domain sequence:
(DNA)
agaagcaagcggtctcggctcctgcattctgattacatgaacatgaccccaagaagaccaggccccaccaggaaacat
taccagccctacgctccgccacgcgacttcgctgcctaccggtcc (SEQ ID NO:377)

(amino acids)
RSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS (SEQ ID NO:378)

4-1BB domain sequence:
(DNA)
aaaaggggccgcaaaaaactcctttacatttttaagcagccttttatgaggccagtacagacgactcaagaggaagac
gggtgctcatgccgctttcctgaggaggaggaaggagggtgcgaactg (SEQ ID NO:379)

(amino acids)
KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL (SEQ ID NO:380)

HumanizeE6 scFV (VH-VL) sequence:

(DNA)
gaggtgcagctggtggagtctgggggaggcctggtcaagcctggggggtccctgagactctcctgtgcagcctctgga
ttcaccttcagtaggtatggcatgagctgggtccgccaggctccagggaagaggctggagtgggtctcaaccattagt
ggcggaggcacctacatatactacccagactcagtgaagggccgattcaccatctccagagacaacgccaagaacacc
ctgtatctgcaaatgaacagcctgagagccgaggacacggctgtgtattactgtaccagagataactatggccgcaac
tatgattatggcatggattattggggccagggcaccctggtgaccgtgagcagcggcggtggcggatccggcggtggc
ggatccggcggtggcggatccgaaattgtgttgacacagtctccagccaccctgtctttgtctccaggggaaagagcc
accctcacctgcagcgccaccagcagtgttagctacatccactggtaccaacagaggcctggccagagccccaggctc
ctcatctatagcacctccaacctggccagcggcatcccagccaggttcagtggcagtgggtctgggagcgactacact
ctcaccatcagcagcctagagcctgaagattttgcagtttattactgtcagcagcgtagcagctcccctttcaccttt
ggcagcggcaccaaagtggaaattaaa (SEQ ID NO:391)

(amino acids)
EVQLVESGGGLVKPGGSLRLSCAASGFTFSRYGMSWVRQAPGKRLEWVSTISGGGTYIYYPDSVKGRFTISRDNAKN
TLYLQMNSLRAEDTAVYYCTRDNYGRNYDYGMDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPATLSLSPGE
RATLTCSATSSVSYIHWYQQRPGQSPRLLIYSTSNLASGIPARFSGSGSGSDYTLTISSLEPEDFAVYYCQQRSSSP
FTFGSGTKVEIK (SEQ ID NO:392)

HumanizeE6 scFV (VL-VH) sequence:

(DNA)
gaaattgtgttgacacagtctccagccaccctgtctttgtctccaggggaaagagccaccctcacctgcagcgccacc
agcagtgttagctacatccactggtaccaacagaggcctggccagagccccaggctcctcatctatagcacctccaac
ctggccagcggcatcccagccaggttcagtggcagtgggtctgggagcgactacactctcaccatcagcagcctagag
cctgaagattttgcagtttattactgtcagcagcgtagcagctcccctttcacctttggcagcggcaccaaagtggaa
attaaaggcggtggcggatccggcggtggcggatccggcggtggcggatccgaggtgcagctggtggagtctgggga
ggcctggtcaagcctggggggtccctgagactctcctgtgcagcctctggattcaccttcagtaggtatggcatgagc
tgggtccgccaggctccagggaagaggctggagtgggtctcaaccattagtggcggaggcacctacatatactaccca
gactcagtgaagggccgattcaccatctccagagacaacgccaagaacaccctgtatctgcaaatgaacagcctgaga
gccgaggacacggctgtgtattactgtaccagagataactatggccgcaactatgattatggcatggattattggggc
cagggcaccctggtgaccgtgagcagc (SEQ ID NO:393)

(amino acids)
EIVLTQSPATLSLSPGERATLTCSATSSVSYIHWYQQRPGQSPRLLIYSTSNLASGIPARFSGSGSGSDYTLTISSL
EPEDFAVYYCQQRSSSPFTFGSGTKVEIKGGGGSGGGGSGGGGSEVQLVESGGGLVKPGGSLRLSCAASGFTFSRYG
MSWVRQAPGKRLEWVSTISGGGTYIYYPDSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCTRDNYGRNYDYGMD
YWGQGTLVTVSS(SEQ ID NO:394)

HumanizeC2 scFV (VH-VL) sequence:

(DNA)
gaggtgcagctggtggagtctgggggaggcctggtcaagcctggggggtccctgagactctcctgtgcagcctctgga
ttcaccttcagtggctatgccatgagctgggtccgccaggctccagggaaggggctggagtgggtctcaaccattagt
agtggcggaacctacatatactaccccgactcagtgaagggccgattcaccatctccagagacaacgccaagaactca
ctgtatctgcaaatgaacagcctgagagccgaggacacggccgtgtattactgtgcgagacttgggggggataattac
tacgaatacttcgatgtctggggcaaagggaccacggtcaccgtctcctccggcggtggcggatccggcggtggcgga
tccggcggtggcggatccgacattgtgctgacccagtctccagcctccttggccgtgtctccaggacagagggccacc
atcacctgcagagccagtaagagtgtcagtaccagcggatactcctacatgcactggtatcagcagaaaccaggacaa
cctcctaaactcctgatttacctggcatccaatctggagagcggggtcccagccaggttcagcggcagtgggtctggg
accgatttcaccctcacaattaatcctgtggaagctaatgatactgcaaattattactgtcagcacagtagggagctg
cctttcacattcggcggagggaccaaggtggagatcaaacgaact (SEQ ID NO:395)

(amino acids)
EVQLVESGGGLVKPGGSLRLSCAASGFTFSGYAMSWVRQAPGKGLEWVSTISSGGTYIYYPDSVKGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARLGGDNYYEYFDVWGKGTTVTVSSGGGGSGGGGSGGGGSDIVLTQSPASLAVSPGQR

ATITCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLASNLESGVPARFSGSGSGTDFTLTINPVEANDTANYYCQHS
RELPFTFGGGTKVEIKRT (SEQ ID NO:396)

HumanizeE6 scFV (VL-VH) sequence:
(DNA)
gacattgtgctgacccagtctccagcctccttggccgtgtctccaggacagagggccaccatcacctgcagagccagt
aagagtgtcagtaccagcggatactcctacatgcactggtatcagcagaaaccaggacaacctcctaaactcctgatt
tacctggcatccaatctggagagcggggtcccagccaggttcagcggcagtgggtctgggaccgatttcaccctcaca
attaatcctgtggaagctaatgatactgcaaattattactgtcagcacagtagggagctgcctttcacattcggcgga
gggaccaaggtggagatcaaacgaactggcggtggcggatccggcggtggcggatccggcggtggcggatccgaggtg
cagctggtggagtctgggggaggcctggtcaagcctggggggtccctgagactctcctgtgcagcctctggattcacc
ttcagtggctatgccatgagctgggtccgccaggctccagggaaggggctggagtgggtctcaaccattagtagtggc
ggaacctacatatactaccccgactcagtgaagggccgattcaccatctccagagacaacgccaagaactcactgtat
ctgcaaatgaacagcctgagagccgaggacacggccgtgtattactgtgcgagacttgggggggataattactacgaa
tacttcgatgtctggggcaaagggaccacggtcaccgtctcctcc (SEQ ID NO:397)

(amino acids)
DIVLTQSPASLAVSPGQRATITCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLASNLESGVPARFSGSGSGTDFTL
TINPVEANDTANYYCQHSRELPFTFGGGTKVEIKRTGGGGSGGGGSGGGGSEVQLVESGGGLVKPGGSLRLSCAASG
FTFSGYAMSWVRQAPGKGLEWVSTISSGGTYIYYPDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARLGGDN
YYEYFDVWGKGTTVTVSS (SEQ ID NO:398)

G_4S_1 linker sequence:
(DNA)
ggcggtggcggatcc (SEQ ID NO:399)

(amino acids)
GGGGS (SEQ ID NO:400)

[G_4S_1]x3 linker sequence:
(DNA)
ggcggtggcggatccggcggtggcggatccggcggtggcggatcc (SEQ ID NO:401)

(amino acids)
GGGGSGGGGSGGGGS (SEQ ID NO:402)

8 aa GS linker sequence:
(DNA)
ggcggttccggcggtggatccgga (SEQ ID NO:403)

(amino acids)
GGSGGGSG (SEQ ID NO:404)

12 aa GS linker sequence:
(DNA)
ggcggttccggcggtggatccggcggtggcggatccgga (SEQ ID NO:405)

(amino acids)
GGSGGGSGGGSG (SEQ ID NO:406)

13 aa GS linker sequence:
(DNA)
ggcggtggatccggcggtggcggatccggcggtggatcc (SEQ ID NO:407)

(amino acids)
GGGSGGGGSGGGS (SEQ ID NO:408)

22 aa GS linker sequence:
(DNA)
ggcggtggaagcggcggtggcggatccggcagcggcggaagcggcggtggcggatccggcggtgga (SEQ ID NO:409)

(amino acids)
GGGSGGGGSGSGGSGGGGSGGG (SEQ ID NO:4110)

24 aa GS linker sequence:
(DNA)
ggcggttccggcggtggatccggcggtggcggatccggaggcggttccggcggtggatccggcggtggcggatccgga (SEQ ID NO:411)

(amino acids)
GGSGGGSGGGSGGGSGGGSGGGSG (SEQ ID NO:412)

Mouse C3 Heavy chain variable region sequence:
(DNA)
caggtccagctgcagcagtctgggcctgagctggtgaggcctggggtctcagtgaagatttcctgcaagggttccggc
tacagattcactgattatgctatgaactgggtgaagcagagtcatgcaaagagtctagagtggattggagttattagt
actttctctggtaatacaaacttcaaccagaagtttaagggcaaggccacaatgactgtagacaaatcctccagcaca
gcctatatggaacttgccagattgacatctgaggattctgccatgtattactgtgcaagatcggattactacggccca
tactttgactactggggccaaggcaccactctcacagtctcctca (SEQ ID NO:413)

(amino acids)
QVQLQQSGPELVRPGVSVKISCKGSGYRFTDYAMNWVKQSHAKSLEWIGVISTFSGNTNFNQKFKGKATMTVDKSSST
AYMELARLTSEDSAMYYCARSDYYGPYFDYWGQGTTLTVSS (SEQ ID NO:414)

Mouse C3 heavy chain variable framework region 1 (FWR1) sequence:
(DNA)
caggtccagctgcagcagtctgggcctgagctggtgaggcctggggtctcagtgaagatttcctgcaagggttccgg
ctacagattcact (SEQ ID NO:415)

(amino acids)
QVQLQQSGPELVRPGVSVKISCKGSGYRFT (SEQ ID NO:416)

Mouse C3 heavy chain variable complementarity determining regions 1 (CDR1) sequence:
(DNA)
gattatgctatgaac (SEQ ID NO:417)

(amino acids)
DYAMN (SEQ ID NO:418)

Mouse C3 heavy chain variable framework region 2 (FWR2) sequence:
(DNA)
tgggtgaagcagagtcatgcaaagagtctagagtggattgga (SEQ ID NO:419)

(amino acids)
WVKQSHAKSLEWIG (SEQ ID NO:420)

Mouse C3 heavy chain variable complementarity determining regions 2 (CDR2) sequence:
(DNA)
gttattagtactttctctggtaatacaaacttcaaccagaagtttaagggc (SEQ ID NO:421)

(amino acids)

VISTFSGNTNFNQKFKG (SEQ ID NO:422)

Mouse C3 heavy chain variable framework region 3 (FWR3) acid sequence:
(DNA)
aaggccacaatgactgtagacaaatcctccagcacagcctatatggaacttgccagattgacatctgaggattctgc
catgtattactgtgcaaga (SEQ ID NO:423)

(amino acids)
KATMTVDKSSSTAYMELARLTSEDSAMYYCAR (SEQ ID NO:424)

Mouse C3 heavy chain variable complementarity determining regions 3 (CDR3) sequence:
(DNA)
tcggattactacggcccatactttgactac (SEQ ID NO:425)

(amino acids)
SDYYGPYFDY (SEQ ID NO:426)

Humanized C3 heavy chain variable region sequence from IGHV1-18*04:
(DNA)
caggttcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctgg
ttacacctttaccgactacgccatgaactgggtgcgacaggcccctggacaagggcttgagtggatgggagtgatca
gcaccttcagcggtaacacaaacttcaaccagaagttcaagggcagagtcaccatgaccacagacacatccacgagc
acagcctacatggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgagaagcgactactacgg
cccatacttcgactactggggccagggcaccaccctgaccgtgtccagc (SEQ ID NO:439)

(amino acids)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYAMNWVRQAPGQGLEWMGVISTFSGNTNFNQKFKGRVTMTTDTSTS
TAYMELRSLRSDDTAVYYCARSDYYGPYFDYWGQGTTLTVSS (SEQ ID NO:440)

Humanized C3 heavy chain variable framework region 1 (FWR1) acid sequence:
(DNA)
caggttcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctgg
ttacacctttacc (SEQ ID NO:441)

(amino acids)
QVQLVQSGAEVKKPGASVKVSCKASGYTFT (SEQ ID NO:442)
Humanized C3 heavy chain variable complementarity determining regions 1 (CDR1) sequence:
(DNA)
gactacgccatgaac (SEQ ID NO:443)

(amino acids)
DYAMN (SEQ ID NO:444)

Humanized C3 heavy chain variable framework region 2 (FWR2) acid sequence:
(DNA)
tgggtgcgacaggcccctggacaagggcttgagtggatggga (SEQ ID NO:445)

(amino acids)
WVRQAPGQGLEWMG (SEQ ID NO:446)

Humanized C3 heavy chain variable complementarity determining regions 2 (CDR2) sequence:
(DNA)
gtgatcagcaccttcagcggtaacacaaacttcaaccagaagttcaagggc (SEQ ID NO:447)

(amino acids)
VISTFSGNTNFNQKFKG (SEQ ID NO:448)

Humanized C3 heavy chain variable framework region 3 (FWR3) acid sequence:
(DNA)
agagtcaccatgaccacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacacggcc
gtgtattactgtgcgaga (SEQ ID NO:449)

(amino acids)
RVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR (SEQ ID NO:450)

Humanized C3 heavy chain variable complementarity determining regions 3 (CDR3) sequence:
(DNA)
agcgactactacggcccatacttcgactac (SEQ ID NO:451)

(amino acids)
SDYYGPYFDY (SEQ ID NO:452)

Humanized C3 IgG1 heavy chain sequence
(DNA)
caggttcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggt
tacacctttaccgactacgccatgaactgggtgcgacaggcccctggacaagggcttgagtggatgggagtgatcagc
accttcagcggtaacacaaacttcaaccagaagttcaagggcagagtcaccatgaccacagacacatccacgagcaca
gcctacatggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgagaagcgactactacggccca
tacttcgactactggggccagggcaccaccctgaccgtgtccagcgctagcaccaagggcccatcggtcttccccctg
gcaccctcctccaagagcacctctgggggcacagcggccctgggctgcctggtcaaggactacttccccgaaccggtg
acggtgtcgtggaactcaggcgccctgaccagcggcgtgcacaccttcccggctgtcctacagtcctcaggactctac
tccctcagcagcgtggtgacagtgccctccagcagcttgggcacccagacctacatctgcaacgtgaatcacaagccc
agcaacaccaaggtggacaagaaagttgagcccaaatcttgtgacaaaactcacacatgcccaccgtgcccagcacct
gaactcctggggggaccgtcagtcttcctcttccccccaaaacccaaggacaccctcatgatctcccggacccctgag
gtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtg
cataatgccaagacaaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcac
caggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaaccatc
tccaaagccaaagggcagccccgagaaccacaggtgtacaccctgcccccatcccgggaggagatgaccaagaaccag
gtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggagtgggagagcaatgggcagccggag
aacaactacaagaccacgcctcccgtgctggactccgacggctccttcttcctctacagcaagctcaccgtggacaag
agcaggtggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagc
ctctccctgtctccgggtaaatgataa (SEQ ID NO: 453)

(amino acids)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYAMNWVRQAPGQGLEWMGVISTFSGNTNFNQKFKGRVTMTTDTSTS
TAYMELRSLRSDDTAVYYCARSDYYGPYFDYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC
PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK**(SEQ ID NO:454)

Humanized C3 IgG2 heavy chain sequence
(DNA)
caggttcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaaggcttctggt
tacacctttaccgactacgccatgaactgggtgcgacaggcccctggacaagggcttgagtggatgggagtgatcagc
accttcagcggtaacacaaacttcaaccagaagttcaagggcagagtcaccatgaccacagacacatccacgagcaca
gcctacatggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgagaagcgactactacggccca
tacttcgactactggggccagggcaccaccctgaccgtgtccagcgcctccaccaagggcccatcggtcttccccctg

gcgccctgctccaggagcacctccgagagcacagccgccctgggctgcctggtcaaggactacttccccgaaccggtg
acggtgtcgtggaactcaggcgctctgaccagcggcgtgcacaccttcccagctgtcctacagtcctcaggactctac
tccctcagcagcgtggtgaccgtgccctccagcaacttcggcacccagacctacacctgcaacgtagatcacaagccc
agcaacaccaaggtggacaagacagttgagcgcaaatgttgtgtcgagtgcccaccgtgcccagcaccacctgtggca
ggaccgtcagtcttcctcttccccccaaaacccaaggacaccctcatgatctcccggacccctgaggtcacgtgcgtg
gtggtggacgtgagccacgaagaccccgaggtccagttcaactggtacgtggacggcgtggaggtgcataatgccaag
acaaagccacgggaggagcagttcaacagcacgttccgtgtggtcagcgtcctcaccgttgtgcaccaggactggctg
aacggcaaggagtacaagtgcaaggtctccaacaaaggcctcccagcccccatcgagaaaaccatctccaaaaccaaa
gggcagccccgagaaccacaggtgtacaccctgcccccatcccgggaggagatgaccaagaaccaggtcagcctgacc
tgcctggtcaaaggcttctaccccagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaag
accacacctcccatgctggactccgacggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcag
caggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtct
ccgggtaaatagtaa (SEQ ID NO:455)

(amino acids)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYAMNWVRQAPGQGLEWMGVISTFSGNTNFNQKFKGRVTMTTDTSTS
TAYMELRSLRSDDTAVYYCARSDYYGPYFDYWGQGTTLTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPE
PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAP
PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVH
QDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK**(SEQ ID NO:456)

Mouse C3 Light Chain variable region sequence:
(DNA)
gatgttttgatgacccaaactccactctccctgcctgtcagtcttggagatcaagcctccatctcttgcagatctagt
cagaccattgtacatagtaatggaaacacctatttagaatggtacctgcagaaaccaggccagtctccaaagctcctg
atctacaaagtttccaaccgattttctggggtcccagacaggttcagtggcagtggatcagggacagatttcacactc
aagatcaacagagtggaggctgaggatctgggagtttattactgctttcaaggttcacatgttccattcacgttcggc
tcggggacaaagttggaaataaaa (SEQ ID NO:458)

(amino acids)
DVLMTQTPLSLPVSLGDQASISCRSSQTIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTL
KINRVEAEDLGVYYCFQGSHVPFTFGSGTKLEIK (SEQ ID NO:459)

Mouse C3 light chain variable framework region 1 (FWR1) sequence :
(DNA)
gatgttttgatgacccaaactccactctccctgcctgtcagtcttggagatcaagcctccatctcttgc (SEQ ID NO:460)

(amino acids)
DVLMTQTPLSLPVSLGDQASISC (SEQ ID NO:461)

Mouse C3 light chain variable complementarity determining regions 1 (CDR1) sequence :
(DNA)
agatctagtcagaccattgtacatagtaatggaaacacctatttagaa (SEQ ID NO:462)

(amino acids)
RSSQTIVHSNGNTYLE (SEQ ID NO:463)

Mouse C3 light chain variable framework region 2 (FWR2) sequence:
(DNA)
tggtacctgcagaaaccaggccagtctccaaagctcctgatctac (SEQ ID NO:464)

(amino acids)
WYLQKPGQSPKLLIY (SEQ ID NO:465)

Mouse C3 light chain variable complementarity determining regions 2 (CDR2) sequence:
(DNA)
aaagtttccaaccgattttct (SEQ ID NO:466)

(amino acids)
KVSNRFS (SEQ ID NO:467)

Mouse C3 light chain variable framework region 3 (FWR3) sequence:
(DNA)
ggggtcccagacaggttcagtggcagtggatcagggacagatttcacactcaagatcaacagagtggaggctgagga
tctgggagtttattactgc (SEQ ID NO:468)

(amino acids)
GVPDRFSGSGSGTDFTLKINRVEAEDLGVYYC (SEQ ID NO:469)

Mouse C3 light chain variable complementarity determining regions 3 (CDR3) sequence:
(DNA)
tttcaaggttcacatgttccattcacg (SEQ ID NO:470)

(amino acids)
FQGSHVPFT (SEQ ID NO:471)

Humanized C3 light chain variable region sequence from IGKV2-29*03:
(DNA)
gatattgtgatgacccagactccactctctctgtccgtcacccctggacagccggcctccatctcctgcaggtctagt
cagaccattgtccatagtaatggaaacacctatttggagtggtacctgcagaagccaggccagtctccacagctcctg
atctataaggtttccaaccggttctctggagtgccagataggttcagtggcagcgggtcagggacagatttcacactg
aaaatcagccgggtggaggctgaggatgttggggtttattactgcttccaaggtagccacgtgcctttcaccttcggc
ggagggaccaaggtggagatcaaacgaact (SEQ ID NO:486)

(amino acids)
DIVMTQTPLSLSVTPGQPASISCRSSQTIVHSNGNTYLEWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFT
LKISRVEAEDVGVYYCFQGSHVPFTFGGGTKVEIKRT (SEQ ID NO:487)

Humanized C3 light chain variable framework region 1 (FWR1) acid sequence:
(DNA)
gatattgtgatgacccagactccactctctctgtccgtcacccctggacagccggcctccatctcctgc (SEQ ID NO:488)

(amino acids)
DIVMTQTPLSLSVTPGQPASISC (SEQ ID NO:489)

Humanized C3 light chain variable complementarity determining regions 1 (CDR1) sequence:
(DNA)
ggtctagtcagaccattgtccatagtaatggaaacacctatttggag (SEQ ID NO:490)

(amino acids)
RSSQTIVHSNGNTYLE (SEQ ID NO:491)

Humanized C3 light chain variable framework region 2 (FWR2) acid sequence:
(DNA)
tggtacctgcagaagccaggccagtctccacagctcctgatctat (SEQ ID NO:492)

(amino acids)

WYLQKPGQSPQLLIY (SEQ ID NO:493)

Humanized C3 light chain variable complementarity determining regions 2 (CDR2) sequence:
(DNA)
aaggtttccaaccggttctct (SEQ ID NO:494)

(amino acids)
KVSNRFS (SEQ ID NO:495)

Humanized C3 light chain variable framework region 3 (FWR3) acid sequence:
(DNA)
ggagtgccagataggttcagtggcagcgggtcagggacagatttcacactgaaaatcagccgggtggaggctgaggat
gttggggtttattactgc (SEQ ID NO:496)

(amino acids)
GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC (SEQ ID NO:497)

Humanized C3 light chain variable complementarity determining regions 3 (CDR3) sequence:
(DNA)
ttccaaggtagccacgtgcctttcacc (SEQ ID NO:498)

(amino acids)
FQGSHVPFT (SEQ ID NO:499)

Humanized C3 lambda light chain sequence
(DNA)
gatattgtgatgacccagactccactctctctgtccgtcacccctggacagccggcctccatctcctgcaggtctagt
cagaccattgtccatagtaatggaaacacctatttggagtggtacctgcagaagccaggccagtctccacagctcctg
atctataaggtttccaaccggttctctggagtgccagataggttcagtggcagcgggtcagggacagatttcacactg
aaaatcagccgggtggaggctgaggatgttggggtttattactgcttccaaggtagccacgtgcctttcaccttcggc
ggagggaccaaggtggagatcaaacgaactggtcagcccaaggctgcccccctcggtcactctgttcccgccctcctct
gaggagcttcaagccaacaaggccacactggtgtgtctcataagtgacttctacccgggagccgtgacagtggcctgg
aaggcagatagcagccccgtcaaggcgggagtggagaccaccacaccctccaaacaaagcaacaacaagtacgcggcc
agcagctatctgagcctgacgcctgagcagtggaagtcccacagaagctacagctgccaggtcacgcatgaagggagc
accgtggagaagacagtggcccctacagaatgttcatagtaa (SEQ ID NO:500)

(amino acids)
DIVMTQTPLSLSVTPGQPASISCRSSQTIVHSNGNTYLEWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFT
LKISRVEAEDVGVYYCFQGSHVPFTFGGGTKVEIKRTGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTV
AWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS** (SEQ ID NO:501)

Humanized C3 Kappa light chain
(DNA)
gatattgtgatgacccagactccactctctctgtccgtcacccctggacagccggcctccatctcctgcaggtctagt
cagaccattgtccatagtaatggaaacacctatttggagtggtacctgcagaagccaggccagtctccacagctcctg
atctataaggtttccaaccggttctctggagtgccagataggttcagtggcagcgggtcagggacagatttcacactg
aaaatcagccgggtggaggctgaggatgttggggtttattactgcttccaaggtagccacgtgcctttcaccttcggc
ggagggaccaaggtggagatcaaacgaactacggtggctgcaccatctgtcttcatcttcccgccatctgatgagcag
ttgaaatctggaactgcctctgttgtgtgcctgctgaataacttctatcccagagaggccaaagtacagtggaaggtg
gataacgccctccaatcgggtaactcccaggagagtgtcacagagcaggacagcaaggacagcacctacagcctcagc
agcaccctgacgctgagcaaagcagactacgagaaacacaaagtctacgcctgcgaagtcacccatcagggcctgagc
tcgcccgtcacaaagagcttcaacaggggagagtgttagtaa (SEQ ID NO:502)

(amino acids)

DIVMTQTPLSLSVTPGQPASISCRSSQTIVHSNGNTYLEWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFT
LKISRVEAEDVGVYYCFQGSHVPFTFGGGTKVEIKRTTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC**(SEQ ID
NO: 503)

Mouse C8 heavy chain variable region sequence
(DNA)
gaagtgatggtcgtggaaagcggcggtggtctggtaaagccgggggggatcccttaagctttcttgcgccgcatccggg
ttcacgttctccggctatgccatgtcctgggtccgacagactcccgaaaagcgcttggaatgggtggccactatctcc
tccgggggggacgtacatctactaccccgacagtgtgaaaggaagatttacaatatctcgcgacaacgcaaaaaatacc
ttgtatcttcaaatgagctccctgcggtcagaggacactgccatgtactattgcgcccgcctgggcggcgacaattac
tatgagtat (SEQ ID NO:505)

(amino acids)
EVMVVESGGGLVKPGGSLKLSCAASGFTFSGYAMSWVRQTPEKRLEWVATISSGGTYIYYPDSVKGRFTISRDNAKNT
LYLQMSSLRSEDTAMYYCARLGGDNYYEY (SEQ ID NO:506)

Mouse C8 heavy chain variable complementarity determining region 1 (CDR1) sequence:
(DNA)
ggctatgccatgtcc (SEQ ID NO:507)

(amino acids)
GYAMS (SEQ ID NO:508)

Mouse C8 heavy chain variable complementarity determining region 2 (CDR2) sequence:
(DNA)
actatctcctccgggggggacgtacatctactaccccgacagtgtgaaagga (SEQ ID NO:509)

(amino acids)
TISSGGTYIYYPDSVKG (SEQ ID NO:510)

Mouse C8 heavy chain variable complementarity determining region 3 (CDR3) sequence:
(DNA)
ctgggcggcgacaattactatgagtat (SEQ ID NO:511)

(amino acids)
LGGDNYYEY (SEQ ID NO:512)

Humanized C8 heavy chain variable region sequence from IGHV3-21*04:
(DNA)
gaggtgcagctggtggagtctgggggaggcctggtcaagcctggggggtccctgagactctcctgtgcagcctctgga
ttcaccttcagtggctatgccatgagctgggtccgccaggctccagggaaggggctggagtgggtctcaaccattagt
agtggcggaacctacatatactaccctgactcagtgaagggccgattcaccatctccagagacaacgccaagaactca
ctgtatctgcaaatgaacagcctgagagccgaggacacggccgtgtattactgtgcgagactgggcggcgataactat
tatgaatattggggcaaagggaccacggtcaccgtctcctcc (SEQ ID NO: 525)

(amino acids)
EVQLVESGGGLVKPGGSLRLSCAASGFTFSGYAMSWVRQAPGKGLEWVSTISSGGTYIYYPDSVKGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARLGGDNYYEYWGKGTTVTVSS (SEQ ID NO: 526)

Humanized C8 heavy chain variable framework region 1 (FWR1) sequence:
(DNA)
gaggtgcagctggtggagtctgggggaggcctggtcaagcctggggggtccctgagactctcctgtgcagcctctgga
ttcaccttcagt (SEQ ID NO:527)

(amino acids)
EVQLVESGGGLVKPGGSLRLSCAASGFTFS (SEQ ID NO:528)

Humanized C8 heavy chain variable complementarity determining region 1 (CDR1) sequence:
(DNA)
ggctatgccatgagc (SEQ ID NO:529)

(amino acids)
GYAMS (SEQ ID NO:530)

Humanized C8 heavy chain variable framework region 2 (FWR2) sequence:
(DNA)
tgggtccgccaggctccagggaaggggctggagtgggtctca (SEQ ID NO:531)

(amino acids)
WVRQAPGKGLEWVS (SEQ ID NO:532)

Humanized C8 heavy chain variable complementarity determining region 2 (CDR2) sequence:
(DNA)
accattagtagtggcggaacctacatatactaccctgactcagtgaagggc (SEQ ID NO:533)

(amino acids)
TISSGGTYIYYPDSVKG (SEQ ID NO:534)

Humanized C8 heavy chain variable framework region 3 (FWR3) sequence:
(DNA)
cgattcaccatctccagagacaacgccaagaactcactgtatctgcaaatgaacagcctgagagccgaggacacggcc
gtgtattactgtgcgaga (SEQ ID NO:535)

(amino acids)
RFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR (SEQ ID NO:536)

Humanized C8 heavy chain variable complementarity determining region 3 (CDR3) sequence:
(DNA)
ctgggcggcgataactattatgaatat (SEQ ID NO:537)

(amino acids)
LGGDNYYEY (SEQ ID NO:538)

Humanized C8 IgG1 heavy chain sequence
(DNA)
gaggtgcagctggtggagtctgggggaggcctggtcaagcctggggggtccctgagactctcctgtgcagcctctgga
ttcaccttcagtggctatgccatgagctgggtccgccaggctccagggaaggggctggagtgggtctcaaccattagt
agtggcggaacctacatatactaccctgactcagtgaagggccgattcaccatctccagagacaacgccaagaactca
ctgtatctgcaaatgaacagcctgagagccgaggacacggccgtgtattactgtgcgagactgggcggcgataactat
tatgaatattggggcaaaggaccacggtcaccgtctcctccgctagcaccaagggcccatcggtcttccccctggca
ccctcctccaagagcacctctgggggcacagcggccctgggctgcctggtcaaggactacttccccgaaccggtgacg
gtgtcgtggaactcaggcgccctgaccagcggcgtgcacaccttcccggctgtcctacagtcctcaggactctactcc
ctcagcagcgtggtgacagtgccctccagcagcttgggcacccagacctacatctgcaacgtgaatcacaagcccagc
aacaccaaggtggacaagaaagttgagcccaaatcttgtgacaaaactcacacatgcccaccgtgcccagcacctgaa
ctcctggggggaccgtcagtcttcctcttccccccaaaacccaaggacaccctcatgatctcccggacccctgaggtc
acatgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcat
aatgccaagacaaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccag
gactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaaccatctcc

aaagccaaagggcagccccgagaaccacaggtgtacaccctgcccccatcccgggaggagatgaccaagaaccaggtc
agcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggagtgggagagcaatgggcagccggagaac
aactacaagaccacgcctcccgtgctggactccgacggctccttcttcctctacagcaagctcaccgtggacaagagc
aggtggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcctc
tccctgtctccgggtaaatgataa (SEQ ID NO:539)

(amino acids)
EVQLVESGGGLVKPGGSLRLSCAASGFTFSGYAMSWVRQAPGKGLEWVSTISSGGTYIYYPDSVKGRFTISRDNAKNS
LYLQMNSLRAEDTAVYYCARLGGDNYYEYWGKGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE
LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK** (SEQ ID NO:540)

Humanized C8 IgG2 heavy chain sequence
(DNA)
gaggtgcagctggtggagtctgggggaggcctggtcaagcctggggggtccctgagactctcctgtgcagcctctgga
ttcaccttcagtggctatgccatgagctgggtccgccaggctccagggaaggggctggagtgggtctcaaccattagt
agtggcggaacctacatatactaccctgactcagtgaagggccgattcaccatctccagagacaacgccaagaactca
ctgtatctgcaaatgaacagcctgagagccgaggacacggccgtgtattactgtgcgagactgggcggcgataactat
tatgaatattggggcaaagggaccacggtcaccgtctcctccgcctccaccaagggcccatcggtcttccccctggcg
ccctgctccaggagcacctccgagagcacagccgccctgggctgcctggtcaaggactacttccccgaaccggtgacg
gtgtcgtggaactcaggcgctctgaccagcggcgtgcacaccttcccagctgtcctacagtcctcaggactctactcc
ctcagcagcgtggtgaccgtgccctccagcaacttcggcacccagacctacacctgcaacgtagatcacaagcccagc
aacaccaaggtggacaagacagttgagcgcaaatgttgtgtcgagtgcccaccgtgcccagcaccacctgtggcagga
ccgtcagtcttcctcttccccccaaaacccaaggacaccctcatgatctcccggacccctgaggtcacgtgcgtggtg
gtggacgtgagccacgaagaccccgaggtccagttcaactggtacgtggacggcgtggaggtgcataatgccaagaca
aagccacgggaggagcagttcaacagcacgttccgtgtggtcagcgtcctcaccgttgtgcaccaggactggctgaac
ggcaaggagtacaagtgcaaggtctccaacaaaggcctcccagcccccatcgagaaaaccatctccaaaaccaaaggg
cagccccgagaaccacaggtgtacaccctgcccccatcccgggaggagatgaccaagaaccaggtcagcctgacctgc
ctggtcaaaggcttctaccccagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagacc
acacctcccatgctggactccgacggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcag
gggaacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtctccg
ggtaaatagtaa (SEQ ID NO:541)

(amino acids)
EVQLVESGGGLVKPGGSLRLSCAASGFTFSGYAMSWVRQAPGKGLEWVSTISSGGTYIYYPDSVKGRFTISRDNAKNS
LYLQMNSLRAEDTAVYYCARLGGDNYYEYWGKGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLN
GKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
TPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK** (SEQ ID NO:542)

Mouse C8 light chain variable region sequence
(DNA)
gacatcgtcattacgcagacccctgccagtcttgccgtttctctgggccagagggccactatcagttacagggcgagt
aagtctgtgagtaccagcggctatagttacatgcattggaaccagcagaaaccgggacagccaccacgcctgcttatt
tatctggtgtctaatcttgagtccggggtgcccgccaggttcagcggcagcggctctgggaccgacttcacactcaac
attcatccagtggaagaagaggacgctgctacatactactgtcaacacattcgggaactgaccaggagtgaa (SEQ
ID NO:543)
(amino acids)
DIVITQTPASLAVSLGQRATISYRASKSVSTSGYSYMHWNQQKPGQPPRLLIYLVSNLESGVPARFSGSGSGTDFTLN
IHPVEEEDAATYYCQHIRELTRSE (SEQ ID NO:544)

Mouse C8 light chain variable complementarity determining region 1 (CDR1) sequence:
(DNA)

agggcgagtaagtctgtgagtaccagcggctatagttacatgcat (SEQ ID NO:545)

(amino acids)

RASKSVSTSGYSYMH (SEQ ID NO: 546)

Mouse C8 light chain variable complementarity determining region 2 (CDR2) sequence:

(DNA)

ctggtgtctaatcttgagtcc (SEQ ID NO:547)

(amino acids)

LVSNLES (SEQ ID NO:548)

Mouse C8 light chain variable complementarity determining region 3 (CDR3) sequence:

(DNA)

caacacattcgggaactgaccaggagtgaa (SEQ ID NO:549)

(amino acids)

QHIRELTRSE (SEQ ID NO:550)

Humanized C8 light chain variable region sequence from NCBI germline z00023:

(DNA)

gacatcgtgatgacccagtctccagactccctggctgtgtctctgggcgagagggccaccatcaactgcagggccagcaagagtgttagcaccagcggctacagctacatgcactggtaccagcagaaaccaggacagcctcctaagctgctcatttacctggtgtctaacctggaatccggggtccctgaccgattcagtggcagcgggtctgggacagatttcactctcaccatcagcagcctgcaggctgaagatgtggcagtttattactgtcaacacattcgggaactgaccaggagtgaattcggcggagggaccaaggtggagatcaaacgaact (SEQ ID NO:565)

(amino acids)

DIVMTQSPDSLAVSLGERATINCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLVSNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQHIRELTRSEFGGGTKVEIKRT (SEQ ID NO:566)

Humanized C8 light chain variable framework region 1 (FWR1) sequence:

(DNA)

gacatcgtgatgacccagtctccagactccctggctgtgtctctgggcgagagggccaccatcaactgc (SEQ ID NO:567)

(amino acids)

DIVMTQSPDSLAVSLGERATINC (SEQ ID NO:568)

Humanized C8 light chain variable complementarity determining region 1 (CDR1) sequence:

(DNA)

agggccagcaagagtgttagcaccagcggctacagctacatg (SEQ ID NO:569)

(amino acids)

RASKSVSTSGYSYM (SEQ ID NO:570)

Humanized C8 light chain variable framework region 2 (FWR2) sequence:

(DNA)

cactggtaccagcagaaaccaggacagcctcctaagctgctcatttac (SEQ ID NO:571)

(amino acids)

HWYQQKPGQPPKLLIY (SEQ ID NO:572)

Humanized C8 light chain variable complementarity determining region 2 (CDR2) sequence:
(DNA)
ctggtgtctaacctggaatcc (SEQ ID NO:573)

(amino acids)
LVSNLES (SEQ ID NO:574)

Humanized C8 light chain variable framework region 3 (FWR3) sequence:
(DNA)
ggggtccctgaccgattcagtggcagcgggtctgggacagatttcactctcaccatcagcagcctgcaggctgaagat
gtggcagtttattactgt (SEQ ID NO:575)

(amino acids)
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC (SEQ ID NO:576)

Humanized C8 light chain variable complementarity determining region 3 (CDR3) sequence:
(DNA)
caacacattcgggaactgaccaggagtgaa (SEQ ID NO:577)

(amino acids)
QHIRELTRSE (SEQ ID NO:578)

Humanized C8 Lambda light chain sequence
(DNA)
gacatcgtgatgacccagtctccagactccctggctgtgtctctgggcgagagggccaccatcaactgcagggccagc
aagagtgttagcaccagcggctacagctacatgcactggtaccagcagaaaccaggacagcctcctaagctgctcatt
tacctggtgtctaacctggaatccggggtccctgaccgattcagtggcagcgggtctgggacagatttcactctcacc
atcagcagcctgcaggctgaagatgtggcagtttattactgtcaacacattcgggaactgaccaggagtgaattcggc
ggagggaccaaggtggagatcaaacgaactggtcagcccaaggctgccccctcggtcactctgttcccgccctcctct
gaggagcttcaagccaacaaggccacactggtgtgtctcataagtgacttctacccgggagccgtgacagtggcctgg
aaggcagatagcagccccgtcaaggcgggagtggagaccaccacaccctccaaacaaagcaacaacaagtacgcggcc
agcagctatctgagcctgacgcctgagcagtggaagtcccacagaagctacagctgccaggtcacgcatgaagggagc
accgtggagaagacagtggcccctacagaatgttcatagtaa (SEQ ID NO:579)

(amino acids)
DIVMTQSPDSLAVSLGERATINCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLVSNLESGVPDRFSGSGSGTDFTLT
ISSLQAEDVAVYYCQHIRELTRSEFGGGTKVEIKRTGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAW
KADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS** (SEQ ID
NO:580)

Humanized C8 Kappa light chain sequence
(DNA)
gacatcgtgatgacccagtctccagactccctggctgtgtctctgggcgagagggccaccatcaactgcagggccagc
aagagtgttagcaccagcggctacagctacatgcactggtaccagcagaaaccaggacagcctcctaagctgctcatt
tacctggtgtctaacctggaatccggggtccctgaccgattcagtggcagcgggtctgggacagatttcactctcacc
atcagcagcctgcaggctgaagatgtggcagtttattactgtcaacacattcgggaactgaccaggagtgaattcggc
ggagggaccaaggtggagatcaaacgaactacggtggctgcaccatctgtcttcatcttcccgccatctgatgagcag
ttgaaatctggaactgcctctgttgtgtgcctgctgaataacttctatcccagagaggccaaagtacagtggaaggtg
gataacgccctccaatcgggtaactcccaggagagtgtcacagagcaggacagcaaggacagcacctacagcctcagc
agcaccctgacgctgagcaaagcagactacgagaaacacaaagtctacgcctgcgaagtcacccatcagggcctgagc
tcgcccgtcacaaagagcttcaacaggggagagtgttagtaa (SEQ ID NO:581)

(amino acids)
DIVMTQSPDSLAVSLGERATINCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLVSNLESGVPDRFSGSGSGTDFTLT
ISSLQAEDVAVYYCQHIRELTRSEFGGGTKVEIKRTTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV

DNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC** (SEQ ID NO:582)

CAR-T E6 CD8 sequence:

(DNA)
gaggtccagctggttgagagtggcggtgggctggttaagcctggcggctccctgcggctgagctgcgccgcgagtgga
tttactttcagccgatatgggatgagttgggtgcggcaagctcccgggaagaggctggaatgggtctcaacaatctcc
gggggggcacttacatctattaccccgactcagtcaaggggagatttaccatttcacgagacaacgctaagaatacc
ctgtatttgcagatgaattctctgagagcagaggacacagctgtttactattgtacccgcgacaactatggcaggaac
tacgactacggtatggactattggggacaagggacattggttacagtgagcagtggcggcgggggcagcggaggagga
ggcagcggtgggggggcagcgagatagtgctcacgcagtcacccgcgactctcagtctctcacctggggaacgagct
accctgacgtgctctgctacctcctcagtgtcatatattcactggtatcagcaacggcccgggcagtcccctagattg
ctcatttatagtacctctaatctggcctcaggtatccctgcacgattttctggatctggttcaggttctgattacacc
ctcactatctctagcctggagcctgaagactttgccgtttattactgccagcagaggtctagctccccattcacttt
gggagtgggaccaaggttgaaattaaaacgacaaccccggcccccagaccaccaacgccagcccccaccatcgccagc
caacccctgtctctgagaccagaagcctgtaggcctgccgccggtggagctgtgcacacaagaggactggatttcgcc
tgtgatatctacatttgggccccgctcgcaggcacatgtggagtgctcctcctctccctggtgattaccctgtactgc
tgataa (SEQ ID NO:584)
(amino acids)
EVQLVESGGGLVKPGGSLRLSCAASGFTFSRYGMSWVRQAPGKRLEWVSTISGGGTYIYYPDSVKGRFTISRDNAKN
TLYLQMNSLRAEDTAVYYCTRDNYGRNYDYGMDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPATLSLSPGE
RATLTCSATSSVSYIHWYQQRPGQSPRLLIYSTSNLASGIPARFSGSGSGSDYTLTISSLEPEDFAVYYCQQRSSSP
FTFGSGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVI
TLYC** (SEQ ID NO:585)

CAR-T C2 CD8 CD8 sequence:

N-CD8ls-huMNC2scFv-CD8ecd fragment- CD8 transmembrane-C
(DNA)
gaagtgcagctcgtagagagtggcggggactggtgaagcccggtggaagcctcagactcagttgcgccgcctcaggt
ttcactttttcaggttacgccatgtcctgggtaagacaggcaccggggaaaggactcgagtgggtgtctactatcagc
tcaggaggcacttatatatattatcctgactctgtaaaaggccgatttacgatttctcgcgacaatgcaaagaactcc
ctctacctccaaatgaacagtcttagggcagaagacactgctgtatactattgtgcacgcctcggcggcgacaactac
tacgagtactttgacgtgtgggggaaagggactaccgtgacagtttcaagcggaggaggtggctcaggtggaggcggg
tcaggggggggaggaagtgatattgtgctcacacaatccccagcctccctggctgtgtctcccggccaacgcgctaca
attacatgtcgggcctccaaaagcgtgagcaccagcggctacagctacatgcactggtatcaacagaaaccaggacaa
ccccccaaactgttgatttatctcgcttcaaacttggagtccggcgtgcctgcgcgcttttcagggagtgggagcggc
acagattttacgctgactatcaaccccgtagaagcaaacgatacagcgaattattattgtcaacattcccgggaactc
ccctttacgttcggcgggggcacaaaggtcgaaattaagagaaccacgacaaccccggcccccagaccaccaacgcca
gcccccaccatcgccagccaacccctgtctctgagaccagaagcctgtaggcctgccgccggtggagctgtgcacaca
agaggactggatttcgcctgtgatatctacatttgggccccgctcgcaggcacatgtggagtgctcctcctctccctg
gtgattaccctgtactgctgataa (SEQ ID NO:586)

(amino acids)
EVQLVESGGGLVKPGGSLRLSCAASGFTFSGYAMSWVRQAPGKGLEWVSTISSGGTYIYYPDSVKGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARLGGDNYYEYFDVWGKGTTVTVSSGGGGSGGGGSGGGGSDIVLTQSPASLAVSPGQR
ATITCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLASNLESGVPARFSGSGSGTDFTLTINPVEANDTANYYCQHS
RELPFTFGGGTKVEIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVL
LLSLVITLYC** (SEQ ID NO:587)

CD8/4-1BB sequence

N- CD8 transmembrane- 4-1BB-C
(DNA)
acgacaaccccggcccccagaccaccaacgccagcccccaccatcgccagccaacccctgtctctgagaccagaagcc
tgtaggcctgccgccggtggagctgtgcacacaagaggactggatttcgcctgtgatatctacatttgggccccgctc
gcaggcacatgtggagtgctcctcctctccctggtgattaccctgtactgcaaaaggggccgcaaaaaactcctttac

atttttaagcagccttttatgaggccagtacagacgactcaagaggaagacgggtgctcatgccgctttcctgaggag
gaggaaggagggtgcgaactgtgataa (SEQ ID NO:588)

(amino acids)
TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLL
YIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL** (SEQ ID NO:589)

CD8/CD28 sequence
N- CD8 transmembrane- CD28-C
(DNA)
acgacaaccccggcccccagaccaccaacgccagcccccaccatcgccagccaacccctgtctctgagaccagaagcc
tgtaggcctgccgccggtggagctgtgcacacaagaggactggatttcgcctgtgatatctacatttgggccccgctc
gcaggcacatgtggagtgctcctcctctccctggtgattaccctgtactgcagaagcaagcggtctcggctcctgcat
tctgattacatgaacatgaccccaagaagaccaggccccaccaggaaacattaccagccctacgctccgccacgcgac
ttcgctgcctaccggtcctgataa (SEQ ID NO: 590)

(amino acids)
TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLL
HSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS** (SEQ ID NO:591)

CD8/CD3z sequence:
N- CD8 transmembrane- CD3zeta-C
(DNA)
acgacaaccccggcccccagaccaccaacgccagcccccaccatcgccagccaacccctgtctctgagaccagaagcc
tgtaggcctgccgccggtggagctgtgcacacaagaggactggatttcgcctgtgatatctacatttgggccccgctc
gcaggcacatgtggagtgctcctcctctccctggtgattaccctgtactgccgcgttaagttctcccgatcagccgac
gcgcctgcttacaagcagggccagaaccaactgtacaacgagctgaatctcggtagacgggaagagtacgacgtgttg
gacaaacggagaggccgcgacccagaaatgggcggcaagcctcgcaggaaaaaccccaggagggactgtacaatgag
ttgcagaaagataagatggcagaagcttatagcgagatcggaatgaaggggggaaaggagacgagggaaaggacacgac
ggcctttatcagggcctgtccacagcaacaaaagatacgtatgacgccctccatatgcaggcacttccaccacggtga
taa (SEQ ID NO:592)

(amino acids)
TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRVKFSRSA
DAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKG
HDGLYQGLSTATKDTYDALHMQALPPR** (SEQ ID NO:593)

CD8/CD28/CD3z sequence:
N- CD8 transmembrane- CD28- CD3zeta-C
(DNA)
acgacaaccccggcccccagaccaccaacgccagcccccaccatcgccagccaacccctgtctctgagaccagaagcc
tgtaggcctgccgccggtggagctgtgcacacaagaggactggatttcgcctgtgatatctacatttgggccccgctc
gcaggcacatgtggagtgctcctcctctccctggtgattaccctgtactgcagaagcaagcggtctcggctcctgcat
tctgattacatgaacatgaccccaagaagaccaggccccaccaggaaacattaccagccctacgctccgccacgcgac
ttcgctgcctaccggtcccgcgttaagttctcccgatcagccgacgcgcctgcttacaagcagggccagaaccaactg
tacaacgagctgaatctcggtagacgggaagagtacgacgtgttggacaaacggagaggccgcgacccagaaatgggc
ggcaagcctcgcaggaaaaaccccaggagggactgtacaatgagttgcagaaagataagatggcagaagcttatagc
gagatcggaatgaaggggggaaaggagacgagggaaaggacacgacggcctttatcagggcctgtccacagcaacaaaa
gatacgtatgacgccctccatatgcaggcacttccaccacggtgataa (SEQ ID NO:594)

(amino acids)
TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLL
HSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPE
MGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR** (SEQ
ID NO:595)

CD8/4-1BB/CD3z sequence:

N- CD8 transmembrane- 4-1BB- CD3zeta-C
(DNA)
acgacaaccccggcccccagaccaccaacgccagcccccaccatcgccagccaacccctgtctctgagaccagaagcc
tgtaggcctgccgccggtggagctgtgcacacaagaggactggatttcgcctgtgatatctacatttgggccccgctc
gcaggcacatgtggagtgctcctcctctccctggtgattaccctgtactgcaaaaggggccgcaaaaaactcctttac
atttttaagcagccttttatgaggccagtacagacgactcaagaggaagacgggtgctcatgccgctttcctgaggag
gaggaaggagggtgcgaactgcgcgttaagttctcccgatcagccgacgcgcctgcttacaagcagggccagaaccaa
ctgtacaacgagctgaatctcggtagacgggaagagtacgacgtgttggacaaacggagaggccgcgacccagaaatg
ggcggcaagcctcgcaggaaaaacccccaggagggactgtacaatgagttgcagaaagataagatggcagaagcttat
agcgagatcggaatgaaggggggaaaggagacgagggaaaggacacgacggcctttatcagggcctgtccacagcaaca
aaagatacgtatgacgccctccatatgcaggcacttccaccacggtgataa (SEQ ID NO:596)

(amino acids)
TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLL
YIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDP
EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR** (SEQ
ID NO:597)

CD8/CD28/4-1BB/CD3z sequence:
N- CD8 transmembrane- CD28- 4-1BB- CD3zeta-C
(DNA)
acgacaaccccggcccccagaccaccaacgccagcccccaccatcgccagccaacccctgtctctgagaccagaagcc
tgtaggcctgccgccggtggagctgtgcacacaagaggactggatttcgcctgtgatatctacatttgggccccgctc
gcaggcacatgtggagtgctcctcctctccctggtgattaccctgtactgcagaagcaagcggtctcggctcctgcat
tctgattacatgaacatgaccccaagaagaccaggccccaccaggaaacattaccagccctacgctccgccacgcgac
ttcgctgcctaccggtccaaaaggggccgcaaaaaactcctttacatttttaagcagccttttatgaggccagtacag
acgactcaagaggaagacgggtgctcatgccgctttcctgaggaggaggaaggagggtgcgaactgcgcgttaagttc
tcccgatcagccgacgcgcctgcttacaagcagggccagaaccaactgtacaacgagctgaatctcggtagacgggaa
gagtacgacgtgttggacaaacggagaggccgcgacccagaaatgggcggcaagcctcgcaggaaaaacccccaggag
ggactgtacaatgagttgcagaaagataagatggcagaagcttatagcgagatcggaatgaaggggggaaaggagacga
gggaaaggacacgacggcctttatcagggcctgtccacagcaacaaaagatacgtatgacgccctccatatgcaggca
cttccaccacggtgataa (SEQ ID NO:598)

(amino acids)
TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLL
HSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRV
KFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGE
RRRGKGHDGLYQGLSTATKDTYDALHMQALPPR** (SEQ ID NO: 599)

CAR-T C2 CD8/CD8/CD28/CD3z sequence:
N-CD8ls-huMNC2scFv-CD8ecd fragment- CD8 transmembrane- CD28- CD3zeta-C
(DNA)
atggccttgccagtgacggccctgctgctgccattggctcttctgttgcacgctgccaggcctgaagtgcagctcgta
gagagtggcggggggactggtgaagcccggtggaagcctcagactcagttgcgccgcctcaggtttcacttttttcaggt
tacgccatgtcctgggtaagacaggcaccggggaaaggactcgagtgggtgtctactatcagctcaggaggcacttat
atatattatcctgactctgtaaaaggccgatttacgatttctcgcgacaatgcaaagaactccctctacctccaaatg
aacagtcttagggcagaagacactgctgtatactattgtgcacgcctcggcggcgacaactactacgagtactttgac
gtgtgggggaaagggactaccgtgacagtttcaagcggaggaggtggctcaggtggaggcgggtcagggggggggagga
agtgatattgtgctcacacaatccccagcctccctggctgtgtctcccggccaacgcgctacaattacatgtcgggcc
tccaaaagcgtgagcaccagcggctacagctacatgcactggtatcaacagaaaccaggacaacccccaaactgttg
atttatctcgcttcaaacttggagtccggcgtgcctgcgcgcttttcagggagtgggagcggcacagattttacgctg
actatcaaccccgtagaagcaaacgatacagcgaattattattgtcaacattcccgggaactcccctttacgttcggc
gggggcacaaaggtcgaaattaagagaaccacgacaaccccggcccccagaccaccaacgccagcccccaccatcgcc
agccaacccctgtctctgagaccagaagcctgtaggcctgccgccggtggagctgtgcacacaagaggactggatttc
gcctgtgatatctacatttgggccccgctcgcaggcacatgtggagtgctcctcctctccctggtgattaccctgtac

tgcagaagcaagcggtctcggctcctgcattctgattacatgaacatgaccccaagaagaccaggccccaccaggaaa
cattaccagccctacgctccgccacgcgacttcgctgcctaccggtcccgcgttaagttctcccgatcagccgacgcg
cctgcttacaagcagggccagaaccaactgtacaacgagctgaatctcggtagacgggaagagtacgacgtgttggac
aaacggagaggccgcgacccagaaatgggcggcaagcctcgcaggaaaaaccccaggagggactgtacaatgagttg
cagaaagataagatggcagaagcttatagcgagatcggaatgaaggggaaaggagacgagggaaaggacacgacggc
ctttatcagggcctgtccacagcaacaaaagatacgtatgacgccctccatatgcaggcacttccaccacggtgataa
(SEQ ID NO:608)

(amino acids)
MALPVTALLLPLALLLHAARPEVQLVESGGGLVKPGGSLRLSCAASGFTFSGYAMSWVRQAPGKGLEWVSTISSGGT
YIYYPDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARLGGDNYYEYFDVWGKGTTVTVSSGGGGSGGGGSGG
GGSDIVLTQSPASLAVSPGQRATITCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLASNLESGVPARFSGSGSGTD
FTLTINPVEANDTANYYCQHSRELPFTFGGGTKVEIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTR
GLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFS
RSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRR
GKGHDGLYQGLSTATKDTYDALHMQALPPR** (SEQ ID NO:609)

CAR-T C2 CD8/CD8/4-1BB/CD3z sequence #13:
N-CD8ls-huMNC2scFv-CD8ecd fragment- CD8 transmembrane- 4-1BB- CD3zeta-C
(DNA)
atggccttgccagtgacggccctgctgctgccattggctcttctgttgcacgctgccaggcctgaagtgcagctcgta
gagagtggcgggggactggtgaagcccggtggaagcctcagactcagttgcgccgcctcaggtttcactttttcaggt
tacgccatgtcctgggtaagacaggcaccggggaaaggactcgagtgggtgtctactatcagctcaggaggcacttat
atatattatcctgactctgtaaaaggccgatttacgatttctcgcgacaatgcaaagaactccctctacctccaaatg
aacagtcttagggcagaagacactgctgtatactattgtgcacgcctcggcggcgacaactactacgagtactttgac
gtgtgggggaaagggactaccgtgacagtttcaagcggaggaggtggctcaggtggaggcgggtcagggggggggagga
agtgatattgtgctcacacaatccccagcctccctggctgtgtctcccggccaacgcgctacaattacatgtcgggcc
tccaaaagcgtgagcaccagcggctacagctacatgcactggtatcaacagaaaccaggacaacccccaaactgttg
atttatctcgcttcaaacttggagtccggcgtgcctgcgcgcttttcagggagtgggagcggcacagattttacgctg
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MUC1 truncated extra cellular domain sequence
(amino acids)
SNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTEAASRY (SEQ ID NO:620)

MUC1 truncated extra cellular domain sequence
(amino acids)
SVVVQLTLAFREGTINVHDVETQFNQYKTEAASRY (SEQ ID NO:621)

MUC1 truncated extra cellular domain sequence
(amino acids)
VQLTLAFREGTINVHDVETQFNQY (SEQ ID NO:622)

MUC1 truncated extra cellular domain sequence
(amino acids)
SNIKFRPGSVVVQLTLAFREGTIN (SEQ ID NO:623)

Primers
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MMP9 catalytic domain
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NO:784)

NFAT consensus sequence:
(A/T)GGAAA(A/N)(A/T/C)N (SEQ ID NO:804)

Current NFAT RE (Form System Biosciences. The sequence is from the mouse IL2 promoter
(DNA)
aagaggaaaatttgtttcatacagaaggcgtt (SEQ ID NO:805)

Mouse IL2 Promoter (highlighted in green the NFAT RE used, highlighted in yellow is the start codon)
(DNA)
aactagagacatataaaataacaccaacatccttagatacaacccttcctgagaatttattggacatcatactcttt
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tcctgcaggcatgtacagcatgcagctcgcatcctgtgtcac (SEQ ID NO:806)

NFAT RE (Form PRomega. The sequence is from the humane IL2 promoter
(DNA)
ggaggaaaaactgtttcatacagaaggcgt (SEQ ID NO:807)

Possible NFAT RE from ET-1 promoter
(DNA)
tccagggaaaatcggagtagaacaagagggatg (SEQ ID NO:808)

Possible NFAT RE from ET-1 promoter
(DNA)

actgttggaaaacgtaaacacgttattaaacggt (SEQ ID NO:809)

Possible NFAT RE from human CD3γ
(DNA)
tccttaacggaaaaacaaaa (SEQ ID NO:810)

Possible NFAT RE from human CD3γ
(DNA)
aaaggaaaaagtatatgttc (SEQ ID NO:811)

Possible NFAT RE from human IL3 promoter
(DNA)
atgccatggaaagggtg (SEQ ID NO:812)

Possible NFAT RE from human GPC6
(DNA)
aaggggaaatgttgagtctaga (SEQ ID NO:813)

Possible NFAT RE from human growth hormone-releasing hormone
(DNA)
AACTTGGAAAAGCATAG (SEQ ID NO:814)

NFATc1 promoter large
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cggggcgcgggcagggctcggagccaccgcgcaggtcctagggccgcggccgggccccgccacgcgcgcacacgccc
ctcgatg (SEQ ID NO:815)

NFATc3 promoter sequence
(DNA)
gcagccaggcagggtgggcgcgcgtagggggcggggccgggcgcgcggcagggcgcgagagcgcacccgcggcggcg
gtggcggcgactgtgggggggcggcggggaacattggctaagccgacagtggaggcttaggcaccggtggcgggcgg
ctgcggttcctggtgctgctcggcgcgcggccagctttcggaacggaacgctcggcgtcgcgggccccgcccggaaa
gtttgccgtggagtcgcgacctcttggcccgcgcggcccggcatgaagcggcgttgaggagctgctgccgccgcttg
ccgctgccgccgccgccgcctgaggaggagctgcagcaccctgggccacgccg (SEQ ID NO:816)

NFATc2 promoter sequence 1
(DNA)
cagagagaggctgcgttcagactggggcactgccatcccctccgcatca
tggggtctgtggaccaaggtaactgactctcgatcccttccagccttttccgctcgctcctcccggccctttcctgc
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aactttacgcgggggcagggaagtgtcccaggccgggattccctaggccagtctgtcgggaggattttcctctccac
gggacaccgggagggattctcgctactaaccgctggctgtttaaccgtttcagcactcggcttttgacagcaa
(SEQ ID NO:817)

NFATc2 promoter sequence 2

(DNA)
catcatggggtctgtggaccaaggtaactgactctcgatcccttccagccttttccgctcgctc (SEQ ID NO:818)

NFATc1 response element consensus
(DNA)
catttttccat (SEQ ID NO:819)

NFATc1 response element consensus
(DNA)
tttttcca (SEQ ID NO:820)

NFAT response elements contained within the Foxp3 enhancer region
(DNA)
acttgaaaatgagataaatgttcacctatgttggcttctagtctcttttatggcttcatt
ttttccatttactatagaggttaagagtgtgggtactggagccagactgtctgggacaa (SEQ ID NO:821)

N+20
SNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA (SEQ ID NO:822)

N+20/C-27
SNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTE (SEQ ID NO:823)

N+9/C-9
VQLTLAFREGTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVP(SEQ ID NO:824)

C-10
GTINVHDVETQFNQYKTEAASRYNLTISDVSVSDV(SEQ ID NO:825)

NME7-AB
(DNA)
atggaaaaaacgctggccctgattaaaccggatgcaatctccaaagctggcgaaattatcgaaattatcaacaaagcg
ggtttcaccatcacgaaactgaaaatgatgatgctgagccgtaaagaagccctggattttcatgtcgaccaccagtct
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cagaacgctgtgcactgtaccgatctgccggaagacggtctgctggaagttcaatacttttcaaaattctggataat
ctcgagcaccaccaccaccaccactga(SEQ ID NO:826)

NME7AB
(amino acids)
MEKTLALIKPDAISKAGEIIEIINKAGFTITKLKMMMLSRKEALDFHVDHQSRPFFNELIQFITTGPIIAMEILRDD
AICEWKRLLGPANSGVARTDASESIRALFGTDGIRNAAHGPDSFASAAREMELFFPSSGGCGPANTAKFTNCTCCIV
KPHAVSEGLLGKILMAIRDAGFEISAMQMFNMDRVNVEEFYEVYKGVVTEYHDMVTEMYSGPCVAMEIQQNNATKTF
REFCGPADPEIARHLRPGTLRAIFGKTKIQNAVHCTDLPEDGLLEVQYFFKILDNLEHHHHHH(SEQ ID NO:827)

Human NME7 x1
(DNA)
atgatgatgctttcaaggaaagaagcattggattttcatgtagatcaccagtcaagacccttttcaatgagctgat
ccagtttattacaactggtcctattattgccatggagattttaagagatgatgctatatgtgaatggaaaagactgc

tgggacctgcaaactctggagtggcacgcacagatgcttctgaaagcattagagccctctttggaacagatggcata
agaaatgcagcgcatggccctgattcttttgcttctgcggccagagaaatggagttgtttttccttcaagtggagg
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tgtactgatctgccagaggatggcctattagaggttcaatacttcttcaagatcttggataatctcgagcaccacca
ccaccaccactga(SEQ ID NO:828)

(amino acids)
MMMLSRKEALDFHVDHQSRPFFNELIQFITTGPIIAMEILRDDAICEWKRLLGPANSGVARTDASESIRALFGTDGIR
NAAHGPDSFASAAREMELFFPSSGGCGPANTAKFTNCTCCIVKPHAVSEGLLGKILMAIRDAGFEISAMQMFNMDRVN
VEEFYEVYKGVVTEYHDMVTEMYSGPCVAMEIQQNNATKTFREFCGPADPEIARHLRPGTLRAIFGKTKIQNAVHCTD
LPEDGLLEVQYFFKILDNLEHHHHHH*(SEQ ID NO:829)

Mouse Antibody **17H6 Heavy chain: DNA sequence**
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGAAGTTGTGGCTGAACTGGATTTTCCTTGTAACACTTTTAAATGGTATCCAGTGTGAGGTGAAGCTGGTGGAGTCT
GGAGGAGGCTTGGTACAGCCTGGGGGTTCTCTGAGACTCTCCTGTGCAACTTCTGGGTTCACCTTCACTGATTACTAC
ATGAGCTGGGTCCGCCAGCCTCCAAGAAAGGCACTTGAGTGGTTGGGTTTTATTAGAAACAAAGCTAATGGTTACACA
GCAGAGTACAGTGCGTCTGTGAAGGGTCGGTTCACCATCTCCAGAGATGTTTCCCAAAACCTCCTCTATCTTCAAATG
AACATCCTGAGAGCTGAGGACAGTGCCACTTATTACTGTGCAAAAGATTACTACGGTAGTAACCCTGCCTGGTTTGCT
TACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA (SEQ ID NO:830)

Mouse Antibody **17H6 Heavy chain: Amino acid sequence**
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
MKLWLNWIFLVTLLNGIQCEVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMSWVRQPPRKALEWLGFIRNKANGYT
AEYSASVKGRFTISRDVSQNLLYLQMNILRAEDSATYYCAKDYYGSNPAWFAYWGQGTLVTVSA (SEQ ID
NO:831)

Mouse 17H6 heavy chain variable *framework 1* (*FW1*) sequence:
(DNA)
GAGGTGAAGCTGGTGGAGTCTGGAGGAGGCTTGGTACAGCCTGGGGGTTCTCTGAGACTCTCCTGTGCAACTTCTGGG
TTCACCTTCACT (SEQ ID NO:832)

(amino acids)
EVKLVESGGGLVQPGGSLRLSCATSGFTFT(SEQ ID NO:833)

Mouse 17H6 heavy chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
GATTACTACATGAGC (SEQ ID NO:834)

(amino acids)
DYYMS(SEQ ID NO:835)

Mouse 17H6 heavy chain variable *framework 2* (*FW2*) sequence:
(DNA)
GAGGTGAAGCTGGTGGAGTCTGGAGGAGGCTTGGTACAGCCTGGGGGTTCTCTGAGACTCTCCTGTGCAACTTCTGGG
TTCACCTTCACT (SEQ ID NO:836)

(amino acids)
WVRQPPRKALEWLG(SEQ ID NO:837)

Mouse 17H6 heavy chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
TTTATTAGAAACAAAGCTAATGGTTACACAGCAGAGTACAGTGCGTCTGTGAAGGGT (SEQ ID NO:838)

(amino acids)
FIRNKANGYTAEYSASVKG (SEQ ID NO:839)

Mouse 17H6 heavy chain variable *framework 3* (*FW3*) sequence:
(DNA)
CGGTTCACCATCTCCAGAGATGTTTCCCAAAACCTCCTCTATCTTCAAATGAACATCCTGAGAGCTGAGGACAGTGCCACTTATTACTGTGCAAAA (SEQ ID NO:840)

(amino acids)
RFTISRDVSQNLLYLQMNILRAEDSATYYCAK (SEQ ID NO:841)

Mouse 17H6 heavy chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
GATTACTACGGTAGTAACCCTGCCTGGTTTGCTTAC (SEQ ID NO:842)
(amino acids)
DYYGSNPAWFAY (SEQ ID NO:1)

Mouse 17H6 heavy chain variable *framework 4* (*FW4*) sequence:
(DNA)
TGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA (SEQ ID NO:843)
(amino acids)
WGQGTLVTVSA (SEQ ID NO:1)

Mouse Antibody **17H6 Light chain: DNA sequence**
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGAAGTTGCCTGTGAGGCTGTTGGTGCTGATGTTCTGGATTCCTGCTTCCAACAGTGATATTTTGATGACCCAGACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCTCCATCTCTTGCAGATCTAGTCAGAGCATTGTACATAGTAGTGGAAACACCTTTTTAGAATGGTACCTGCAGAAACCTGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAACCGATTTTCTGGGGTCCCAGACAGGTTCAGTGGCAGTGGATCAGGGATAGATTTCACACTCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTACTGCTTTCAAGGTTCACATGTTCCTTTCACGTTCGGCTCGGGGACAAAGTTGGAAATAAAA (SEQ ID NO:844)

Mouse Antibody **17H6 Light chain: Amino acid sequence**
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
MKLPVRLLVLMFWIPASNSDILMTQTPLSLPVSLGDQASISCRSSQSIVHSSGNTFLEWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGIDFTLKISRVEAEDLGVYYCFQGSHVPFTFGSGTKLEIK (SEQ ID NO:845)

Mouse 17H6 light chain variable *framework 1* (*FW1*) sequence:
(DNA)
GATATTTTGATGACCCAGACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCTCCATCTCTTGC (SEQ ID NO:846)

(amino acids)
DILMTQTPLSLPVSLGDQASISC (SEQ ID NO:847)

Mouse 17H6 light chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
AGATCTAGTCAGAGCATTGTACATAGTAGTGGAAACACCTTTTTAGAA (SEQ ID NO:848)
(amino acids)

RSSQSIVHSSGNTFLE (SEQ ID NO:849)

Mouse 17H6 light chain variable *framework 2* (*FW2*) sequence:
(DNA)
TGGTACCTGCAGAAACCTGGCCAGTCTCCAAAGCTCCTGATCTAC (SEQ ID NO:850)
(amino acids)

WYLQKPGQSPKLLIY (SEQ ID NO:851)

Mouse 17H6 light chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
AAAGTTTCCAACCGATTTTCT (SEQ ID NO:852)

(amino acids)
KVSNRFS (SEQ ID NO:853)

Mouse 17H6 light chain variable *framework 3* (*FW3*) sequence:
(DNA)
GGGGTCCCAGACAGGTTCAGTGGCAGTGGATCAGGGATAGATTTCACACTCAAGATCAGCAGAGTGGAGGCTGAGGAT
CTGGGAGTTTATTACTGC (SEQ ID NO:854)

(amino acids)
GVPDRFSGSGSGIDFTLKISRVEAEDLGVYYC (SEQ ID NO:855)

Mouse 17H6 light chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
TTTCAAGGTTCACATGTTCCTTTCACG (SEQ ID NO:856)

(amino acids)
FQGSHVPFT (SEQ ID NO:857)

Mouse 17H6 light chain variable *framework 4* (*FW4*) sequence:
(DNA)
TTCGGCTCGGGGACAAAGTTGGAAATAAAA (SEQ ID NO:858)

(amino acids)
FGSGTKLEIK (SEQ ID NO:859)

Mouse antibody 39H5 Heavy chain: DNA sequence
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGGCTTGGGTGTGGACCTTGCTATTCCTGATGGCAGCTGCCCAAAGTGCCCAAGCACAGATCCAGTTGGTGCAGTCT
GGACCTGAGCTGAAGAAGCCTGGAGAGACAGTCAAGATCTCCTGCAAGGCTTCTGGGTATACCTTCACAAACTATGGA
ATGAACTGGGTGAAGCAGGCTCCAGGAAAGGGTTTAAAGTGGATGGGCTGGATAAACACCTACACTGGAGAGCCAACA
TATGTTGGTGACTTCAAGGGACGGTTTGCCTTCTCTTTGGAGACCTCTGCCAGCACTGCCTATTTGCAGATCAACAAC
CTCAAAAATGAGGACACGGCTACATATTTTTGTGTTAGAGGTATCCACGGCTACGTGGACTACTGGGGCCAAGGCACC
ACTCTCACAGTCTCCTCA (SEQ ID NO:860)

Mouse antibody 39H5 Heavy chain: Amino acid sequence
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
MAWVWTLLFLMAAAQSAQAQIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTYTGEPT
YVGDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCVRGIHGYVDYWGQGTTLTVSS (SEQ ID NO:861)

Mouse antibody 39H5 heavy chain variable *framework 1* (*FW1*) sequence:
(DNA)

CAGATCCAGTTGGTGCAGTCTGGACCTGAGCTGAAGAAGCCTGGAGAGACAGTCAAGATCTCCTGCAAGGCTTCTGGG
TATACCTTCACA (SEQ ID NO:862)
(amino acids)

QIQLVQSGPELKKPGETVKISCKASGYTFT (SEQ ID NO:863)

Mouse antibody 39H5 heavy chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
AACTATGGAATGAAC (SEQ ID NO:864)
(amino acids)
NYGMN (SEQ ID NO:865)

Mouse antibody 39H5 heavy chain variable *framework 2* (*FW2*) sequence:
(DNA)
TGGGTGAAGCAGGCTCCAGGAAAGGGTTTAAAGTGGATGGGC (SEQ ID NO:866)
(amino acids)
WVKQAPGKGLKWMG (SEQ ID NO:867)

Mouse antibody 39H5 heavy chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
TGGATAAACACCTACACTGGAGAGCCAACATATGTTGGTGACTTCAAGGGA (SEQ ID NO:868)

(amino acids)
WINTYTGEPTYVGDFKG (SEQ ID NO:869)

Mouse antibody 39H5 heavy chain variable *framework 3* (*FW3*) sequence:
(DNA)
CGGTTTGCCTTCTCTTTGGAGACCTCTGCCAGCACTGCCTATTTGCAGATCAACAACCTCAAAAATGAGGACACGGCT
ACATATTTTTGTGTTAGA (SEQ ID NO:870)
(amino acids)
RFAFSLETSASTAYLQINNLKNEDTATYFCVR (SEQ ID NO:871)

Mouse antibody 39H5 heavy chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
GGTATCCACGGCTACGTGGACTAC (SEQ ID NO:872)
(amino acids)
GIHGYVDY (SEQ ID NO:873)

Mouse antibody 39H5 heavy chain variable *framework 4* (*FW4*) sequence:
(DNA)
TGGGGCCAAGGCACCACTCTCACAGTCTCCTCA (SEQ ID NO:874)
(amino acids)
WGQGTTLTVSS (SEQ ID NO:875)

Mouse antibody 39H5 Light chain: DNA sequence
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGAAGTTGCCTGTTAGGCTGTTGGTGCTGATGTTCTGGATTCCTGCTTCCAGCAGTGATGTTTTGATGACCCAAACT
CCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCTCCATCTCTTGCAGATCTAGTCAGAGCATTGTACATAGAAAT
GGAAACACCTATTTAGAATGGTACCTGCAGAAACCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAACCGA
TTTTCTGGGGTCCCAGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACACTCAAGATCAGCAGAGTGGAGGCT
GAGGATCTGGGAGTTTATTACTGCTTTCAAGGTTCACATCTTCCGTGGACGTTCGGTGGAGGCACCAAGCTGGAAATC
AAA (SEQ ID NO:876)

Mouse antibody 39H5 Light chain: Amino acid sequence

Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
MKLPVRLLVLMFWIPASSSDVLMTQTPLSLPVSLGDQASISCRSSQSIVHRNGNTYLEWYLQKPGQSPKLLIYKVSNR
FSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHLPWTFGGGTKLEIK (SEQ ID NO:877)

Mouse antibody 39H5 light chain variable *framework 1* (*FW1*) sequence:
(DNA)
GATGTTTTGATGACCCAAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCTCCATCTCTTGC (SEQ ID NO:878)
(amino acids)
DVLMTQTPLSLPVSLGDQASISC (SEQ ID NO:879)
Mouse antibody 39H5 light chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
AGATCTAGTCAGAGCATTGTACATAGAAATGGAAACACCTATTTAGAA (SEQ ID NO:880)
(amino acids)

RSSQSIVHRNGNTYLE (SEQ ID NO:881)

Mouse antibody 39H5 light chain variable *framework 2* (*FW2*) sequence:
(DNA)
TGGTACCTGCAGAAACCAGGCCAGTCTCCAAAGCTCCTGATCTAC (SEQ ID NO:882)

(amino acids)
WYLQKPGQSPKLLIY (SEQ ID NO:883)

Mouse antibody 39H5 light chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
AAAGTTTCCAACCGATTTTCT (SEQ ID NO:884)
(amino acids)
KVSNRFS (SEQ ID NO:885)

Mouse antibody 39H5 light chain variable *framework 3* (*FW3*) sequence:
(DNA)
GGGGTCCCAGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACACTCAAGATCAGCAGAGTGGAGGCTGAGGAT
CTGGGAGTTTATTACTGC (SEQ ID NO:886)
(amino acids)
GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYC (SEQ ID NO:887)

Mouse antibody 39H5 light chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
TTTCAAGGTTCACATCTTCCGTGGACG (SEQ ID NO:888)
(amino acids)
FQGSHLPWT (SEQ ID NO:889)

Mouse antibody 39H5 light chain variable *framework 4* (*FW4*) sequence:
(DNA)
TTCGGTGGAGGCACCAAGCTGGAAATCAAA (SEQ ID NO:890)
(amino acids)
FGGGTKLEIK (SEQ ID NO:891)

Antibody 3C5 Heavy chain: DNA sequence
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGGCTTGGGTGTGGACCTTGCTGTTCCTGATGGCAGCTGCCCAAAGTGCCCAAGCACAGATCCAGTTGGTGCAGTCT
GGACCTGAGCTGAAGAAGCCTGGAGAGACAGTCAAGATCTCCTGCAAGGCTTCTGGGTATACCTTCACAAACTATGGA
ATGAACTGGGTGAAGCAGGCTCCAGGAAAGGGTTTAAAGTGGATGGGCTGGATAAACACCTACACTGGAAAGCCAACA

TATGCTGATGACTTCAAGGGACGGTTTGCCTTCTCTTTGGAGACCTCTGCCAGCACTGCCTATTTGCAGATCAACAAC
CTCAAAAATGAGGACACGGCTACATATTTCTGTGCAAGAGGGGGACTAGATGGTTACTACGGCTACTGGGGCCAAGGC
ACCACTCTCACAGTCTCCTCA (SEQ ID NO:892)

Antibody 3C5 Heavy chain: Amino acid sequence
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
MAWVWTLLFLMAAAQSAQAQIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTYTGKPT
YADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCARGGLDGYYGYWGQGTTLTVSS (SEQ ID NO:893)

Mouse antibody 3C5 heavy chain variable *framework 1* (*FW1*) sequence:
(DNA)
CAGATCCAGTTGGTGCAGTCTGGACCTGAGCTGAAGAAGCCTGGAGAGACAGTCAAGATCTCCTGCAAGGCTTCTGGG
TATACCTTCACA (SEQ ID NO:894)
(amino acids)
QIQLVQSGPELKKPGETVKISCKASGYTFT (SEQ ID NO:895)

Mouse antibody 3C5 heavy chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
AACTATGGAATGAAC (SEQ ID NO:896)
(amino acids)
NYGMN (SEQ ID NO:897)

Mouse antibody 3C5 heavy chain variable *framework 2* (*FW2*) sequence:
(DNA)
TGGGTGAAGCAGGCTCCAGGAAAGGGTTTAAAGTGGATGGGC (SEQ ID NO:898)
(amino acids)
WVKQAPGKGLKWMG (SEQ ID NO:899)

Mouse antibody 3C5 heavy chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
TGGATAAACACCTACACTGGAAAGCCAACATATGCTGATGACTTCAAGGGA (SEQ ID NO:900)
(amino acids)
WINTYTGKPTYADDFKG (SEQ ID NO:901)

Mouse antibody 3C5 heavy chain variable *framework 3* (*FW3*) sequence:
(DNA)
CGGTTTGCCTTCTCTTTGGAGACCTCTGCCAGCACTGCCTATTTGCAGATCAACAACCTCAAAAATGAGGACACGGCT
ACATATTTCTGTGCAAGA (SEQ ID NO:902)
(amino acids)
RFAFSLETSASTAYLQINNLKNEDTATYFCAR (SEQ ID NO:903)

Mouse antibody 3C5 heavy chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
GGGGGACTAGATGGTTACTACGGCTAC (SEQ ID NO:904)
(amino acids)
GGLDGYYGY (SEQ ID NO:905)

Mouse antibody 3C5 heavy chain variable *framework 4* (*FW4*) sequence:
(DNA)
TGGGGCCAAGGCACCACTCTCACAGTCTCCTCA (SEQ ID NO:906)
(amino acids)
WGQGTTLTVSS (SEQ ID NO:907)

Antibody 3C5 Light chain: DNA sequence (393 bp)

Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGAGTCCTGCCCAGTTCCTGTTTCTGCTAGTGCTCTCGATTCAGGAAACCAACGGTGATGTTGTGATGGCTCAGACC
CCACTCACTTTGTCGGTTACCATTGGACAACCAGCCTCCATCTCTTGCAAATCAAGTCAGAGCCTCTTACATAGTAAA
GGAAAGACATATTTGAATTGGTTATTACAGAGGCCAGGCCAGTCTCCAAAGCTCCTAATCTATCTGGTGTCTAAACTG
GAATCTGGAGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACACTGAAAATCAGCAGAGTGGAGGCT
GAAGATTTGGGAGTTTATTACTGCTTGCAAACTACACATTTTCCGTGGACGTTCGGTGGAGGCACCAAGCTGGAAATC
AAA (SEQ ID NO:908)

Antibody 3C5 Light chain: Amino acid sequence (131 aa)
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
MSPAQFLFLLVLSIQETNGDVVMAQTPLTLSVTIGQPASISCKSSQSLLHSKGKTYLNWLLQRPGQSPKLLIYLVSKL
ESGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCLQTTHFPWTFGGGTKLEIK (SEQ ID NO:909)

Mouse antibody 3C5 light chain variable *framework 1* (*FW1*) sequence:
(DNA)
GATGTTGTGATGGCTCAGACCCCACTCACTTTGTCGGTTACCATTGGACAACCAGCCTCCATCTCTTGC (SEQ ID NO:910)
(amino acids)
DVVMAQTPLTLSVTIGQPASISC (SEQ ID NO:911)
Mouse antibody 39H5 light chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
AAATCAAGTCAGAGCCTCTTACATAGTAAAGGAAAGACATATTTGAAT (SEQ ID NO:912)
(amino acids)
KSSQSLLHSKGKTYLN (SEQ ID NO:913)

Mouse antibody 3C5 light chain variable *framework 2* (*FW2*) sequence:
(DNA)
TGGTTATTACAGAGGCCAGGCCAGTCTCCAAAGCTCCTAATCTAT (SEQ ID NO:914)
(amino acids)
WLLQRPGQSPKLLIY (SEQ ID NO:915)

Mouse antibody 3C5 light chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
CTGGTGTCTAAACTGGAATCT (SEQ ID NO:916)
(amino acids)
LVSKLES (SEQ ID NO:917)

Mouse antibody 3C5 light chain variable *framework 3* (*FW3*) sequence:
(DNA)
GGAGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACACTGAAAATCAGCAGAGTGGAGGCTGAAGAT
TTGGGAGTTTATTACTGC (SEQ ID NO:918)
(amino acids)
GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYC (SEQ ID NO:919)

Mouse antibody 3C5 light chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
TTGCAAACTACACATTTTCCGTGGACG (SEQ ID NO:920)
(amino acids)
LQTTHFPWT (SEQ ID NO:921)

Mouse antibody 3C5 light chain variable *framework 4* (*FW4*) sequence:
(DNA)
TTCGGTGGAGGCACCAAGCTGGAAATCAAA (SEQ ID NO:922)
(amino acids)

FGGGTKLEIK (SEQ ID NO:923)

Mouse antibody 8A9 Heavy chain: DNA sequence (420 bp)
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGAAGTTGTGGCTGAACTGGATTTTCCTTGTAACACTTTTAAATGGTATCCAGTGTGAGGTGGAGCTGGTGGAGTCT
GGAGGAGGCTTGGTACAGCCTGGGGGTTCTCTGAGACTCTCCTGTGCAACTTCTGGGTTCACCTTCACTGATCACTAC
ATGAGCTGGGTCCGCCAGCCTCCAGGAAAGGCACTTGAGTGGTTGGGATTTATTAGAAACAAAGCTAATGGTTACACA
ACAGAGTACAGTGCATCTGTGAAGGGTCGGTTCACCATCTCCAGAGATAATTCCCAAAGCATCCTCTATCTTCAAATG
AAAACCCTGAGAACTGAGGACAGTGCCACTTATTACTGTGCAAGACCTTCTGACTGGGACTCCTGGTTTGCTTACTGG
GGCCAAGGGACTCTGGTCACTGTCTCTGCA (SEQ ID NO:924)
Mouse antibody 8A9 Heavy chain: Amino acid sequence (140 aa)
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
MKLWLNWIFLVTLLNGIQCEVELVESGGGLVQPGGSLRLSCATSGFTFTDHYMSWVRQPPGKALEWLGFIRNKANGYT
TEYSASVKGRFTISRDNSQSILYLQMKTLRTEDSATYYCARPSDWDSWFAYWGQGTLVTVSA (SEQ ID NO:925)

Mouse antibody 8A9 heavy chain variable *framework 1* (*FW1*) sequence:
(DNA)
GAGGTGGAGCTGGTGGAGTCTGGAGGAGGCTTGGTACAGCCTGGGGGTTCTCTGAGACTCTCCTGTGCAACTTCTGGG
TTCACCTTCACT (SEQ ID NO:926)
(amino acids)
EVELVESGGGLVQPGGSLRLSCATSGFTFT (SEQ ID NO:927)

Mouse antibody 8A9 heavy chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
GATCACTACATGAGC (SEQ ID NO:928)
(amino acids)
DHYMS (SEQ ID NO:929)

Mouse antibody 8A9 heavy chain variable *framework 2* (*FW2*) sequence:
(DNA)
TGGGTCCGCCAGCCTCCAGGAAAGGCACTTGAGTGGTTGGGA (SEQ ID NO:930)
(amino acids)
WVRQPPGKALEWLG (SEQ ID NO:931)

Mouse antibody 8A9 heavy chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
TTTATTAGAAACAAAGCTAATGGTTACACAACAGAGTACAGTGCATCTGTGAAGGGT (SEQ ID NO:932)
(amino acids)
FIRNKANGYTTEYSASVKG (SEQ ID NO:933)

Mouse antibody 8A9 heavy chain variable *framework 3* (*FW3*) sequence:
(DNA)
CGGTTCACCATCTCCAGAGATAATTCCCAAAGCATCCTCTATCTTCAAATGAAAACCCTGAGAACTGAGGACAGTGCC
ACTTATTACTGTGCAAGA (SEQ ID NO:934)
(amino acids)
RFTISRDNSQSILYLQMKTLRTEDSATYYCAR (SEQ ID NO:935)

Mouse antibody 8A9 heavy chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
CCTTCTGACTGGGACTCCTGGTTTGCTTAC (SEQ ID NO:936)
(amino acids)
PSDWDSWFAY (SEQ ID NO:937)

Mouse antibody 8A9 heavy chain variable *framework 4* (*FW4*) sequence:

(DNA)
TGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA (SEQ ID NO:938)
(amino acids)
WGQGTLVTVSA (SEQ ID NO:939)

Mouse antibody 8A9 Light chain: DNA sequence (393 bp)
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGAAGTTGCCTGTTAGGCTGTTGGTGCTGATGTTCTGGATTCCTGCTTCCAGCAGTGATGTTTTGATGACCCAAACT
CCACTCTCCCTGCCTGTCAGTCTTGGTGATCAAGCCTCCATCTCTTGCAGATCTAGTCAGAGCATTGTACATAGTAAT
GGCAACACCTATTTAGATTGGTACTTGCAGAAACCAGGCCAGTCTCCAAAGCTCCTGATCTACAGAGTTTCCAACCGA
TTTTCTGGGGTCCCAGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACACTCAAGATCAGCAGAGTGGAGGCT
GAGGATCTGGGACTTTATTACTGTTTTCAAGGTTCACATGTTCCGTGGGCGTTCGGTGGAGGCACCAAGCTGGAAATC
AAA (SEQ ID NO:940)

Mouse antibody 8A9 Light chain: Amino acid sequence (131 aa)
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
MKLPVRLLVLMFWIPASSSDVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLDWYLQKPGQSPKLLIYRVSNR
FSGVPDRFSGSGSGTDFTLKISRVEAEDLGLYYCFQGSHVPWAFGGGTKLEIK (SEQ ID NO:941)

Mouse antibody 8A9 light chain variable *framework 1* (*FW1*) sequence:
(DNA)
GATGTTTTGATGACCCAAACTCCACTCTCCCTGCCTGTCAGTCTTGGTGATCAAGCCTCCATCTCTTGC (SEQ ID NO:942)
(amino acids)
DVLMTQTPLSLPVSLGDQASISC (SEQ ID NO:943)
Mouse antibody 8A9 light chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
AGATCTAGTCAGAGCATTGTACATAGTAATGGCAACACCTATTTAGAT (SEQ ID NO:944)
(amino acids)
RSSQSIVHSNGNTYLD (SEQ ID NO:945)

Mouse antibody 8A9 light chain variable *framework 2* (*FW2*) sequence:
(DNA)
TGGTACTTGCAGAAACCAGGCCAGTCTCCAAAGCTCCTGATCTAC (SEQ ID NO:946)
(amino acids)
WYLQKPGQSPKLLIY (SEQ ID NO:947)

Mouse antibody 8A9 light chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
AGAGTTTCCAACCGATTTTCT (SEQ ID NO:948)
(amino acids)
RVSNRFS (SEQ ID NO:949)

Mouse antibody 8A9 light chain variable *framework 3* (*FW3*) sequence:
(DNA)
GGGGTCCCAGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACACTCAAGATCAGCAGAGTGGAGGCTGAGGAT
CTGGGACTTTATTACTGT (SEQ ID NO:950)
(amino acids)
GVPDRFSGSGSGTDFTLKISRVEAEDLGLYYC (SEQ ID NO:951)

Mouse antibody 8A9 light chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
TTTCAAGGTTCACATGTTCCGTGGGCG (SEQ ID NO:952)

(amino acids)
FQGSHVPWA (SEQ ID NO:953)

Mouse antibody 8A9 light chain variable *framework 4* (*FW4*) sequence:
(DNA)
TTCGGTGGAGGCACCAAGCTGGAAATCAAA (SEQ ID NO:954)
(amino acids)
FGGGTKLEIK (SEQ ID NO:955)

Mouse antibody 18G12 Heavy chain: DNA sequence (399 bp)
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGGGATGGAGCTATATCATCCTCTTTTTGGTCGCAACAGCTACAGGTGTCCACTCCCAGGTCCAACTGCAGCAGTCT
GGGGCTGAACTGGTGAAGCCTGGGGCTTCAGTGAAGTTGTCCTGCAAGGCTTCTGGCTACACCTTCACCGGCTACTTT
TTGTACTGGGTGAAGCAGAGGCCTGGACAAGGCCTTGAGTGGATTGGGGGGATTAATCCTGACAATGGTGGTATTGAC
TTCAATGAGAAGTTCAGGAACAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTACATGCAACTCAGCAGC
CTGACATCTGAGGACTCTGCGGTCTATTATTGTACATTACTAATAGGGAACTATTGGGGCCAAGGCACCACTCTCACA
GTCTCCTCA (SEQ ID NO:956)

Mouse antibody 18G12 Heavy chain: Amino acid sequence (133 aa)
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
MGWSYIILFLVATATGVHSQVQLQQSGAELVKPGASVKLSCKASGYTFTGYFLYWVKQRPGQGLEWIGGINPDNGGID
FNEKFRNKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTLLIGNYWGQGTTLTVSS (SEQ ID NO:957)

Mouse antibody 18G12 heavy chain variable *framework 1* (*FW1*) sequence:
(DNA)
CAGGTCCAACTGCAGCAGTCTGGGGCTGAACTGGTGAAGCCTGGGGCTTCAGTGAAGTTGTCCTGCAAGGCTTCTGGC
TACACCTTCACC (SEQ ID NO:958)
(amino acids)
QVQLQQSGAELVKPGASVKLSCKASGYTFT (SEQ ID NO:959)

Mouse antibody 39H5 heavy chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
GGCTACTTTTTGTAC (SEQ ID NO:960)
(amino acids)
GYFLY (SEQ ID NO:961)

Mouse antibody 18G12 heavy chain variable *framework 2* (*FW2*) sequence:
(DNA)
TGGGTGAAGCAGAGGCCTGGACAAGGCCTTGAGTGGATTGGG (SEQ ID NO:962)
(amino acids)
WVKQRPGQGLEWIG (SEQ ID NO:963)

Mouse antibody 18G12 heavy chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
GGGATTAATCCTGACAATGGTGGTATTGACTTCAATGAGAAGTTCAGGAAC (SEQ ID NO:964)
(amino acids)
GINPDNGGIDFNEKFRN (SEQ ID NO:965)

Mouse antibody 18G12 heavy chain variable *framework 3* (*FW3*) sequence:
(DNA)
AAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTGACATCTGAGGACTCTGCG
GTCTATTATTGTACATTA (SEQ ID NO:966)
(amino acids)
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCTL (SEQ ID NO:967)

Mouse antibody 18G12 heavy chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
CTAATAGGGAACTAT (SEQ ID NO:968)
(amino acids)
LIGNY (SEQ ID NO:969)

Mouse antibody 18G12 heavy chain variable *framework 4* (*FW4*) sequence:
(DNA)
TGGGGCCAAGGCACCACTCTCACAGTCTCCTCA (SEQ ID NO:970)
(amino acids)
WGQGTTLTVSS (SEQ ID NO:971)

Mouse antibody 18G12 Light chain: DNA sequence (393 bp)
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGAGTCCTGCCCAGTTCCTGTTTCTGTTAGTGCTCTGGATTCGGGAAACCAATGGTGATGTTGTGATGACCCAGACT
CCACTCACTTTGTCGGTAACCATTGGACAGCCAGCCTCCATCTCTTGCAAGTCAAGTCAGAGCCTCTTACATAGTGAT
GGAAAGACATATTTGATTTGGTTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCTAAACTG
GACTCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTCACACTGAAAATCAGCAGAGTGGAGGCT
GAGGATTTGGGAGTTTATTTTTGCTGTCAAGGTACACATTTTCCGTGGACGTTCGGTGGAGGCACCATGCTGGAAATC
AAA (SEQ ID NO:972)

Mouse antibody 18G12 Light chain: Amino acid sequence (131 aa)
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
MSPAQFLFLLVLWIRETNGDVVMTQTPLTLSVTIGQPASISCKSSQSLLHSDGKTYLIWLLQRPGQSPKRLIYLVSKL
DSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYFCCQGTHFPWTFGGGTMLEIK (SEQ ID NO:973)

Mouse antibody 18G12 light chain variable *framework 1* (*FW1*) sequence:
(DNA)
GATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTAACCATTGGACAGCCAGCCTCCATCTCTTGC (SEQ ID NO:974)

(amino acids)
DVVMTQTPLTLSVTIGQPASISC (SEQ ID NO:975)

Mouse antibody 18G12 light chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
AAGTCAAGTCAGAGCCTCTTACATAGTGATGGAAAGACATATTTGATT (SEQ ID NO:976)

(amino acids)
KSSQSLLHSDGKTYLI(SEQ ID NO:977)

Mouse antibody 18G12 light chain variable *framework 2* (*FW2*) sequence:
(DNA)
TGGTTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTAT (SEQ ID NO:978)

(amino acids)
WLLQRPGQSPKRLIY(SEQ ID NO:979)

Mouse antibody 18G12 light chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
CTGGTGTCTAAACTGGACTCT (SEQ ID NO:980)

(amino acids)

LVSKLDS(SEQ ID NO:981)

Mouse antibody 18G12 light chain variable *framework 3* (*FW3*) sequence:
(DNA)
GGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTCACACTGAAAATCAGCAGAGTGGAGGCTGAGGAT
TTGGGAGTTTATTTTTGC (SEQ ID NO:982)

(amino acids)
GVPDRFTGSGSGTDFTLKISRVEAEDLGVYFC (SEQ ID NO:983)

Mouse antibody 18G12 light chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
TGTCAAGGTACACATTTTCCGTGGACG (SEQ ID NO:984)

(amino acids)
CQGTHFPWT (SEQ ID NO:985)

Mouse antibody 18G12 light chain variable *framework 4* (*FW4*) sequence:
(DNA)
TTCGGTGGAGGCACCATGCTGGAAATCAAA (SEQ ID NO:986)

(amino acids)
FGGGTMLEIK (SEQ ID NO:987)

Mouse antibody 20A10 Heavy chain: DNA sequence (417 bp)
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGAACTTCGGGTTCAGCTTGATTTTCCTTGTCCTTGTTTTAAAAGGTGTCCAGTGTGAAGTGATGCTGGTGGAGTCT
GGGGGAGGCTTAGTGAAGCCTGGAGGGTCCCTGAAACTCTCCTGTCAGCCTCTGGATTCACTTTCAGTACCTATGCCA
TGTCTTGGATTCGCCAGACTCCAGAGAAGAGGCTGGAGTGGGTCGCATCCATTGGTCGTGCTGGTTCCACCTACTATT
CAGACAGTGTGAAGGGCCGATTCACCATCTCCAGAGATAATGTCCGGAACATCCTGTACCTGCAAATGAGCAGTCTGA
GGTCTGAGGACACGGCCATGTATTACTGTGCTAGAGGCCCGATCTACAATGATTACGACGAGTTTGCTTACTGGGGCC
AAGGGACTCTGGTCACTGTCTCTGCA (SEQ ID NO:988)

Mouse antibody 20A10 Heavy chain: Amino acid sequence (139 aa)
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
MNFGFSLIFLVLVLKGVQCEVMLVESGGGLVKPGGSLKLSCAASGFTFSTYAMSWIRQTPEKRLEWVASIGRAGSTYY
SDSVKGRFTISRDNVRNILYLQMSSLRSEDTAMYYCARGPIYNDYDEFAYWGQGTLVTVSA (SEQ ID NO:989)

Mouse antibody 20A10 heavy chain variable *framework 1* (*FW1*) sequence:
(DNA)
GAAGTGATGCTGGTGGAGTCTGGGGGAGGCTTAGTGAAGCCTGGAGGGTCCCTGAAACTCTCCTGTGCAGCCTCTGGA
TTCACTTTCAGT (SEQ ID NO:990)

(amino acids)
EVMLVESGGGLVKPGGSLKLSCAASGFTFS (SEQ ID NO:991)

Mouse antibody 20A10 heavy chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
ACCTATGCCATGTCT (SEQ ID NO:992)

(amino acids)
TYAMS (SEQ ID NO:993)

Mouse antibody 20A10 heavy chain variable *framework 2* (*FW2*) sequence:
(DNA)

TGGATTCGCCAGACTCCAGAGAAGAGGCTGGAGTGGGTCGCA (SEQ ID NO:994)

(amino acids)
WIRQTPEKRLEWVA (SEQ ID NO:995)

Mouse antibody 20A10 heavy chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
TCCATTGGTCGTGCTGGTTCCACCTACTATTCAGACAGTGTGAAGGGC (SEQ ID NO:996)

(amino acids)
SIGRAGSTYYSDSVKG (SEQ ID NO:997)

Mouse antibody 20A10 heavy chain variable *framework 3* (*FW3*) sequence:
(DNA)
CGATTCACCATCTCCAGAGATAATGTCCGGAACATCCTGTACCTGCAAATGAGCAGTCTGAGGTCTGAGGACACGGCC
ATGTATTACTGTGCTAGA (SEQ ID NO:998)

(amino acids)
RFTISRDNVRNILYLQMSSLRSEDTAMYYCAR (SEQ ID NO:999)

Mouse antibody 20A10 heavy chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
GGCCCGATCTACAATGATTACGACGAGTTTGCTTAC (SEQ ID NO:1000)

(amino acids)
GPIYNDYDEFAY (SEQ ID NO:1001)

Mouse antibody 20A10 heavy chain variable *framework 4* (*FW4*) sequence:
(DNA)
TGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA (SEQ ID NO:1002)

(amino acids)
WGQGTLVTVSA (SEQ ID NO:1003)

Mouse antibody 20A10 Light chain: DNA sequence (396 bp)
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGGAATCACAGACTCAGGTCTTCCTCTCCCTGCTGCTCTGGGTATCTGGTACCTGTGGGAACATTATGATGACACAG
TCGCCATCATCTCTGGCTGTGTCTGCAGGAGAAAAGGTCACTATGAGCTGTAAGTCCAGTCAAAGTGTTTTATACAGT
TCAAATCAGAAGAACTATTTGGCCTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCC
ACTAGGGAATCTGGTGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTTACTCTTACCATCAGCAGTGTA
CAAGCTGAAGACCTGGCAGTTTATTACTGTCATCAATACCTCTCCTCGCTCACGTTCGGTGCTGGGACCAAGCTGGAG
CTGAAA (SEQ ID NO:1004)

Mouse antibody 20A10 Light chain: Amino acid sequence (132 aa)
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
MESQTQVFLSLLLWVSGTCGNIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWAS
TRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCHQYLSSLTFGAGTKLELK (SEQ ID NO:1005)

Mouse antibody 20A10 light chain variable *framework 1* (*FW1*) sequence:
(DNA)
AACATTATGATGACACAGTCGCCATCATCTCTGGCTGTGTCTGCAGGAGAAAAGGTCACTATGAGCTGT (SEQ ID NO:1006)
(amino acids)
NIMMTQSPSSLAVSAGEKVTMSC (SEQ ID NO:1007)

Mouse antibody 20A10 light chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
AAGTCCAGTCAAAGTGTTTTATACAGTTCAAATCAGAAGAACTATTTGGCC (SEQ ID NO:1008)
(amino acids)
KSSQSVLYSSNQKNYLA (SEQ ID NO:1009)

Mouse antibody 20A10 light chain variable *framework 2* (*FW2*) sequence:
(DNA)
TGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTAC (SEQ ID NO:1010)
(amino acids)
WYQQKPGQSPKLLIY (SEQ ID NO:1011)

Mouse antibody 20A10 light chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
TGGGCATCCACTAGGGAATCT (SEQ ID NO:1012)
(amino acids)
WASTRES (SEQ ID NO:1013)

Mouse antibody 20A10 light chain variable *framework 3* (*FW3*) sequence:
(DNA)
GGTGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTTACTCTTACCATCAGCAGTGTACAAGCTGAAGAC
CTGGCAGTTTATTACTGT (SEQ ID NO:1014)
(amino acids)
GVPDRFTGSGSGTDFTLTISSVQAEDLAVYYC (SEQ ID NO:1015)

Mouse antibody 20A10 light chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
CATCAATACCTCTCCTCGCTCACG (SEQ ID NO:1016)
(amino acids)
HQYLSSLT (SEQ ID NO:1017)

Mouse antibody 20A10 light chain variable *framework 4* (*FW4*) sequence:
(DNA)
TTCGGTGCTGGGACCAAGCTGGAGCTGAAA (SEQ ID NO:1018)
(amino acids)
FGAGTKLELK (SEQ ID NO:1019)

Mouse antibody 25E6 Heavy chain: DNA sequence (414 bp)
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGAACTTCGGGCTCAGCTTGATTTTCCTTGCCCTCATTTTAAAAGGTGTCCAGTGTGAGGTGCAGCTGGTGGAGTCT
GGGGGAGACTTAGTGAAGCCTGGAGGGTCCCTGAAACTCTCCTGTGCAGCCTCTGGTTTCACTTTCAGTAGTTATGGA
ATGTCTTGGGTTCGCCAGACTCCAGACAAGAGGCTGGAGTGGGTCGCAACCATTAGTAATGGTGGTAGACACACCTTC
TATCCAGACAGTGTGAAGGGGCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCTGTATCTGCAAATGAGCAGT
CTGAAGTTGAGGACACAGCCATGTATTTATGTGTAAGACAGACTGGGACGGAGGGCTGGTTTGCTTACTGGGGCCAAG
GGACTCTGGTCACTGTCTCTGCA (SEQ ID NO:1020)

Mouse antibody 25E6 Heavy chain: Amino acid sequence (138 aa)
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
MNFGLSLIFLALILKGVQCEVQLVESGGDLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISNGGRHTF
YPDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYLCVRQTGTEGWFAYWGQGTLVTVSA (SEQ ID NO:1021)

Mouse antibody 25E6 heavy chain variable *framework 1* (*FW1*) sequence:
(DNA)

GAGGTGCAGCTGGTGGAGTCTGGGGGAGACTTAGTGAAGCCTGGAGGGTCCCTGAAACTCTCCTGTGCAGCCTCTGGT
TTCACTTTCAGT (SEQ ID NO:1022)
(amino acids)
EVQLVESGGDLVKPGGSLKLSCAASGFTFS (SEQ ID NO:1023)

Mouse antibody 25E6 heavy chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
AGTTATGGAATGTCT (SEQ ID NO:1024)
(amino acids)
SYGMS (SEQ ID NO:1025)

Mouse antibody 25E6 heavy chain variable *framework 2* (*FW2*) sequence:
(DNA)
TGGGTTCGCCAGACTCCAGACAAGAGGCTGGAGTGGGTCGCA (SEQ ID NO:1026)
(amino acids)
WVRQTPDKRLEWVA (SEQ ID NO:1027)

Mouse antibody 25E6 heavy chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
ACCATTAGTAATGGTGGTAGACACACCTTCTATCCAGACAGTGTGAAGGGG (SEQ ID NO:1028)
(amino acids)
TISNGGRHTFYPDSVKG (SEQ ID NO:1029)

Mouse antibody 25E6 heavy chain variable *framework 3* (*FW3*) sequence:
(DNA)
CGATTCACCATCTCCAGAGACAATGCCAAGAACACCCTGTATCTGCAAATGAGCAGTCTGAAGTCTGAGGACACAGCC
ATGTATTTATGTGTAAGA (SEQ ID NO:1030)
(amino acids)
RFTISRDNAKNTLYLQMSSLKSEDTAMYLCVR (SEQ ID NO:1031)

Mouse antibody 25E6 heavy chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
CAGACTGGGACGGAGGGCTGGTTTGCTTAC (SEQ ID NO:1032)
(amino acids)
QTGTEGWFAY (SEQ ID NO:1033)

Mouse antibody 25E6 heavy chain variable *framework 4* (*FW4*) sequence:
(DNA)
TGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA (SEQ ID NO:1034)
(amino acids)
WGQGTLVTVSA (SEQ ID NO:1035)

Mouse antibody 25E6 Light chain: DNA sequence (393 bp)
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGAGTCCTGCCCAGTTCCTGTTTCTGTTAGTGCTCTGGATTCGGGAAACCAACGGTGATGTTGTGATGACCCAGACT
CCACTCACTTTGTCGGTTACCATTGGACAACCAGCCTCCATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGAT
GGAAAGACATATTTGAATTGGTTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCTAAACTG
GACTCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTCACACTGAAAATCAGCAGAGGGAGGCTG
AGGATTTGGGAGTTTATTATTGCTGGCAAGGTACACATTTTCCTCAGACGTTCGGTGGAGGCACCAAGCTGGAAATCA
AA (SEQ ID NO:1036)

Mouse antibody 25E6 Light chain: Amino acid sequence (131 aa)
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4

MSPAQFLFLLVLWIRETNGDVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPQTFGGGTKLEIK (SEQ ID NO:1037)

Mouse antibody 25E6 light chain variable *framework 1* (*FW1*) sequence:
(DNA)
GATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCCTCCATCTCTTGC (SEQ ID NO:1038)
(amino acids)
DVVMTQTPLTLSVTIGQPASISC (SEQ ID NO:1039)
Mouse antibody 25E6 light chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
AAGTCAAGTCAGAGCCTCTTAGATAGTGATGGAAAGACATATTTGAAT (SEQ ID NO:1040)
(amino acids)
KSSQSLLDSDGKTYLN (SEQ ID NO:1041)

Mouse antibody 25E6 light chain variable *framework 2* (*FW2*) sequence:
(DNA)
TGGTTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTAT (SEQ ID NO:1042)
(amino acids)
WLLQRPGQSPKRLIY (SEQ ID NO:1043)

Mouse antibody 25E6 light chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
CTGGTGTCTAAACTGGACTCT (SEQ ID NO:1044)
(amino acids)
LVSKLDS (SEQ ID NO:1045)

Mouse antibody 25E6 light chain variable *framework 3* (*FW3*) sequence:
(DNA)
GGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTCACACTGAAAATCAGCAGAGTGGAGGCTGAGGATTTGGGAGTTTATTATTGC (SEQ ID NO:1046)
(amino acids)
GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYC (SEQ ID NO:1047)

Mouse antibody 25E6 light chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
TGGCAAGGTACACATTTTCCTCAGACG (SEQ ID NO:1048)
(amino acids)
WQGTHFPQT (SEQ ID NO:1049)

Mouse antibody 25E6 light chain variable *framework 4* (*FW4*) sequence:
(DNA)
TTCGGTGGAGGCACCAAGCTGGAAATCAAA (SEQ ID NO:1050)
(amino acids)
FGGGTKLEIK (SEQ ID NO:1051)

Mouse antibody 28F9 Heavy chain: DNA sequence (399 bp)
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGGGATGGAGCTATATCATCCTCTTTTTGGTAGCAACAGCTACAGGTGTCCACTCCCAGGTCCAACTGCAGCAGCCT
GGGGCTGAACTGGTGCAGCCTGGGGCTTCAGTGAAGTTGTCCTGCAAGGCTTCTGGCTACACCTTCACCGGCTACTTT
TTGTACTGGGTGAAGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGGGGAATTCATCCTAGCAATGGTGATACTGAC
TTCAATGAGAAGTTCAAGAACAAGGCCACACTGACTGTAGACATATCCTCCAGCACTGCCTACATGCAACTCAGCAGC
CTGACATCTGAGGACTCTGCGGTCTATTATTGTACATTACTAATAGGGGTCTACTGGGGCCAAGGCACCACTCTCACA
GTCTCCTCA (SEQ ID NO:1052)

Mouse antibody 28F9 Heavy chain: Amino acid sequence (133 aa)
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
MGWSYIILFLVATATGVHSQVQLQQPGAELVQPGASVKLSCKASGYTFTGYFLYWVKQRPGHGLEWIGGIHPSNGDTD
FNEKFKNKATLTVDISSSTAYMQLSSLTSEDSAVYYCTLLIGVYWGQGTTLTVSS (SEQ ID NO:1053)

Mouse antibody 28F9 heavy chain variable *framework 1* (*FW1*) sequence:
(DNA)
CAGGTCCAACTGCAGCAGCCTGGGGCTGAACTGGTGCAGCCTGGGGCTTCAGTGAAGTTGTCCTGCAAGGCTTCTGGC
TACACCTTCACC (SEQ ID NO:1054)
(amino acids)
QVQLQQPGAELVQPGASVKLSCKASGYTFT (SEQ ID NO:1055)

Mouse antibody 28F9 heavy chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
GGCTACTTTTTGTAC (SEQ ID NO:1056)
(amino acids)
GYFLY (SEQ ID NO:1057)

Mouse antibody 28F9 heavy chain variable *framework 2* (*FW2*) sequence:
(DNA)
TGGGTGAAGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGG (SEQ ID NO:1058)
(amino acids)
WVKQRPGHGLEWIG (SEQ ID NO:1059)

Mouse antibody 28F9 heavy chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
GGAATTCATCCTAGCAATGGTGATACTGACTTCAATGAGAAGTTCAAGAAC (SEQ ID NO:1060)
(amino acids)
GIHPSNGDTDFNEKFKN (SEQ ID NO:1061)

Mouse antibody 28F9 heavy chain variable *framework 3* (*FW3*) sequence:
(DNA)
AAGGCCACACTGACTGTAGACATATCCTCCAGCACTGCCTACATGCAACTCAGCAGCCTGACATCTGAGGACTCTGCG
GTCTATTATTGTACATTA (SEQ ID NO:1062)
(amino acids)
KATLTVDISSSTAYMQLSSLTSEDSAVYYCTL (SEQ ID NO:1063)

Mouse antibody 28F9 heavy chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
CTAATAGGGGTCTAC (SEQ ID NO:1064)
(amino acids)
LIGVY (SEQ ID NO:1065)

Mouse antibody 28F9 heavy chain variable *framework 4* (*FW4*) sequence:

(DNA)
TGGGGCCAAGGCACCACTCTCACAGTCTCCTCA (SEQ ID NO:1066)
(amino acids)
WGQGTTLTVSS (SEQ ID NO:1067)

Mouse antibody 28F9 Light chain: DNA sequence (393 bp)
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGAGTCCTGCCCAGTTCCTGTTTCTGTTAGTGCTCTGGATTCGGGAAACCAACGGTGATGTTGTGATGACCCAGACT
CCACTCACTTTGTCGGTTACCATTGGACAACCAGCCTCCATCTCTTGCAAGTCAAGTCAGAGCCTCTTACATAGTGAT
GGAAAGACATATTTGATTTGGTTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCTAAACTG
GACTCTGGAGTCCCTGACAGGTTCACCGGCAGTGGATCAGGGACAGATTTCACACTGAAAATCAGCAGAGTGGAGGCT
GAGGATTTGGGAGTTTATTTTTGCTGTCAAGGTACACATTTTCCGTGGACGTTCGGTGGAGGCACCATGCTGGAAATC
AAA (SEQ ID NO:1068)

Mouse antibody 28F9 Light chain: Amino acid sequence (131 aa)
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
MSPAQFLFLLVLWIRETNGDVVMTQTPLTLSVTIGQPASISCKSSQSLLHSDGKTYLIWLLQRPGQSPKRLIYLVSKL
DSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYFCCQGTHFPWTFGGGTMLEIK (SEQ ID NO:1069)

Mouse antibody 28F9 light chain variable *framework 1* (*FW1*) sequence:
(DNA)
GATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCCTCCATCTCTTGC (SEQ ID NO:1070)
(amino acids)
DVVMTQTPLTLSVTIGQPASISC (SEQ ID NO:1071)
Mouse antibody 28F9 light chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
AAGTCAAGTCAGAGCCTCTTACATAGTGATGGAAAGACATATTTGATT (SEQ ID NO:1072)
(amino acids)
KSSQSLLHSDGKTYLI (SEQ ID NO:1073)

Mouse antibody 28F9 light chain variable *framework 2* (*FW2*) sequence:
(DNA)
TGGTTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTAT (SEQ ID NO:1074)
(amino acids)
WLLQRPGQSPKRLIY (SEQ ID NO:1075)

Mouse antibody 28F9 light chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
CTGGTGTCTAAACTGGACTCT (SEQ ID NO:1076)
(amino acids)
LVSKLDS (SEQ ID NO:1077)

Mouse antibody 28F9 light chain variable *framework 3* (*FW3*) sequence:
(DNA)
GGAGTCCCTGACAGGTTCACCGGCAGTGGATCAGGGACAGATTTCACACTGAAAATCAGCAGAGTGGAGGCTGAGGAT
TTGGGAGTTTATTTTTGC (SEQ ID NO:1078)
(amino acids)
GVPDRFTGSGSGTDFTLKISRVEAEDLGVYFC (SEQ ID NO:1079)

Mouse antibody 28F9 light chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
TGTCAAGGTACACATTTTCCGTGGACG (SEQ ID NO:1080)
(amino acids)

CQGTHFPWT (SEQ ID NO:1081)

Mouse antibody 28F9 light chain variable *framework 4* (*FW4*) sequence:
(DNA)
TTCGGTGGAGGCACCATGCTGGAAATCAAA (SEQ ID NO:1082)
(amino acids)
FGGGTMLEIK (SEQ ID NO:1083)

Mouse antibody 18B4 Heavy chain: DNA sequence (411 bp)
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGTACTTGGGACTGAACTATGTATTCATAGTTTTTCTCTTAAATGGTGTCCAGAGTGAAGTGAAACTTGAGGAGTCT
GGAGGAGGCTTGGTGCAACCTGGGGGATCCATGAAACTCTCTTGTGCTGCCTCTGGATTCACTTTTAATGACGCCTGG
ATGGACTGGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGAAGCACAGCTAATATTCATACA
ACATACTATGCTGAGTCTGTCCAAGGGAGGTTCACCATCTCAAGAGATGATTCCAAAAGTAGTGTCTACCTGCAAATG
AACAGCTTGAGAGCTGAAGACACTGGCATTTATTATTGTACCCCATTACTCTACGGATTTGCTTACTGGGGCCAAGGG
ACTCTGGTCACTGTCTCTGCA (SEQ ID NO:1084)

Mouse antibody 18B4 Heavy chain: Amino acid sequence (137 aa)
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
MYLGLNYVFIVFLLNGVQSEVKLEESGGGLVQPGGSMKLSCAASGFTFNDAWMDWVRQSPEKGLEWVAEIRSTANIHT
TYYAESVQGRFTISRDDSKSSVYLQMNSLRAEDTGIYYCTPLLYGFAYWGQGTLVTVSA (SEQ ID NO:1085)

Mouse antibody 18B4 heavy chain variable *framework 1* (*FW1*) sequence:
(DNA)
GAAGTGAAACTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGGGGATCCATGAAACTCTCTTGTGCTGCCTCTGGA
TTCACTTTTAAT (SEQ ID NO:1086)
(amino acids)
EVKLEESGGGLVQPGGSMKLSCAASGFTFN (SEQ ID NO:1087)

Mouse antibody 18B4 heavy chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
GACGCCTGGATGGAC (SEQ ID NO:1088)
(amino acids)
DAWMD (SEQ ID NO:1089)

Mouse antibody 18B4 heavy chain variable *framework 2* (*FW2*) sequence:
(DNA)
TGGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTGCT (SEQ ID NO:1090)
(amino acids)
WVRQSPEKGLEWVA (SEQ ID NO:1091)

Mouse antibody 18B4 heavy chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
GAAATTAGAAGCACAGCTAATATTCATACAACATACTATGCTGAGTCTGTCCAAGGG (SEQ ID NO:1092)
(amino acids)
EIRSTANIHTTYYAESVQG (SEQ ID NO:1093)

Mouse antibody 18B4 heavy chain variable *framework 3* (*FW3*) sequence:
(DNA)
AGGTTCACCATCTCAAGAGATGATTCCAAAAGTAGTGTCTACCTGCAAATGAACAGCTTGAGAGCTGAAGACACTGGC
ATTTATTATTGTACCCCA (SEQ ID NO:1094)
(amino acids)
RFTISRDDSKSSVYLQMNSLRAEDTGIYYCTP (SEQ ID NO:1095)

Mouse antibody 18B4 heavy chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
TTACTCTACGGATTTGCTTAC (SEQ ID NO:1096)
(amino acids)
LLYGFAY (SEQ ID NO:1097)

Mouse antibody 18B4 heavy chain variable *framework 4* (*FW4*) sequence:
(DNA)
TGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA (SEQ ID NO:1098)
(amino acids)
WGQGTLVTVSA (SEQ ID NO:1099)

Mouse antibody 18B4 Light chain: DNA sequence (393 bp)
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGAAGTTGCCTGTTAGGCTGTTGGTGCTGATGTTCTGGATTCCTGCTTCCAGCAGTGATGTTGTGATGACCCAAAGT
CCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCTCCATCTCTTGCAGAACTAGTCAGAGCCTTGTACACAGTAAT
GGAAACACCTATTTACATTGGCACCTGCAGAAGCCAGGCCAGTCTCCAAAGGTCCTGATCTACAAAGTTTCCAGCCGA
TTTTCTGGGGTCCCAGACAGGTTCAGTGGCAGTGGATCGGGGACAGATTTCACACTCAAGATCAGCAGAGTGGAGGCT
GAGGATCTGGGAGTTTATTTCTGCTCTCAAAATACACATGTTCCGTACACGTTCGGAGGGGGGACCAAGCTGGAAATA
AAA (SEQ ID NO:1100)

Mouse antibody 18B4 Light chain: Amino acid sequence (131 aa)
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
MKLPVRLLVLMFWIPASSSDVVMTQSPLSLPVSLGDQASISCRTSQSLVHSNGNTYLHWHLQKPGQSPKVLIYKVSSR
FSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQNTHVPYTFGGGTKLEIK (SEQ ID NO:1101)

Mouse antibody 18B4 light chain variable *framework 1* (*FW1*) sequence:
(DNA)
GATGTTGTGATGACCCAAAGTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCTCCATCTCTTGC (SEQ ID NO:1102)
(amino acids)
DVVMTQSPLSLPVSLGDQASISC (SEQ ID NO:1103)
Mouse antibody 18B4 light chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
AGAACTAGTCAGAGCCTTGTACACAGTAATGGAAACACCTATTTACAT (SEQ ID NO:1104)
(amino acids)
RTSQSLVHSNGNTYLH (SEQ ID NO:1105)

Mouse antibody 18B4 light chain variable *framework 2* (*FW2*) sequence:
(DNA)
TGGCACCTGCAGAAGCCAGGCCAGTCTCCAAAGGTCCTGATCTAC (SEQ ID NO:1106)
(amino acids)
WHLQKPGQSPKVLIY (SEQ ID NO:1107)

Mouse antibody 18B4 light chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
AAAGTTTCCAGCCGATTTTCT (SEQ ID NO:1108)
(amino acids)
KVSSRFS (SEQ ID NO:1109)

Mouse antibody 18B4 light chain variable *framework 3* (*FW3*) sequence:
(DNA)
GGGGTCCCAGACAGGTTCAGTGGCAGTGGATCGGGGACAGATTTCACACTCAAGATCAGCAGAGTGGAGGCTGAGGAT
CTGGGAGTTTATTTCTGC (SEQ ID NO:1110)

(amino acids)
GVPDRFSGSGSGTDFTLKISRVEAEDLGVYFC (SEQ ID NO:1111)

Mouse antibody 18B4 light chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
TCTCAAAATACACATGTTCCGTACACG (SEQ ID NO:1112)
(amino acids)
SQNTHVPYT (SEQ ID NO:1113)

Mouse antibody 18B4 light chain variable *framework 4* (*FW4*) sequence:
(DNA)
TTCGGAGGGGGGACCAAGCTGGAAATAAAA (SEQ ID NO:1114)
(amino acids)
FGGGTKLEIK (SEQ ID NO:1115)

Mouse Antibody IE4 Heavy chain: DNA sequence (408 bp)
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGGAATGGCCTTGTATCTTTCTCTTCCTCCTGTCAGTAACTGAAGGTGTCCACTCCCAGGTTCAGCTGCAGCAGTCT
GGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGTAAGGCTTCTGGCTATGCATTCAGTACCTACTGG
ATGAACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGATTGGACAGATTTATCCTGGAGATAGTGATACTAAC
TACAATGGAAAGTTCAAGGGTAAAGCCACACTGACTGCAGACAAGTCCTCCAACACAGCCTACATGCAGCTCAGCAGC
CTAACATCTGAGGACTCTGCGGTCTTTTTCTGTGCAAGAGGTAACCACGCCTCTATGGACTACTGGGGTCAAGGAACC
TCAGTCACCGTCTCCTCA (SEQ ID NO:1116)

Mouse Antibody IE4 Heavy chain: Amino acid sequence (136 aa)
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
MEWPCIFLFLLSVTEGVHSQVQLQQSGAELVRPGSSVKISCKASGYAFSTYWMNWVKQRPGQGLEWIGQIYPGDSDTN
YNGKFKGKATLTADKSSNTAYMQLSSLTSEDSAVFFCARGNHASMDYWGQGTSVTVSS (SEQ ID NO:1117)

Mouse Antibody IE4 heavy chain variable *framework 1* (*FW1*) sequence:
(DNA)
CAGGTTCAGCTGCAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGTAAGGCTTCTGGC
TATGCATTCAGT (SEQ ID NO:1118)
(amino acids)
QVQLQQSGAELVRPGSSVKISCKASGYAFS (SEQ ID NO:1119)

Mouse antibody IE4 heavy chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
ACCTACTGGATGAAC (SEQ ID NO:1200)
(amino acids)
TYWMN (SEQ ID NO:1201)

Mouse antibody IE4 heavy chain variable *framework 2* (*FW2*) sequence:
(DNA)
TGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGATTGGA (SEQ ID NO:1202)
(amino acids)
WVKQRPGQGLEWIG (SEQ ID NO:1203)

Mouse antibody IE4 heavy chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
CAGATTTATCCTGGAGATAGTGATACTAACTACAATGGAAAGTTCAAGGGT (SEQ ID NO:1204)
(amino acids)
QIYPGDSDTNYNGKFKG (SEQ ID NO:1205)

Mouse antibody IE4 heavy chain variable *framework 3* (*FW3*) sequence:
(DNA)
AAAGCCACACTGACTGCAGACAAGTCCTCCAACACAGCCTACATGCAGCTCAGCAGCCTAACATCTGAGGACTCTGCG
GTCTTTTTCTGTGCAAGA (SEQ ID NO:1206)
(amino acids)
KATLTADKSSNTAYMQLSSLTSEDSAVFFCAR (SEQ ID NO:1207)

Mouse antibody IE4 heavy chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
GGTAACCACGCCTCTATGGACTAC (SEQ ID NO:1208)
(amino acids)
GNHASMDY (SEQ ID NO:1209)

Mouse antibody IE4 heavy chain variable *framework 4* (*FW4*) sequence:
(DNA)
TGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA (SEQ ID NO:1210)
(amino acids)
WGQGTSVTVSS (SEQ ID NO:1211)

Mouse Antibody IE4 Light chain: DNA sequence (393 bp)
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGAAGTTGCCTGTTAGGCTGTTGGTGCTGATGTTCTGGATTCCTGCTTCCAGCAGTGATGTTGTGATGACCCAAACT
CCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCTCCATCTCTTGCAGATCTAGTCAGAGCCTTGTACACAGTAAT
GGAAACACCTATTTACATTGGTACCTGCAGAAGCCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAACCGA
TTTTCTGGGGTCCCAGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACACTCAAGATCAGCAGAGTGGAGGCT
GAGGATCTGGGAGTTTATTTCTGCTCTCAAAAAACACATGTTCCGTGGACGTTCGGTGGAGGCACCAAGCTGGAAATC
AAA (SEQ ID NO:1212)

Mouse Antibody IE4 Light chain: Amino acid sequence (131 aa)
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
MKLPVRLLVLMFWIPASSSDVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNR
FSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQKTHVPWTFGGGTKLEIK (SEQ ID NO:1213)

Mouse antibody IE4 light chain variable *framework 1* (*FW1*) sequence:
(DNA)
GATGTTGTGATGACCCAAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCTCCATCTCTTGC (SEQ ID NO:1214)
(amino acids)
DVVMTQTPLSLPVSLGDQASISC (SEQ ID NO:1215)
Mouse antibody IE4 light chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
AGATCTAGTCAGAGCCTTGTACACAGTAATGGAAACACCTATTTACAT (SEQ ID NO:1216)
(amino acids)
RSSQSLVHSNGNTYLH (SEQ ID NO:1217)

Mouse antibody IE4 light chain variable *framework 2* (*FW2*) sequence:
(DNA)
TGGTACCTGCAGAAGCCAGGCCAGTCTCCAAAGCTCCTGATCTAC (SEQ ID NO:1218)
(amino acids)
WYLQKPGQSPKLLIY (SEQ ID NO:1219)

Mouse antibody IE4 light chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)

AAAGTTTCCAACCGATTTTCT (SEQ ID NO:1220)
 (amino acids)
KVSNRFS (SEQ ID NO:1221)

Mouse antibody IE4 light chain variable *framework 3* (*FW3*) sequence:
(DNA)
GGGGTCCCAGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACACTCAAGATCAGCAGAGTGGAGGCTGAGGAT
CTGGGAGTTTATTTCTGC (SEQ ID NO:1222)
 (amino acids)
GVPDRFSGSGSGTDFTLKISRVEAEDLGVYFC (SEQ ID NO:1223)

Mouse antibody IE4 light chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
TCTCAAAAAACACATGTTCCGTGGACG (SEQ ID NO:1224)
 (amino acids)
SQKTHVPWT (SEQ ID NO:1225)

Mouse antibody IE4 light chain variable *framework 4* (*FW4*) sequence:
(DNA)
TTCGGTGGAGGCACCAAGCTGGAAATCAAA (SEQ ID NO:1226)
 (amino acids)
FGGGTKLEIK (SEQ ID NO:1227)

Mouse antibody 29H1 Heavy chain: DNA sequence (411 bp)
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGTACTTGGGACTGAACTATGTATTCATAGTTTTTCTCTTAAATGGTGTCCAGAGTGAAGTGAAGCTTGAGGAGTCT
GGAGGAGGCTTGGTACAACCTGGAGGATCCATGAAACTCTCTTGTGCTGCCTCTGGATTCACTTTTAGTGACGCCTGG
ATGGACTGGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAATGGGTTGCTGAAATTAGAAGCAAAGCTACTAATCATGCA
ACATACTATGCTGAGTCTGTGAAAGGGAGGTTCACCATCTCAAGAGATGATTCCAAAAGTAGTGTCTACCTGCAAATG
AACAGCTTAAGAGCTGAAGACACTGGCATTTATTACTGTACCCCCCTACTTTACGGGTTTGCTTACTGGGGCCAAGGG
ACTCTGGTCACTGTCTCTGCA (SEQ ID NO:1228)

Mouse antibody 29H1 Heavy chain: Amino acid sequence (137 aa)
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
MYLGLNYVFIVFLLNGVQSEVKLEESGGGLVQPGGSMKLSCAASGFTFSDAWMDWVRQSPEKGLEWVAEIRSKATNHA
TYYAESVKGRFTISRDDSKSSVYLQMNSLRAEDTGIYYCTPLLYGFAYWGQGTLVTVSA (SEQ ID NO:1229)

Mouse antibody 29H1 heavy chain variable *framework 1* (*FW1*) sequence:
(DNA)
GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTACAACCTGGAGGATCCATGAAACTCTCTTGTGCTGCCTCTGGA
TTCACTTTTAGT (SEQ ID NO:1230)
 (amino acids)
EVKLEESGGGLVQPGGSMKLSCAASGFTFS (SEQ ID NO:1231)

Mouse antibody 29H1 heavy chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
GACGCCTGGATGGAC (SEQ ID NO:1232)
 (amino acids)
DAWMD (SEQ ID NO:1233)

Mouse antibody 29H1 heavy chain variable *framework 2* (*FW2*) sequence:
(DNA)
TGGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAATGGGTTGCT (SEQ ID NO:1234)
 (amino acids)

WVRQSPEKGLEWVA (SEQ ID NO:1235)

Mouse antibody 29H1 heavy chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
GAAATTAGAAGCAAAGCTACTAATCATGCAACATACTATGCTGAGTCTGTGAAAGGG (SEQ ID NO:1236)
(amino acids)
EIRSKATNHATYYAESVKG (SEQ ID NO:1237)

Mouse antibody 29H1 heavy chain variable *framework 3* (*FW3*) sequence:
(DNA)
AGGTTCACCATCTCAAGAGATGATTCCAAAAGTAGTGTCTACCTGCAAATGAACAGCTTAAGAGCTGAAGACACTGGC
ATTTATTACTGTACCCCC (SEQ ID NO:1238)
(amino acids)
RFTISRDDSKSSVYLQMNSLRAEDTGIYYCTP (SEQ ID NO:1239)

Mouse antibody 29H1 heavy chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
CTACTTTACGGGTTTGCTTAC (SEQ ID NO:1240)

(amino acids)
LLYGFAY (SEQ ID NO:1241)

Mouse antibody 29H1 heavy chain variable *framework 4* (*FW4*) sequence:
(DNA)
TGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA (SEQ ID NO:1242)

(amino acids)
WGQGTLVTVSA (SEQ ID NO:1243)

Mouse antibody 29H1 Light chain: DNA sequence (393 bp)
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGAAGTTGCCTGTTAGGCTGTTGGTGCTGATGTTCTGGATTCCTGCTTCCAGCAGTGATGTTGTGATGACCCAAACT
CCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCTCCATCTCTTGCAGATCTGGTCAGAGCCTTGTACACAGTAAT
GGACACACCTATTTACATTGGTACCTGCAGAAGCCAGGCCAGTCTCCAAGGCTCCTGATCTACAAAGTTTCCAACCGA
TTTTCTGGGGTCCCAGACAGGTTCAGTGGCAGTGGATCAAGGGCAGATTTCACACTCAAGATCAGCAGAGTGGAGGCT
GAGGATCTGGGAGTTTATTTCTGCTCTCAAACTACACATGTTCCGTGGACGTTCGGTGGAGGCACCAAGCTGGAAATC
AAA (SEQ ID NO:1244)

Mouse antibody 29H1 Light chain: Amino acid sequence (131 aa)
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
MKLPVRLLVLMFWIPASSSDVVMTQTPLSLPVSLGDQASISCRSGQSLVHSNGHTYLHWYLQKPGQSPRLLIYKVSNR
FSGVPDRFSGSGSRADFTLKISRVEAEDLGVYFCSQTTHVPWTFGGGTKLEIK (SEQ ID NO:1245)

Mouse antibody 29H1 light chain variable *framework 1* (*FW1*) sequence:
(DNA)
GATGTTGTGATGACCCAAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCTCCATCTCTTGC (SEQ ID NO:1246)

(amino acids)
DVVMTQTPLSLPVSLGDQASISC (SEQ ID NO:1247)

Mouse antibody 29H1 light chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)

AGATCTGGTCAGAGCCTTGTACACAGTAATGGACACACCTATTTACAT (SEQ ID NO:1248)

(amino acids)
RSGQSLVHSNGHTYLH (SEQ ID NO:1249)

Mouse antibody 29H1 light chain variable *framework 2* (*FW2*) sequence:
(DNA)
TGGTACCTGCAGAAGCCAGGCCAGTCTCCAAGGCTCCTGATCTAC (SEQ ID NO:1250)

(amino acids)
WYLQKPGQSPRLLIY (SEQ ID NO:1251)

Mouse antibody 29H1 light chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
AAAGTTTCCAACCGATTTTCT (SEQ ID NO:1252)

(amino acids)
KVSNRFS (SEQ ID NO:1253)

Mouse antibody 29H1 light chain variable *framework 3* (*FW3*) sequence:
(DNA)
GGGGTCCCAGACAGGTTCAGTGGCAGTGGATCAAGGGCAGATTTCACACTCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTTCTGC (SEQ ID NO:1254)

(amino acids)
GVPDRFSGSGSRADFTLKISRVEAEDLGVYFC (SEQ ID NO:1255)

Mouse antibody 29H1 light chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
TCTCAAACTACACATGTTCCGTGGACG (SEQ ID NO:1256)

(amino acids)
SQTTHVPWT (SEQ ID NO:1257)

Mouse antibody 29H1 light chain variable *framework 4* (*FW4*) sequence:
(DNA)
TTCGGTGGAGGCACCAAGCTGGAAATCAAA (SEQ ID NO:1258)

(amino acids)
FGGGTKLEIK (SEQ ID NO:1259)

Mouse antibody 31A1 Heavy chain: DNA sequence (399 bp)
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGGAAAGGCACTGGATCTTTCTCTTCCTGTTTTCAGTAACTGCAGGTGTCCACTCCCAGGTCCAGCTTCAGCAGTCTGGGGCTGAACTGGCAAAACCTGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACTGGATGCACTGGGTAAAACAGAGGCCTGGACAGGGTCTGGAATGGATTGGATACATTAATCCTAGCACTGGTTATACTGAGTACAATCAGAAGTTCAAGGACAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTACATGCAACTGAGCAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGAGCCTACATTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA (SEQ ID NO:1260)

Mouse antibody 31A1 Heavy chain: Amino acid sequence (133 aa)
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4

MERHWIFLFLFSVTAGVHSQVQLQQSGAELAKPGASVKMSCKASGYTFTSYWMHWVKQRPGQGLEWIGYINPSTGYTE
YNQKFKDKATLTADKSSSTAYMQLSSLTSEDSAVYYCARAYIDYWGQGTTLTVSS (SEQ ID NO:1261)

Mouse antibody 31A1 heavy chain variable *framework 1* (*FW1*) sequence:
(DNA)
CAGGTCCAGCTTCAGCAGTCTGGGGCTGAACTGGCAAAACCTGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCTGGC
TACACCTTTACT (SEQ ID NO:1262)

(amino acids)
QVQLQQSGAELAKPGASVKMSCKASGYTFT (SEQ ID NO:1263)

Mouse antibody 31A1 heavy chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
AGCTACTGGATGCAC (SEQ ID NO:1264)

(amino acids)
SYWMH (SEQ ID NO:1265)

Mouse antibody 31A1 heavy chain variable *framework 2* (*FW2*) sequence:
(DNA)
TGGGTAAAACAGAGGCCTGGACAGGGTCTGGAATGGATTGGA (SEQ ID NO:1266)

(amino acids)
WVKQRPGQGLEWIG (SEQ ID NO:1267)

Mouse antibody 31A1 heavy chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
TACATTAATCCTAGCACTGGTTATACTGAGTACAATCAGAAGTTCAAGGAC (SEQ ID NO:1268)

(amino acids)
YINPSTGYTEYNQKFKD (SEQ ID NO:1269)

Mouse antibody 31A1 heavy chain variable *framework 3* (*FW3*) sequence:
(DNA)
AAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTACATGCAACTGAGCAGCCTGACATCTGAGGACTCTGCA
GTCTATTACTGTGCAAGA (SEQ ID NO:1270)

(amino acids)
KATLTADKSSSTAYMQLSSLTSEDSAVYYCAR (SEQ ID NO:1271)

Mouse antibody 31A1 heavy chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
GCCTACATTGACTAC (SEQ ID NO:1272)

(amino acids)
AYIDY (SEQ ID NO:1273)

Mouse antibody 31A1 heavy chain variable *framework 4* (*FW4*) sequence:
(DNA)
TGGGGCCAAGGCACCACTCTCACAGTCTCCTCA (SEQ ID NO:1274)

(amino acids)

WGQGTTLTVSS (SEQ ID NO:1275)

Mouse antibody 31A1 Light chain: DNA sequence (393 bp)
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGAAGTTGCCTGTTAGGCTGTTGGTGCTGATGTTCTGGATTCCTGCTTCCAGCAGTGATGTTTTGATGACCCAAACT
CCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCTCCTTCTCTTGCAGATCTAGTCAGAGCATTGTACATAGTAAT
GGAAACACCTATTTAGAATGGTACCTGCAGAAACCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAACCGA
TTTTCTGGGGTCCCAGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACACTCAAGATCAACAGAGTGGAGGCT
GAGGATCTGGGAGTTTATTACTGCTTTCAAGTTTCACATTTTCCGTGGACGTTCGGTGGAGGCACCAAGCTGGAAATC
AAA (SEQ ID NO:1276)

Mouse antibody 31A1 Light chain: Amino acid sequence (131 aa)
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
MKLPVRLLVLMFWIPASSSDVLMTQTPLSLPVSLGDQASFSCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNR
FSGVPDRFSGSGSGTDFTLKINRVEAEDLGVYYCFQVSHFPWTFGGGTKLEIK (SEQ ID NO:1277)

Mouse antibody 31A1 light chain variable *framework 1* (*FW1*) sequence:
(DNA)
GATGTTTTGATGACCCAAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCTCCTTCTCTTGC (SEQ ID NO:1278)

(amino acids)
DVLMTQTPLSLPVSLGDQASFSC (SEQ ID NO:1279)

Mouse antibody 31A1 light chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
AGATCTAGTCAGAGCATTGTACATAGAAATGGAAACACCTATTTAGAA (SEQ ID NO:1280)

(amino acids)
RSSQSIVHRNGNTYLE (SEQ ID NO:1281)

Mouse antibody 31A1 light chain variable *framework 2* (*FW2*) sequence:
(DNA)
TGGTACCTGCAGAAACCAGGCCAGTCTCCAAAGCTCCTGATCTAC (SEQ ID NO:1282)

(amino acids)
WYLQKPGQSPKLLIY (SEQ ID NO:1283)

Mouse antibody 31A1 light chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
AAAGTTTCCAACCGATTTTCT (SEQ ID NO:1284)

(amino acids)
KVSNRFS (SEQ ID NO:1285)

Mouse antibody 31A1 light chain variable *framework 3* (*FW3*) sequence:
(DNA)
GGGGTCCCAGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACACTCAAGATCAACAGAGTGGAGGCTGAGGAT
CTGGGAGTTTATTACTGC (SEQ ID NO:1286)

(amino acids)
GVPDRFSGSGSGTDFTLKINRVEAEDLGVYYC (SEQ ID NO:1287)

Mouse antibody 31A1 light chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
TTTCAAGTTTCACATTTTCCGTGGACG (SEQ ID NO:1288)

(amino acids)
FQVSHFPWT (SEQ ID NO:1289)

Mouse antibody 31A1 light chain variable *framework 4* (*FW4*) sequence:
(DNA)
TTCGGTGGAGGCACCAAGCTGGAAATCAAA (SEQ ID NO:1290)

(amino acids)
FGGGTKLEIK (SEQ ID NO:1291)

Mouse antibody 32C1 Heavy chain: DNA sequence (411 bp)
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGTACTTGGGACTGAACTGTGTATTCATAGTTTTTCTCTTAAAAGGTGTCCAGAGTGAAGTGAAGCTTGAGGAGTCT
GGAGGAGGCTTGGTGCAATCTGGAGGATCCATGAAACTCTCCTGTGTTGCCTCTGGATTCACTTTCAGTAATTACTGG
ATGAACTGGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGATTGAAATCTAATAATTATGCA
ATACATTATGCGGAGTCTGTGAAGGGGAGGTTCACCATCTCAAGAGATGATTCCAAAAGTAGTGTCTACCTGCAAATG
AACAACTTAAGAGCTGAAGACACTGGCATTTATTACTGTACCAGGGTCCCGGGACTGGATGCTTACTGGGGCCAAGGG
ACTCTGGTCACTGTCTCTGCA (SEQ ID NO:1292)

Mouse antibody 32C1 Heavy chain: Amino acid sequence (137 aa)
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
MYLGLNCVFIVFLLKGVQSEVKLEESGGGLVQSGGSMKLSCVASGFTFSNYWMNWVRQSPEKGLEWVAEIRLKSNNYA
IHYAESVKGRFTISRDDSKSSVYLQMNNLRAEDTGIYYCTRVPGLDAYWGQGTLVTVSA (SEQ ID NO:1293)

Mouse antibody 32C1 heavy chain variable *framework 1* (*FW1*) sequence:
(DNA)
GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAATCTGGAGGATCCATGAAACTCTCCTGTGTTGCCTCTGGA
TTCACTTTCAGT (SEQ ID NO:1294)

(amino acids)
EVKLEESGGGLVQSGGSMKLSCVASGFTFS (SEQ ID NO:1295)

Mouse antibody 32C1 heavy chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
AATTACTGGATGAAC (SEQ ID NO:1296)

(amino acids)
NYWMN (SEQ ID NO:1297)

Mouse antibody 32C1 heavy chain variable *framework 2* (*FW2*) sequence:
(DNA)
TGGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTGCT (SEQ ID NO:1298)

(amino acids)
WVRQSPEKGLEWVA (SEQ ID NO:1299)

Mouse antibody 32C1 heavy chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)

GAAATTAGATTGAAATCTAATAATTATGCAATACATTATGCGGAGTCTGTGAAGGGG (SEQ ID NO:1300)

(amino acids)
EIRLKSNNYAIHYAESVKG (SEQ ID NO:1301)

Mouse antibody 32C1 heavy chain variable *framework 3* (*FW3*) sequence:
(DNA)
AGGTTCACCATCTCAAGAGATGATTCCAAAAGTAGTGTCTACCTGCAAATGAACAACTTAAGAGCTGAAGACACTGGC
ATTTATTACTGTACCAGG (SEQ ID NO:1302)

(amino acids)
RFTISRDDSKSSVYLQMNNLRAEDTGIYYCTR (SEQ ID NO:1303)

Mouse antibody 32C1 heavy chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
GTCCCGGGACTGGATGCTTAC (SEQ ID NO:1304)

(amino acids)
VPGLDAY (SEQ ID NO:1305)

Mouse antibody 32C1 heavy chain variable *framework 4* (*FW4*) sequence:
(DNA)
TGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA (SEQ ID NO:1306)

(amino acids)
WGQGTLVTVSA (SEQ ID NO:1307)

Mouse antibody 32C1 Light chain: DNA sequence (393 bp)
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGAAGTTGCCTGTTAGGCTGTTGGTGCTGATGTTCTGGATTCCTGCTTCCAGCAGTGATGTTGTGATGACCCAAACT
CCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCTCCATCTCTTGCAGATCTAGTCAGAGCCTTGTACACAGTAAT
GGAAACACCTATTTACATTGGTACCTGCAGAAGCCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAACCGA
TTTTCTGGGGTCCCAGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACACTCAAGATCAGCAGTGTGGAGGCT
GAGGATCTGGGAGTTTATTTCTGCTCTCAAATTACACATGTTCCGTACACGTTCGGAGGGGGGACCAATCTGGAAATA
AAA (SEQ ID NO:1308)

Mouse antibody 32C1 Light chain: Amino acid sequence (131 aa)
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
MKLPVRLLVLMFWIPASSSDVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNR
FSGVPDRFSGSGSGTDFTLKISSVEAEDLGVYFCSQITHVPYTFGGGTNLEIK (SEQ ID NO:1309)

Mouse antibody 32C1 light chain variable *framework 1* (*FW1*) sequence:
(DNA)
GATGTTGTGATGACCCAAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCTCCATCTCTTGC (SEQ ID NO:1310)
(amino acids)
DVVMTQTPLSLPVSLGDQASISC (SEQ ID NO:1311)
Mouse antibody 32C1 light chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
AGATCTAGTCAGAGCCTTGTACACAGTAATGGAAACACCTATTTACAT (SEQ ID NO:1312)
(amino acids)
RSSQSLVHSNGNTYLH (SEQ ID NO:1313)

Mouse antibody 32C1 light chain variable *framework 2* (*FW2*) sequence:

(DNA)
TGGTACCTGCAGAAGCCAGGCCAGTCTCCAAAGCTCCTGATCTAC (SEQ ID NO:1314)
(amino acids)
WYLQKPGQSPKLLIY (SEQ ID NO:1315)

Mouse antibody 32C1 light chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
AAAGTTTCCAACCGATTTTCT (SEQ ID NO:1316)
(amino acids)
KVSNRFS (SEQ ID NO:1317)

Mouse antibody 32C1 light chain variable *framework 3* (*FW3*) sequence:
(DNA)
GGGGTCCCAGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACACTCAAGATCAGCAGTGTGGAGGCTGAGGAT
CTGGGAGTTTATTTCTGC (SEQ ID NO:1318)
(amino acids)
GVPDRFSGSGSGTDFTLKISSVEAEDLGVYFC (SEQ ID NO:1319)

Mouse antibody 32C1 light chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
TCTCAAATTACACATGTTCCGTACACG (SEQ ID NO:1320)
(amino acids)
SQITHVPYT (SEQ ID NO:1321)

Mouse antibody 32C1 light chain variable *framework 4* (*FW4*) sequence:
(DNA)
TTCGGAGGGGGGACCAATCTGGAAATAAAA (SEQ ID NO:1322)
(amino acids)
FGGGTNLEIK (SEQ ID NO:1323)

Mouse antibody 45C11 Heavy chain: DNA sequence (423 bp)
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGAAATGCAGCTGGGTTATCTTCTTCCTGATGGCAGTGGTTACAGGGGTCAATTCAGAGGTTCAGCTGCAGCAGTCT
GGGGCAGACCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCTTT
ATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAATGGTAATACTAAA
TATGACCCGAAATTCCAGGGCAAGGCCACTATAACAGCAGACACATCCTCCAACACAGCCTACCTGCAGCTCAGCAGC
CTGACATCTGAGGACACTGCCGTCTATTACTGTGCTAAACCGTATGGTAACTACGGCTATTACTATGCTTTGGACTAC
TGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA (SEQ ID NO:1324)

Mouse antibody 45C11 Heavy chain: Amino acid sequence (141 aa)
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
MKCSWVIFFLMAVVTGVNSEVQLQQSGADLVKPGASVKLSCTASGFNIKDTFMHWVKQRPEQGLEWIGRIDPANGNTK
YDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCAKPYGNYGYYYALDYWGQGTSVTVSS (SEQ ID NO:1325)

Mouse antibody 45C11 heavy chain variable *framework 1* (*FW1*) sequence:
(DNA)
GAGGTTCAGCTGCAGCAGTCTGGGGCAGACCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGC
TTCAACATTAAA (SEQ ID NO:1326)
(amino acids)
EVQLQQSGADLVKPGASVKLSCTASGFNIK (SEQ ID NO:1327)

Mouse antibody 45C11 heavy chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)

GACACCTTTATGCAC (SEQ ID NO:1328)
 (amino acids)
DTFMH (SEQ ID NO:1329)

Mouse antibody 45C11 heavy chain variable *framework 2* (*FW2*) sequence:
(DNA)
TGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGA (SEQ ID NO:1330)
 (amino acids)
WVKQRPEQGLEWIG (SEQ ID NO:1331)

Mouse antibody 45C11 heavy chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
AGGATTGATCCTGCGAATGGTAATACTAAATATGACCCGAAATTCCAGGGC (SEQ ID NO:1332)
 (amino acids)
RIDPANGNTKYDPKFQG (SEQ ID NO:1333)

Mouse antibody 45C11 heavy chain variable *framework 3* (*FW3*) sequence:
(DNA)
AAGGCCACTATAACAGCAGACACATCCTCCAACACAGCCTACCTGCAGCTCAGCAGCCTGACATCTGAGGACACTGCC
GTCTATTACTGTGCTAAA (SEQ ID NO:1334)
 (amino acids)
KATITADTSSNTAYLQLSSLTSEDTAVYYCAK (SEQ ID NO:1335)

Mouse antibody 45C11 heavy chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
CCGTATGGTAACTACGGCTATTACTATGCTTTGGACTAC (SEQ ID NO:1336)
 (amino acids)
PYGNYGYYYALDY (SEQ ID NO:1337)

Mouse antibody 45C11 heavy chain variable *framework 4* (*FW4*) sequence:
(DNA)
TGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA (SEQ ID NO:1338)
 (amino acids)
WGQGTSVTVSS (SEQ ID NO:1339)

Mouse antibody 45C11 Light chain: DNA sequence (381 bp)
Signal sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
ATGAGGTTCCAGGTTCAGGTTCTGGGGCTCCTTCTGCTCTGGATATCAGGTGCCCAGTGTGATGTCCAGATAACCCAG
TCTCCATCTTATCTTGCTGCATCTCCTGGAGAAACCATTACTATTAATTGCAGGGCAAGTAAGAGCATTAGCAAATAT
TTAGCCTGGTATCAAGAGAAACCTGGGAAAACTAATAAGCTTCTTATCTACTCTGGATCCACTTTGCAATCTGGAATT
CCATCAAGGTTCAGTGGCAGTGGATCTGGTACAGATTTCACTCTCACCATCAGTAGCCTGGAGCCTGAAGATTTTGCA
ATGTATTACTGTCAACAGCATAATGAATTCCCGTGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA (SEQ ID NO:1340)

Mouse antibody 45C11 Light chain: Amino acid sequence (127 aa)
Signal peptide-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4
MRFQVQVLGLLLLWISGAQCDVQITQSPSYLAASPGETITINCRASKSISKYLAWYQEKPGKTNKLLIYSGSTLQSGI
PSRFSGSGSGTDFTLTISSLEPEDFAMYYCQQHNEFPWTFGGGTKLEIK (SEQ ID NO:1341)

Mouse antibody 45C11 light chain variable *framework 1* (*FW1*) sequence:
(DNA)
GATGTCCAGATAACCCAGTCTCCATCTTATCTTGCTGCATCTCCTGGAGAAACCATTACTATTAATTGC (SEQ ID NO:1342)
 (amino acids)
DVQITQSPSYLAASPGETITINC (SEQ ID NO:1343)

Mouse antibody 45C11 light chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
AGGGCAAGTAAGAGCATTAGCAAATATTTAGCC (SEQ ID NO:1344)
(amino acids)
RASKSISKYLA (SEQ ID NO:1345)

Mouse antibody 45C11 light chain variable *framework 2* (*FW2*) sequence:
(DNA)
TGGTATCAAGAGAAACCTGGGAAAACTAATAAGCTTCTTATCTAC (SEQ ID NO:1346)
(amino acids)
WYQEKPGKTNKLLIY (SEQ ID NO:1347)

Mouse antibody 45C11 light chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
TCTGGATCCACTTTGCAATCT (SEQ ID NO:1348)
(amino acids)
SGSTLQS (SEQ ID NO:1349)

Mouse antibody 45C11 light chain variable *framework 3* (*FW3*) sequence:
(DNA)
GGAATTCCATCAAGGTTCAGTGGCAGTGGATCTGGTACAGATTTCACTCTCACCATCAGTAGCCTGGAGCCTGAAGAT
TTTGCAATGTATTACTGT (SEQ ID NO:1350)
(amino acids)
GIPSRFSGSGSGTDFTLTISSLEPEDFAMYYC (SEQ ID NO:1351)

Mouse antibody 45C11 light chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
CAACAGCATAATGAATTCCCGTGGACG (SEQ ID NO:1352)
(amino acids)
QQHNEFPWT (SEQ ID NO:1353)

Mouse antibody 45C11 light chain variable *framework 4* (*FW4*) sequence:
(DNA)
TTCGGTGGAGGCACCAAGCTGGAAATCAAA (SEQ ID NO:1354)
(amino acids)
FGGGTKLEIK (SEQ ID NO:1355)

5C6F3
Mouse 5C6F3 heavy chain variable *framework 1* (*FW1*) sequence:
(DNA)
Gaagtgatgctggtggagtctgggggaggcttagtgaagcctggagggtccctgaaactctcctgtgcagcctctgga
ttcactttcagt (SEQ ID NO:1356)
(amino acids)
EVMLVESGGGLVKPGGSLKLSCAASGFTFS (SEQ ID NO:1357)

Mouse 5C6F3 heavy chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
acctatgccatgtct (SEQ ID NO:1358)
(amino acids)
TYAMS (SEQ ID NO:1359)

Mouse 5C6F3 heavy chain variable *framework 2* (*FW2*) sequence:
(DNA)

tgggttcgccagactccggagaagaggctggagtgggtcgca (SEQ ID NO:1360)
(amino acids)
WVRQTPEKRLEWVA (SEQ ID NO:1361)

Mouse 5C6F3 heavy chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
gccattagtaatggtggtggttacacctactatccagacagtctgaagggg (SEQ ID NO:1362)
(amino acids)
AISNGGGYTYYPDSLKG (SEQ ID NO:1363)

Mouse 5C6F3 heavy chain variable *framework 3* (*FW3*) sequence:
(DNA)
cgattcaccatctccagagacaatgccaagaacaccctgtacctgcaaatgagcagtctgaggtctgaggacacggccacgtattactgtgcaaga (SEQ ID NO:1364)
(amino acids)
RFTISRDNAKNTLYLQMSSLRSEDTATYYCAR (SEQ ID NO:1365)

Mouse 5C6F3 heavy chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
cgttactatgatcactactttgactac (SEQ ID NO:1366)
(amino acids)
RYYDHYFDY (SEQ ID NO:1367)

Mouse 5C6F3 heavy chain variable *framework 4* (*FW4*) sequence:
(DNA)
tggggccaaggcaccgctctcacggtctcctca (SEQ ID NO:1368)
(amino acids)
WGQGTALTVSS (SEQ ID NO:1369)

Mouse 5C6F3 light chain variable *framework 1* (*FR1*) sequence:
(DNA)
gatgttttgatgacccaaactccactctccctgcctgtcagtcttggagatcaagcctccatctcttgc (SEQ ID NO:1370)
(amino acids)
DVLMTQTPLSLPVSLGDQASISC (SEQ ID NO:1371)

Mouse 5C6F3 light chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
agatctagtcagaccattgtacatagtaatggaaacacctatttagaa (SEQ ID NO:1372)
(amino acids)
RSSQTIVHSNGNTYLE (SEQ ID NO:1373)

Mouse 5C6F3 light chain variable *framework 2* (*FR2*) sequence:
(DNA)
tggtacctgcagaaaccaggccagtctccaaagctcctgatctac (SEQ ID NO:1374)
(amino acids)
WYLQKPGQSPKLLIY (SEQ ID NO:1375)

Mouse 5C6F3 light chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
aaagtttccaaccgattttct (SEQ ID NO:1376)
(amino acids)
KVSNRFS (SEQ ID NO:1377)

Mouse 5C6F3 light chain variable *framework 3* (*FR3*) sequence:
(DNA)
ggggtcccagacaggttcagtggcagtggatcagggacagatttcacactcaagatcagcagggtggaggctgaggat
ctgggagtttattactgc (SEQ ID NO:1378)
(amino acids)
GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYC (SEQ ID NO:1379)

Mouse 5C6F3 light chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
tttcaagattcacatgttcctctcacg (SEQ ID NO:1380)
(amino acids)
FQDSHVPLT (SEQ ID NO:1381)

Mouse 5C6F3 light chain variable *framework 4* (*FR4*) sequence:
(DNA)
ttcggtgctgggaccaagctggagctgaaa (SEQ ID NO:1382)
(amino acids)
FGAGTKLELK (SEQ ID NO:1383)

mu5C6F3 scFv sequence
(DNA)
gaagtgatgctggtggagtctgggggaggcttagtgaagcctggagggtccctgaaactctcctgtgcagcctctgga
ttcactttcagtacctatgccatgtcttgggttcgccagactccggagaagaggctggagtgggtcgcagccattagt
aatggtggtggttacacctactatccagacagtctgaaggggcgattcaccatctccagagacaatgccaagaacacc
ctgtacctgcaaatgagcagtctgaggtctgaggacacggccacgtattactgtgcaagacgttactatgatcactac
tttgactactggggccaaggcaccgctctcacggtctcctcaggtggcggaggatctggcggaggtggaagcggcgga
ggcggatccgatgttttgatgacccaaactccactctccctgcctgtcagtcttggagatcaagcctccatctcttgc
agatctagtcagaccattgtacatagtaatggaaacacctatttagaatggtacctgcagaaaccaggccagtctcca
aagctcctgatctacaaagtttccaaccgattttctggggtcccagacaggttcagtggcagtggatcagggacagat
ttcacactcaagatcagcagggtggaggctgaggatctgggagtttattactgctttcaagattcacatgttcctctc
acgttcggtgctgggaccaagctggagctgaaa (SEQ ID NO:1384)
(amino acids)
EVMLVESGGGLVKPGGSLKLSCAASGFTFSTYAMSWVRQTPEKRLEWVAAISNGGGYTYYPDSLKGRFTISRDNAKN
TLYLQMSSLRSEDTATYYCARRYYDHYFDYWGQGTALTVSSGGGGSGGGGSGGGGSDVLMTQTPLSLPVSLGDQASI
SCRSSQTIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQDSH
VPLTFGAGTKLELK (SEQ ID NO:1385)

3C2B1

Mouse 3C2B1 heavy chain variable *framework 1* (*CDR1*) sequence:
(DNA)
gaagtgatgctggtggagtctgggggaggcttagtgaagcctggagggtccctgaaactctcctgtgcagcctctgga
atcactttcagt (SEQ ID NO:1386)
(amino acids)
EVMLVESGGGLVKPGGSLKLSCAASGITFS (SEQ ID NO:1387)

Mouse 3C2B1 heavy chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
acctataccatgtcg (SEQ ID NO:1388)
(amino acids)
TYTMS (SEQ ID NO:1389)

Mouse 3C2B1 heavy chain variable *framework 2* (*CDR2*) sequence:
(DNA)

tgggttcgccagactccggagaagaggctggagtgggtcgca (SEQ ID NO:1390)
(amino acids)
WVRQTPEKRLEWVA (SEQ ID NO:1391)

Mouse 3C2B1 heavy chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
accattagtactggtggtgataaaacctactattcagacagtgtgaagggt (SEQ ID NO:1392)
(amino acids)
TISTGGDKTYYSDSVKG (SEQ ID NO:1393)

Mouse 3C2B1 heavy chain variable *framework 3* (*CDR3*) sequence:
(DNA)
cgattcaccatctccagagacaatgccaagaacaacctgtacctccaaatgagcagtctgaggtctgaggacacggcc ttgtattactgtgcaagg (SEQ ID NO:1394)
(amino acids)
RFTISRDNAKNNLYLQMSSLRSEDTALYYCAR (SEQ ID NO:1395)

Mouse 3C2B1 heavy chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
ggaaccacggctatgtattactatgctatggactac (SEQ ID NO:1396)
(amino acids)
GTTAMYYYAMDY (SEQ ID NO:1397)

Mouse 3C2B1 heavy chain variable *framework 4* (*CDR4*) sequence:
(DNA)
tggggtcaaggaacctcagtcaccgtctcctca (SEQ ID NO:1398)
(amino acids)
WGQGTSVTVSS (SEQ ID NO:1399)

Mouse 3C2B1 light chain variable *framework 1* (*FW1*) sequence:
(DNA)
gacattgtgctgacacagtctcctgcttccttagctgtatctctggggcagagggccaccatctcatgc (SEQ ID NO:1400)
(amino acids)
DIVLTQSPASLAVSLGQRATISC (SEQ ID NO:1401)

Mouse 3C2B1 light chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
agggccagcaaaagtatcagtacatctgactataattatattcac (SEQ ID NO:1402)
(amino acids)
RASKSISTSDYNYIH (SEQ ID NO:1403)

Mouse 3C2B1 light chain variable *framework 2* (*FW2*) sequence:
(DNA)
tggtaccaacagaaaccaggacagccacccaaactcctcatctat (SEQ ID NO:1404)
(amino acids)
WYQQKPGQPPKLLIY (SEQ ID NO:1405)

Mouse 3C2B1 light chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
CTTGCATCCAACCTAGAATCT (SEQ ID NO:1406)
(amino acids)
LASNLES (SEQ ID NO:1407)

Mouse 3C2B1 light chain variable *framework 3* (*FW3*) sequence:
(DNA)
gggtccctgccaggttcagtggcagtgggtctgggacagacttcaccctcaacatccatcctgtggaggaagaagatg
ctgcaacctattactgt (SEQ ID NO:1408)
(amino acids)
GVPARFSGSGSGTDFTLNIHPVEEEDAATYYC (SEQ ID NO:1409)

Mouse 3C2B1 light chain variable *complementarity determining regions 3* (*CDR3*)
sequence:
(DNA)
cagcacagtagggagcttcctctcacg (SEQ ID NO:1410)
(amino acids)
QHSRELPLT (SEQ ID NO:1411)

Mouse 3C2B1 light chain variable *framework 4* (*FW4*) sequence:
(DNA)
ttcggtgctgggaccaagctggagctgaaa (SEQ ID NO:1412)
(amino acids)
FGAGTKLELK (SEQ ID NO:1413)

Mouse B12 heavy chain variable *framework 1* (*FW1*) sequence:
(DNA)
Caggcgcagctgaaggagtcaggacctggcctggtggcgccctcacagagcctgtccatcacttgcactgtctctggg
ttttcattaacc (SEQ ID NO:1414)
(amino acids)
QAQLKESGPGLVAPSQSLSITCTVSGFSLT (SEQ ID NO:1415)

Mouse B12 heavy chain variable *complementarity determining regions 1* (*CDR1*)
sequence:
(DNA)
agctatggtgtacac (SEQ ID NO:1416)
(amino acids)
SYGVH (SEQ ID NO:1417)

Mouse B12 heavy chain variable *framework 2* (*FW2*) sequence:
(DNA)
tgggttcgccagcctccaggaaagggtctggagtggctggga (SEQ ID NO:1418)
(amino acids)
WVRQPPGKGLEWLG (SEQ ID NO:1419)

Mouse B12 heavy chain variable *complementarity determining regions 2* (*CDR2*)
sequence:
(DNA)
gtaatatggcctggtggaagcacaaattataattcgactctcatgtccagaatg (SEQ ID NO:1420)
(amino acids)
VIWPGGSTNYNSTLMSRM (SEQ ID NO:1421)

Mouse B12 heavy chain variable *framework 3* (*FW3*) sequence:
(DNA)
cggatcatcaaagacaactccaagagccaagttttcttaaaaatgaacagtctgcaaattgatgacacagccatgtac
tactgtgccaga (SEQ ID NO:1422)
(amino acids)
RIIKDNSKSQVFLKMNSLQIDDTAMYYCAR (SEQ ID NO:1423)

Mouse B12 heavy chain variable *complementarity determining regions 3* (*CDR3*)
sequence:

(DNA)
gatcggacacctcgggtgggggcctggtttgcttac (SEQ ID NO:1424)
(amino acids)
DRTPRVGAWFAY (SEQ ID NO:1425)

Mouse B12 heavy chain variable *framework 4* (*FW4*) sequence:
(DNA)
tggggccaagggactctggtcactgtctctgcag (SEQ ID NO:1426)
(amino acids)
WGQGTLVTVSA (SEQ ID NO:1427)

Mouse B12 light chain variable *framework 1* (*FR1*) sequence:
(DNA)
atcattgtgctgacccaatctccagcttctttggctgtgtctctagggcagagggccaccatatcctgc (SEQ ID NO:1428)
(amino acids)
IIVLTQSPASLAVSLGQRATISC (SEQ ID NO:1429)

Mouse B12 light chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
agagccagtgagagtgttgctacttatggcaataattttatgcag (SEQ ID NO:1430)
(amino acids)
RASESVATYGNNFMQ (SEQ ID NO:1431)

Mouse B2 heavy chain variable *framework 1* (*FW1*) sequence:
(DNA)
gaagtggtgctggtggagtctgggggaggcttagtggagcctggagggtccctgaaactctcctgtgtagcctctggattcgctttcagt (SEQ ID NO:1432)
(amino acids)
EVVLVESGGGLVEPGGSLKLSCVASGFAFS (SEQ ID NO:1433)

Mouse B2 heavy chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
acctttgccatgtct (SEQ ID NO:1434)
(amino acids)
TFAMS (SEQ ID NO:1435)

Mouse B2 heavy chain variable *framework 2* (*FW2*) sequence:
(DNA)
tggattcgccagactccggagaagaggctggagtgggtcgca (SEQ ID NO:1436)
(amino acids)
WIRQTPEKRLEWVA (SEQ ID NO:1437)

Mouse B2 heavy chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
gccattagtaatggtggtggttacacctactatccagacactctgaagggg (SEQ ID NO:1438)
(amino acids)
AISNGGGYTYYPDTLKG (SEQ ID NO:1439)

Mouse B2 heavy chain variable *framework 3* (*FW3*) sequence:
(DNA)
cgattctccatctccagagacaatgccaagaataccctgtacctgcaaatgagtagtctgaggtctgaggacacggccgtgtattactgtgcaaga (SEQ ID NO:1440)
(amino acids)

RFSISRDNAKNTLYLQMSSLRSEDTAVYYCAR (SEQ ID NO:1441)

Mouse B2 heavy chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
cgctactatgatctctactttgactta (SEQ ID NO:1442)
(amino acids)
RYYDLYFDL (SEQ ID NO:1443)

Mouse B2 heavy chain variable *framework 4* (*FW4*) sequence:
(DNA)
Tggggccgaggcacctctctcatagtctcctca (SEQ ID NO:1444)
(amino acids)
WGRGTSLIVSS (SEQ ID NO:1445)

Mouse B2 light chain variable *framework 1* (*FR1*) sequence:
(DNA)
gatattctgatgacccaaactccactctccctgcctgtcagtcttggagatcaagcctccatttcttgc (SEQ ID NO:1446)
(amino acids)
DILMTQTPLSLPVSLGDQASISC (SEQ ID NO:1447)
Mouse B2 light chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
agatctagtcagaacattgtacatagtaatggaaacacctatttagaa (SEQ ID NO:1448)
(amino acids)
RSSQNIVHSNGNTYLE (SEQ ID NO:1449)

Mouse B2 light chain variable *framework 2* (*FR2*) sequence:
(DNA)
tggtacctgcagaaaccaggccagtctccaaagctcctgatctac (SEQ ID NO:1450)
(amino acids)
WYLQKPGQSPKLLIY (SEQ ID NO:1451)

Mouse B2 light chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
aaagtttccaaccgattttct (SEQ ID NO:1452)
(amino acids)
KVSNRFS (SEQ ID NO:1453)

Mouse B2 light chain variable *framework 3* (*FR3*) sequence:
(DNA)
ggggtccccgacaggttcagtggtagtgggtcagggacagatttcacactcaagatcagcagagtggaggctgaggatctgggagtttattactgc (SEQ ID NO:1454)
(amino acids)
GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYC (SEQ ID NO:1455)

Mouse B2 light chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
tttcaagattcacatgttcctctcacg (SEQ ID NO:1456)
(amino acids)
FQDSHVPLT (SEQ ID NO:1457)

Mouse B2 light chain variable *framework 4* (*FR4*) sequence:
(DNA)

ttcggtgctgggaccaggctggagctgaaa (SEQ ID NO:1458)
(amino acids)
FGAGTRLELK (SEQ ID NO:1459)

Mouse B7 heavy chain variable *framework 1* (*FW1*) sequence:
(DNA)
gaggtgcaggtggtggagtctgggggagacttagtgaagcctggagggtccctgaaactctcctgtgcagcctctggattcactttcagt (SEQ ID NO:1460)
(amino acids)
EVQVVESGGDLVKPGGSLKLSCAASGFTFS (SEQ ID NO:1461)

Mouse B7 heavy chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
agatatggcatgtct (SEQ ID NO:1462)
(amino acids)
RYGMS (SEQ ID NO:1463)

Mouse B7 heavy chain variable *framework 2* (*FW2*) sequence:
(DNA)
tgggttcgccagactccagacaagaggctggagtgggtcgca (SEQ ID NO:1464)
(amino acids)
WVRQTPDKRLEWVA (SEQ ID NO:1465)

Mouse B7 heavy chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
accattagtagtggtggtacttacatctactatccagacagtgtgaagggg (SEQ ID NO:1466)
(amino acids)
TISSGGTYIYYPDSVKG (SEQ ID NO:1467)

Mouse B7 heavy chain variable *framework 3* (*FW3*) sequence:
(DNA)
cgattcaccatctccagagacaatgccaagaacaccctgtacctgcaaatgagcagtctgaagtctgaggacacagccatgtattactgtgcaagg (SEQ ID NO:1468)
(amino acids)
RFTISRDNAKNTLYLQMSSLKSEDTAMYYCAR (SEQ ID NO:1469)

Mouse B7 heavy chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
gataactacggtagtagctacgactatgctatggactac (SEQ ID NO:1470)
(amino acids)
DNYGSSYDYAMDY (SEQ ID NO:1471)

Mouse B7 heavy chain variable *framework 4* (*FW4*) sequence:
(DNA)
tggggtcaaggaacctcagtcaccgtctcctca (SEQ ID NO:1472)
(amino acids)
WGQGTSVTVSS (SEQ ID NO:1473)

Mouse B7 light chain variable *framework 1* (*FR1*) sequence:
(DNA)
gatgttttgatgacccaaactccactctccctgcctgtcagtcttggagatcaagcctccatctcttgc (SEQ ID NO:1474)
(amino acids)
DVLMTQTPLSLPVSLGDQASISC (SEQ ID NO:1475)

Mouse B7 light chain variable *complementarity determining regions 1* (*CDR1*)
sequence:
(DNA)
agatctagtcagaccattgtacatagtaatggaaacacctatttagaa (SEQ ID NO:1476)
(amino acids)
RSSQTIVHSNGNTYLE (SEQ ID NO:1477)

Mouse B7 light chain variable *framework 2* (*FR2*) sequence:
(DNA)
tggtacctgcaaaaaccaggccagtctccaaagctcctgatctac (SEQ ID NO:1478)
(amino acids)
WYLQKPGQSPKLLIY (SEQ ID NO:1479)

Mouse B7 light chain variable *complementarity determining regions 2* (*CDR2*)
sequence:
(DNA)
aaagtttccaaccgattttct (SEQ ID NO:1480)
(amino acids)
KVSNRFS (SEQ ID NO:1481)

Mouse B7 light chain variable *framework 3* (*FR3*) sequence:
(DNA)
ggggtcccagacaggttcagtggcagtggatcagggacagatttcacactcaagatcagcagggtggaggctgaggat
ctgggagtttattactgc (SEQ ID NO:1482)
(amino acids)
GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYC (SEQ ID NO:1483)

Mouse B7 light chain variable *complementarity determining regions 3* (*CDR3*)
sequence:
(DNA)
tttcaagattcacatgttcctctcacg (SEQ ID NO:1484)
(amino acids)
FQDSHVPLT (SEQ ID NO:1485)

Mouse B7 light chain variable *framework 4* (*FR4*) sequence:
(DNA)
ttcggtgctgggaccaagctggagctgaaa (SEQ ID NO:1486)
(amino acids)
FGAGTKLELK (SEQ ID NO:1487)

Mouse 8C7F3 heavy chain variable *framework 1* (*FW1*) sequence:
(DNA)
gaagtgatgctggtggagtctgggggaggcttagtgaagcctggagggtccctgaaactctcctgtgcagcctctgga
ttcactttcagt (SEQ ID NO:1488)
(amino acids)
EVMLVESGGGLVKPGGSLKLSCAASGFTFS (SEQ ID NO:1489)

Mouse 8C7F3 heavy chain variable *complementarity determining regions 1* (*CDR1*)
sequence:
(DNA)
acctatgccatgtct (SEQ ID NO:1490)
(amino acids)
TYAMS (SEQ ID NO:1491)

Mouse 8C7F3 heavy chain variable *framework 2* (*FW2*) sequence:
(DNA)

tgggttcgccagactccggagaagaggctggagtgggtcgca (SEQ ID NO:1492)
(amino acids)
WVRQTPEKRLEWVA (SEQ ID NO:1493)

Mouse 8C7F3 heavy chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
gccattagtaatggtggtggttacacctactatccagacagtctgaagggg (SEQ ID NO:1494)
(amino acids)
AISNGGGYTYYPDSLKG (SEQ ID NO:1495)

Mouse 8C7F3 heavy chain variable *framework 3* (*FW3*) sequence:
(DNA)
cgattcaccatctccagagacaatgccaagaacaccctgtacctgcaaatgagcagtctgaggtctgaggacacggccacgtattactgtgcaaga (SEQ ID NO:1496)
(amino acids)
RFTISRDNAKNTLYLQMSSLRSEDTATYYCAR (SEQ ID NO:1497)

Mouse 8C7F3 heavy chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
cgttactatgatcactactttgactac (SEQ ID NO:1498)
(amino acids)
RYYDHYFDY (SEQ ID NO:1499)

Mouse 8C7F3 heavy chain variable *framework 4* (*FW4*) sequence:
(DNA)
tggggccaaggcaccgctctcacggtctcctca (SEQ ID NO:1500)
(amino acids)
WGQGTALTVSS (SEQ ID NO:1501)
Mouse 8C7F3 light chain variable *framework 1* (*FR1*) sequence:
(DNA)
atcattgtgctgacccaatctccagcttctttggctgtgtctctagggcagagggccaccatatcctgc (SEQ ID NO:1502)
(amino acids)
IIVLTQSPASLAVSLGQRATISC (SEQ ID NO:1503)

Mouse 8C7F3 light chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
agagccagtgagagtgttgctacttatggcaataattttatgcag (SEQ ID NO:1504)
(amino acids)
RASESVATYGNNFMQ (SEQ ID NO:1505)

Mouse 8C7F3 light chain variable *framework 2* (*FR2*) sequence:
(DNA)
tggtatcagcagaaaccaggacagccacccaaactcctcatctat (SEQ ID NO:1506)
(amino acids)
WYQQKPGQPPKLLIY (SEQ ID NO:1507)

Mouse 8C7F3 light chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
cttgcatccaccctagattct (SEQ ID NO:1508)
(amino acids)
LASTLDS (SEQ ID NO:1509)

Mouse 8C7F3 light chain variable *framework 3* (*FR3*) sequence:
(DNA)
ggggtccctgccaggttcagtggcagtgggtctaggacagacttcaccctcaccattgatcctgtggaggctgatgatgctgcaacctattactgt (SEQ ID NO:1510)
(amino acids)
GVPARFSGSGSRTDFTLTIDPVEADDAATYYC (SEQ ID NO:1511)

Mouse 8C7F3 light chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
cagcaaaataatgaggatcctccgacg (SEQ ID NO:1512)
(amino acids)
QQNNEDPPT (SEQ ID NO:1513)

Mouse 8C7F3 light chain variable *framework 4* (*FR4*) sequence:
(DNA)
ttcggtggaggcaccaagctggaaatcaag (SEQ ID NO:1514)
(amino acids)
FGGGTKLEIK (SEQ ID NO:1515)

Mouse H11 heavy chain variable *framework 1* (*FW1*) sequence:
(DNA)
gaagtggtgctggtggagtctgggggaggcttagtggagcctggagggtccctgaaactctcctgtgtagcctctgga
ttcgcttttagt (SEQ ID NO:1516)
(amino acids)
EVVLVESGGGLVEPGGSLKLSCVASGFAFS (SEQ ID NO:1517)

Mouse H11 heavy chain variable *complementarity determining regions 1* (*CDR1*)
sequence:
(DNA)
acctttgccatgtct (SEQ ID NO:1518)
(amino acids)
TFAMS (SEQ ID NO:1519)

Mouse H11 heavy chain variable *framework 2* (*FW2*) sequence:
(DNA)
tggattcgccagactccggagaagaggctggagtgggtcgca (SEQ ID NO:1520)
(amino acids)
WIRQTPEKRLEWVA (SEQ ID NO:1521)

Mouse H11 heavy chain variable *complementarity determining regions 2* (*CDR2*)
sequence:
(DNA)
gccattagtaatggtggtggttacacttactatccagacactctgaagggg (SEQ ID NO:1522)
(amino acids)
AISNGGGYTYYPDTLKG (SEQ ID NO:1523)

Mouse H11 heavy chain variable *framework 3* (*FW3*) sequence:
(DNA)
cgattcaccatctccagagacaatgccaagaataccctgtacctgcaaatgagtagtctgaggtctgaggacacggcc
gtgtattactgtgcaaga (SEQ ID NO:1524)
(amino acids)
RFTISRDNAKNTLYLQMSSLRSEDTAVYYCAR (SEQ ID NO:1525)

Mouse H11 heavy chain variable *complementarity determining regions 3* (*CDR3*)
sequence:
(DNA)
cgctactatgatctctactttgactta (SEQ ID NO:1526)
(amino acids)
RYYDLYFDL (SEQ ID NO:1527)

Mouse H11 heavy chain variable *framework 4* (*FW4*) sequence:
(DNA)
tggggccaaggcacctctctcatagtctcctca (SEQ ID NO:1528)
(amino acids)
WGQGTSLIVSS (SEQ ID NO:1529)

Mouse H11 light chain variable *framework 1* (*FR1*) sequence:
(DNA)
gatattctgatgacccaaactccactctccctgcctgtcagtcttggagatcaagcctccatttcttgc (SEQ ID
NO:1530)
(amino acids)
DILMTQTPLSLPVSLGDQASISC (SEQ ID NO:1531)

Mouse H11 light chain variable *complementarity determining regions 1* (*CDR1*)
sequence:

(DNA)
agatctagtcagaacattgtacatagtaatggaaacacctatttagaa (SEQ ID NO:1532)
(amino acids)
RSSQNIVHSNGNTYLE (SEQ ID NO:1533)

Mouse H11 light chain variable *framework 2* (*FR2*) sequence:
(DNA)
tggtacctgcagaaaccaggccagtctccaaagctcctgatctac (SEQ ID NO:1534)
(amino acids)
WYLQKPGQSPKLLIY (SEQ ID NO:1535)

Mouse H11 light chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
aaagtttccaaccgattttct (SEQ ID NO:1536)
(amino acids)
KVSNRFS (SEQ ID NO:1537)

Mouse H11 light chain variable *framework 3* (*FR3*) sequence:
(DNA)
ggggtccccgacaggttcagtggtagtgggtcagggacagatttcacactcaagatcagcagagtggaggctgaggatctgggagtttattactgc (SEQ ID NO:1538)
(amino acids)
GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYC (SEQ ID NO:1539)

Mouse H11 light chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
tttcaagattcacatgttcctctcacg (SEQ ID NO:1540)
(amino acids)
FQDSHVPLT (SEQ ID NO:1541)

Mouse H11 light chain variable *framework 4* (*FR4*) sequence:
(DNA)
ttcggtgctgggaccaggctggagctgaaa (SEQ ID NO:1542)
(amino acids)
FGAGTRLELK (SEQ ID NO:1543)

Mouse B9 heavy chain variable *framework 1* (*FW1*) sequence:
(DNA)
gaggtgcaggtggtggagtctgggggagacttagtgaagcctggagggtccctgaaactctcctgtgcagcctctggattcactttcagt (SEQ ID NO:1544)
(amino acids)
EVQVVESGGDLVKPGGSLKLSCAASGFTFS (SEQ ID NO:1545)

Mouse B9 heavy chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
agatatggcatgtct (SEQ ID NO:1546)
(amino acids)
RYGMS (SEQ ID NO:1547)

Mouse B9 heavy chain variable *framework 2* (*FW2*) sequence:
(DNA)
tgggttcgccagactccagacaagaggctggagtgggtcgca (SEQ ID NO:1548)
(amino acids)
WVRQTPDKRLEWVA (SEQ ID NO:1549)

Mouse B9 heavy chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
accattagtagtggtggtacttacatctactatccagacagtgtgaagggg (SEQ ID NO:1550)
(amino acids)
TISSGGTYIYYPDSVKG (SEQ ID NO:1551)

Mouse B9 heavy chain variable *framework 3* (*FW3*) sequence:
(DNA)
cgattcaccatctccagagacaatgccaagaacaccctgtacctgcaaatgagcagtctgaagtctgaggacacagccatgtattactgtgca (SEQ ID NO:1552)
(amino acids)
RFTISRDNAKNTLYLQMSSLKSEDTAMYYCAR (SEQ ID NO:1553)

Mouse B9 heavy chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
agggataactacggtagtagctacgactatgctatggactac (SEQ ID NO:1554)
(amino acids)
DNYGSSYDYAMDY (SEQ ID NO:1555)

Mouse B9 heavy chain variable *framework 4* (*FW4*) sequence:
(DNA)
tggggtcaaggaacctcagtcaccgtctcctct (SEQ ID NO:1556)
(amino acids)
WGQGTSVTVSS (SEQ ID NO:1557)

Mouse B9 light chain variable *framework 1* (*FR1*) sequence:
(DNA)
caaattgttctcacccagtctccagcaatcatgtctgcatctccaggggaggaggtcaccctaacctgc (SEQ ID NO:1558)
(amino acids)
QIVLTQSPAIMSASPGEEVTLTC (SEQ ID NO:1559)

Mouse B9 light chain variable *complementarity determining regions 1* (*CDR1*) sequence:
(DNA)
agtgccagctcaagtgtaagttacatgcac (SEQ ID NO:1560)
(amino acids)
SASSSVSYMH (SEQ ID NO:1561)

Mouse B9 light chain variable *framework 2* (*FR2*) sequence:
(DNA)
tggttccagcagaggccaggcacttctcccaaactctggatttat (SEQ ID NO:1562)
(amino acids)
WFQQRPGTSPKLWIY (SEQ ID NO:1563)

Mouse B9 light chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
accacatccaacctggcttct (SEQ ID NO:1564)
(amino acids)
TTSNLAS (SEQ ID NO:1565)

Mouse B9 light chain variable *framework 3* (*FR3*) sequence:
(DNA)

ggagtccctgctcgcttcagtggcagtggatctgggacctcttactctctcacaatcagccgaatggaggctgaagat
gctgccacttattactgc (SEQ ID NO:1566)
(amino acids)
GVPARFSGSGSGTSYSLTISRMEAEDAATYYC (SEQ ID NO:1567)

Mouse B9 light chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
cagcaaaggagtagttacccattc (SEQ ID NO:1568)
(amino acids)
QQRSSYPF (SEQ ID NO:1569)

Mouse B9 light chain variable *framework 4* (*FR4*) sequence:
(DNA)
acgttcggctcggggacaaagttggaaataaaa (SEQ ID NO:1570)
(amino acids)
TFGSGTKLEIK (SEQ ID NO:1571)

mu3C2B1 scFv sequence
(DNA)
Gaagtgatgctggtggagtctgggggaggcttagtgaagcctggagggtccctgaaactctcctgtgcagcctctgga
atcactttcagtacctataccatgtcgtgggttcgccagactccggagaagaggctggagtgggtcgcaaccattagt
actggtggtgataaaacctactattcagacagtgtgaagggtcgattcaccatctccagagacaatgccaagaacaac
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cctctcacgttcggtgctgggaccaagctggagctgaaa (SEQ ID NO:1572)
(amino acids)
EVMLVESGGGLVKPGGSLKLSCAASGITFSTYTMSWVRQTPEKRLEWVATISTGGDKTYYSDSVKGRFTISRDNAKN
NLYLQMSSLRSEDTALYYCARGTTAMYYYAMDYWGQGTSVTVSSGGGGSGGGGSGGGGSDIVLTQSPASLAVSLGQR
ATISCRASKSISTSDYNYIHWYQQKPGQPPKLLIYLASNLESGVPARFSGSGSGTDFTLNIHPVEEEDAATYYCQHS
RELPLTFGAGTKLELK (SEQ ID NO:1573)

mu20A10 scFv full sequence
(DNA)
gaagtgatgctggtggaatctggcggcggactggttaagcctggcggatctctgaagctgagctgtgccgccagcggc
ttcacctttagcacatacgccatgagctggatccggcagacccctgagaagagactggaatgggttgccagcatcggc
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agcctgacctttggcgccggaacaaagctggaactgaag (SEQ ID NO:1574)
(amino acids)
EVMLVESGGGLVKPGGSLKLSCAASGFTFSTYAMSWIRQTPEKRLEWVASIGRAGSTYYSDSVKGRFTISRDNVRNI
LYLQMSSLRSEDTAMYYCARGPIYNDYDEFAYWGQGTLVTVSAGGGGSGGGGSGGGGSNIMMTQSPSSLAVSAGEKV
TMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCHQ
YLSSLTFGAGTKLELK (SEQ ID NO:1575)

hu20A10M scFV
(DNA
gaggtgcagctggttgaatctggcggcggacttgtgaagcctggcggatctctgagactgagctgtgccgccagcggc
ttcacctttagcacatacgccatgagctgggtccgacaggcccctggaaaaggccttgaatgggttgcctctatcggc
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agcctgacctttggcggcggaacaaaggtggaaatcaag (SEQ ID NO:1576)
(amino acids)
EVQLVESGGGLVKPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVASIGRAGSTYYSDSVKGRFTISRDNAKNS
LYLQMNSLRAEDTAVYYCARGPIYNDYDEFAYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPSSLAVSLGERA
TISCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSLQAEDVAVYYCHQ
YLSSLTFGGGTKVEIK (SEQ ID NO:1577)

hu20A10C2 scFV
(DNA)
gaggtgcagctggttgaatctggcggcggacttgtgaagcctggcggatctctgagactgagctgtgccgccagcggc
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(amino acids)
EVQLVESGGGLVKPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVASIGRAGSTYYSDSVKGRFTISRDNAKNS
LYLQMNSLRAEDTAVYYCARGPIYNDYDEFAYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVLTQSPASLAVSPGQRA
TITCKSSQSVLYSSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPARFSGSGSGTDFTLTINPVEANDTANYYCHQ
YLSSLTFGGGTKVEIKR (SEQ ID NO:1579)

hu20A10N scFV
(DNA)
caggtgcagctggttgaatctggcggcggacttgtgaagcctggcggatctctgagactgagctgtgccgccagcggc
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ggcaccgatttcaccctgaccataagcagcctggaacctgaggacttcgccgtgtattactgccaccagtacctgagc
agcctgacctttggcggaggcaccaaggtggaaatcaagcgg (SEQ ID NO:1580)
(amino acids)
QVQLVESGGGLVKPGGSLRLSCAASGFTFSTYAMSWIRQAPGKGLEWVASIGRAGSTYYSDSVKGRFTISRDNAKNS
LYLQMNSLRAEDTAVYYCARGPIYNDYDEFAYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPATLSLSPGERA
TLSCKSSQSVLYSSNQKNYLAWYQQKPGQAPRLLIYWASTRESGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCHQ
YLSSLTFGGGTKVEIKR (SEQ ID NO:1581)

mu20A10-CAR T-8-4-1BB-3z
(DNA)

atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccggaagtgatgctggtg
gaatctggcggcggactggttaagcctggcggatctctgaagctgagctgtgccgccagcggcttcacctttagcaca
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(SEQ ID NO:1582)
(amino acis)
MALPVTALLLPLALLLHAARPEVMLVESGGGLVKPGGSLKLSCAASGFTFSTYAMSWIRQTPEKRLEWVASIGRAGS
TYYSDSVKGRFTISRDNVRNILYLQMSSLRSEDTAMYYCARGPIYNDYDEFAYWGQGTLVTVSAGGGGSGGGGSGGG
GSNIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGT
DFTLTISSVQAEDLAVYYCHQYLSSLTFGAGTKLELKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGL
DFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSR
SADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRG
KGHDGLYQGLSTATKDTYDALHMQALPPR** (SEQ ID NO:1583)

hu20A10-CAR T-8-4-1BB-3z
(DNA)
atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccggaggtgcagctggtt
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(SEQ ID NO:1584)
(amino acids)
MALPVTALLLPLALLLHAARPEVQLVESGGGLVKPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVASIGRAGS
TYYSDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGPIYNDYDEFAYWGQGTLVTVSSGGGGSGGGGSGGG
GSDIVLTQSPASLAVSPGQRATITCKSSQSVLYSSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPARFSGSGSGT
DFTLTINPVEANDTANYYCHQYLSSLTFGGGTKVEIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRG
LDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFS

RSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRR
GKGHDGLYQGLSTATKDTYDALHMQALPPR** (SEQ ID NO:1585)

mu20A10-CAR T-8-28-3z
(DNA)
atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccggaagtgatgctggtg
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ID NO:1586)
(amino acids)
MALPVTALLLPLALLLHAARPEVMLVESGGGLVKPGGSLKLSCAASGFTFSTYAMSWIRQTPEKRLEWVASIGRAGS
TYYSDSVKGRFTISRDNVRNILYLQMSSLRSEDTAMYYCARGPIYNDYDEFAYWGQGTLVTVSAGGGGSGGGGSGGG
GSNIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGT
DFTLTISSVQAEDLAVYYCHQYLSSLTFGAGTKLELKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGL
DFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRS
ADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK
GHDGLYQGLSTATKDTYDALHMQALPPR** (SEQ ID NO:1587)

hu20A10-CAR T-8-28-3z
(DNA)
atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccggaggtgcagctggtt
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(SEQ ID NO:1588)
(amino acids)

MALPVTALLLPLALLLHAARPEVQLVESGGGLVKPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVASIGRAGS
TYYSDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGPIYNDYDEFAYWGQGTLVTVSSGGGGSGGGGSGGG
GSDIVLTQSPASLAVSPGQRATITCKSSQSVLYSSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPARFSGSGSGT
DFTLTINPVEANDTANYYCHQYLSSLTFGGGTKVEIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRG
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SADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRG
KGHDGLYQGLSTATKDTYDALHMQALPPR** (SEQ ID NO:1589)

mu20A10-CAR T-8-4-1BB-3z-1XX
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(SEQ ID NO:1590)
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GSNIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGT
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SADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLFNELQKDKMAEAFSEIGMKGERRRG
KGHDGLFQGLSTATKDTFDALHMQALPPR** (SEQ ID NO:1591)

hu20A10-CAR T-8-4-1BB-3z-1XX
(DNA)
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(SEQ ID NO:1592)
(amino acids)
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GSDIVLTQSPASLAVSPGQRATITCKSSQSVLYSSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPARFSGSGSGT
DFTLTINPVEANDTANYYCHQYLSSLTFGGGTKVEIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRG
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RSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLFNELQKDKMAEAFSEIGMKGERRR
GKGHDGLFQGLSTATKDTFDALHMQALPPR** (SEQ ID NO:1593)

mu20A10-CAR T-8-28-3z-1XX
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(amino acids)
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GSNIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGT
DFTLTISSVQAEDLAVYYCHQYLSSLTFGAGTKLELKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGL
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ADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLFNELQKDKMAEAFSEIGMKGERRRGK
GHDGLFQGLSTATKDTFDALHMQALPPR** (SEQ ID NO:1595)

hu20A10-CAR T-8-28-3z-1XX
(DNA)
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(SEQ ID NO:1596)
(amino acids)
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TYYSDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGPIYNDYDEFAYWGQGTLVTVSSGGGGSGGGGSGGG
GSDIVLTQSPASLAVSPGQRATITCKSSQSVLYSSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPARFSGSGSGT
DFTLTINPVEANDTANYYCHQYLSSLTFGGGTKVEIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRG
LDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSR
SADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLFNELQKDKMAEAFSEIGMKGERRRG
KGHDGLFQGLSTATKDTFDALHMQALPPR** (SEQ ID NO:1597)

25E6
mu25E6 scFv full sequence
(DNA)
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(amino acids)
EVQLVESGGDLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISNGGRHTFYPDSVKGRFTISRDNAKN
TLYLQMSSLKSEDTAMYLCVRQTGTEGWFAYWGQGTLVTVSAGGGGSGGGGSGGGGSDVVMTQTPLTLSVTIGQPAS
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hu25E6 full sequence
(DNA)
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(amino acids)
EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYGMSWVRQAPGKGLEWVSTISNGGRHTFYPDSVKGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARQTGTEGWFAYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPAS
ISCKSSQSLLDSDGKTYLNWYLQKPGQSPQLLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGT
HFPQTFGQGTKVEIK (SEQ ID NO:1601)

mu25E6-CAR T-8-4-1BB-3z

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ID NO:1602)
(amino acids)
MALPVTALLLPLALLLHAARPEVQLVESGGDLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISNGGR
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ADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK
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(amino acids)
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SDIVMTQTPLSLSVTPGQPASISCKSSQSLLDSDGKTYLNWYLQKPGQSPQLLIYLVSKLDSGVPDRFSGSGSGTDF
TLKISRVEAEDVGVYYCWQGTHFPQTFGQGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLD
FACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRS

ADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK
GHDGLYQGLSTATKDTYDALHMQALPPR** (SEQ ID NO:1605)

mu25E6-CAR T-8-28-3z
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NO:1606)
(amino acids)
MALPVTALLLPLALLLHAARPEVQLVESGGDLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISNGGR
HTFYPDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYLCVRQTGTEGWFAYWGQGTLVTVSAGGGGSGGGGSGGGG
SDVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDF
TLKISRVEAEDLGVYYCWQGTHFPQTFGGGTKLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLD
FACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSA
DAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKG
HDGLYQGLSTATKDTYDALHMQALPPR** (SEQ ID NO:1607)

hu25E6-CAR T-8-28-3z
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NO:1608)
(amino acids)

MALPVTALLLPLALLLHAARPEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYGMSWVRQAPGKGLEWVSTISNGGR
HTFYPDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARQTGTEGWFAYWGQGTLVTVSSGGGGSGGGGSGGGG
SDIVMTQTPLSLSVTPGQPASISCKSSQSLLDSDGKTYLNWYLQKPGQSPQLLIYLVSKLDSGVPDRFSGSGSGTDF
TLKISRVEAEDVGVYYCWQGTHFPQTFGQGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLD
FACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSA
DAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKG
HDGLYQGLSTATKDTYDALHMQALPPR** (SEQ ID NO:1609)

mu25E6-CAR T-8-4-1BB-3z-1XX
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ID NO:1610)
(amino acids)
MALPVTALLLPLALLLHAARPEVQLVESGGDLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISNGGR
HTFYPDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYLCVRQTGTEGWFAYWGQGTLVTVSAGGGGSGGGGSGGGG
SDVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDF
TLKISRVEAEDLGVYYCWQGTHFPQTFGGGTKLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLD
FACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRS
ADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLFNELQKDKMAEAFSEIGMKGERRRGK
GHDGLFQGLSTATKDTFDALHMQALPPR** (SEQ ID NO:1611)

hu25E6-CAR T-8-4-1BB-3z-1XX
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(amino acids)
MALPVTALLLPLALLLHAARPEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYGMSWVRQAPGKGLEWVSTISNGGR
HTFYPDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARQTGTEGWFAYWGQGTLVTVSSGGGGSGGGGSGGGG
SDIVMTQTPLSLSVTPGQPASISCKSSQSLLDSDGKTYLNWYLQKPGQSPQLLIYLVSKLDSGVPDRFSGSGSGTDF
TLKISRVEAEDVGVYYCWQGTHFPQTFGQGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLD
FACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRS
ADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLFNELQKDKMAEAFSEIGMKGERRRGK
GHDGLFQGLSTATKDTFDALHMQALPPR** (SEQ ID NO:1613)

mu25E6-CAR T-8-28-3z-1XX
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(amino acids)
MALPVTALLLPLALLLHAARPEVQLVESGGDLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISNGGR
HTFYPDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYLCVRQTGTEGWFAYWGQGTLVTVSAGGGGSGGGGSGGGG
SDVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDF
TLKISRVEAEDLGVYYCWQGTHFPQTFGGGTKLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLD
FACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSA
DAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLFNELQKDKMAEAFSEIGMKGERRRGKG
HDGLFQGLSTATKDTFDALHMQALPPR** (SEQ ID NO:1615)

hu25E6-CAR T-8-28-3z-1XX
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NO:1616)
(amino acids)
MALPVTALLLPLALLLHAARPEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYGMSWVRQAPGKGLEWVSTISNGGR
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SDIVMTQTPLSLSVTPGQPASISCKSSQSLLDSDGKTYLNWYLQKPGQSPQLLIYLVSKLDSGVPDRFSGSGSGTDF
TLKISRVEAEDVGVYYCWQGTHFPQTFGQGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLD
FACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSA
DAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLFNELQKDKMAEAFSEIGMKGERRRGKG
HDGLFQGLSTATKDTFDALHMQALPPR** (SEQ ID NO:1617)

MNC2-1XX
muMNC2-CAR T-8-4-1BB-3z-1XX
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(amino acids)
MALPVTALLLPLALLLHAARPEVQLEESGGGLVKPGGSLKLSCAASGFTFSGYAMSWVRQTPEKRLEWVATISSGGT
YIYYPDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCARLGGDNYYEYFDVWGAGTTVTVSSAKTTPPSVYGGG
GSGGGGSGGGGSDIVITQSTASLGVSLGQRATISCRASKSVSTSGYSYMHWYQQRPGQPPKLLIYLASNLESGVPAR
FSGSGSGTDFTLNIHPVEEEDAATYYCQHSRELPFTFGGGTKLEIKRADAAPTVSTTTPAPRPPTPAPTIASQPLSL
RPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSC
RFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLFNELQKD
KMAEAFSEIGMKGERRRGKGHDGLFQGLSTATKDTFDALHMQALPPR** (SEQ ID NO:1619)

huMNC2-CAR T-8-4-1BB-3z-1XX
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taa (SEQ ID NO:1620)
(amino acids)
MALPVTALLLPLALLLHAARPEVQLVESGGGLVKPGGSLRLSCAASGFTFSGYAMSWVRQAPGKGLEWVSTISSGGT
YIYYPDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARLGGDNYYEYFDVWGKGTTVTVSSGGGGSGGGGSGG
GGSDIVLTQSPASLAVSPGQRATITCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLASNLESGVPARFSGSGSGTD
FTLTINPVEANDTANYYCQHSRELPFTFGGGTKVEIKRTTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTR
GLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKF
SRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLFNELQKDKMAEAFSEIGMKGERR
RGKGHDGLFQGLSTATKDTFDALHMQALPPR** (SEQ ID NO:1621)

muMNC2-CAR T-8-28-3z-1XX
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(amino acids)
MALPVTALLLPLALLLHAARPEVQLEESGGGLVKPGGSLKLSCAASGFTFSGYAMSWVRQTPEKRLEWVATISSGGT
YIYYPDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCARLGGDNYYEYFDVWGAGTTVTVSSAKTTPPSVYGGG
GSGGGGSGGGGSDIVITQSTASLGVSLGQRATISCRASKSVSTSGYSYMHWYQQRPGQPPKLLIYLASNLESGVPAR
FSGSGSGTDFTLNIHPVEEEDAATYYCQHSRELPFTFGGGTKLEIKRADAAPTVSTTTPAPRPPTPAPTIASQPLSL
RPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPY
APPRDFAAYRSRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLFNELQKDK
MAEAFSEIGMKGERRRGKGHDGLFQGLSTATKDTFDALHMQALPPR** (SEQ ID NO:1623)

huMNC2-CAR T-8-28-3z-1XX
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(SEQ ID NO:1624)
(amino acids)
MALPVTALLLPLALLLHAARPEVQLVESGGGLVKPGGSLRLSCAASGFTFSGYAMSWVRQAPGKGLEWVSTISSGGT
YIYYPDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARLGGDNYYEYFDVWGKGTTVTVSSGGGGSGGGGSGG
GGSDIVLTQSPASLAVSPGQRATITCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLASNLESGVPARFSGSGSGTD
FTLTINPVEANDTANYYCQHSRELPFTFGGGTKVEIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTR
GLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFS
RSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLFNELQKDKMAEAFSEIGMKGERRR
GKGHDGLFQGLSTATKDTFDALHMQALPPR** (SEQ ID NO:1625)

MNE6-1XX
muMNE6-CAR T-8-4-1BB-3z-1XX
atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccggaggtgaaggtggtg
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NO:1626)
(amino acids)
MALPVTALLLPLALLLHAARPEVKVVESGGDLVKPGGSLKLSCVVSGFTFSRYGMSWVRQTPGKRLEWVATISGGGT
YIYYPDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYHCTRDNYGRNYDYGMDYWGQGTSVTVSSGGGGSGGGGSG
GGGSQIVLTQSPAIMSASPGEEVTLTCSATSSVSYIHWFQQRPGTSPKLWIYSTSNLASGVPVRFSGSGYGTSYSLT
ISRMEAEDAATYYCQQRSSSPFTFGSGTKLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFAC
DIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADA
PAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLFNELQKDKMAEAFSEIGMKGERRRGKGHD
GLFQGLSTATKDTFDALHMQALPPR** (SEQ ID NO:1627)

huMNE6-CAR T-8-4-1BB-3z-1XX
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NO:1628)
(amino acids)
MALPVTALLLPLALLLHAARPEVQLVESGGGLVKPGGSLRLSCAASGFTFSRYGMSWVRQAPGKRLEWVSTISGGGT
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GGGSEIVLTQSPATLSLSPGERATLTCSATSSVSYIHWYQQRPGQSPRLLIYSTSNLASGIPARFSGSGSGSDYTLT
ISSLEPEDFAVYYCQQRSSSPFTFGSGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFAC
DIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADA
PAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLFNELQKDKMAEAFSEIGMKGERRRGKGHD
GLFQGLSTATKDTFDALHMQALPPR** (SEQ ID NO:1629)

muMNE6-CAR T-8-4-28-3z-1XX
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(amino acids)
MALPVTALLLPLALLLHAARPEVKVVESGGDLVKPGGSLKLSCVVSGFTFSRYGMSWVRQTPGKRLEWVATISGGGT
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GGGSQIVLTQSPAIMSASPGEEVTLTCSATSSVSYIHWFQQRPGTSPKLWIYSTSNLASGVPVRFSGSGYGTSYSLT
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DIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAP
AYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLFNELQKDKMAEAFSEIGMKGERRRGKGHDG
LFQGLSTATKDTFDALHMQALPPR** (SEQ ID NO:1631)

huMNE6-CAR T-8-4-28-3z-1XX

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(amino acids)
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GGGSEIVLTQSPATLSLSPGERATLTCSATSSVSYIHWYQQRPGQSPRLLIYSTSNLASGIPARFSGSGSGSDYTLT
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AYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLFNELQKDKMAEAFSEIGMKGERRRGKGHDG
LFQGLSTATKDTFDALHMQALPPR** (SEQ ID NO:1633)

Minimal CMV promoter (mCMV)
(DNA)
taggcgtgtacggtgggaggcctatataagcagagctcgtttagtgaaccgtcagatcgcctggagacgccatccacg
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Minimal IL2 promoter (mIL2P)
cattttgacacccccataatatttttccagaattaacagtataaattgcatctcttgttcaagagttccctatcactc
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Minimal promoter, miniP
(DNA)
Agagggtatataatggaagctcgacttccag (SEQ ID NO:1636)

IL-18 activated
(DNA)
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Best antibodies with inducible IL-18 +/- 1XX mutations in ITAMs of CD3-zeta
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hu25E6-8-28-3z1XX-Foxp3-NFAT-IL-18
(DNA)
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tcaccgtgcagaacgaggactgataa (SEQ ID NO:1674)

Construct Name:	**pCDH MSCV h20A10-O CAR 41BB**
Construct backbone:	**pCDH CMV MCS (SBI)**
Promoter	**MSCV**
Leader sequence:	**Human CD8 alpha (1- 63)**
scFv Name:	**Humanized 20A10-O (64 - 807)**
Hinge region:	**Human CD8 alpha (808 - 942)**
Transmembrane Domain:	**Human CD8 alpha (943 - 1014)**
Costimulatory Domains:	**Human 41BB (1015 - 1140) and CD3 zeta (1141 - 1476)**

atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccggaggtgcagctggtt
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cccgcgtacaagcagggccagaaccagctctataacgagctcaatctaggacgaagagaggagtacgatgttttggac
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cagaaagataagatggcggaggcctacagtgagattgggatgaaaggcgagcgccggaggggcaaggggcacgatggc
ctttaccagggtctcagtacagccaccaaggacacctacgacgcccttcacatgcaggccctgccccctcgctgataa
(SEQ ID NO:1675)

CD8 leader sequence
ATGGCCTTACCAGTGACCGCCTTGCTCCTGCCGCTGGCCTTGCTGCTCCACGCCGCCAGGCCG (SEQ ID NO:1676)

h20A10-O scFV
GAGGTGCAGCTGGTTGAATCTGGCGGCGGACTTGTGAAGCCTGGCGGATCTCTGAGACTGAGCTGTGCCGCCAGCGGC
TTCACCTTTAGCACATACGCCATGAGCTGGGTCCGACAGGCCCCTGGAAAAGGCCTTGAATGGGTTGCCTCTATCGGC
AGAGCCGGCAGCACCTACTACAGCGATTCTGTGAAGGGCAGATTCACCATCAGCCGGGACAACGCCAAGAACAGCCTG
TACCTGCAGATGAACTCCCTGAGAGCCGAGGACACCGCCGTGTACTATTGTGCCAGAGGACCCATCTACAACGACTAC
GACGAGTTCGCCTATTGGGGCCAGGGCACACTGGTCACAGTCAGCTCTGGCGGTGGCGGAagcGGAGGCGGTGGCtcc
GGTGGCGGAGGCagcGACATCGTGATGACACAGAGCCCTGATAGCCTGGCCGTGTCTCTGGGAGAGAGAGCCACCATC
AACTGCAAGAGCAGCCAGAGCGTGCTGTACTCCAGCAACCAGAAGAACTACCTGGCCTGGTATCAGCAGAAGCCCGGC
CAGCCTCCTAAGCTGCTGATCTACTGGGCCAGCACCAGAGAAAGCGGCGTGCCCGATAGATTTTCTGGCAGCGGCTCT
GGCACCGACTTCACCCTGACAATTAGCTCCCTGCAGGCCGAGGATGTGGCCGTGTACTACTGTCACCAGTACCTGAGC
AGCCTGACCTTTGGCGGCGGAACAAAGGTGGAAATCAAGcga (SEQ ID NO:1677)
CD8 hinge region
ACAACAACCCCTGCCCCCAGACCTCCTACCCCAGCCCCTACAATTGCCAGCCAGCCTCTGAGCCTGAGGCCCGAGGCT
TGTAGACCTGCTGCTGGCGGAGCCGTGCACACCAGAGGACTGGATTTCGCCTGCGAC(SEQ ID NO:1678)
CD8 transmembrane domain
ATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCCTTCTCCTGTCACTGGTTATCACCCTTTACTGC(SEQ ID NO:1675)
41BB
AAACGGGGCAGAAAGAAACTCCTGTATATATTCAAACAACCATTTATGAGACCAGTACAAACTACTCAAGAGGAAGAT
GGCTGTAGCTGCCGATTTCCAGAAGAAGAAGAAGGAGGATGTGAACTG(SEQ ID NO:1676)
CD3
AGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGCGTACAAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATCTA
GGACGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAG
AACCCTCAGGAAGGCCTGTACAATGAACTGCAGAAAGATAAGATGGCGGAGGCCTACAGTGAGATTGGGATGAAAGGC
GAGCGCCGGAGGGGCAAGGGGCACGATGGCCTTTACCAGGGTCTCAGTACAGCCACCAAGGACACCTACGACGCCCTT
CACATGCAGGCCCTGCCCCCTCGCTGATAA (SEQ ID NO:1677)

Construct Name:	**pCDH MSCV h20A10-N CAR 41BB**
Construct backbone:	**pCDH CMV MCS (SBI)**
Promoter	**MSCV**
Leader sequence:	**Human CD8 alpha (1- 63)**
scFv Name:	**Humanized 20A10-N (64 - 807)**
Hinge region:	**Human CD8 alpha (808 - 942)**
Transmembrane Domain:	**Human CD8 alpha (943 - 1014)**
Costimulatory Domains:	**Human 41BB (1015 - 1140) and CD3 zeta (1141 - 1476)**

ATGGCCTTACCAGTGACCGCCTTGCTCCTGCCGCTGGCCTTGCTGCTCCACGCCGCCAGGCCGCAGGTGCAGCTGGTT
GAATCTGGCGGCGGACTTGTGAAGCCTGGCGGATCTCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCTTTAGCACA
TACGCCATGAGCTGGATCAGACAGGCCCCTGGCAAAGGCCTGGAATGGGTGgcgTCTATTGGCAGAGCCGGCAGCACC
TACTACAGCGACTCTGTGAAGGGCAGATTCACCATCAGCCGGGACAACGCCAAGAACAGCCTGTACCTGCAGATGAAC
TCCCTGAGAGCCGAGGACACCGCCGTGTACTATTGTGCCAGAGGACCCATCTACAACGACTACGACGAGTTCGCCTAT
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CAGAGCGTGCTGTACTCCAGCAACCAGAAGAACTACCTGGCCTGGTATCAGCAGAAGCCCGGCCAAGCTCCTCGGCTG
CTGATCTATTGGGCCAGCACAAGAGAGAGCGGCATCCCTGCCAGATTTTCTGGCAGCGGCTCTGGCACCGATTTCACC
CTGACCATAAGCAGCCTGGAACCTGAGGACTTCGCCGTGTATTACTGCCACCAGTACCTGAGCAGCCTGACCTTTGGC
GGAGGCACCAAGGTGGAAATCAAGCGGACAACAACCCCTGCCCCCAGACCTCCTACCCCAGCCCCTACAATTGCCAGC
CAGCCTCTGAGCCTGAGGCCCGAGGCTTGTAGACCTGCTGCTGGCGGAGCCGTGCACACCAGAGGACTGGATTTCGCC
TGCGACATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCCTTCTCCTGTCACTGGTTATCACCCTTTACTGC
AAACGGGGCAGAAAGAAACTCCTGTATATATTCAAACAACCATTTATGAGACCAGTACAAACTACTCAAGAGGAAGAT
GGCTGTAGCTGCCGATTTCCAGAAGAAGAAGAAGGAGGATGTGAACTGAGAGTGAAGTTCAGCAGGAGCGCAGACGCC
CCCGCGTACAAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATCTAGGACGAAGAGAGGAGTACGATGTTTTGGAC
AAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGAACCCTCAGGAAGGCCTGTACAATGAACTG
CAGAAAGATAAGATGGCGGAGGCCTACAGTGAGATTGGGATGAAAGGCGAGCGCCGGAGGGGCAAGGGGCACGATGGC
CTTTACCAGGGTCTCAGTACAGCCACCAAGGACACCTACGACGCCCTTCACATGCAGGCCCTGCCCCCTCGCTGATAA
(SEQ ID NO: 1678)

CD8 leader sequence
ATGGCCTTACCAGTGACCGCCTTGCTCCTGCCGCTGGCCTTGCTGCTCCACGCCGCCAGGCCG (SEQ ID NO: 1679)
h20A10-N scFV
CAGGTGCAGCTGGTTGAATCTGGCGGCGGACTTGTGAAGCCTGGCGGATCTCTGAGACTGAGCTGTGCCGCCAGCGGC
TTCACCTTTAGCACATACGCCATGAGCTGGATCAGACAGGCCCCTGGCAAAGGCCTGGAATGGGTGgcgTCTATTGGC
AGAGCCGGCAGCACCTACTACAGCGACTCTGTGAAGGGCAGATTCACCATCAGCCGGGACAACGCCAAGAACAGCCTG
TACCTGCAGATGAACTCCCTGAGAGCCGAGGACACCGCCGTGTACTATTGTGCCAGAGGACCCATCTACAACGACTAC
GACGAGTTCGCCTATTGGGGCCAGGGCACACTGGTCACAGTTTCTAGCGGCGGTGGCGGAagcGGAGGCGGTGGCtcc
GGTGGCGGAGGCagcGAAATTGTGCTGACACAGAGCCCCGCCACACTGTCACTTTCTCCAGGCGAAAGAGCCACACTG
AGCTGCAAGAGCAGCCAGAGCGTGCTGTACTCCAGCAACCAGAAGAACTACCTGGCCTGGTATCAGCAGAAGCCCGGC
CAAGCTCCTCGGCTGCTGATCTATTGGGCCAGCACAAGAGAGAGCGGCATCCCTGCCAGATTTTCTGGCAGCGGCTCT
GGCACCGATTTCACCCTGACCATAAGCAGCCTGGAACCTGAGGACTTCGCCGTGTATTACTGCCACCAGTACCTGAGC
AGCCTGACCTTTGGCGGAGGCACCAAGGTGGAAATCAAGCGG (SEQ ID NO: 1680)
CD8 hinge region
ACAACAACCCCTGCCCCCAGACCTCCTACCCCAGCCCCTACAATTGCCAGCCAGCCTCTGAGCCTGAGGCCCGAGGCT
TGTAGACCTGCTGCTGGCGGAGCCGTGCACACCAGAGGACTGGATTTCGCCTGCGAC (SEQ ID NO: 1681)
CD8 transmembrane domain
ATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCCTTCTCCTGTCACTGGTTATCACCCTTTACTGC (SEQ ID NO: 1682)
41BB
AAACGGGGCAGAAAGAAACTCCTGTATATATTCAAACAACCATTTATGAGACCAGTACAAACTACTCAAGAGGAAGAT
GGCTGTAGCTGCCGATTTCCAGAAGAAGAAGAAGGAGGATGTGAACTG (SEQ ID NO: 1683)
CD3

AGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGCGTACAAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATCTAGGACGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGAACCCTCAGGAAGGCCTGTACAATGAACTGCAGAAAGATAAGATGGCGGAGGCCTACAGTGAGATTGGGATGAAAGGCGAGCGCCGGAGGGGCAAGGGGCACGATGGCCTTTACCAGGGTCTCAGTACAGCCACCAAGGACACCTACGACGCCCTTCACATGCAGGCCCTGCCCCCTCGCTGATAA (SEQ ID NO: 1684)

Construct Name:	**pCDH MSCV h20A10-C2 CAR 41BB**
Construct backbone:	**pCDH CMV MCS (SBI)**
Promoter	**MSCV**
Leader sequence:	**Human CD8 alpha (1- 63)**
scFv Name:	**Humanized 20A10-C2 (64 - 807)**
Hinge region:	**Human CD8 alpha (808 - 942)**
Transmembrane Domain:	**Human CD8 alpha (943 - 1014)**
Costimulatory Domains:	**Human 41BB (1015 - 1140) and CD3 zeta (1141 - 1476)**

ATGGCCTTACCAGTGACCGCCTTGCTCCTGCCGCTGGCCTTGCTGCTCCACGCCGCCAGGCCGGAGGTGCAGCTGGTT
GAATCTGGCGGCGGACTTGTGAAGCCTGGCGGATCTCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCTTTAGCACA
TACGCCATGAGCTGGGTCCGACAGGCCCCTGGAAAAGGCCTTGAATGGGTTGCCTCTATCGGCAGAGCCGGCAGCACC
TACTACAGCGATTCTGTGAAGGGCAGATTCACCATCAGCCGGGACAACGCCAAGAACAGCCTGTACCTGCAGATGAAC
TCCCTGAGAGCCGAGGACACCGCCGTGTACTATTGTGCCAGAGGACCCATCTACAACGACTACGACGAGTTCGCCTAT
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ctcacaattaatcctgtggaagctaatgatactgcaaattattactgtCACCAGTACCTGAGCAGCCTGACCTTCGGC
GGAGGGACCAAGGTGGAGATCAAACGAACAACAACCCCTGCCCCCAGACCTCCTACCCCAGCCCCTACAATTGCCAGC
CAGCCTCTGAGCCTGAGGCCCGAGGCTTGTAGACCTGCTGCTGGCGGAGCCGTGCACACCAGAGGACTGGATTTCGCC
TGCGACATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCCTTCTCCTGTCACTGGTTATCACCCTTTACTGC
AAACGGGGCAGAAAGAAACTCCTGTATATATTCAAACAACCATTTATGAGACCAGTACAAACTACTCAAGAGGAAGAT
GGCTGTAGCTGCCGATTTCCAGAAGAAGAAGAAGGAGGATGTGAACTGAGAGTGAAGTTCAGCAGGAGCGCAGACGCC
CCCGCGTACAAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATCTAGGACGAAGAGAGGAGTACGATGTTTTGGAC
AAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGAACCCTCAGGAAGGCCTGTACAATGAACTG
CAGAAAGATAAGATGGCGGAGGCCTACAGTGAGATTGGGATGAAAGGCGAGCGCCGGAGGGGCAAGGGGCACGATGGC
CTTTACCAGGGTCTCAGTACAGCCACCAAGGACACCTACGACGCCCTTCACATGCAGGCCCTGCCCCCTCGCTGATAA
(SEQ ID NO:1685)

CD8 leader sequence
ATGGCCTTACCAGTGACCGCCTTGCTCCTGCCGCTGGCCTTGCTGCTCCACGCCGCCAGGCCG (SEQ ID NO: 1686)

h20A10-C2 scFV
GAGGTGCAGCTGGTTGAATCTGGCGGCGGACTTGTGAAGCCTGGCGGATCTCTGAGACTGAGCTGTGCCGCCAGCGGC
TTCACCTTTAGCACATACGCCATGAGCTGGGTCCGACAGGCCCCTGGAAAAGGCCTTGAATGGGTTGCCTCTATCGGC
AGAGCCGGCAGCACCTACTACAGCGATTCTGTGAAGGGCAGATTCACCATCAGCCGGGACAACGCCAAGAACAGCCTG
TACCTGCAGATGAACTCCCTGAGAGCCGAGGACACCGCCGTGTACTATTGTGCCAGAGGACCCATCTACAACGACTAC
GACGAGTTCGCCTATTGGGGCCAGGGCACACTGGTCACAGTCAGCTCTGGCGGTGGCGGAagcGGAGGCGGTGGCtcc
GGTGGCGGAGGCagcgacattgtgctgacccagtctccagcctccttggccgtgtctccaggacagagggccaccatc
acctgcAAGAGCAGCCAGAGCGTGCTGTACTCCAGCAACCAGAAGAACTACCTGGCCtggtatcagcagaaaccagga
caacctcctaaactcctgatttacTGGGCCAGCACCAGAGAAAGCggggtcccagccaggttcagcggcagtgggtct
gggaccgatttcaccctcacaattaatcctgtggaagctaatgatactgcaaattattactgtCACCAGTACCTGAGC
AGCCTGACCTTCGGCGGAGGGACCAAGGTGGAGATCAAACGA (SEQ ID NO: 1687)

CD8 hinge region
ACAACAACCCCTGCCCCCAGACCTCCTACCCCAGCCCCTACAATTGCCAGCCAGCCTCTGAGCCTGAGGCCCGAGGCT
TGTAGACCTGCTGCTGGCGGAGCCGTGCACACCAGAGGACTGGATTTCGCCTGCGAC (SEQ ID NO: 1688)

CD8 transmembrane region
ATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCCTTCTCCTGTCACTGGTTATCACCCTTTACTGC (SEQ ID NO: 1689)

41BB
AAACGGGGCAGAAAGAAACTCCTGTATATATTCAAACAACCATTTATGAGACCAGTACAAACTACTCAAGAGGAAGAT
GGCTGTAGCTGCCGATTTCCAGAAGAAGAAGAAGGAGGATGTGAACTG (SEQ ID NO: 1690)

CD3

AGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGCGTACAAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATCTA
GGACGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAG
AACCCTCAGGAAGGCCTGTACAATGAACTGCAGAAAGATAAGATGGCGGAGGCCTACAGTGAGATTGGGATGAAAGGC
GAGCGCCGGAGGGGCAAGGGGCACGATGGCCTTTACCAGGGTCTCAGTACAGCCACCAAGGACACCTACGACGCCCTT
CACATGCAGGCCCTGCCCCCTCGCTGATAA (SEQ ID NO: 1691)

Construct Name:	**pCDH MSCV h20A10-O CAR CD28 1XX**
Construct backbone:	**pCDH CMV MCS (SBI)**
Promoter	**MSCV**
Leader sequence:	**Human CD8 alpha (1- 63)**
scFv Name:	**Humanized 20A10-O (64 - 807)**
Hinge region:	**Human CD8 alpha (808 - 942)**
Transmembrane Domain:	**Human CD8 alpha (943 - 1014)**
Costimulatory Domains:	**Human CD28 (1015 - 1137) and CD3 zeta 1XX (1138 - 1473)**

ATGGCCTTACCAGTGACCGCCTTGCTCCTGCCGCTGGCCTTGCTGCTCCACGCCGCCAGGCCGGAGGTGCAGCTGGTT
GAATCTGGCGGCGGACTTGTGAAGCCTGGCGGATCTCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCTTTAGCACA
TACGCCATGAGCTGGGTCCGACAGGCCCCTGGAAAAGGCCTTGAATGGGTTGCCTCTATCGGCAGAGCCGGCAGCACC
TACTACAGCGATTCTGTGAAGGGCAGATTCACCATCAGCCGGGACAACGCCAAGAACAGCCTGTACCTGCAGATGAAC
TCCCTGAGAGCCGAGGACACCGCCGTGTACTATTGTGCCAGAGGACCCATCTACAACGACTACGACGAGTTCGCCTAT
TGGGGCCAGGGCACACTGGTCACAGTCAGCTCTGGCGGTGGCGGAagcGGAGGCGGTGGCtccGGTGGCGGAGGCagc
GACATCGTGATGACACAGAGCCCTGATAGCCTGGCCGTGTCTCTGGGAGAGAGAGCCACCATCAACTGCAAGAGCAGC
CAGAGCGTGCTGTACTCCAGCAACCAGAAGAACTACCTGGCCTGGTATCAGCAGAAGCCCGGCCAGCCTCCTAAGCTG
CTGATCTACTGGGCCAGCACCAGAGAAAGCGGCGTGCCCGATAGATTTTCTGGCAGCGGCTCTGGCACCGACTTCACC
CTGACAATTAGCTCCCTGCAGGCCGAGGATGTGGCCGTGTACTACTGTCACCAGTACCTGAGCAGCCTGACCTTTGGC
GGCGGAACAAAGGTGGAAATCAAGcgaACAACAACCCCTGCCCCCAGACCTCCTACCCCAGCCCCTACAATTGCCAGC
CAGCCTCTGAGCCTGAGGCCCGAGGCTTGTAGACCTGCTGCTGGCGGAGCCGTGCACACCAGAGGACTGGATTTCGCC
TGCGACATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCCTTCTCCTGTCACTGGTTATCACCCTTTACTGC
AGGAGTAAGAGGAGCAGGCTCCTGCACAGTGACTACATGAACATGACTCCTAGAAGACCTGGGCCTACCAGAAAGCAT
TACCAGCCCTATGCCCCACCACGCGACTTCGCAGCCTATCGCTCCAGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCC
GCGTACAAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATCTAGGACGAAGAGAGGAGTACGATGTTTTGGACAAG
AGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGAACCCTCAGGAAGGCCTGTtCAATGAACTGCAG
AAAGATAAGATGGCGGAGGCCTtCAGTGAGATTGGGATGAAAGGCGAGCGCCGGAGGGGCAAGGGGCACGATGGCCTT
TtCCAGGGTCTCAGTACAGCCACCAAGGACACCTtCGACGCCCTTCACATGCAGGCCCTGCCCCCTCGCTGATAA
(SEQ ID NO:1692)

CD8 leader sequence
ATGGCCTTACCAGTGACCGCCTTGCTCCTGCCGCTGGCCTTGCTGCTCCACGCCGCCAGGCCG (SEQ ID NO: 1693)
h20A10-O scFV
GAGGTGCAGCTGGTTGAATCTGGCGGCGGACTTGTGAAGCCTGGCGGATCTCTGAGACTGAGCTGTGCCGCCAGCGGC
TTCACCTTTAGCACATACGCCATGAGCTGGGTCCGACAGGCCCCTGGAAAAGGCCTTGAATGGGTTGCCTCTATCGGC
AGAGCCGGCAGCACCTACTACAGCGATTCTGTGAAGGGCAGATTCACCATCAGCCGGGACAACGCCAAGAACAGCCTG
TACCTGCAGATGAACTCCCTGAGAGCCGAGGACACCGCCGTGTACTATTGTGCCAGAGGACCCATCTACAACGACTAC
GACGAGTTCGCCTATTGGGGCCAGGGCACACTGGTCACAGTCAGCTCTGGCGGTGGCGGAagcGGAGGCGGTGGCtcc
GGTGGCGGAGGCagcGACATCGTGATGACACAGAGCCCTGATAGCCTGGCCGTGTCTCTGGGAGAGAGAGCCACCATC
AACTGCAAGAGCAGCCAGAGCGTGCTGTACTCCAGCAACCAGAAGAACTACCTGGCCTGGTATCAGCAGAAGCCCGGC
CAGCCTCCTAAGCTGCTGATCTACTGGGCCAGCACCAGAGAAAGCGGCGTGCCCGATAGATTTTCTGGCAGCGGCTCT
GGCACCGACTTCACCCTGACAATTAGCTCCCTGCAGGCCGAGGATGTGGCCGTGTACTACTGTCACCAGTACCTGAGC
AGCCTGACCTTTGGCGGCGGAACAAAGGTGGAAATCAAGcga (SEQ ID NO: 1694)
CD8 hinge region
ACAACAACCCCTGCCCCCAGACCTCCTACCCCAGCCCCTACAATTGCCAGCCAGCCTCTGAGCCTGAGGCCCGAGGCT
TGTAGACCTGCTGCTGGCGGAGCCGTGCACACCAGAGGACTGGATTTCGCCTGCGAC (SEQ ID NO: 1695)
CD8 transmembrane region
ATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCCTTCTCCTGTCACTGGTTATCACCCTTTACTGC (SEQ ID NO: 1696)
CD28
AGGAGTAAGAGGAGCAGGCTCCTGCACAGTGACTACATGAACATGACTCCTAGAAGACCTGGGCCTACCAGAAAGCAT
TACCAGCCCTATGCCCCACCACGCGACTTCGCAGCCTATCGCTCC (SEQ ID NO: 1697)
CD3 1XX

AGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGCGTACAAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATCTA
GGACGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAG
AACCCTCAGGAAGGCCTGTtCAATGAACTGCAGAAAGATAAGATGGCGGAGGCCTtCAGTGAGATTGGGATGAAAGGC
GAGCGCCGGAGGGGCAAGGGGCACGATGGCCTTTtCCAGGGTCTCAGTACAGCCACCAAGGACACCTtCGACGCCCTT
CACATGCAGGCCCTGCCCCCTCGCTGATAA (SEQ ID NO: 1698)

Construct Name:	**pCDH MSCV h20A10-N CAR CD28 1XX**
Construct backbone:	**pCDH CMV MCS (SBI)**
Promoter	**MSCV**
Leader sequence:	**Human CD8 alpha (1- 63)**
scFv Name:	**Humanized 20A10-N (64 - 807)**
Hinge region:	**Human CD8 alpha (808 - 942)**
Transmembrane Domain:	**Human CD8 alpha (943 - 1014)**
Costimulatory Domains:	**Human CD28 (1015 - 1137) and CD3 zeta 1XX (1138 - 1473)**

ATGGCCTTACCAGTGACCGCCTTGCTCCTGCCGCTGGCCTTGCTGCTCCACGCCGCCAGGCCGCAGGTGCAGCTGGTT
GAATCTGGCGGCGGACTTGTGAAGCCTGGCGGATCTCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCTTTAGCACA
TACGCCATGAGCTGGATCAGACAGGCCCCTGGCAAAGGCCTGGAATGGGTGgcgTCTATTGGCAGAGCCGGCAGCACC
TACTACAGCGACTCTGTGAAGGGCAGATTCACCATCAGCCGGGACAACGCCAAGAACAGCCTGTACCTGCAGATGAAC
TCCCTGAGAGCCGAGGACACCGCCGTGTACTATTGTGCCAGAGGACCCATCTACAACGACTACGACGAGTTCGCCTAT
TGGGGCCAGGGCACACTGGTCACAGTTTCTAGCGGCGGTGGCGGAagcGGAGGCGGTGGCTccGGTGGCGGAGGCagc
GAAATTGTGCTGACACAGAGCCCCGCCACACTGTCACTTTCTCCAGGCGAAAGAGCCACACTGAGCTGCAAGAGCAGC
CAGAGCGTGCTGTACTCCAGCAACCAGAAGAACTACCTGGCCTGGTATCAGCAGAAGCCCGGCCAAGCTCCTCGGCTG
CTGATCTATTGGGCCAGCACAAGAGAGAGCGGCATCCCTGCCAGATTTTCTGGCAGCGGCTCTGGCACCGATTTCACC
CTGACCATAAGCAGCCTGGAACCTGAGGACTTCGCCGTGTATTACTGCCACCAGTACCTGAGCAGCCTGACCTTTGGC
GGAGGCACCAAGGTGGAAATCAAGCGGACAACAACCCCTGCCCCCAGACCTCCTACCCCAGCCCCTACAATTGCCAGC
CAGCCTCTGAGCCTGAGGCCCGAGGCTTGTAGACCTGCTGCTGGCGGAGCCGTGCACACCAGAGGACTGGATTTCGCC
TGCGACATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCCTTCTCCTGTCACTGGTTATCACCCTTTACTGC
AGGAGTAAGAGGAGCAGGCTCCTGCACAGTGACTACATGAACATGACTCCTAGAAGACCTGGGCCTACCAGAAAGCAT
TACCAGCCCTATGCCCCACCACGCGACTTCGCAGCCTATCGCTCCAGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCC
GCGTACAAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATCTAGGACGAAGAGAGGAGTACGATGTTTTGGACAAG
AGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGAACCCTCAGGAAGGCCTGTtCAATGAACTGCAG
AAAGATAAGATGGCGGAGGCCTtCAGTGAGATTGGGATGAAAGGCGAGCGCCGGAGGGGCAAGGGGCACGATGGCCTT
TtCCAGGGTCTCAGTACAGCCACCAAGGACACCTtCGACGCCCTTCACATGCAGGCCCTGCCCCCTCGCTGATAA
(SEQ ID NO:1699)

CD8 leader sequence
ATGGCCTTACCAGTGACCGCCTTGCTCCTGCCGCTGGCCTTGCTGCTCCACGCCGCCAGGCCG (SEQ ID NO: 1700)
h20A10-N scFV
CAGGTGCAGCTGGTTGAATCTGGCGGCGGACTTGTGAAGCCTGGCGGATCTCTGAGACTGAGCTGTGCCGCCAGCGGC
TTCACCTTTAGCACATACGCCATGAGCTGGATCAGACAGGCCCCTGGCAAAGGCCTGGAATGGGTGgcgTCTATTGGC
AGAGCCGGCAGCACCTACTACAGCGACTCTGTGAAGGGCAGATTCACCATCAGCCGGGACAACGCCAAGAACAGCCTG
TACCTGCAGATGAACTCCCTGAGAGCCGAGGACACCGCCGTGTACTATTGTGCCAGAGGACCCATCTACAACGACTAC
GACGAGTTCGCCTATTGGGGCCAGGGCACACTGGTCACAGTTTCTAGCGGCGGTGGCGGAagcGGAGGCGGTGGCTcc
GGTGGCGGAGGCagcGAAATTGTGCTGACACAGAGCCCCGCCACACTGTCACTTTCTCCAGGCGAAAGAGCCACACTG
AGCTGCAAGAGCAGCCAGAGCGTGCTGTACTCCAGCAACCAGAAGAACTACCTGGCCTGGTATCAGCAGAAGCCCGGC
CAAGCTCCTCGGCTGCTGATCTATTGGGCCAGCACAAGAGAGAGCGGCATCCCTGCCAGATTTTCTGGCAGCGGCTCT
GGCACCGATTTCACCCTGACCATAAGCAGCCTGGAACCTGAGGACTTCGCCGTGTATTACTGCCACCAGTACCTGAGC
AGCCTGACCTTTGGCGGAGGCACCAAGGTGGAAATCAAGCGG (SEQ ID NO: 1701)
CD8 hinge region
ACAACAACCCCTGCCCCCAGACCTCCTACCCCAGCCCCTACAATTGCCAGCCAGCCTCTGAGCCTGAGGCCCGAGGCT
TGTAGACCTGCTGCTGGCGGAGCCGTGCACACCAGAGGACTGGATTTCGCCTGCGAC (SEQ ID NO: 1702)
CD8 transmembrane domain
ATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCCTTCTCCTGTCACTGGTTATCACCCTTTACTGC (SEQ ID NO: 1703)
CD28
AGGAGTAAGAGGAGCAGGCTCCTGCACAGTGACTACATGAACATGACTCCTAGAAGACCTGGGCCTACCAGAAAGCAT
TACCAGCCCTATGCCCCACCACGCGACTTCGCAGCCTATCGCTCC (SEQ ID NO: 1704)
CD3 1XX

AGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGCGTACAAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATCTA
GGACGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAG
AACCCTCAGGAAGGCCTGTtCAATGAACTGCAGAAAGATAAGATGGCGGAGGCCTtCAGTGAGATTGGGATGAAAGGC
GAGCGCCGGAGGGGCAAGGGGCACGATGGCCTTTtCCAGGGTCTCAGTACAGCCACCAAGGACACCTtCGACGCCCTT
CACATGCAGGCCCTGCCCCCTCGCTGATAA (SEQ ID NO: 1705)

Construct Name:	**pCDH MSCV h20A10-C2 CAR CD28 1XX**
Construct backbone:	**pCDH CMV MCS (SBI)**
Promoter	**MSCV**
Leader sequence:	**Human CD8 alpha (1- 63)**
scFv Name:	**Humanized 20A10-C2 (64 - 807)**
Hinge region:	**Human CD8 alpha (808 - 942)**
Transmembrane Domain:	**Human CD8 alpha (943 - 1014)**
Costimulatory Domains:	**Human CD28 (1015 - 1137) and CD3 zeta 1XX (1138 - 1473)**

ATGGCCTTACCAGTGACCGCCTTGCTCCTGCCGCTGGCCTTGCTGCTCCACGCCGCCAGGCCGGAGGTGCAGCTGGTT
GAATCTGGCGGCGGACTTGTGAAGCCTGGCGGATCTCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCTTTAGCACA
TACGCCATGAGCTGGGTCCGACAGGCCCCTGGAAAAGGCCTTGAATGGGTTGCCTCTATCGGCAGAGCCGGCAGCACC
TACTACAGCGATTCTGTGAAGGGCAGATTCACCATCAGCCGGGACAACGCCAAGAACAGCCTGTACCTGCAGATGAAC
TCCCTGAGAGCCGAGGACACCGCCGTGTACTATTGTGCCAGAGGACCCATCTACAACGACTACGACGAGTTCGCCTAT
TGGGGCCAGGGCACACTGGTCACAGTCAGCTCTGGCGGTGGCGGAagcGGAGGCGGTGGCtccGGTGGCGGAGGCagc
gacattgtgctgacccagtctccagcctccttggccgtgtctccaggacagagggccaccatcacctgcAAGAGCAGC
CAGAGCGTGCTGTACTCCAGCAACCAGAAGAACTACCTGGCCtggtatcagcagaaaccaggacaacctcctaaactc
ctgatttacTGGGCCAGCACCAGAGAAAGCggggtcccagccaggttcagcggcagtgggtctgggaccgatttcacc
ctcacaattaatcctgtggaagctaatgatactgcaaattattactgtCACCAGTACCTGAGCAGCCTGACCTTCGGC
GGAGGGACCAAGGTGGAGATCAAACGAACAACAACCCCTGCCCCCAGACCTCCTACCCCAGCCCCTACAATTGCCAGC
CAGCCTCTGAGCCTGAGGCCCGAGGCTTGTAGACCTGCTGCTGGCGGAGCCGTGCACACCAGAGGACTGGATTTCGCC
TGCGACATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCCTTCTCCTGTCACTGGTTATCACCCTTTACTGC
AGGAGTAAGAGGAGCAGGCTCCTGCACAGTGACTACATGAACATGACTCCTAGAAGACCTGGCCCTACCAGAAAGCAT
TACCAGCCCTATGCCCCACCACGCGACTTCGCAGCCTATCGCTCCAGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCC
GCGTACAAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATCTAGGACGAAGAGAGGAGTACGATGTTTTGGACAAG
AGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGAACCCTCAGGAAGGCCTGTtCAATGAACTGCAG
AAAGATAAGATGGCGGAGGCCTtCAGTGAGATTGGGATGAAAGGCGAGCGCCGGAGGGGCAAGGGGCACGATGGCCTT
TtCCAGGGTCTCAGTACAGCCACCAAGGACACCTtCGACGCCCTTCACATGCAGGCCCTGCCCCCTCGCTGATAA
(SEQ ID NO:1706)

CD8 leader sequence
ATGGCCTTACCAGTGACCGCCTTGCTCCTGCCGCTGGCCTTGCTGCTCCACGCCGCCAGGCCG (SEQ ID NO: 1707)

h20A10-C2 scFV
GAGGTGCAGCTGGTTGAATCTGGCGGCGGACTTGTGAAGCCTGGCGGATCTCTGAGACTGAGCTGTGCCGCCAGCGGC
TTCACCTTTAGCACATACGCCATGAGCTGGGTCCGACAGGCCCCTGGAAAAGGCCTTGAATGGGTTGCCTCTATCGGC
AGAGCCGGCAGCACCTACTACAGCGATTCTGTGAAGGGCAGATTCACCATCAGCCGGGACAACGCCAAGAACAGCCTG
TACCTGCAGATGAACTCCCTGAGAGCCGAGGACACCGCCGTGTACTATTGTGCCAGAGGACCCATCTACAACGACTAC
GACGAGTTCGCCTATTGGGGCCAGGGCACACTGGTCACAGTCAGCTCTGGCGGTGGCGGAagcGGAGGCGGTGGCtcc
GGTGGCGGAGGCagcgacattgtgctgacccagtctccagcctccttggccgtgtctccaggacagagggccaccatc
acctgcAAGAGCAGCCAGAGCGTGCTGTACTCCAGCAACCAGAAGAACTACCTGGCCtggtatcagcagaaaccagga
caacctcctaaactcctgatttacTGGGCCAGCACCAGAGAAAGCggggtcccagccaggttcagcggcagtgggtct
gggaccgatttcaccctcacaattaatcctgtggaagctaatgatactgcaaattattactgtCACCAGTACCTGAGC
AGCCTGACCTTCGGCGGAGGGACCAAGGTGGAGATCAAACGA (SEQ ID NO: 1708)

CD8 hinge region
ACAACAACCCCTGCCCCCAGACCTCCTACCCCAGCCCCTACAATTGCCAGCCAGCCTCTGAGCCTGAGGCCCGAGGCT
TGTAGACCTGCTGCTGGCGGAGCCGTGCACACCAGAGGACTGGATTTCGCCTGCGAC (SEQ ID NO: 1709)

CD8 transmembrane region
ATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCCTTCTCCTGTCACTGGTTATCACCCTTTACTGC (SEQ ID NO: 1710)

CD28
AGGAGTAAGAGGAGCAGGCTCCTGCACAGTGACTACATGAACATGACTCCTAGAAGACCTGGCCCTACCAGAAAGCAT
TACCAGCCCTATGCCCCACCACGGGACTTCGCAGCCTATCGCTCC (SEQ ID NO: 1711)

CD3 1XX
AGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGCGTACAAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATCTA
GGACGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAG
AACCCTCAGGAAGGCCTGTtCAATGAACTGCAGAAAGATAAGATGGCGGAGGCCTtCAGTGAGATTGGGATGAAAGGC
GAGCGCCGGAGGGGCAAGGGGCACGATGGCCTTTtCCAGGGTCTCAGTACAGCCACCAAGGACACCTtCGACGCCCTT
CACATGCAGGCCCTGCCCCCTCGCTGATAA (SEQ ID NO: 1712)

Construct Name:	**pCDH MSCV hC2 CAR 41BB 6xNFATFoxP3 IL18**
Construct backbone:	**pCDH CMV MCS (SBI)**
Promoter	**MSCV**
Leader sequence:	**Human CD8 alpha (1- 63)**
scFv Name:	**Humanized C2 (64 - 8010)**
Hinge region:	**Human CD8 alpha (811 - 945)**
Transmembrane Domain:	**Human CD8 alpha (946 - 1017)**
Costimulatory Domains:	**Human 41BB (1018 - 1143) and CD3 zeta (1144 - 1479)**
NFAT response element:	**Human FoxP3 NFAT (6x) response element (1530 - 1691)**
Minimal promoter:	**mCMV (1698 - 1815)**
Leader sequence:	**Human CD8 alpha (1841- 1903)**
Cytokine:	**Human IL18(1904 - 2374)**

ATGGCCTTACCAGTGACCGCCTTGCTCCTGCCGCTGGCCTTGCTGCTCCACGCCGCCAGGCCGGAGGTGCAGCTGGTG
GAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTGGC
TATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAACCATTAGTAGTGGCGGAACCTAC
ATATACTACCCCGACTCAGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATG
AACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGACTTGGGGGGGATAATTACTACGAATACTTCGAT
GTCTGGGGCAAAGGGACCACGGTCACCGTCTCCTCCGGCGGTGGCGGATCCGGCGGTGGCGGATCCGGCGGTGGCGGA
TCCGACATTGTGCTGACCCAGTCTCCAGCCTCCTTGGCCGTGTCTCCAGGACAGAGGGCCACCATCACCTGCAGAGCC
AGTAAGAGTGTCAGTACCAGCGGATACTCCTACATGCACTGGTATCAGCAGAAACCAGGACAACCTCCTAAACTCCTG
ATTTACCTGGCATCCAATCTGGAGAGCGGGGTCCCAGCCAGGTTCAGCGGCAGTGGGTCTGGGACCGATTTCACCCTC
ACAATTAATCCTGTGGAAGCTAATGATACTGCAAATTATTACTGTCAGCACAGTAGGGAGCTGCCTTTCACATTCGGC
GGAGGGACCAAGGTGGAGATCAAACGAACTACAACAACCCCTGCCCCCAGACCTCCTACCCCAGCCCCTACAATTGCC
AGCCAGCCTCTGAGCCTGAGGCCCGAGGCTTGTAGACCTGCTGCTGGCGGAGCCGTGCACACCAGAGGACTGGATTTC
GCCTGCGACATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCCTTCTCCTGTCACTGGTTATCACCCTTTAC
TGCAAACGGGGCAGAAAGAAACTCCTGTATATATTCAAACAACCATTTATGAGACCAGTACAAACTACTCAAGAGGAA
GATGGCTGTAGCTGCCGATTTCCAGAAGAAGAAGAAGGAGGATGTGAACTGAGAGTGAAGTTCAGCAGGAGCGCAGAC
GCCCCCGCGTACAAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATCTAGGACGAAGAGAGGAGTACGATGTTTTG
GACAAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGAACCCTCAGGAAGGCCTGTACAATGAA
CTGCAGAAAGATAAGATGGCGGAGGCCTACAGTGAGATTGGGATGAAAGGCGAGCGCCGGAGGGGCAAGGGGCACGAT
GGCCTTTACCAGGGTCTCAGTACAGCCACCAAGGACACCTACGACGCCCTTCACATGCAGGCCCTGCCCCCTCGCTGA
TAAGTTTAAACTGCCAGAACATTTCTCTGGCCTAACTGGCCGGTACCGGCTTTCATTTTTCCATTTACTGCAGAGGCT
TTCATTTTTCCATTTACTGCAGAGGCTTTCATTTTTCCATTTACTGCAGAGGCTTTCATTTTTCCATTTACTGCAGAG
GCTTTCATTTTTCCATTTACTGCAGAGGCTTTCATTTTTCCATTTACTGCAGAactagttaggcgtgtacggtgggag
gcctatataagcagagctcgtttagtgaaccgtcagatcgcctggagacgccatccacgctgttttgacctccataga
agacaccgggaccgatccagcCTCGAGAGACCCAATGCTAGCCACCATGGCCTTACCAGTGACCGCCTTGCTCCTGCC
GCTGGCCTTGCTGCTCCACGCCGCCAGGCCG[illegible]TGAtaa (SEQ ID NO:1713)

CD8 leader sequence
ATGGCCTTACCAGTGACCGCCTTGCTCCTGCCGCTGGCCTTGCTGCTCCACGCCGCCAGGCCG (SEQ ID NO: 1714)

C2 scFV
GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGA
TTCACCTTCAGTGGCTATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAACCATTAGT
AGTGGCGGAACCTACATATACTACCCCGACTCAGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCA

CTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGACTTGGGGGGGATAATTAC
TACGAATACTTCGATGTCTGGGGCAAAGGGACCACGGTCACCGTCTCCTCCGGCGGTGGCGGATCCGGCGGTGGCGGA
TCCGGCGGTGGCGGATCCGACATTGTGCTGACCCAGTCTCCAGCCTCCTTGGCCGTGTCTCCAGGACAGAGGGCCACC
ATCACCTGCAGAGCCAGTAAGAGTGTCAGTACCAGCGGATACTCCTACATGCACTGGTATCAGCAGAAACCAGGACAA
CCTCCTAAACTCCTGATTTACCTGGCATCCAATCTGGAGAGCGGGGTCCCAGCCAGGTTCAGCGGCAGTGGGTCTGGG
ACCGATTTCACCCTCACAATTAATCCTGTGGAAGCTAATGATACTGCAAATTATTACTGTCAGCACAGTAGGGAGCTG
CCTTTCACATTCGGCGGAGGGACCAAGGTGGAGATCAAACGAACT (SEQ ID NO: 1715)

CD8 hinge region
ACAACAACCCCTGCCCCCAGACCTCCTACCCCAGCCCCTACAATTGCCAGCCAGCCTCTGAGCCTGAGGCCCGAGGCT
TGTAGACCTGCTGCTGGCGGAGCCGTGCACACCAGAGGACTGGATTTCGCCTGCGAC (SEQ ID NO: 1716)
CD8 transmembrane region
ATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCCTTCTCCTGTCACTGGTTATCACCCTTTACTGC (SEQ ID NO: 1717)
41BB
AAACGGGGCAGAAAGAAACTCCTGTATATATTCAAACAACCATTTATGAGACCAGTACAAACTACTCAAGAGGAAGAT
GGCTGTAGCTGCCGATTTCCAGAAGAAGAAGAAGGAGGATGTGAACTG (SEQ ID NO: 1718)
CD3
AGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGCGTACAAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATCTA
GGACGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAG
AACCCTCAGGAAGGCCTGTACAATGAACTGCAGAAAGATAAGATGGCGGAGGCCTACAGTGAGATTGGGATGAAAGGC
GAGCGCCGGAGGGGCAAGGGGCACGATGGCCTTTACCAGGGTCTCAGTACAGCCACCAAGGACACCTACGACGCCCTT
CACATGCAGGCCCTGCCCCCTCGC (SEQ ID NO: 1719)

plasmid
TGATAAGTTTAAACTGCCAGAACATTTCTCTGGCCTAACTGGCCGGTACC (SEQ ID NO: 1720)

6xNFAT FoxP3
GGCTTCATTTTTTCCATTTACTGCAGAGGCTTCATTTTTTCCATTTACTGCAGAGGCTTCATTTTTTCCATTTACTGC
AGAGGCTTCATTTTTTCCATTTACTGCAGAGGCTTCATTTTTTCCATTTACTGCAGAGGCTTCATTTTTTCCATTTAC
TGCAGAactagt (SEQ ID NO: 1721)

mCMV
Taggcgtgtacggtgggaggcctatataagcagagctcgtttagtgaaccgtcagatcgcctggagacgccatccacg
ctgttttgacctccatagaagacaccgggaccgatccagc (SEQ ID NO: 1722)

plasmid
CTCGAGAGACCCAATGCTAGCCACC (SEQ ID NO: 1723)

CD8 leader sequence
ATGGCCTTACCAGTGACCGCCTTGCTCCTGCCGCTGGCCTTGCTGCTCCACGCCGCCAGGCCG (SEQ ID NO: 1724)

[illegible]
[illegible]TGAtaa (SEQ ID NO: 1725)

Construct Name:	**pCDH MSCV hC2 CAR CD28 1XX**
Construct backbone:	**pCDH CMV MCS (SBI)**
Promoter	**MSCV**
Leader sequence:	**Human CD8 alpha (1- 63)**
scFv Name:	**Humanized C2 (64 - 8010)**
Hinge region:	**Human CD8 alpha (811 - 945)**
Transmembrane Domain:	**Human CD8 alpha (946 - 1017)**
Costimulatory Domains:	**Human CD28 (1018 - 1140) and CD3 zeta 1XX (1141 - 1476)**

ATGGCCTTACCAGTGACCGCCTTGCTCCTGCCGCTGGCCTTGCTGCTCCACGCCGCCAGGCCGGAGGTGCAGCTGGTG
GAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTGGC
TATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAACCATTAGTAGTGGCGGAACCTAC
ATATACTACCCCGACTCAGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATG
AACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGACTTGGGGGGGATAATTACTACGAATACTTCGAT
GTCTGGGGCAAAGGGACCACGGTCACCGTCTCCTCCGGCGGTGGCGGATCCGGCGGTGGCGGATCCGGCGGTGGCGGA
TCCGACATTGTGCTGACCCAGTCTCCAGCCTCCTTGGCCGTGTCTCCAGGACAGAGGGCCACCATCACCTGCAGAGCC
AGTAAGAGTGTCAGTACCAGCGGATACTCCTACATGCACTGGTATCAGCAGAAACCAGGACAACCTCCTAAACTCCTG
ATTTACCTGGCATCCAATCTGGAGAGCGGGGTCCCAGCCAGGTTCAGCGGCAGTGGGTCTGGGACCGATTTCACCCTC
ACAATTAATCCTGTGGAAGCTAATGATACTGCAAATTATTACTGTCAGCACAGTAGGGAGCTGCCTTTCACATTCGGC
GGAGGGACCAAGGTGGAGATCAAACGAACTACAACAACCCCTGCCCCCAGACCTCCTACCCCAGCCCCTACAATTGCC
AGCCAGCCTCTGAGCCTGAGGCCCGAGGCTTGTAGACCTGCTGCTGGCGGAGCCGTGCACACCAGAGGACTGGATTTC
GCCTGCGACATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCCTTCTCCTGTCACTGGTTATCACCCTTTAC
TGCAGGAGTAAGAGGAGCAGGCTCCTGCACAGTGACTACATGAACATGACTCCTAGAAGACCTGGGCCTACCAGAAAG
CATTACCAGCCCTATGCCCCACCACGCGACTTCGCAGCCTATCGCTCCAGAGTGAAGTTCAGCAGGAGCGCAGACGCC
CCCGCGTACAAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATCTAGGACGAAGAGAGGAGTACGATGTTTTGGAC
AAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGAACCCTCAGGAAGGCCTGTtCAATGAACTG
CAGAAAGATAAGATGGCGGAGGCCTtCAGTGAGATTGGGATGAAAGGCGAGCGCCGGAGGGGCAAGGGGCACGATGGC
CTTTtCCAGGGTCTCAGTACAGCCACCAAGGACACCTtCGACGCCCTTCACATGCAGGCCCTGCCCCCTCGCTGATAA
(SEQ ID NO:1726)

CD8 leader sequence
ATGGCCTTACCAGTGACCGCCTTGCTCCTGCCGCTGGCCTTGCTGCTCCACGCCGCCAGGCCG (SEQ ID NO: 1727)

C2 scFV
GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGA
TTCACCTTCAGTGGCTATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAACCATTAGT
AGTGGCGGAACCTACATATACTACCCCGACTCAGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCA
CTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGACTTGGGGGGGATAATTAC
TACGAATACTTCGATGTCTGGGGCAAAGGGACCACGGTCACCGTCTCCTCCGGCGGTGGCGGATCCGGCGGTGGCGGA
TCCGGCGGTGGCGGATCCGACATTGTGCTGACCCAGTCTCCAGCCTCCTTGGCCGTGTCTCCAGGACAGAGGGCCACC
ATCACCTGCAGAGCCAGTAAGAGTGTCAGTACCAGCGGATACTCCTACATGCACTGGTATCAGCAGAAACCAGGACAA
CCTCCTAAACTCCTGATTTACCTGGCATCCAATCTGGAGAGCGGGGTCCCAGCCAGGTTCAGCGGCAGTGGGTCTGGG
ACCGATTTCACCCTCACAATTAATCCTGTGGAAGCTAATGATACTGCAAATTATTACTGTCAGCACAGTAGGGAGCTG
CCTTTCACATTCGGCGGAGGGACCAAGGTGGAGATCAAACGAACT (SEQ ID NO: 1728)

CD8 hinge region
ACAACAACCCCTGCCCCCAGACCTCCTACCCCAGCCCCTACAATTGCCAGCCAGCCTCTGAGCCTGAGGCCCGAGGCT
TGTAGACCTGCTGCTGGCGGAGCCGTGCACACCAGAGGACTGGATTTCGCCTGCGAC (SEQ ID NO: 1729)

CD8 transmembrane region
ATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCCTTCTCCTGTCACTGGTTATCACCCTTTACTGC (SEQ ID NO: 1730)

CD28
AGGAGTAAGAGGAGCAGGCTCCTGCACAGTGACTACATGAACATGACTCCTAGAAGACCTGGGCCTACCAGAAAGCAT
TACCAGCCCTATGCCCCACCACGCGACTTCGCAGCCTATCGCTCC (SEQ ID NO: 1731)

CD3 1XX
AGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGCGTACAAGCAGGGCCAGAACCAGCTCTATAACGAGCTCAATCTA
GGACGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAG
AACCCTCAGGAAGGCCTGTtCAATGAACTGCAGAAAGATAAGATGGCGGAGGCCTtCAGTGAGATTGGGATGAAAGGC
GAGCGCCGGAGGGGCAAGGGGCACGATGGCCTTTtCCAGGGTCTCAGTACAGCCACCAAGGACACCTtCGACGCCCTT
CACATGCAGGCCCTGCCCCCTCGCTGATAA (SEQ ID NO: 1732)

Mouse B12 light chain variable *framework 2* (*FR2*) sequence:
(DNA)
tggtatcagcagaaaccaggacagccacccaaactcctcatctat (SEQ ID NO: 1733)
(amino acids)
WYQQKPGQPPKLLIY (SEQ ID NO: 1734)

Mouse B12 light chain variable *complementarity determining regions 2* (*CDR2*) sequence:
(DNA)
cttgcatccaccctagattct (SEQ ID NO: 1735)
(amino acids)
LASTLDS (SEQ ID NO: 1736)

Mouse B12 light chain variable *framework 3* (*FR3*) sequence:
(DNA)
ggggtccctgccaggttcagtggcagtgggtctaggacagacttcaccctcaccattgatcctgtggaggctgatgatgctgcaacctattactgt (SEQ ID NO: 1737)
(amino acids)
GVPARFSGSGSRTDFTLTIDPVEADDAATYYC (SEQ ID NO: 1738)

Mouse B12 light chain variable *complementarity determining regions 3* (*CDR3*) sequence:
(DNA)
cagcaaaataatgaggatcctccgacg (SEQ ID NO: 1739)
(amino acids)
QQNNEDPPT (SEQ ID NO: 1740)

Mouse B12 light chain variable *framework 4* (*FR4*) sequence:
(DNA)
ttcggtggaggcaccaagctggaaatcaagg (SEQ ID NO: 1741)
(amino acids)
FGGGTKLEIK (SEQ ID NO: 1742)

epitope to which NME1 and NME7$_{AB}$ bind part of the 10 membrane proximal amino acids
PFPFSAQSGA (SEQ ID NO:1743)

SNIKFRPGSVV (SEQ ID NO:1744)

ASRYNLT (SEQ ID NO:1745)

Fragment of PSMGFR
GTINVHDVET (SEQ ID NO:1746)

Fragment of PSMGFR
FPFS (SEQ ID NO:1747)

Fragment of PSMGFR
SNIKFRPGSVVVQLTLAFRE (SEQ ID NO:1748)

Fragment of PSMGFR
QFNQYKTEA (SEQ ID NO:1749)

Fragment of PSMGFR
VQLTLAFRE (SEQ ID NO:1750)

Fragment of PSMGFR
SVSDV (SEQ ID NO:1751)

[00820] IL18 sequence

[00821] (DNA)

[00822] Atagaagacaccgggaccgatccagcctcgagagacccaatgctagccaccatggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccgtacttcggcaagctggaaagcaagctgagcgtgatccggaacctgaacgaccaggtgctgttcatcgatcagggcaacagacccctgttcgaggacatgaccgacagcgactgcagagacaacgcccctcggaccatcttcatcatcagcatgtacaaggacagccagcctagaggcatggccgtgaccatctctgtgaagtgcgagaagatcagcaccctgagctgcgagaacaagatcatcagcttcaaagagatgaacccgccggacaacatcaaggacaccaagagcgacatcatattcttccagcggagcgtgcccggccacgacaacaagatgcagtttgagagcagcagctacgagggctacttcctggcctgcgagaaagagcgggacctgttcaagctgatcctgaagaaagaggacgaactgggcgaccgcagcatcatgttcaccgtgcagaacgaggactgataaaagcttggcaatccggtactgttggtaaagccacca (SEQ ID NO:1752)

[00823] (amino acids)

IEDTGTDPASRDPMLATMALPVTALLLPLALLLHAARPYFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGMAVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSYEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED**KLGNPVLLVKPP (SEQ ID NO:1753)

primer

5′- agggagacccaagctggctagttaagcttggatggccttaccagtgaccgccttgc-3′ (SEQ ID NO:1754)

primer

5′- taggccagagaaatgttctggcattatcagcgagggggcagggcctgc-3′ (SEQ ID NO:1755).

5′- tgccagaacatttctctgg-3′ (SEQ ID NO:1756)

5′- acagtcgaggctgatcagcgggtttaaacttatcagtcctcgttctgcacgg-3′ (SEQ ID NO: 1757)

5′-atgcaggccctgccccctcgctgataagtttaaactgccagaacatttctctggcctaac-3′ (SEQ ID NO:1758)

5′- accggagcgatcgcagatccttcgcggccgcttatcagtcctcgttctgcacggtgaac-3′ (SEQ ID NO:1759)

5′- attgcactagttgaaagaccccacctgtagg-3′ (SED ID NO:1760)

5′- aatgctctagaatacgggtatccagg-3′ (SEQ ID NO:1761)

5′ atagcgaattcgtaccgagggccaccatgg-3′ (SEQ ID NO:1762)

5′- taggcctcccaccgtacacgcctaggtaccacgccttctgtatg-3′ (SEQ ID NO:1763)

5′- taggcctcccaccgtacacgcctaggtacctctgcagtaaatgg-3′ (SEQ ID NO:1764)

5′- taaggccatggtggctagc-3′ (SEQ ID NO:1765)

5′- aataagtttaaactgccagaacatttctctgg-3′ (SEQ ID NO:1766)

5′- atatagcggccgcttatcagtcctcgttctgcacgg-3′ (SEQ ID NO:1767)

[00824] 6x FoxP3NFAT mCMV

[00825] (DNA)

[00826] Agaacatttctctggcctaactggccggtaccggcttcattttttccatttactgcagaggcttcattttttccatttactgcagaggcttcattttttccatttactgcagaggcttcattttttccatttactgcagaggcttcattttttccatttactgcagaggcttcattttttccatttactgcagaactagttaggcgtgtacggtgggaggcctatataagcagagctcgtttagtgaaccgtcagatcgcctggagacgccatccacgctgttttgacctccatagaagacaccgggaccgatccagcctcgagagacccaatgctagccaccatgg (SEQ ID NO:1768)

[00827] (amino acids)

[00828] RTFLWPNWPVPASFFPFTAEASFFPFTAEASFFPFTAEASFFPFTAEASFFPFTAEASFFPFTAELVRRVRWEAYISRARLVNRQIAWRRHPRCFDLHRRHRDRSSLERPNASHHG (SEQ ID NO:1769)

[00829] 6x FoxP3NFAT mIL2P

[00830] (DNA)

[00831] Agaacatttctctggcctaactggccggtaccggcttcattttttccatttactgcagaggcttcattttttccatttactgcagaggcttcattttttccatttactgcagaggcttcattttttccatttactgcagaggcttcattttttccatttactgcagaggcttcattttttccatttactgcagaactagtcattttgacacccccataatattttccagaattaacagtataaattgcatctcttgttcaagagttccctatcactctctttaatcactactcacagtaacctcaactcctgcctcgagagacccaatgctagccaccatgg (SEQ ID NO:1770)

[00832] (amino acids)

[00833] RTFLWPNWPVPASFFPFTAEASFFPFTAEASFFPFTAEASFFPFTAEASFFPFTAEASFFPFTAELVILTPP*YFSRINSINCISCSRVPYHSL*SLLTVTSTPASRDPMLATMX (SEQ ID NO:1771)

[00834] 6x FoxP3NFAT miniP

[00835] (DNA)

[00836] Agaacatttctctggcctaactggccggtaccggcttcattttttccatttactgcagaggcttcattttttccatttactgcagaggcttcattttttccatttactgcagaggcttcattttttccatttactgcagaggcttcattttttccatttactgcagaggcttcattttttccatttactgcagaactagtagagggtatataatggaagctcgacttccagctcgagagacccaatgctagccaccatgg (SEQ ID NO:1772)

[00837] (amino acids)

[00838] RTFLWPNWPVPASFFPFTAEASFFPFTAEASFFPFTAEASFFPFTAEASFFPFTAEASFFPFTAELVEGI*WKLDFQLERPNASHHG (SEQ ID NO:1773)

[00839] 6x IL2NFAT mCMV

[00840] (DNA)

[00841] Agaacatttctctggcctaactggccggtaccggaggaaaaactgtttcatacagaaggcgtggaggaaaaactgtttcatacagaaggcgtggaggaaaaactgtttcatacagaaggcgtggaggaaaaactgtttcatacagaaggcgtggaggaaaaactgtttcatacagaaggcgtggaggaaaaactgtttcatacagaaggcgtactagttaggcgtgtacggtgggaggcctatataagcagagctcgtttagtgaaccgtcagatcgcctggagacgccatccacgctgttttgacctccatagaagacaccgggaccgatccagcctcgagagacccaatgctagccaccatgg (SEQ ID NO:1774)

[00842] (amino acids)

[00843] RTFLWPNWPVPEEKLFHTEGVEEKLFHTEGVEEKLFHTEGVEEKLFHTEGVEEKLFHTEGVEEKLFHTEGVLVRRVRWEAYISRARLVNRQIAWRRHPRCFDLHRRHRDRSSLERPNASHHG (SEQ ID NO:1775)

[00844] 6x IL2NFAT mIL2P

[00845] (DNA)

[00846] Agaacatttctctggcctaactggccggtaccggaggaaaaactgtttcatacagaaggcgtggaggaaaaactgtttcatacagaaggcgtggaggaaaaactgtttcatacagaaggcgtggaggaaaaactgtttcatacagaaggcgtggaggaaaaactgtttcatacagaaggcgtggaggaaaaactgtttcatacagaaggcgtactagtcatttgacacccccataatatttttccagaattaacagtataaattgcatctcttgttcaagagttccctatcactctcttaatcactactcacagtaacctcaactcctgcctcgagagacccaatgctagccaccatgg (SEQ ID NO:1776)

[00847] (amino acids)

[00848] RTFLWPNWPVPEEKLFHTEGVEEKLFHTEGVEEKLFHTEGVEEKLFHTEGVEEKLFHTEGVEEKLFHTEGVLVILTPP*YFSRINSINCISCSRVPYHSL*SLLTVTSTPASRDPMLATMX (SEQ ID NO:1777)

[00849] 6x IL2NFAT miniP

[00850] (DNA)

[00851] Agaacatttctctggcctaactggccggtaccggaggaaaaactgtttcatacagaaggcgtggaggaaaaactgtttcatacagaaggcgtggaggaaaaactgtttcatacagaaggcgtggaggaaaaactgtttcatacagaaggcgtggaggaaaaactgtttcatacagaaggcgtggaggaaaaactgtttcatacagaaggcgtactagtagagggtatataatggaagctcgacttccagctcgagagacccaatgctagccaccatgg (SEQ ID NO:1778)

[00852] (amino acids)

[00853] RTFLWPNWPVPEEKLFHTEGVEEKLFHTEGVEEKLFHTEGVEEKLFHTEGVEEKLFHTEGVEEKLFHTEGVLVEGI*WKLDFQLERPNASHHG (SEQ ID NO:1779)

Human NME1
(DNA)
atggccaactgtgagcgtaccttcattgcgatcaaaccagatggggtccagcggggtcttgtgggagagattatcaa
gcgttttgagcagaaaggattccgccttgttggtctgaaattcatgcaagcttccgaagatcttctcaaggaacact
acgttgacctgaaggaccgtccattctttgccggcctggtgaaatacatgcactcagggccggtagttgccatggtc
tgggaggggctgaatgtggtgaagacgggccgagtcatgctcggggagaccaaccctgcagactccaagcctgggac
catccgtggagacttctgcatacaagttggcaggaacattatacatggcagtgattctgtggagagtgcagagaagg
agatcggcttgtggtttcaccctgaggaactggtagattacacgagctgtgctcagaactggatctatgaatga
(SEQ ID NO:1780)

(amino acids)
MANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFMQASEDLLKEHYVDLKDRPFFAGLVKYMHSGPVVAMV
WEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSDSVESAEKEIGLWFHPEELVDYTSCAQNWIYE-
(SEQ ID NO:1781)

Human NME7
(DNA)
atgaatcatagtgaaagattcgttttcattgcagagtggtatgatccaaatgcttcacttcttcgacgttatgagct
tttattttacccaggggatggatctgttgaaatgcatgatgtaaagaatcatcgcacctttttaaagcggaccaaat
atgataacctgcacttggaagatttatttataggcaacaaagtgaatgtcttttctcgacaactggtattaattgac
tatggggatcaatatacagctcgccagctgggcagtaggaaagaaaaaacgctagccctaattaaaccagatgcaat
atcaaaggctggagaaataattgaaataataaacaaagctggatttactataaccaaactcaaaatgatgatgcttt
caaggaaagaagcattggattttcatgtagatcaccagtcaagacccttttcaatgagctgatccagtttattaca
actggtcctattattgccatggagattttaagagatgatgctatatgtgaatggaaaagactgctgggacctgcaaa
ctctggagtggcacgcacagatgcttctgaaagcattagagccctctttggaacagatggcataagaaatgcagcgc
atggccctgattcttttgcttctgcggccagagaaatggagttgtttttccttcaagtggaggttgtgggccggca
aacactgctaaatttactaattgtacctgttgcattgttaaaccccatgctgtcagtgaaggactgttgggaaagat
cctgatggctatccgagatgcaggttttgaaatctcagctatgcagatgttcaatatggatcgggttaatgttgagg
aattctatgaagtttataaaggagtagtgaccgaatatcatgacatggtgacagaaatgtattctggcccttgtgta
gcaatggagattcaacagaataatgctacaaagacatttcgagaattttgtggacctgctgatcctgaaattgcccg
gcatttacgccctggaactctcagagcaatctttggtaaaactaagatccagaatgctgttcactgtactgatctgc
cagaggatggcctattagaggttcaatacttcttcaagatcttggataattag (SEQ ID NO:1782)

[00854] (amino acids)

MNHSERFVFIAEWYDPNASLLRRYELLFYPGDGSVEMHDVKNHRTFLKRTKYDNLHLEDLFIGNKVNVFSRQLVLID
YGDQYTARQLGSRKEKTLALIKPDAISKAGEIIEIINKAGFTITKLKMMMLSRKEALDFHVDHQSRPFFNELIQFIT
TGPIIAMEILRDDAICEWKRLLGPANSGVARTDASESIRALFGTDGIRNAAHGPDSFASAAREMELFFPSSGGCGPA
NTAKFTNCTCCIVKPHAVSEGLLGKILMAIRDAGFEISAMQMFNMDRVNVEEFYEVYKGVVTEYHDMVTEMYSGPCV
AMEIQQNNATKTFREFCGPADPEIARHLRPGTLRAIFGKTKIQNAVHCTDLPEDGLLEVQYFFKILDN- (SEQ ID
NO:1783)

[00855] Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention specifically described herein.

What is claimed is:

1. An antibody, or fragment thereof, for the diagnosis, treatment or prevention of cancers wherein the antibody specifically binds to the PSMGFR peptide (SEQ ID NO:2) or a fragment thereof of the peptide.

2. The antibody, or fragment thereof of claim 1, which binds to the N-10 peptide (SEQ ID NO:3), N-19 peptide (SEQ ID NO:4), N-23 peptide (SEQ ID NO:5), N-26 peptide (SEQ ID NO:6), N-30 peptide (SEQ ID NO:7), N-10/C-5 peptide (SEQ ID NO:8), N-19/C-5 peptide (SEQ ID NO:9), or C-5 peptide (SEQ ID NO:825).

3. The antibody, or fragment thereof, of claim 1, which interacts with a peptide comprising conformational epitope SVSDV (SEQ ID NO:1751) and FPSA (SEQ ID NO:1747) within N-26 sequence ISDVSVSDVPFPFSAQSGA (SEQ ID NO:6), wherein mutation or deletion of FPFS (SEQ ID NO:1747) destroys binding of the antibody or fragment thereof to the N-26 peptide.

4. The antibody, or fragment thereof, of claim 1, which interacts with a peptide comprising conformational epitope ASRYNLT (SEQ ID NO:1745), SVSDV (SEQ ID NO:1751), and FPSA (SEQ ID NO:1747) within the N-19 sequence ASRYNLT ISDVSVSDVPFPFSAQSGA (SEQ ID NO:4), wherein mutation or deletion of ASRYNLT (SEQ ID NO:1745) destroys binding of the antibody or fragment thereof to the N-26 peptide.

5. The antibody, or fragment thereof, of claim 1, which does not bind to the C-10 peptide (SEQ ID NO:825).

6. The antibody, or fragment thereof of claim 5, which binds to the N-10 peptide (SEQ ID NO:3), but not to the C-10 peptide (SEQ ID NO:825).

7. The antibody, or fragment thereof, of claim 1, which inhibits interaction between $NME7_{AB}$ and MUC1*.

8. The antibody, or fragment thereof, of claim 1, which inhibits interaction between $NME7_{AB}$ and PSMGFR peptide (SEQ ID NO:2).

9. The antibody, or fragment thereof, of claim 2, which inhibits interaction between $NME7_{AB}$ and N-10 peptide (SEQ ID NO:3), N-19 peptide (SEQ ID NO:4), N-23 peptide (SEQ ID NO:5), N-26 peptide (SEQ ID NO:6), N-30 peptide (SEQ ID NO:7), N-10/C-5 peptide (SEQ ID NO:8), N-19/C-5 peptide (SEQ ID NO:9), or C-5 peptide (SEQ ID NO:825).

10. An antibody, or fragment thereof, of claim 1, wherein the antibody recognizes a MUC1 transmembrane enzymatic cleavage product.

11. The antibody, or fragment thereof, of claim 10, wherein the cleavage enzyme is MMP14 or MMP9 or a catalytically active fragment thereof of the enzyme.

12. The antibody, or fragment thereof, of claim 1, which binds to PSMGFR (SEQ ID NO:2) or fragment thereof in which presence of an amino acid sequence within PSMGFR (SEQ ID NO:2) induces binding of the antibody to the PSMGFR.

13. The antibody of claim 12, wherein the amino acid sequence of the binding conformationally inducing peptide is present in N-10 peptide (SEQ ID NO:3).

14. The antibody, or fragment thereof, of claim 12, which does not bind to a linear form of the binding conformationally inducing peptide sequence wherein the linear form of the peptide is a denatured form.

15. The antibody, or fragment thereof, of claim 14, wherein the binding conformationally inducing peptide sequence is in the N-26 peptide sequence ISDVSVSDVPFPFSAQSGA (SEQ ID NO:6), wherein mutation or deletion of FPFS (SEQ ID NO:1747) destroys binding of the antibody or fragment thereof to the N-26 peptide.

16. The antibody, or fragment thereof, of claim 14, wherein the binding conformationally inducing peptide sequence is located within the N-19 sequence ASRYNLTISDVSVSDVPFPFSAQSGA (SEQ ID NO:4), wherein mutation or deletion of ASRYNLT (SEQ ID NO:1745) destroys binding of the antibody or fragment thereof to the N-19 peptide.

17. An antibody, or fragment thereof, for the diagnosis, treatment or prevention of cancers wherein a binding inducing peptide sequence is located within the N-26 sequence ISDVSVSDVPFPFSAQSGA

(SEQ ID NO:6), wherein mutation or deletion within FPFS (SEQ ID NO:1747) destroys binding of the antibody or fragment thereof to PSMGFR.

18. The antibody, or fragment thereof of claim 17, wherein

heavy chain CDR1 comprises consensus sequence at least 90% identical to sequence: F or I at position 1, T at position 2, F at position 3, S at position 4, T, G, or R at position 5, Y at position 6, A, G or T at position 7, M at position 8 and S at position 9;

heavy Chain CDR2 comprises consensus sequence at least 90% identical to sequence: T at position 1, I or S at position 2, I or S at position 3, G or R at position 5, G or A at position 6, T or I at position 9, Y at position 10, Y at position 11, P or S at position12 and DSVKG for positions 13-17;

heavy chain CDR3 comprises consensus sequence at least 90% identical to sequence:_ G, L, or N at position 2, G or T at position 4, Y at position 7, D or E at position 12, A at position 14, and Y at position 15;

light chain CDR1 comprises consensus sequence at least 90% identical to sequence: K or R at position 1, A or S at position 2, S at position 3, K or Q at position 4, S at position 5, L or V at position 6, L at position 7, T or S at position 10, Y at position 15, and I, L or M at position 16;

light Chain CDR2 comprises consensus sequence at least 90% identical to sequence: L or W, or S at position 1, A or T at position 2, S at position 3, N or T at position 4, L or R at position 5, E or A at position 6, and S at position 7; and

light chain CDR3 comprises consensus sequence at least 90% identical to sequence: Q at position 1, H or Q at position 2, S, Q or R at position 3, R, S or Y at position 4, E, L, or S at position 5, L or S at position 6, P or S at position 7, F or L at position 8 and T at position 9.

19. An antibody, or fragment thereof, for the diagnosis, treatment or prevention of cancers wherein binding conformationally inducing peptide is within the N-26 sequence ISDVSVSDVPFPFSAQSGA (SEQ ID NO:6), wherein mutation or deletion within FPFS (SEQ ID NO:1747), SVSDV (SEQ ID NO:1751), or ASRYNLT (SEQ ID NO:1745) destroys binding of the antibody or fragment thereof to PSMGFR.

20 The antibody, or fragment thereof of claim 17, wherein
wherein

heavy chain CDR1 comprises consensus sequence at least 90% identical to sequence: F or I at position 1, T or A at position 2, F at position 3, S at position 4, T, G, or R at position 5, Y or F at position 6, A, G or T at position 7, M at position 8 and S at position 9;

heavy Chain CDR2 comprises consensus sequence at least 90% identical to sequence: T or A at position 1, I or S at position 2, I or S at position 3, N, S, T or G at position 4, G or R at position 5, G or A at position 6, G, T, or D at position 7, Y, K, H or S at position 8, T or I at position 9, Y or F at position 10, Y at position 11, P or S at position12 and D at position 13, S or T at position 14, V or L at position 15 and KG for positions 16-17;

heavy chain CDR3 comprises consensus sequence at least 90% identical to sequence: G, L, or N at position 2, G, T, or Y at position 3, G or T at position 4, Y at position 7, Y, A, or G at position 10, M, D or F at position 11, D or E at position 12 and AY at position 14-15;

light chain CDR1 comprises consensus sequence _ at least 90% identical to sequence: K or R at position 1, A or S at position 2, S or R at position 3, S, Y, I or V at position 8, T or S at position 10, G, S, D, or Q at position 12, V, Y, K or N at position 13, N, S, or T at position 14, Y or F at position 15, and I, L or M at position 16;

light Chain CDR2 comprises consensus sequence at least 90% identical to sequence: A, T or V at position 2, S at position 3, N, T, or K at position 4, L or R at position 5, E, A, F or D at position 6, and S at position 7; and

light chain CDR3 comprises consensus sequence at least 90% identical to sequence: Q, F or W at position 1, H or Q at position 2, R, S, T, Y or N at position 4, E, L, S or H at position 5, L, S, V, D or Y at position 6, P or S at position 7, and T at position 9.

21. The antibody, or fragment thereof of claim 17, which is MNC2, having
heavy chain CDR1 comprises consensus sequence FTFSGYAMS;
heavy Chain CDR2 comprises consensus sequence TISSGGTYIYYPDSVKG;
heavy chain CDR3 comprises consensus sequence -LGGDNYYEYFDV--;
light chain CDR1 comprises consensus sequence RASKS--VSTSGYSYMH;
light Chain CDR2 comprises consensus sequence LASNLES; and
light chain CDR3 comprises consensus sequence QHSRELPFT.

22. The antibody, or fragment thereof of claim 17, which is MNE6, having
heavy chain CDR1 comprises consensus sequence FTFSRYGMS;
heavy Chain CDR2 comprises consensus sequence TISGGGTYIYYPDSVKG;
heavy chain CDR3 comprises consensus sequence DNYGRNYDYGMDY--;
light chain CDR1 comprises consensus sequence -------SATSSVSYIH;
light Chain CDR2 comprises consensus sequence STSNLAS; and
light chain CDR3 comprises consensus sequence QQRSSSPFT.

23. The antibody, or fragment thereof of claim 17, which is B2, having
heavy chain CDR1 comprises consensus sequence FAFSTFAMS;
heavy Chain CDR2 comprises consensus sequence AISNGGGYTYYPDTLKG;
heavy chain CDR3 comprises consensus sequence ----RYYDLYFDL--;
light chain CDR1 comprises consensus sequence RSSQNIV-HSNGNTYLE;
light Chain CDR2 comprises consensus sequence KVSNRFS; and
light chain CDR3 comprises consensus sequence FQDSHVPLT.

24. The antibody, or fragment thereof of claim 17, which is B7, having
heavy chain CDR1 comprises consensus sequence FTFSRYGMS;
heavy Chain CDR2 comprises consensus sequence TISSGGTYIYYPDSVKG;
heavy chain CDR3 comprises consensus sequence DNYGSSYDYAMDY--;
light chain CDR1 comprises consensus sequence RSSQTIV-HSNGNTYLE;
light Chain CDR2 comprises consensus sequence KVSNRFS; and
light chain CDR3 comprises consensus sequence FQDSHVPLT.

25. The antibody, or fragment thereof of claim 17, which is B9, having
heavy chain CDR1 comprises consensus sequence FTFSRYGMS;
heavy Chain CDR2 comprises consensus sequence TISSGGTYIYYPDSVKG;
heavy chain CDR3 comprises consensus sequence DNYGSSYDYAMDY--;
light chain CDR1 comprises consensus sequence -------SASSSVSYMH;
light Chain CDR2 comprises consensus sequence TTSNLAS; and
light chain CDR3 comprises consensus sequence QQRSSYPF-.

26. The antibody, or fragment thereof of claim 17, which is 8C7F3, having
heavy chain CDR1 comprises consensus sequence FTFSTYAMS;
heavy Chain CDR2 comprises consensus sequence AISNGGGYTYYPDSLKG;
heavy chain CDR3 comprises consensus sequence ----RYYDHYFDY--;
light chain CDR1 comprises consensus sequence --RASESVATYGNNFMQ;
light Chain CDR2 comprises consensus sequence LASTLDS; and
light chain CDR3 comprises consensus sequence QQNNEDPPT.

27. The antibody, or fragment thereof of claim 17, which is H11, having

heavy chain CDR1 comprises consensus sequence FAFSTFAMS;
heavy Chain CDR2 comprises consensus sequence AISNGGGYTYYPDTLKG;
heavy chain CDR3 comprises consensus sequence ----RYYDLYFDL--;
light chain CDR1 comprises consensus sequence RSSQNIV-HSNGNTYLE;
light Chain CDR2 comprises consensus sequence KVSNRFS; and
light chain CDR3 comprises consensus sequence FQDSHVPLT.

28. The antibody, or fragment thereof of claim 17, which is B12, having
heavy chain CDR1 comprises consensus sequence SYGVH;
heavy Chain CDR2 comprises consensus sequence VIWPGGSTNYNSTLMSRM;
heavy chain CDR3 comprises consensus sequence DRTPRVGAWFAY; and
light chain CDR1 comprises consensus sequence RASESVATYGNNFMQ;
light Chain CDR2 comprises consensus sequence LASTLDS; and
light chain CDR3 comprises consensus sequence QQNNEDPPT.

29. The antibody, or fragment thereof of claim 17, which is 20A10, having
heavy chain CDR1 comprises consensus sequence FTFSTYAMS;
heavy Chain CDR2 comprises consensus sequence -SIGRAGSTYYSDSVKG;
heavy chain CDR3 comprises consensus sequence ---GPIYNDYDEFAY;
light chain CDR1 comprises consensus sequence KSSQSVLYSSNQKNYLA;
light Chain CDR2 comprises consensus sequence WASTRES; and
light chain CDR3 comprises consensus sequence HQYLSSLT.

30. The antibody, or fragment thereof of claim 17, which is 3C2B1, having
heavy chain CDR1 comprises consensus sequence ITFSTYTMS;
heavy Chain CDR2 comprises consensus sequence TISTGGDKTYYSDSVKG;
heavy chain CDR3 comprises consensus sequence -GTTAMYYYAMDY;
light chain CDR1 comprises consensus sequence RASKS---ISTSDYNYIH ;
light Chain CDR2 comprises consensus sequence LASNLES; and
light chain CDR3 comprises consensus sequence QHSRELPLT.

31. An antibody, or fragment thereof, for the diagnosis, treatment or prevention of cancers that requires presence of antibody binding conformationally inducing peptide ASRYNLT (SEQ ID NO:1745) of PSMGFR (SEQ ID NO:2).

32. The antibody, or fragment thereof of claim 31, which is 25E6, having

heavy chain CDR1 comprises consensus sequence FTFSSYGMS;
heavy Chain CDR2 comprises consensus sequence TISNGGRHTFYPDSVKG;
heavy chain CDR3 comprises consensus sequence QTGTEGWFAY;
light chain CDR1 comprises consensus sequence KSSQSLLDSDGKTYLN;
light Chain CDR2 comprises consensus sequence LVSKLDS _; and
light chain CDR3 comprises consensus sequence WQGTHFPQT.

33. An antibody, or fragment thereof, for the diagnosis, treatment or prevention of cancers that requires presence of antibody binding conformationally inducing peptide SVSDV (SEQ ID NO:1761) of PSMGFR (SEQ ID NO:2).

34. The antibody of claim 33, which is 5C6F3, having

heavy chain CDR1 comprises consensus sequence FTFSTYAMS ;
heavy Chain CDR2 comprises consensus sequence AISNGGGYTYYPDSLKG;
heavy chain CDR3 comprises consensus sequence RYYDHYFDY;
light chain CDR1 comprises consensus sequence RSSQTIVHSNGNTYLE;
light Chain CDR2 comprises consensus sequence KVSNRFS; and
light chain CDR3 comprises consensus sequence FQDSHVPLT.

35. The antibody or fragment thereof according to claims 1-34, which is murine, camelid, human or humanized.

36. The antibody or fragment thereof according to claims 1-34, wherein the antibody fragment is scFv or scFv-Fc, which variable regions thereof may be murine, camelid, human or humanized.

37. A chimeric antigen receptor (CAR) comprising the antibody fragment of claim 36.

38. A chimeric antigen receptor (CAR) comprising the antibody fragment of claim 36, further comprising mutations in the co-stimulatory domain or CD3-zeta signaling domain.

39. The CAR of claim 38, wherein tyrosines are mutated in CD28 or 4-1BB.

40. The CAR of claim 38, wherein the CD3-zeta contains 1XX mutations.

41. An immune cell comprising the CAR of claim 37.

42, The immune cell of claim 41, which is a T cell, NK cell, dendritic cell, or mast cell.

43. A cell composition expressed in a cell comprising a CARs of claim 37, and second entity having a biological recognition unit that has a specificity that is different from that of the CAR.

44. The composition of claim 43, wherein the second entity binds PD-1, PDL-1, or other checkpoint inhibitor.

45. The composition of claim 43, wherein the second entity binds to NME7.

46. The composition of claim 43, wherein the second entity is a cytokine.

47. The composition of claim 46, wherein the cytokine is IL-12.

48. The composition of claim 46, wherein the cytokine is IL-18

49. The composition of claim 43, wherein the second entity is c-Jun

50. An immune cell engineered to express a nucleic encoding a CAR of claim 37 and a nucleic acid encoding a second entity as in any of the claims above wherein the second entity expressed from an inducible promoter.

51. The immune cell of claim 50, wherein the second entity is expressed from an inducible promoter that is activated by elements of an activated immune cell.

52. The immune cell of claim 51, wherein the second entity is expressed from an NFAT inducible promoter.

53. The immune cell of claim 52, wherein the NFAT is NFATc1, NFATc3 or NFATc2.

54. The immune cell of claim 50, wherein the second entity is a cytokine.

55. The immune cell of claim 51, wherein the cytokine is IL-7, IL-15, or IL-18.

56. The immune cell of claim 50, wherein the nucleic acids encoding the second entity are inserted into a Foxp3 promoter or enhancer region.

57. The immune cell of claim 56, wherein the cytokine is IL-18.

58. The immune cell of claim 56, wherein the cytokine is expressed from an NFAT inducible promoter.

59. A BiTE construct comprising the antibody fragment of claim 36.

60. An antibody drug conjugate (ADC) comprising the antibody or antibody fragment of claim 35.

61. An antibody or fragment thereof that specifically binds to PSMGFR (SEQ ID NO:2) and N-10 (SEQ ID NO:3); and

(i) does not bind to full-length MUC1;

(ii) does not bind to C-10 (SEQ ID NO:825);

(iii) competitively inhibits binding of NME1 or NME7$_{AB}$ to MUC1* extra cellular domain or a PSMGFR peptide;

(iv) recognizes a MUC1* generated by cleavage by a cleavage enzyme;

(v) recognizes a conformational epitope and not a linear epitope; or

(vi) is cancer selective by immunohistochemistry on tissues.

62. The antibody or fragment thereof of claim 61, wherein four of the criteria (i) – (vi) are satisfied.

63. The antibody or fragment thereof of claim 61, wherein five of the criteria (i) – (vi) are satisfied.

64. The antibody or fragment thereof of claim 61, wherein six of the criteria (i) – (vi) are satisfied.

65. The antibody or fragment thereof of claim 61, wherein at least criteria (vi) is satisfied.

66. The antibody or fragment thereof of claim 61, wherein cleavage enzyme is MMP-9.

67. The antibody or fragment thereof of claims 1-66, wherein the cancer is breast cancer, pancreatic cancer, ovarian cancer, lung cancer, colon cancer, gastric cancer or esophageal cancer.

Fig. 1A

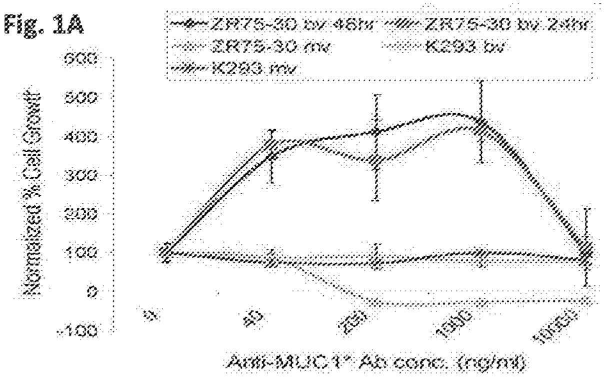


Fig. 1B

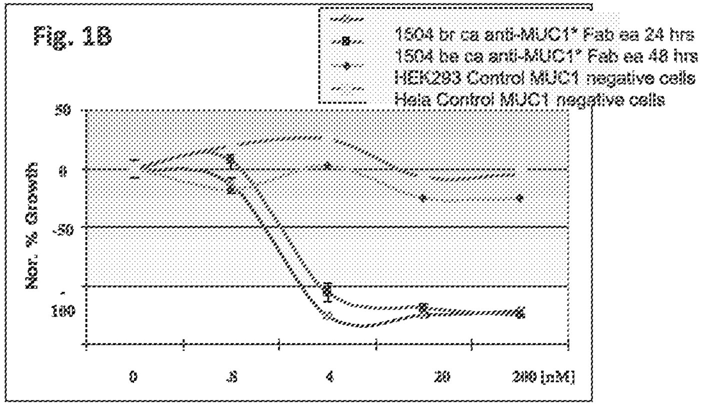


Fig. 1C

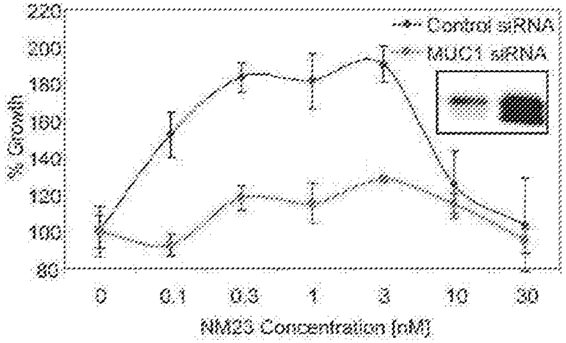


Fig. 1D NME7-AB induces growth of MUC1* positive cells

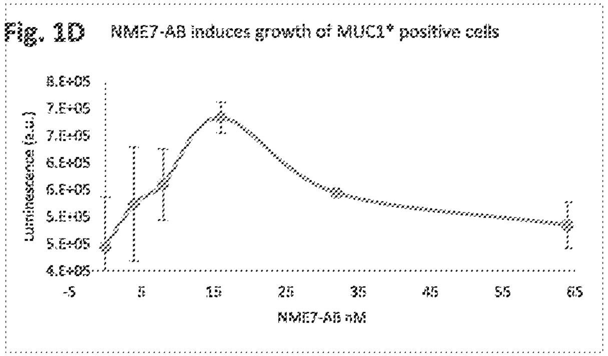


Figure 1A-1D

Fig. 2A

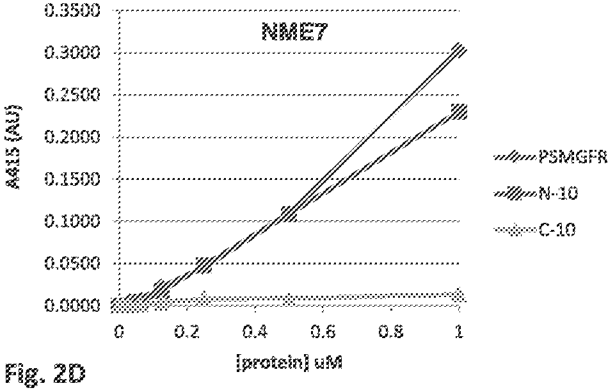


Fig. 2B

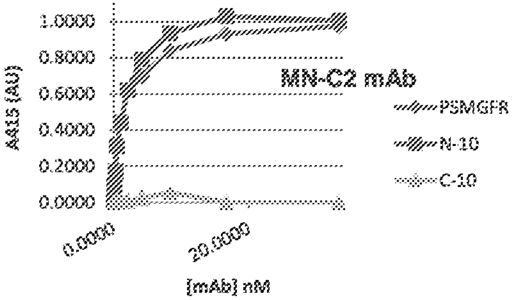


Fig. 2C

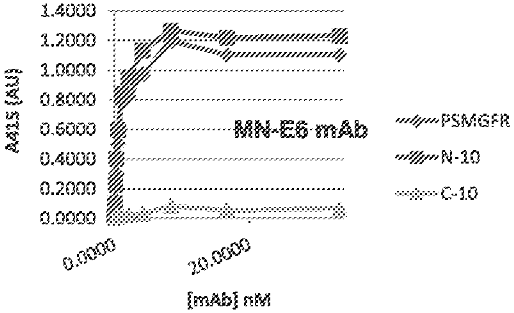


Fig. 2D

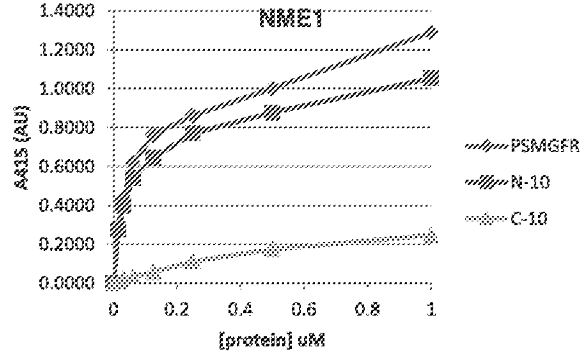


Fig. 2E

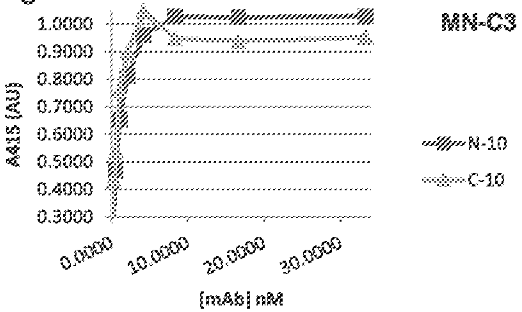


Fig. 2F

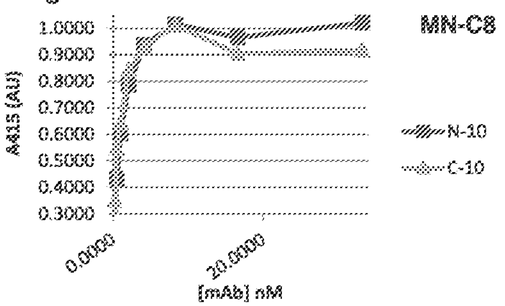


Fig. 2G PSMGFR GTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA

Fig. 2H PSMGFR N-10 QFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA

Fig. 2I PSMGFR C-10 GTINVHDVETQFNQYKTEAASRYNLTISDVSVSDV

Figure 2A-2I

Fig. 3A

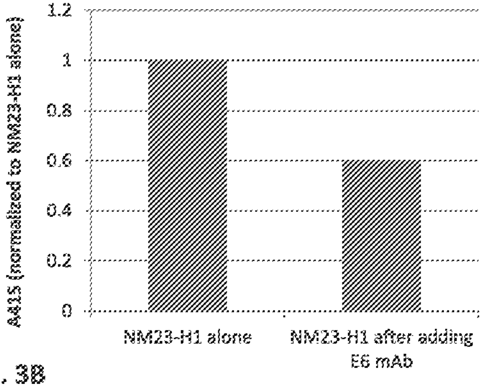


Fig. 3B

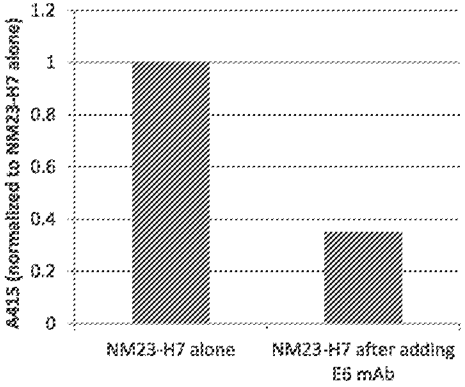


Fig. 3C

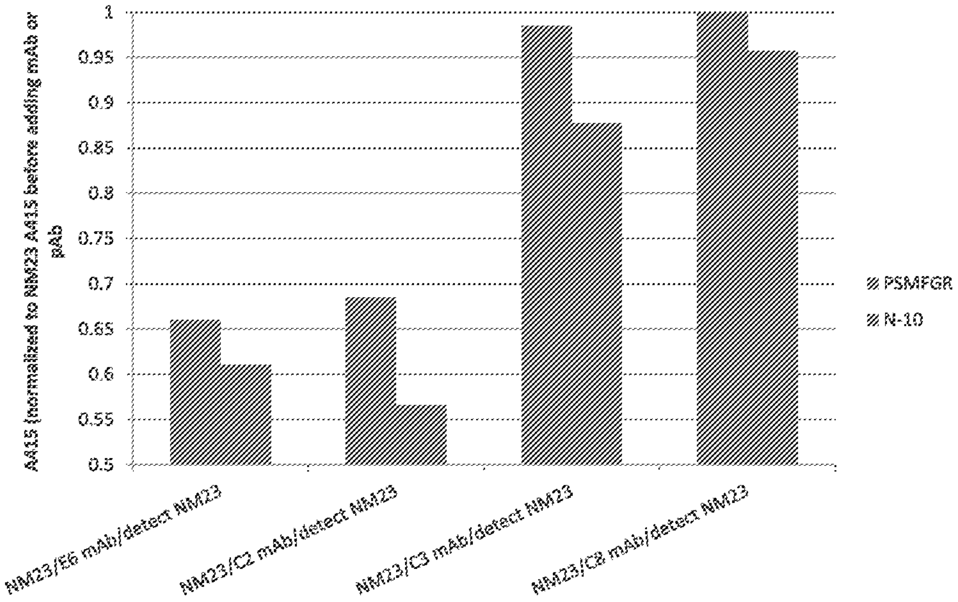


Figure 3A-3C

Humanized MN-C2 scFv binds to ZR-75-1, aka 1500, MUC1* positive breast cancer cells

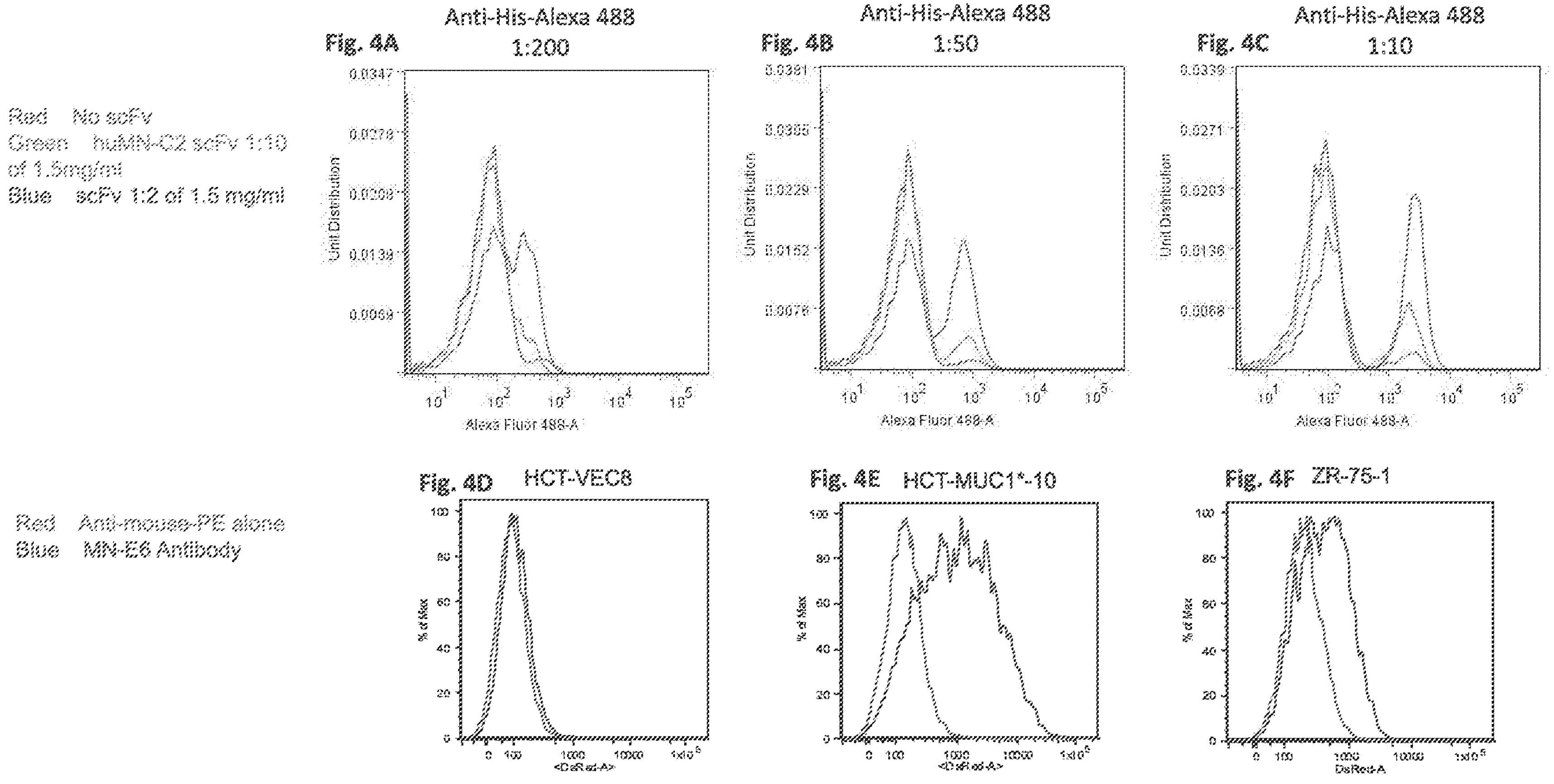


Figure 4A-4F

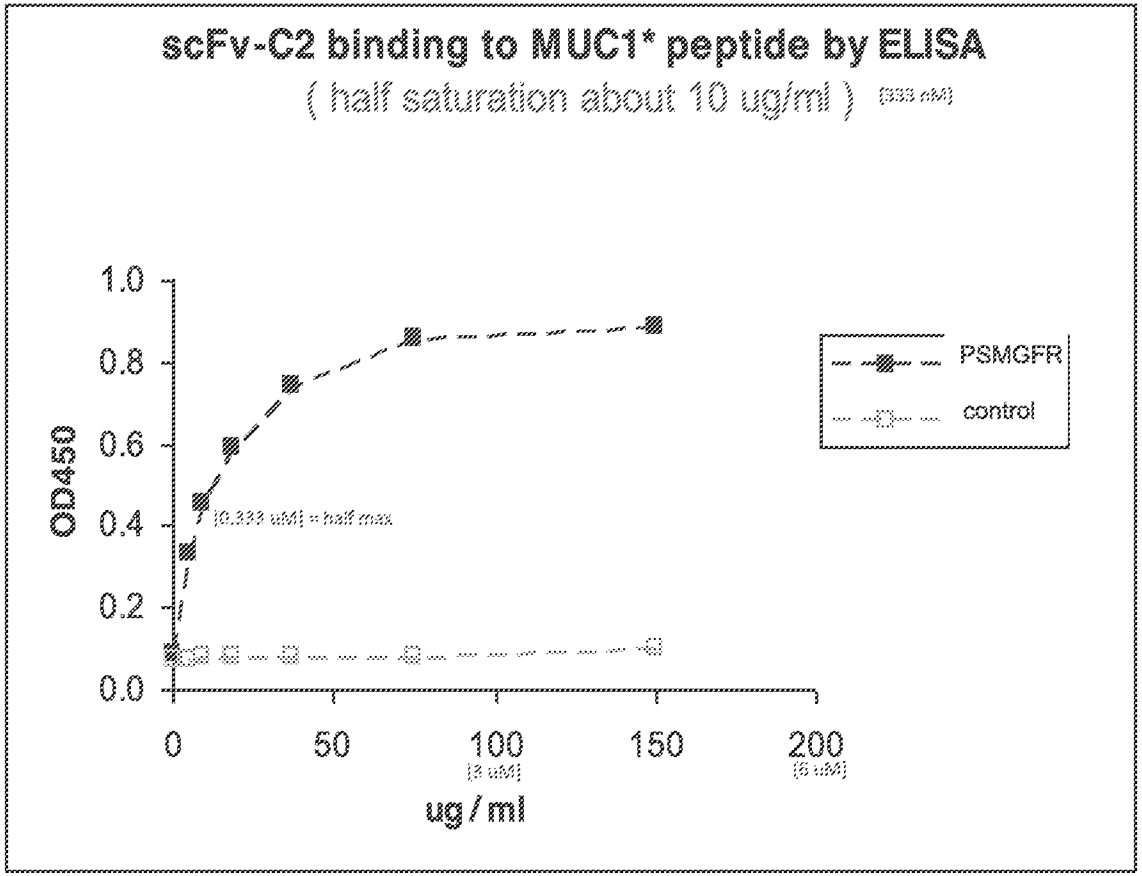

scFv-C2 binding to MUC1* peptide by ELISA
(half saturation about 10 ug/ml) [333 nM]
OD450
1.0
0.8
0.6
0.4
0.2
0.0
[0.333 uM] = half max
0
50
100
[3 uM]
150
200
[6 uM]
ug / ml
PSMGFR
control

Figure 5

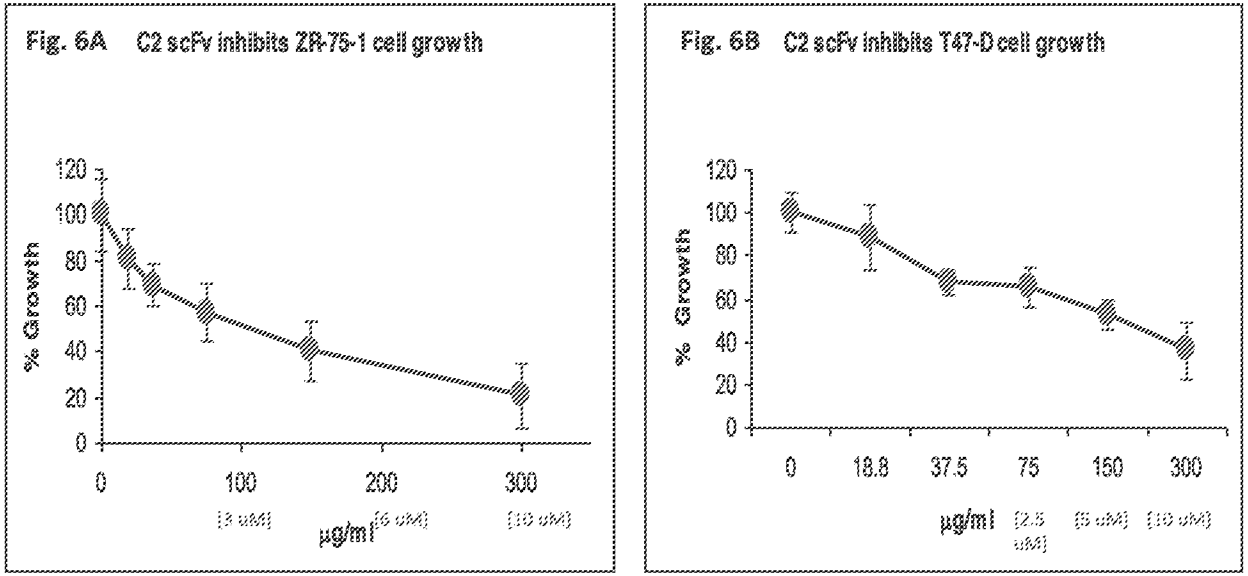


Fig. 6A C2 scFv inhibits ZR-75-1 cell growth

Fig. 6B C2 scFv inhibits T47-D cell growth

Figure 6A-6B

Fig. 7A

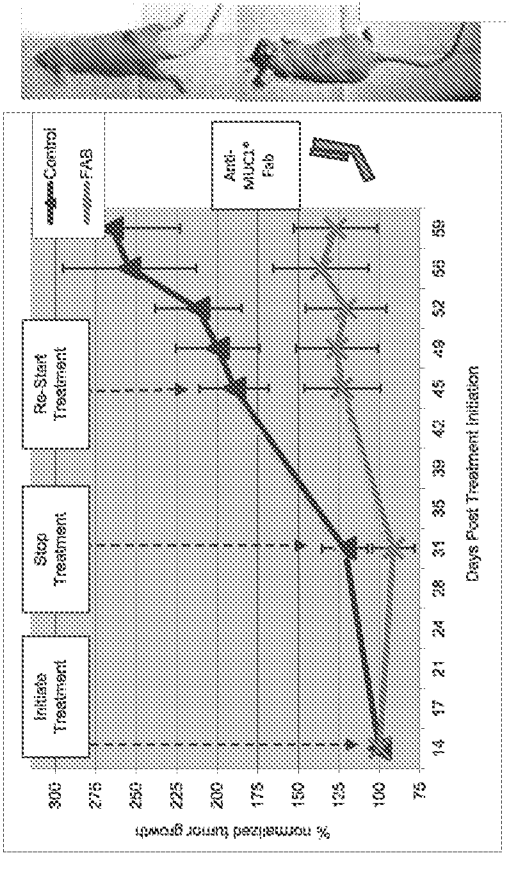


Fig. 7B

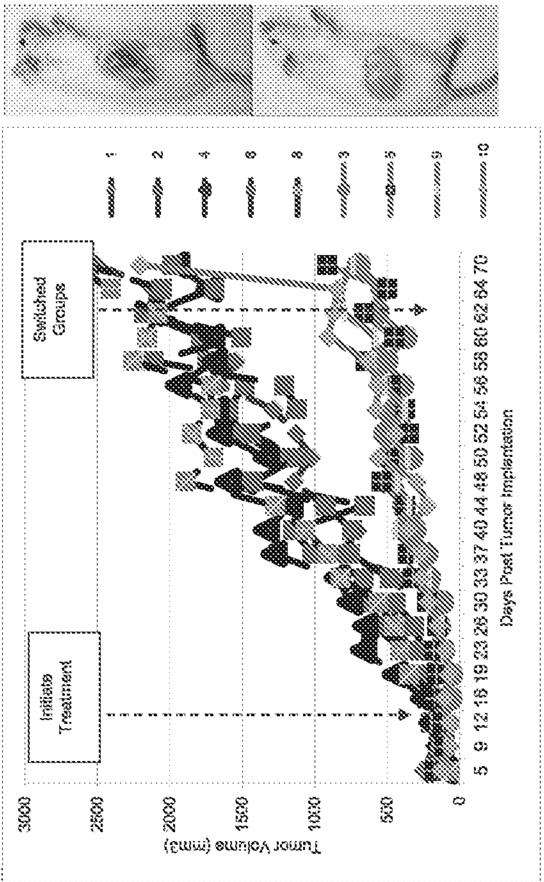


Figure 7A-7B

ELISA – hu MN-E6 scFv-Fc binding to MUC1* peptides PSMGFR, PSMGFR N-10 and PSMGFR C-10

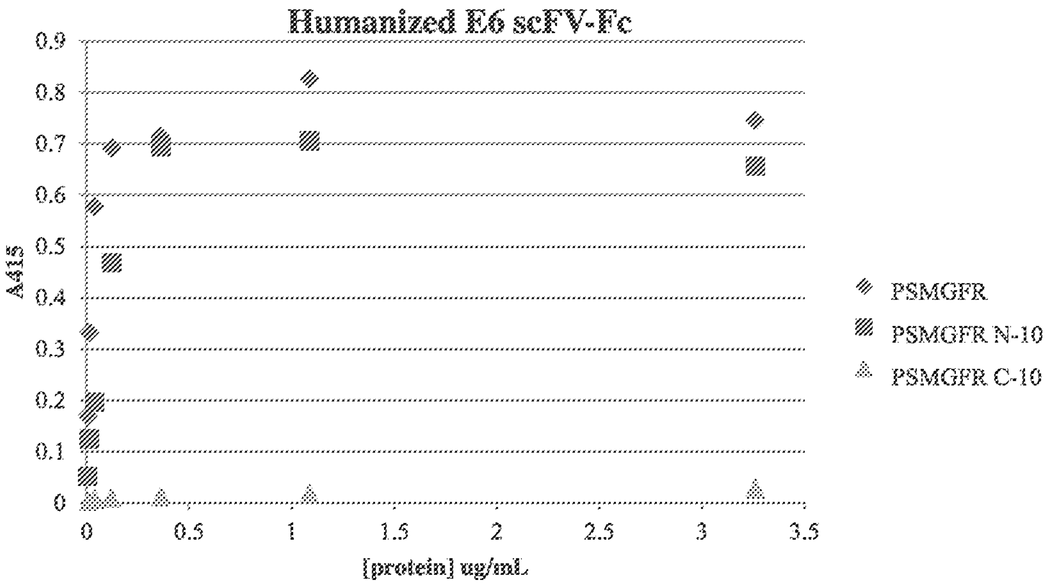


Figure 8

ELISA – mouse monoclonal MN-C3, humanized MN-C3 and humanized MN-C3 scFv-Fc binding to MUC1* peptides PSMGFR, PSMGFR N-10 and PSMGFR C-10

Fig. 9A

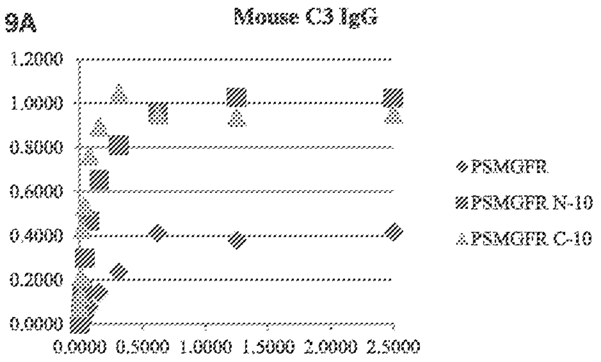


Fig. 9B

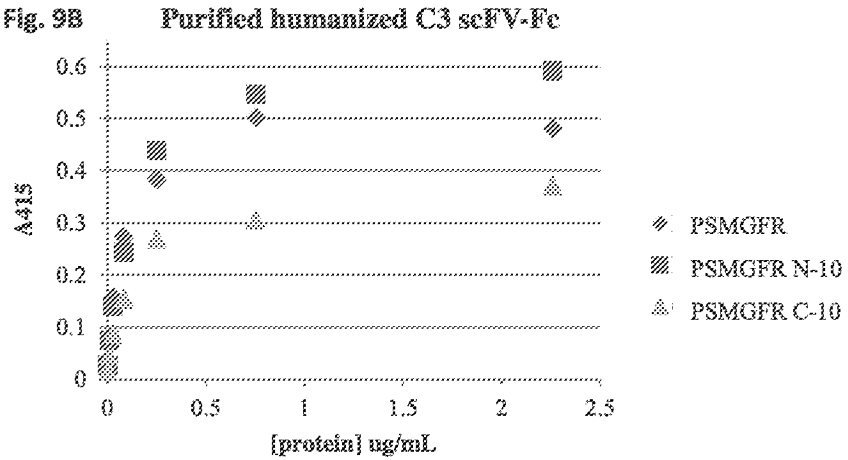


Figure 9A-9B

Tissue arrays comprising specimens from 240 breast cancer patients were stained with an antibody (VU4H5) that recognizes full-length MUC1 (left) or stained with an antibody that recognizes MUC1* (MN-C2). The data show that most or all (green boxes) of the MUC1 on cancerous tissue is MUC1* and not MUC1 full-length (MUC1-FL). The data further show that MN-C2 monoclonal antibody binds to cancerous tissue but not the healthy control tissue.

Fig. 10A

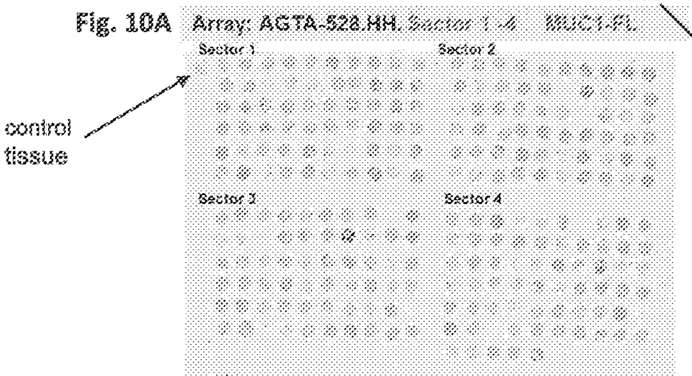


Fig. 10B

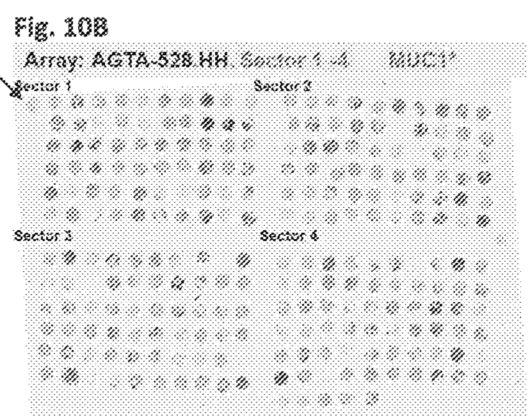


Fig. 10C

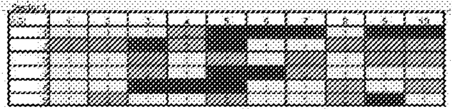


Fig. 10G

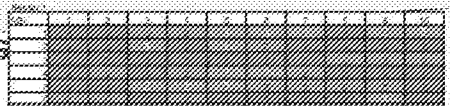


Fig. 10D

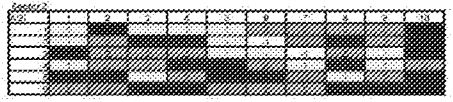


Fig. 10H

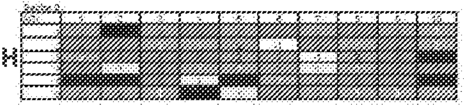


Fig. 10E

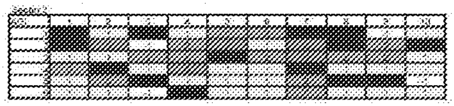


Fig. 10I

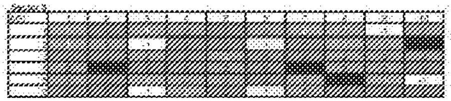


Fig. 10F

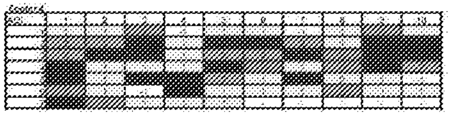
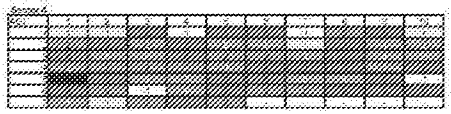


Fig. 10J



Green = MUC1* positive; MUC1 negative

White: no sample

Black: no stain

Yellow: weak stain

Figure 10A-10J

Tissue arrays comprising specimens from 240 breast cancer patients were stained with an antibody (VU4H5) that recognizes full-length MUC1 (left) or stained with an antibody that recognizes MUC1* (MN-C2). The data show that most or all (green boxes) of the MUC1 on cancerous tissue is MUC1* and not MUC1 full-length (MUC1-FL). The data further show that MN-C2 monoclonal antibody binds to cancerous tissue but not the healthy control tissue.

Fig. 11A

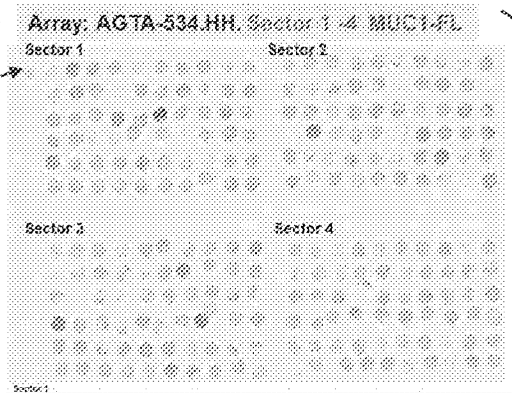


Fig. 11B

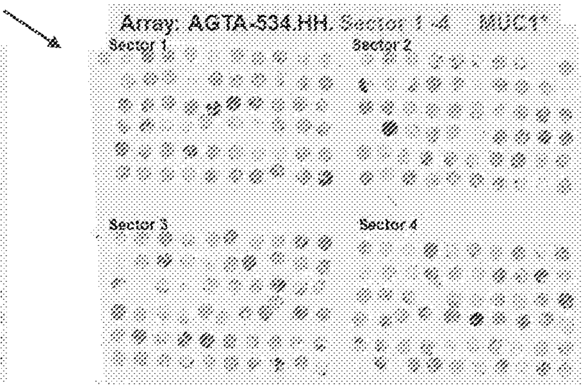


Fig. 11C

Fig. 11D

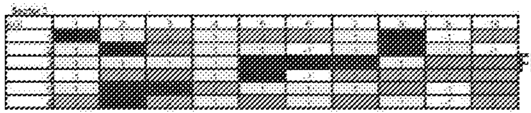


Fig. 11E

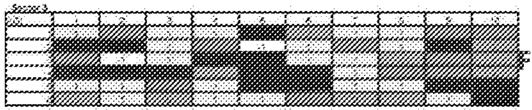


Fig. 11F

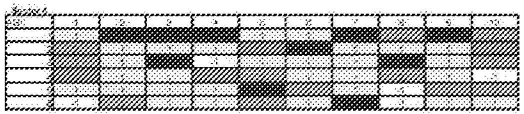


Fig. 11G

Fig. 11H

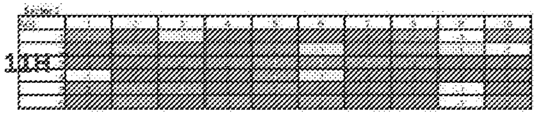


Fig. 11I

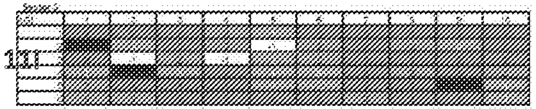
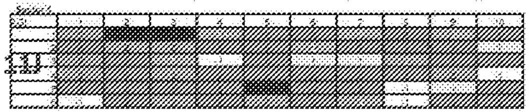


Fig. 11J



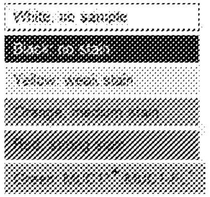


Figure 11A-11J

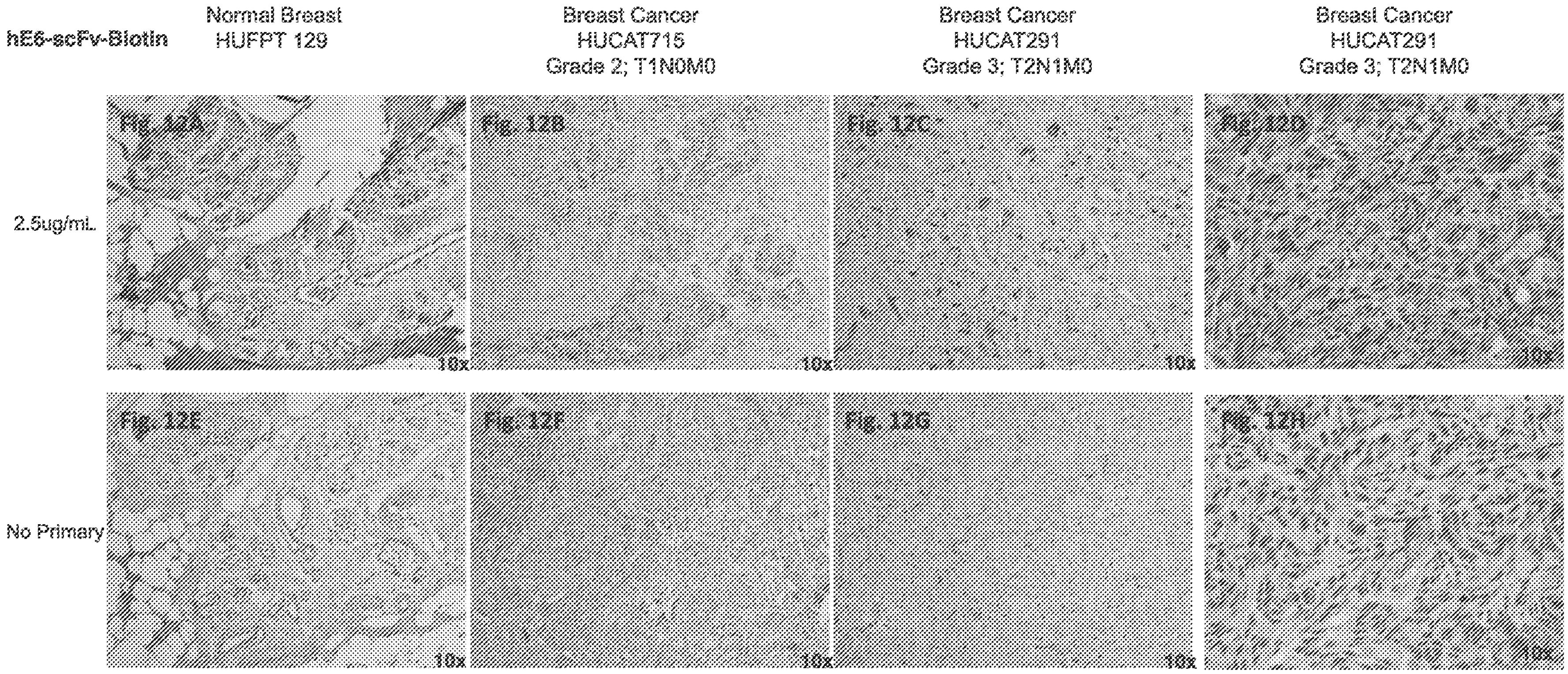


Figure 12A-12H

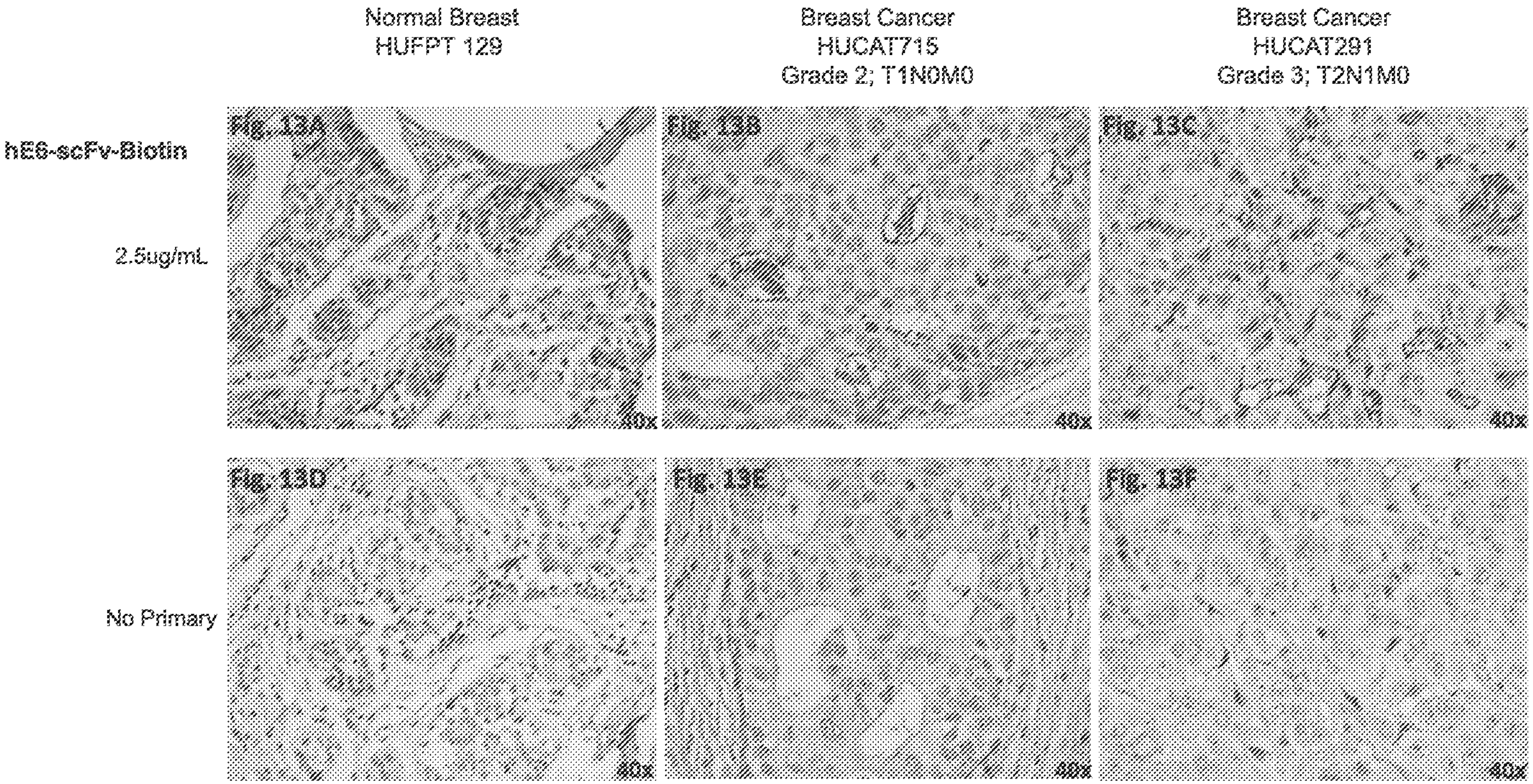


Figure 13A-13F

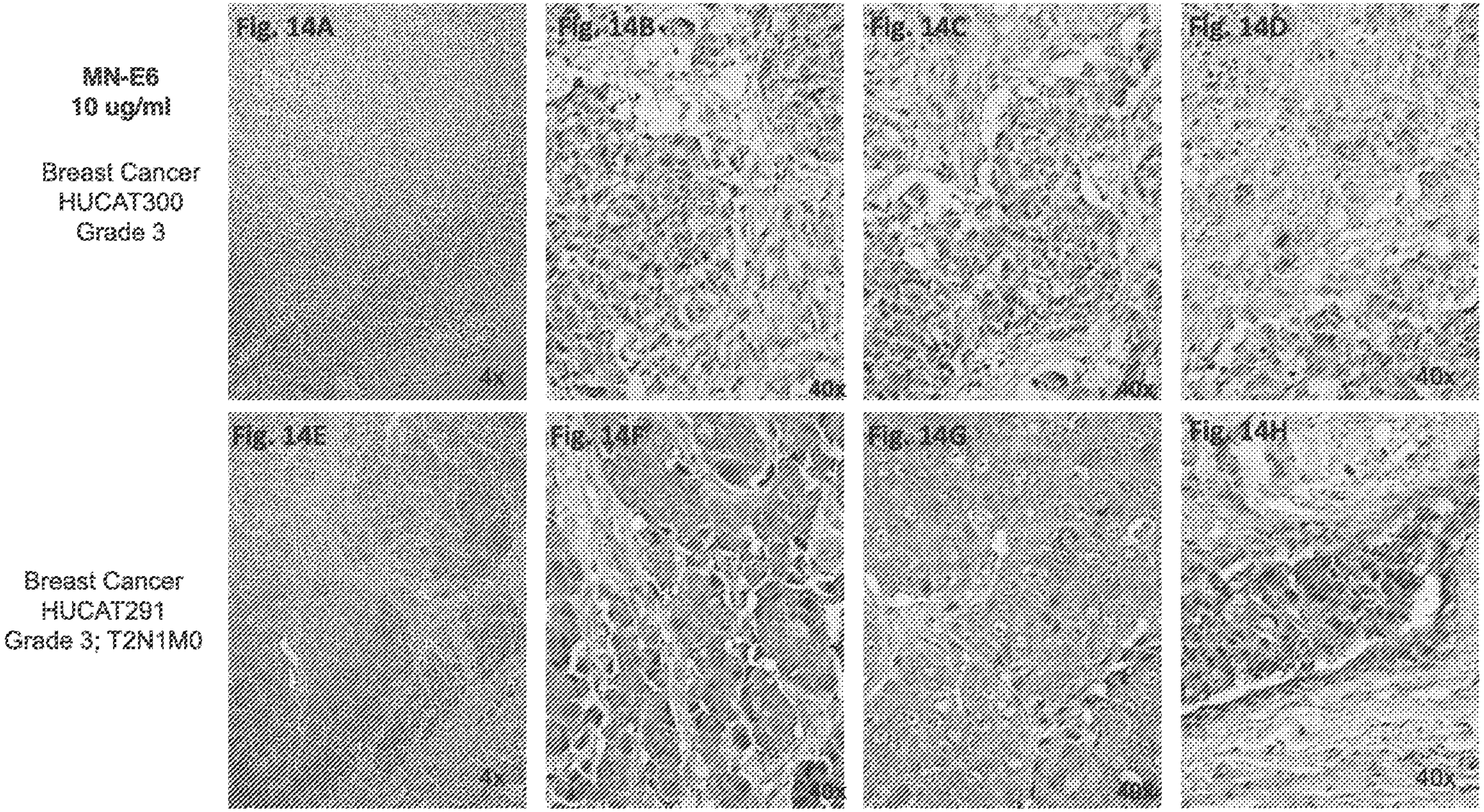


Figure 14A-14H

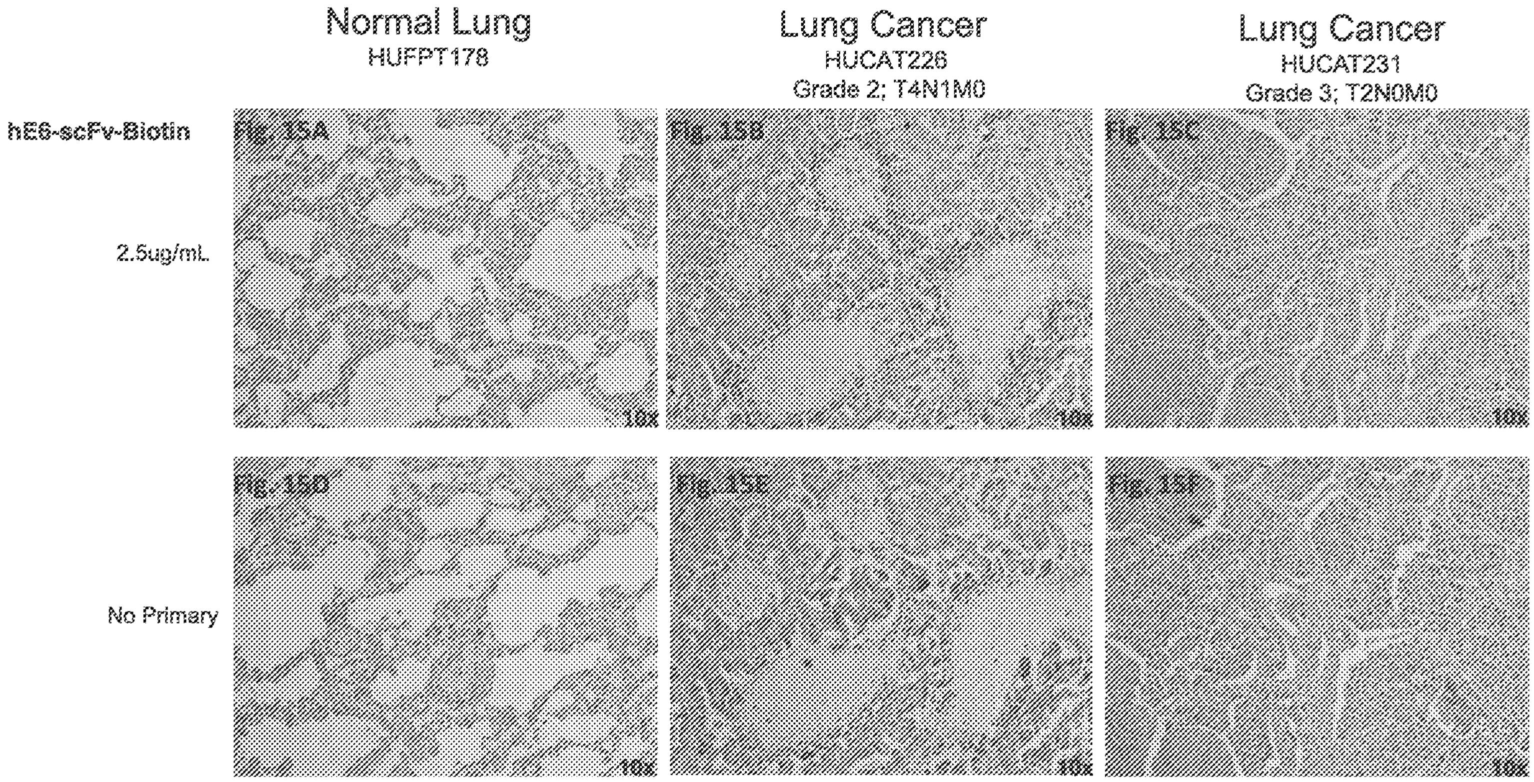


Figure 15A-15F

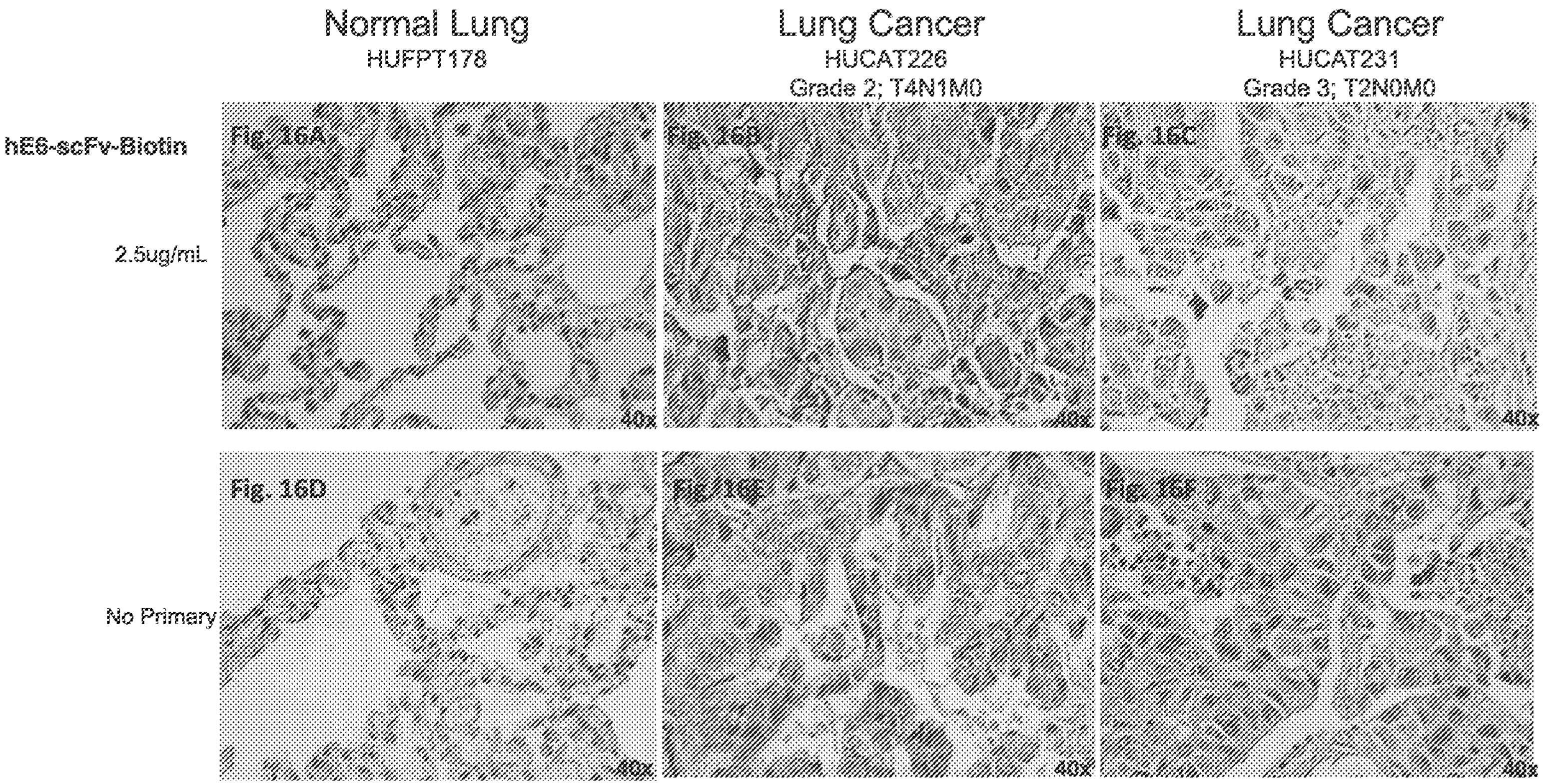


Figure 16A-16F

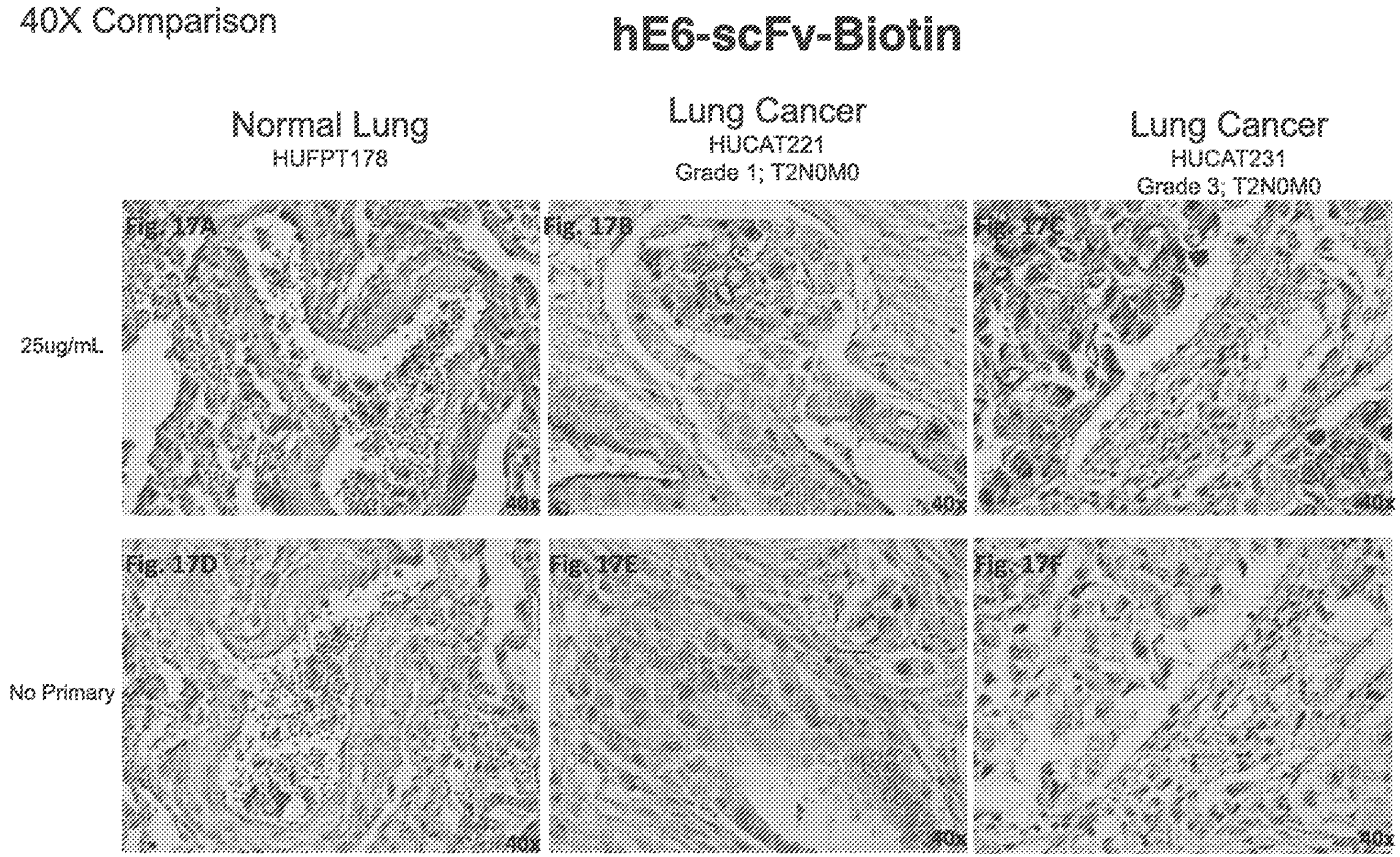


Figure 17A-17F

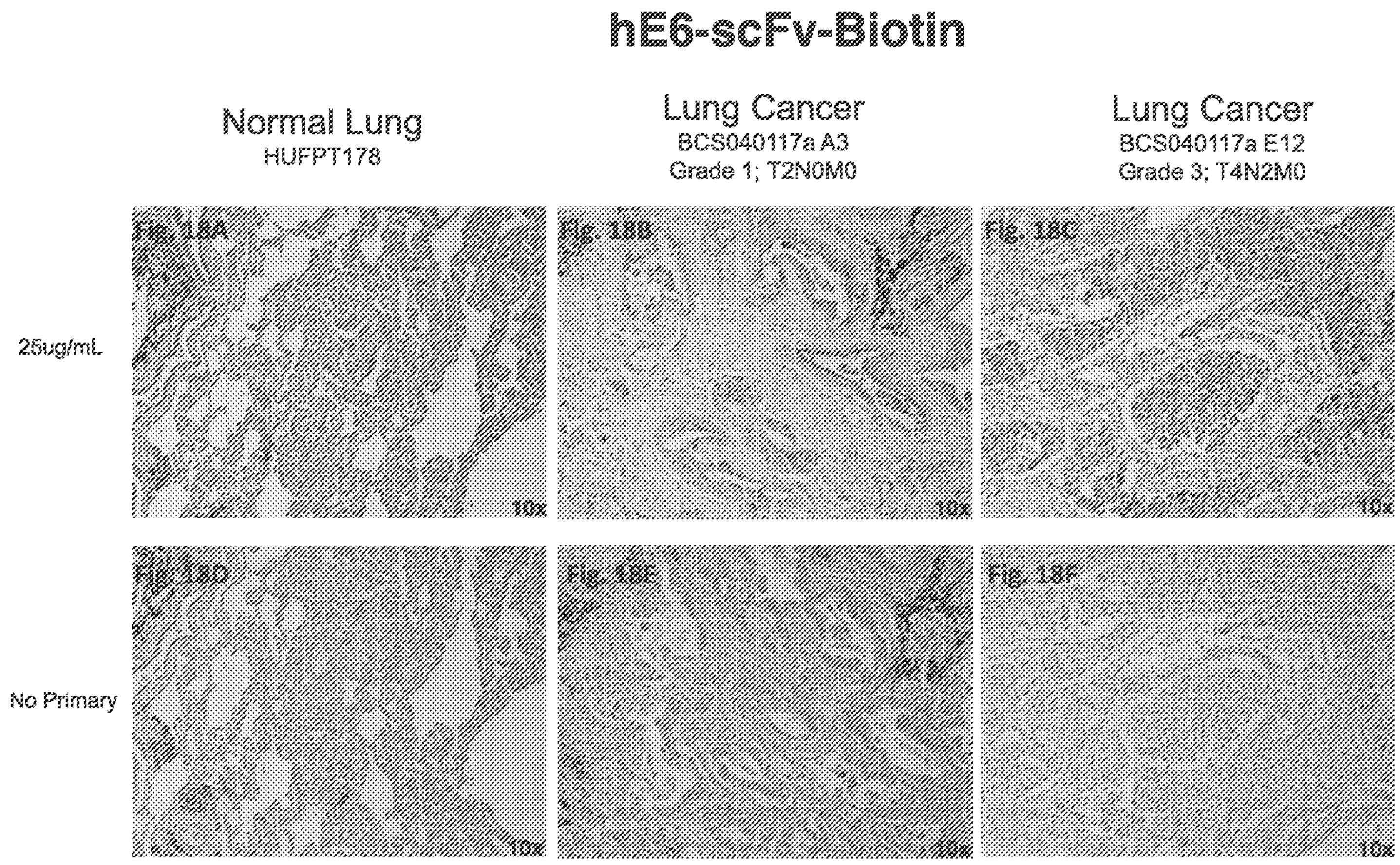


Figure 18A-18F

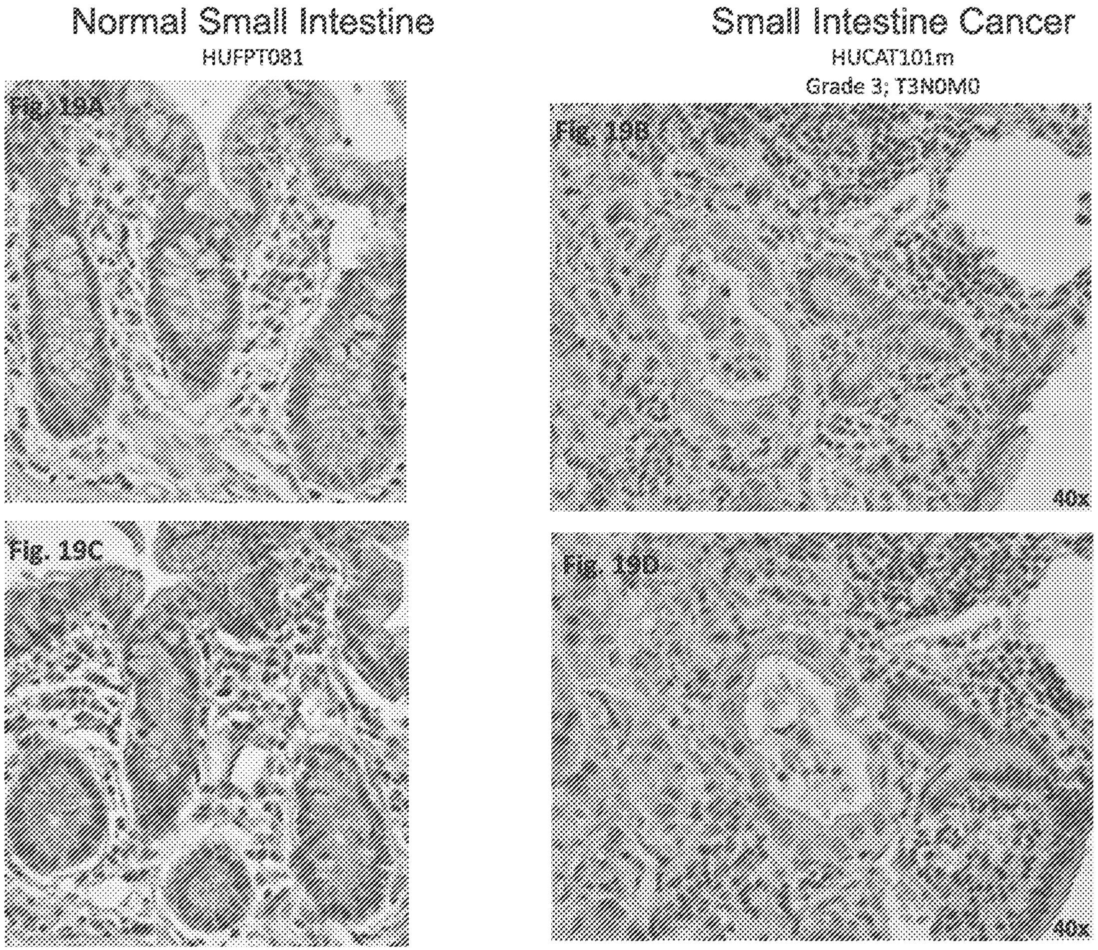


Figure 19A-19D

Small Intestine Normal
HUFPT081

hu-E6
scFv+Fc

50 ug/ml
2' (1:1000)

2' only control
(GaH-HRP)
1:1000

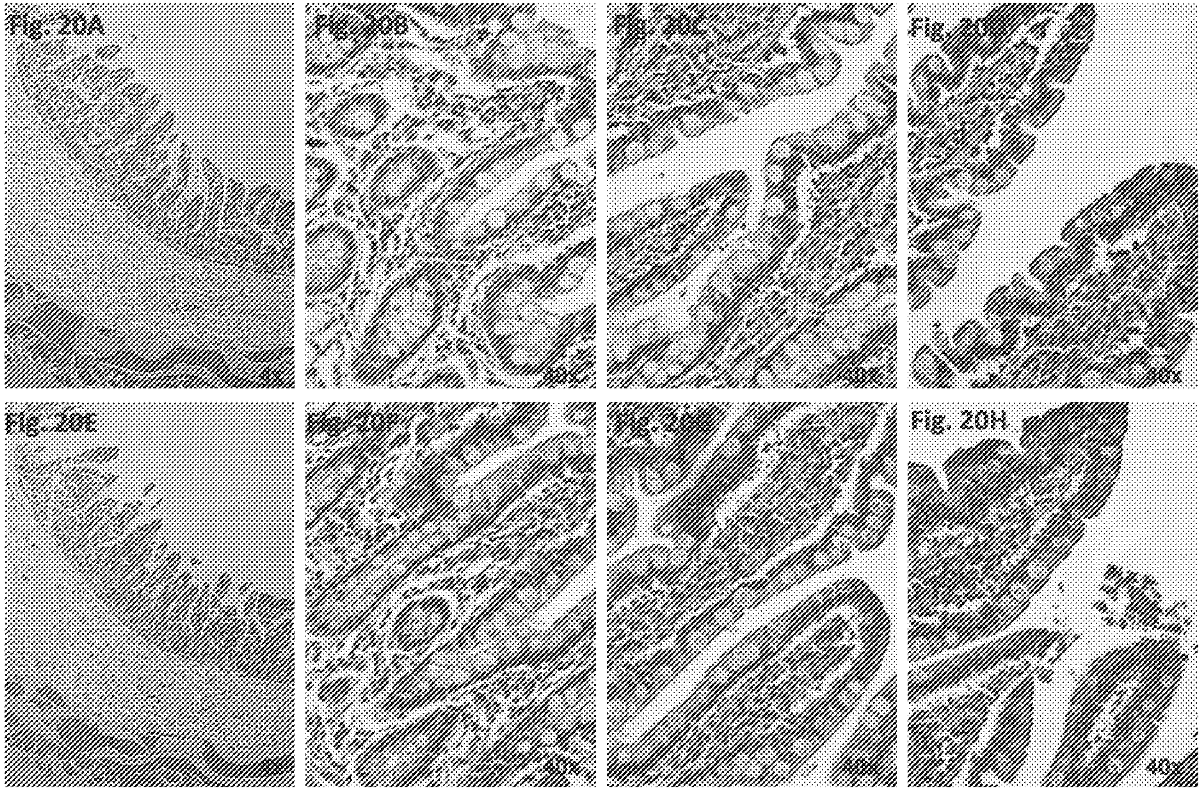
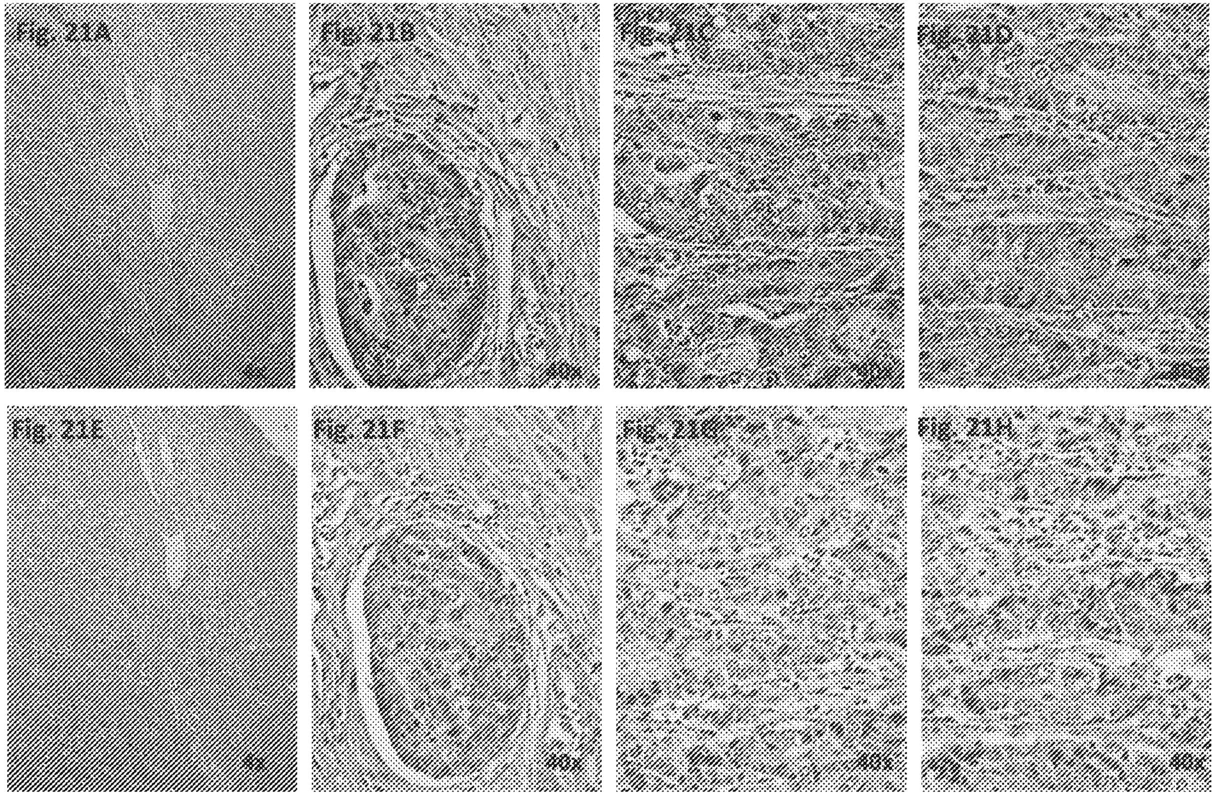


Figure 20A-20H

Small Intestine Cancer
HUCAT096
Grade 3; T3N0M0



hu-E6
scFv+Fc

50 ug/ml
2' (1:1000)

2' only control
(GaH-HRP)

1:1000

Figure 21A-21H

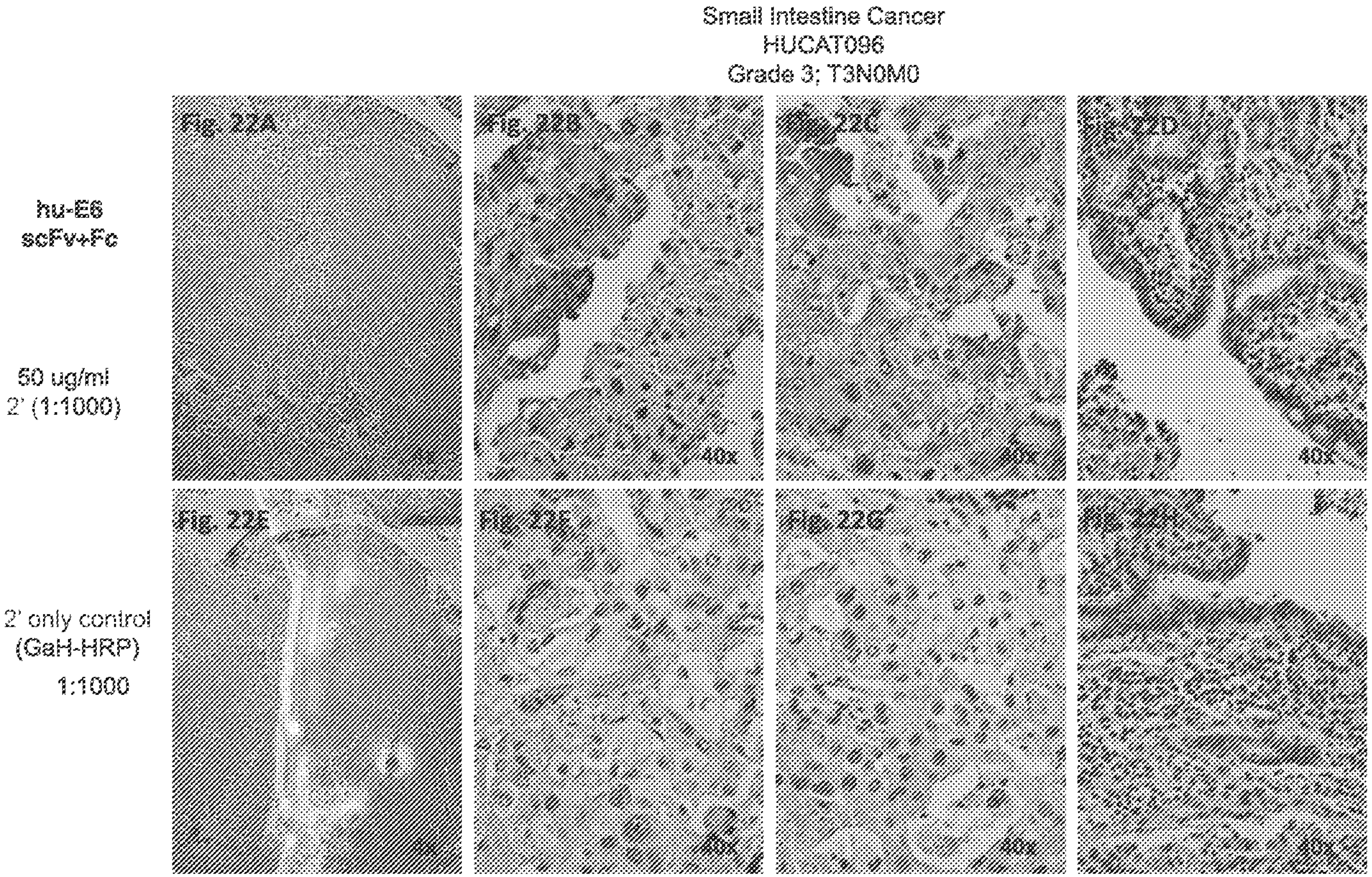


Figure 22A-22H

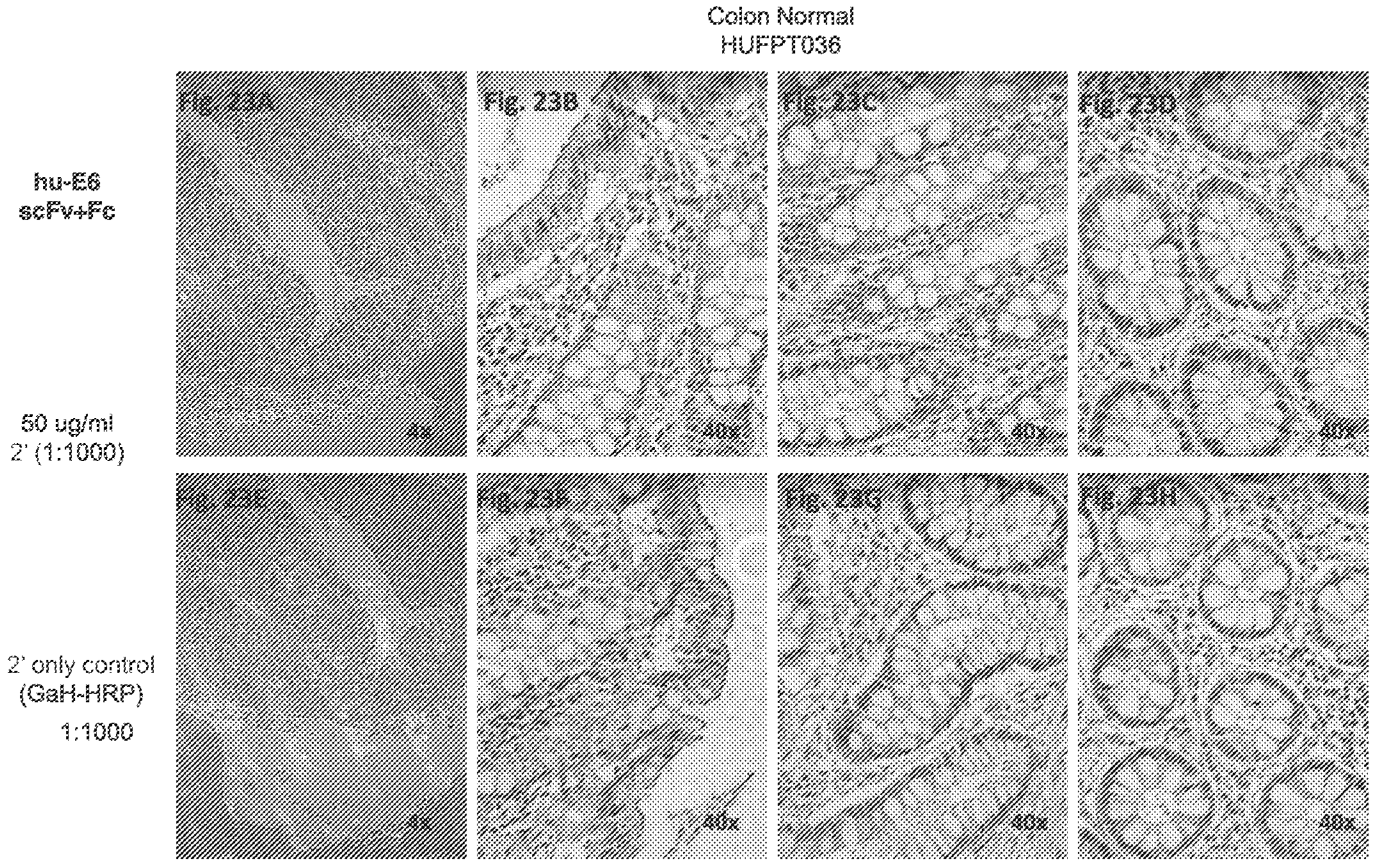


Figure 23A-23H

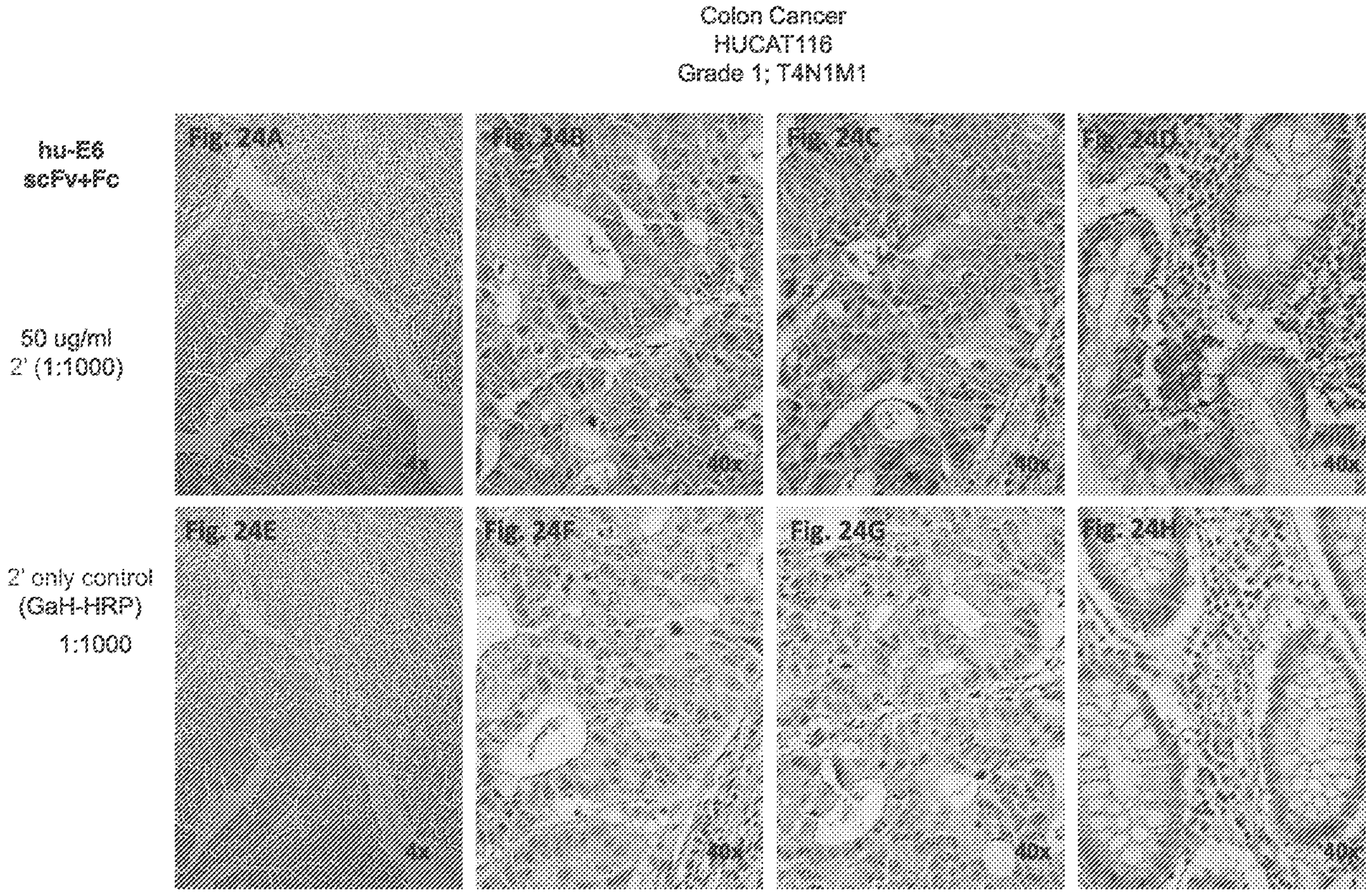


Figure 24A-24H

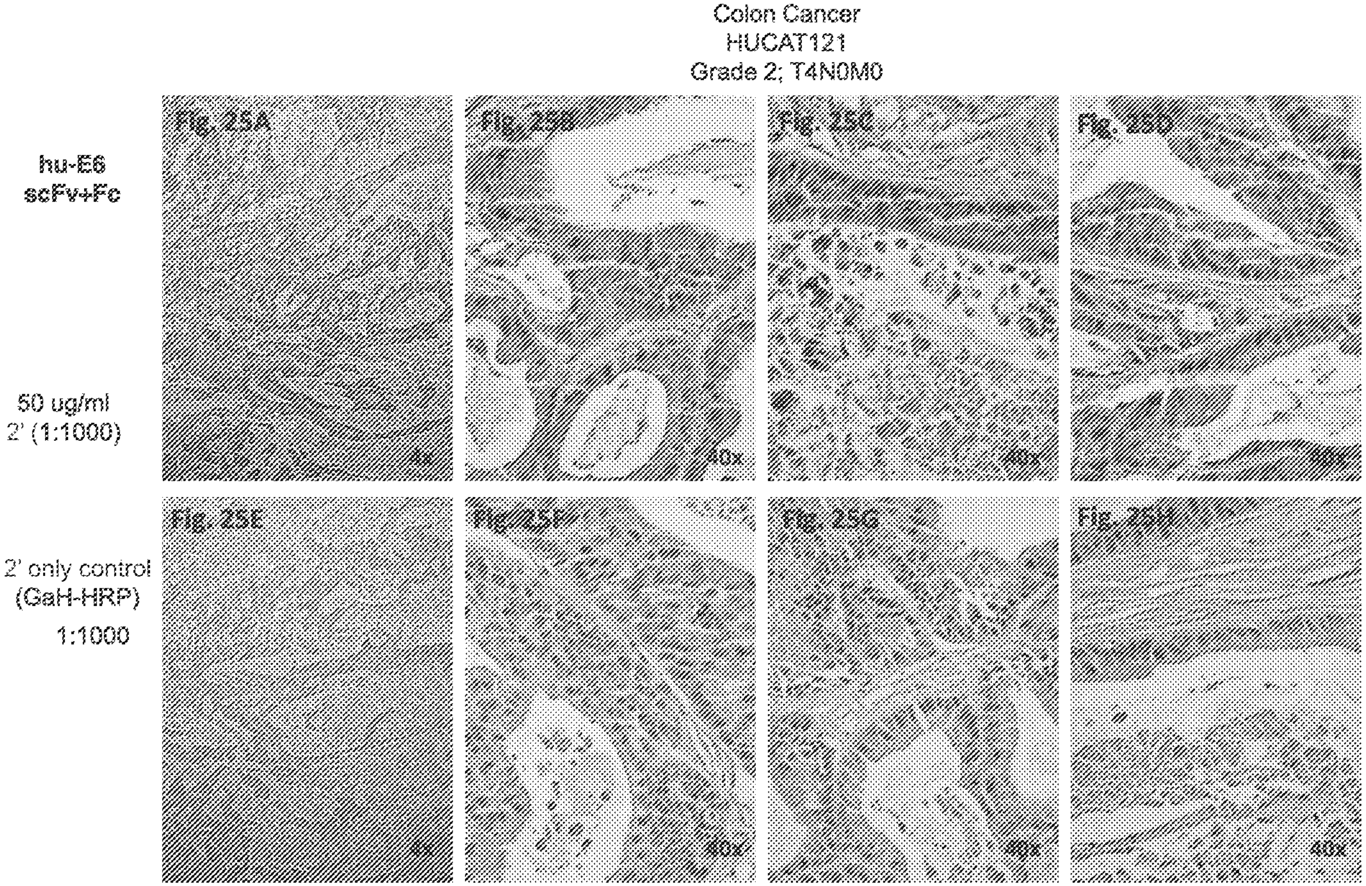


Figure 25A-25H

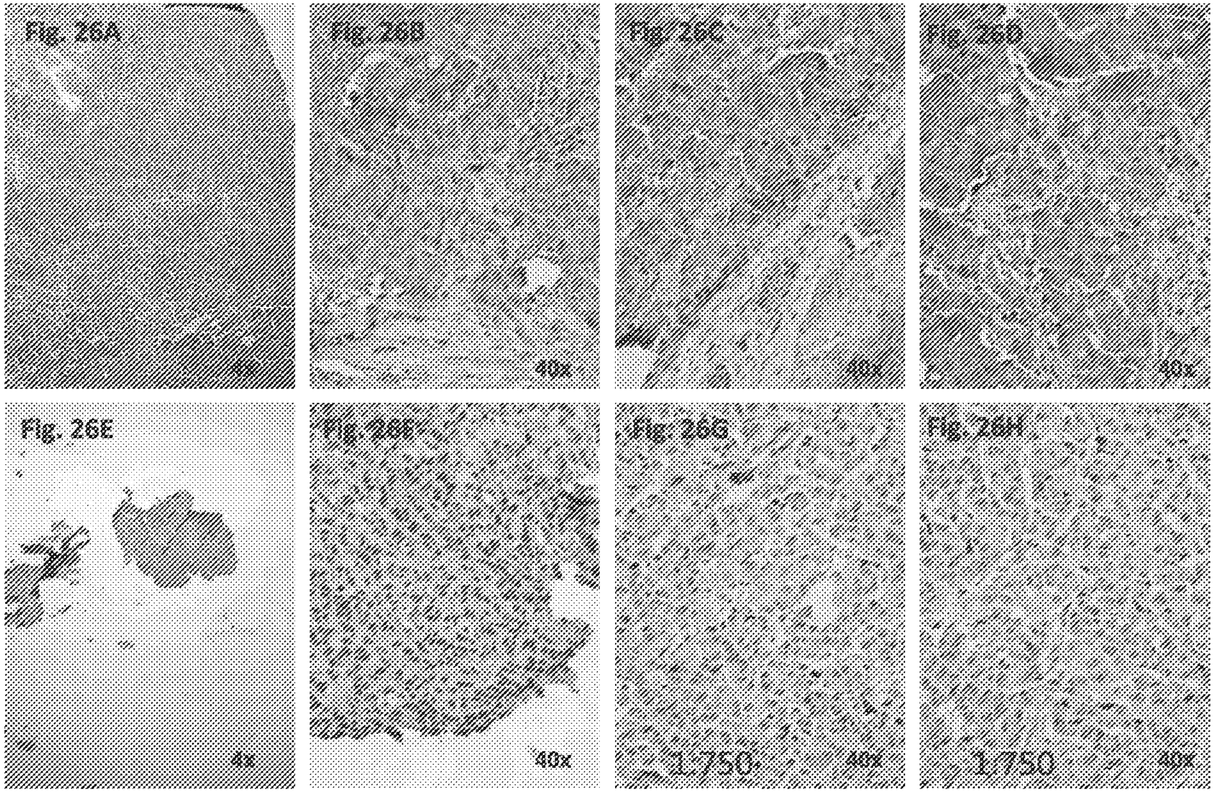


Figure 26A-26H

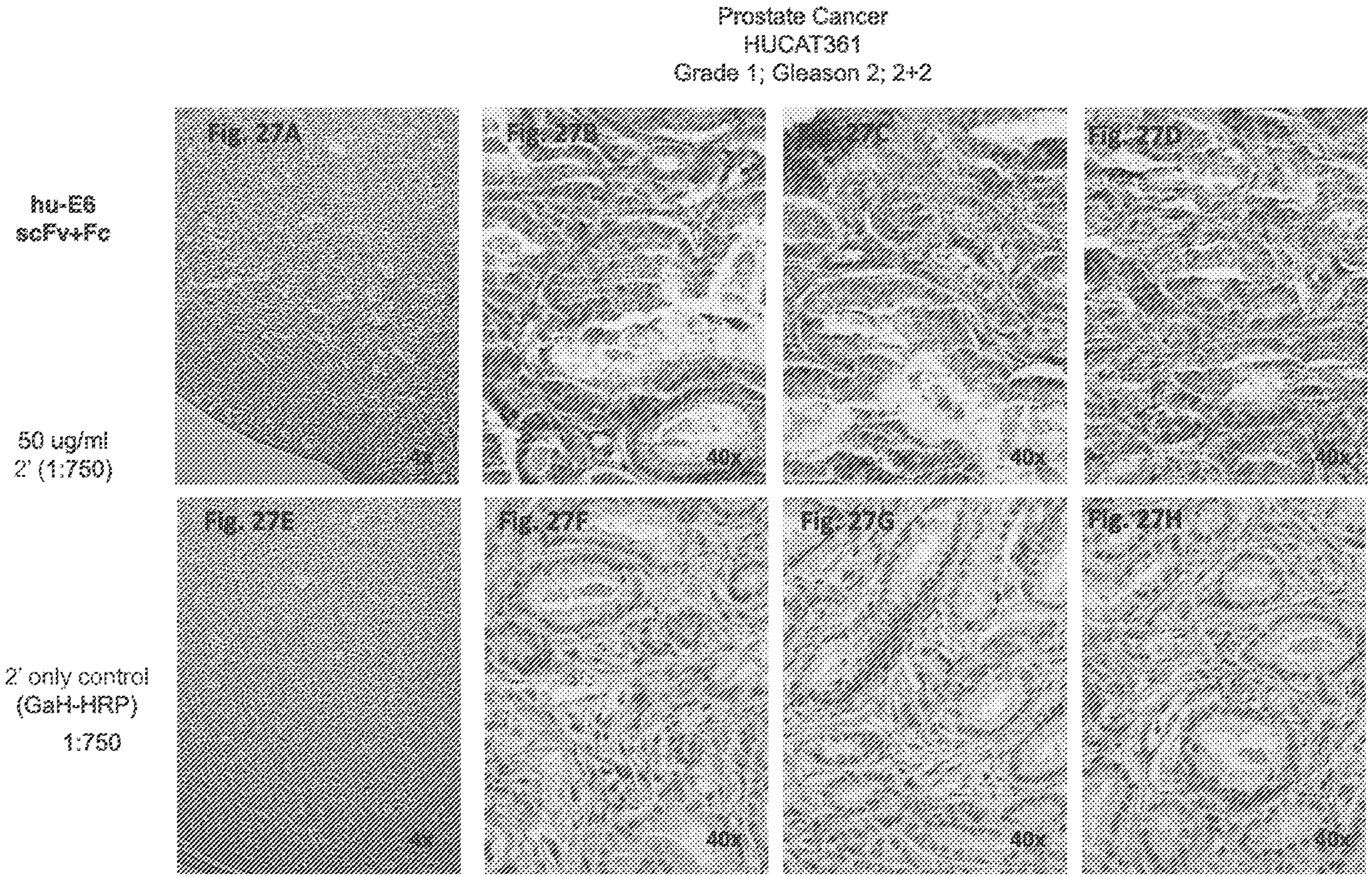


Figure 27A-27H

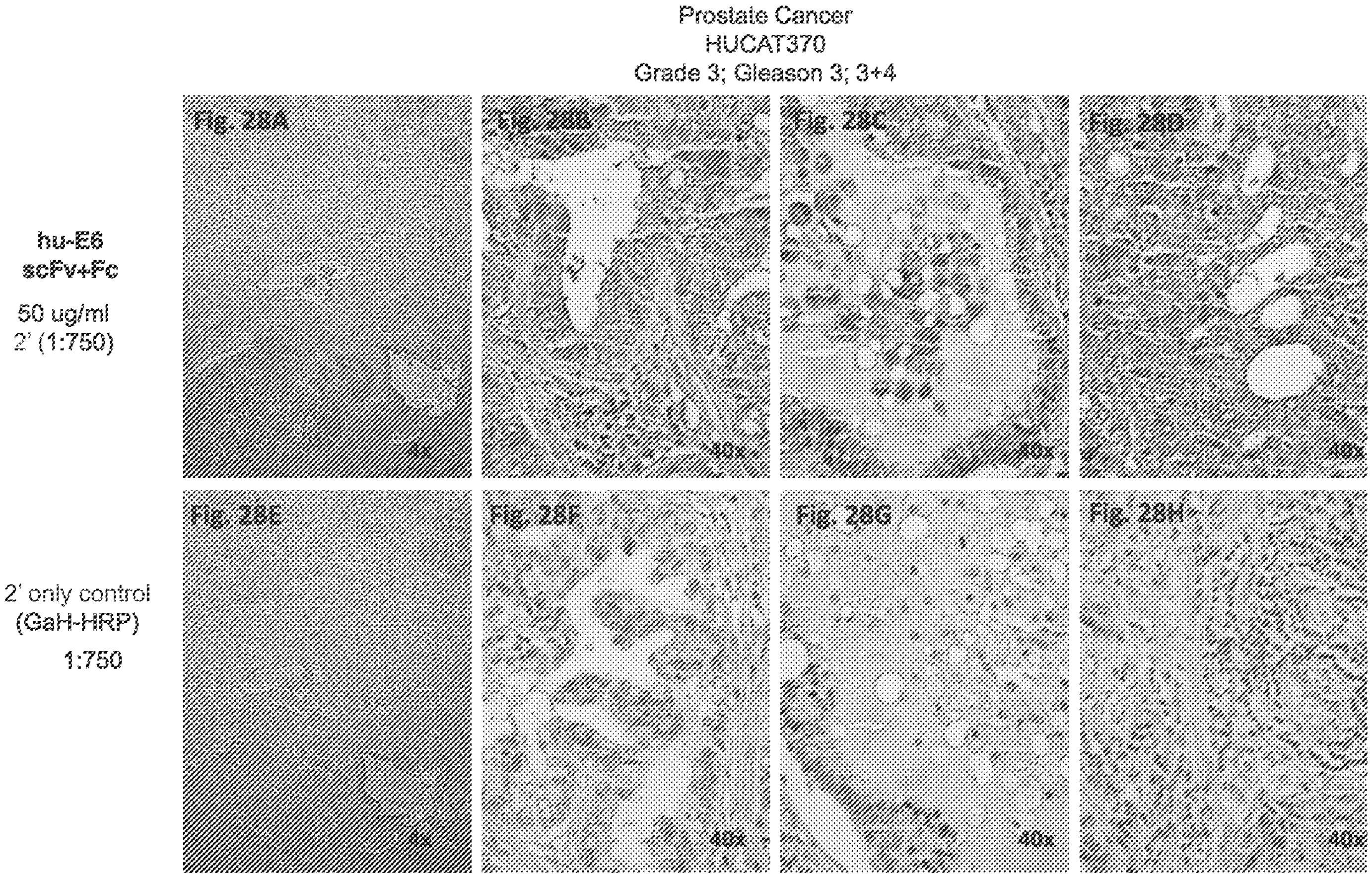


Figure 28A-28H

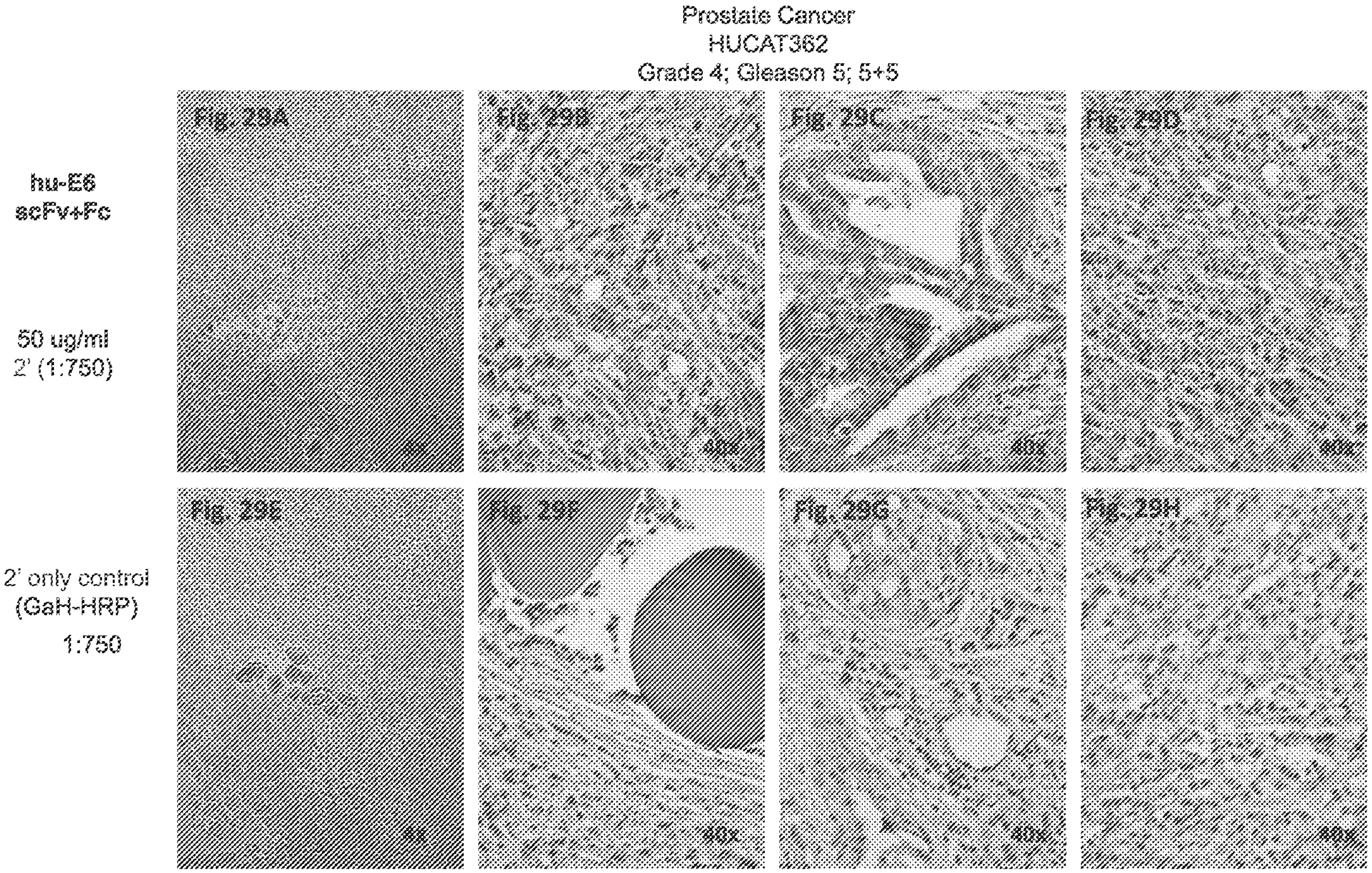


Figure 29A-29H

Triple Negative Breast Cancer 85% Positive

BR487b

Antibody: MN-hC2-scFv-Fc-Biotin 50ug/mL

Fig. 30A

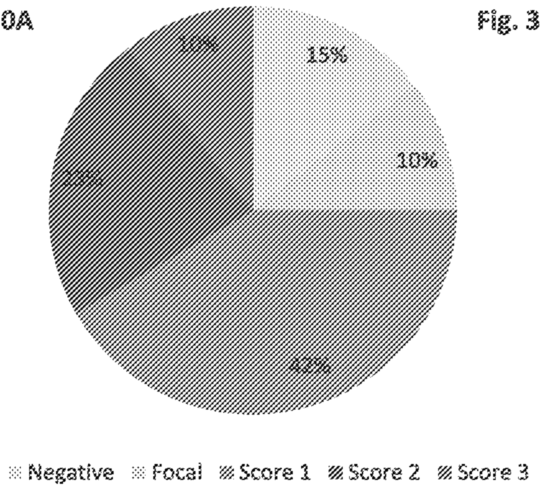
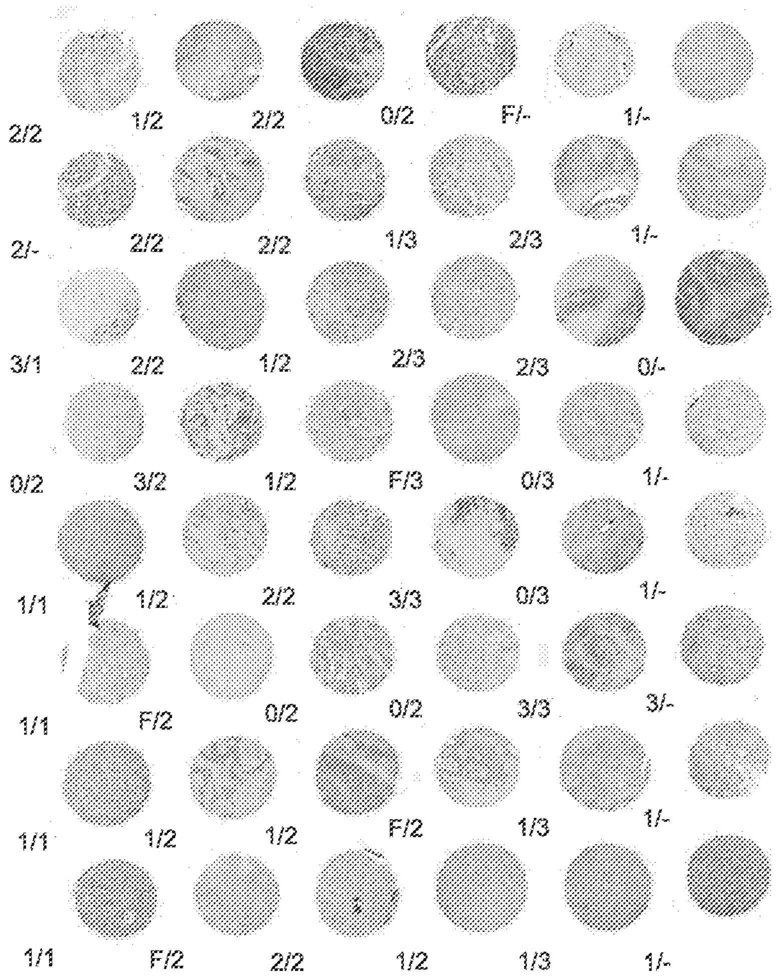


Fig. 30B

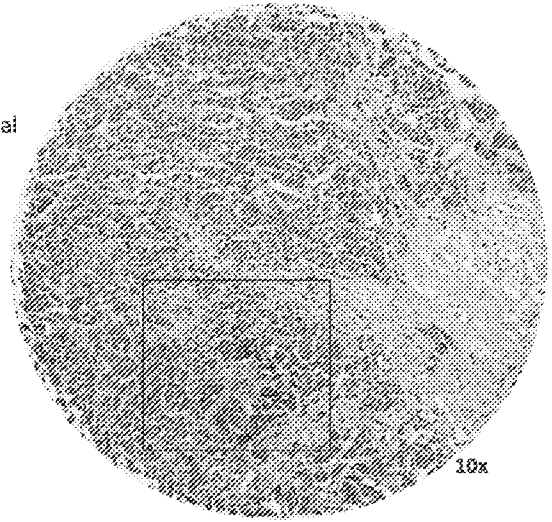


Score/Grade
2/3 = Score 2; Grade 3

Figure 30A-30B

Score 2
Grade 2
T2N0M0
Invasive ductal
Carcinoma
Address C8

Fig. 30C



Score 3
Grade 3
T2N1M0
Invasive ductal
Carcinoma
Address E3

Fig. 30D

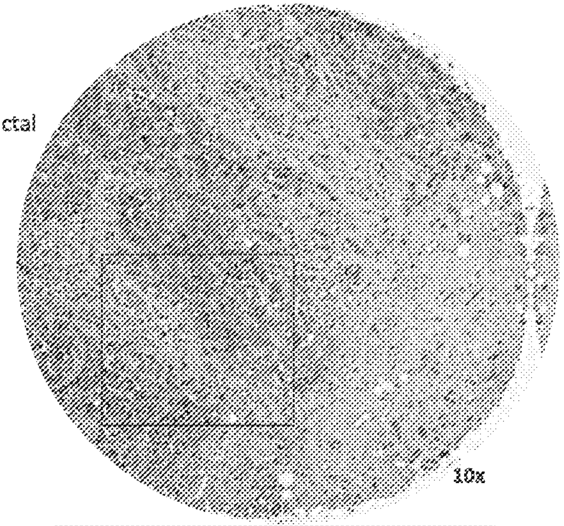


Fig. 30E

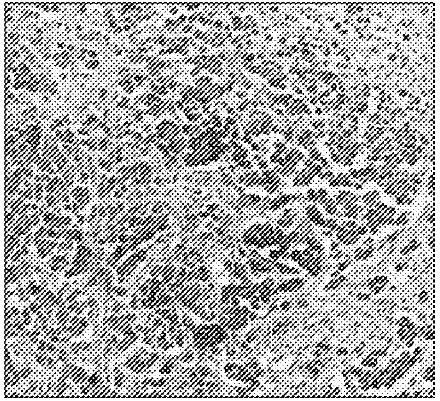


Fig. 30F

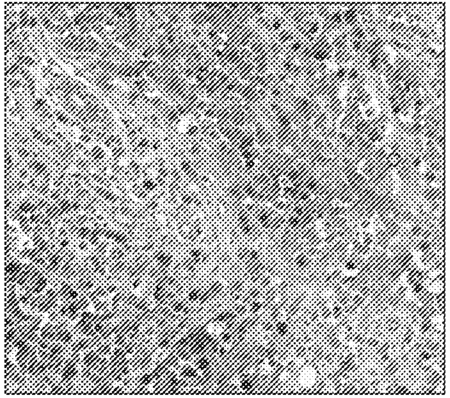


Figure 30C-30F

Ovarian Cancer 83% Positive

Biomax BC1115a
Antibody: MN-hC2-scFv-Fc-Biotin 50ug/mL

Fig. 31A

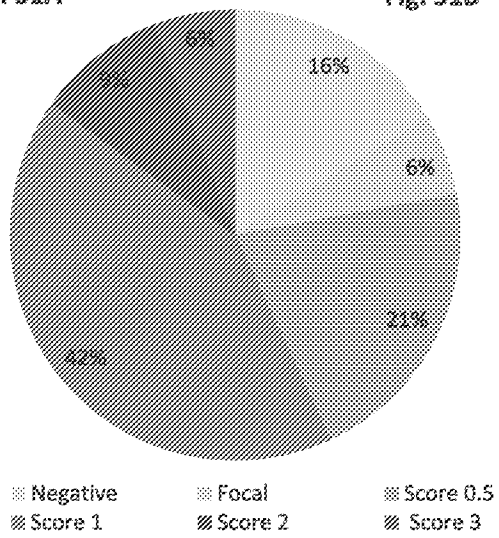


*Chart scores for Ovarian Adenocarcinoma

Score/Grade
2/3 = Score 2;Grade 3

Fig. 31B

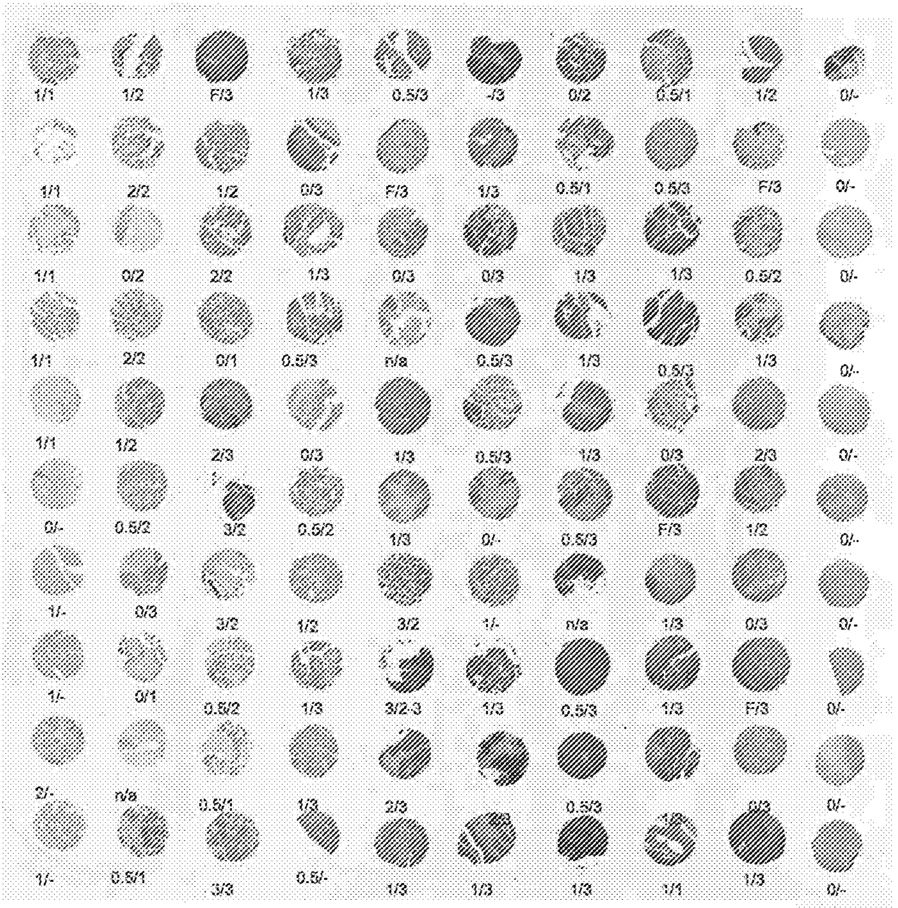
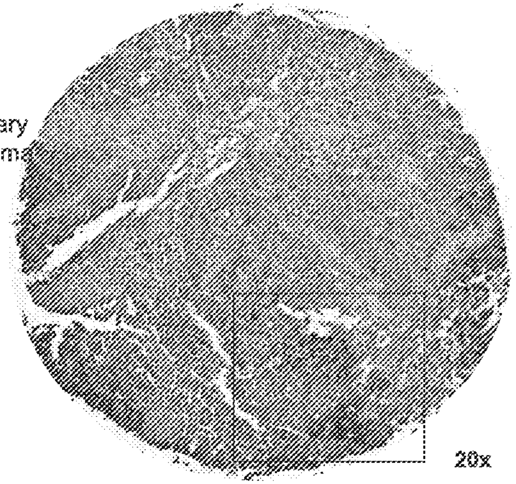
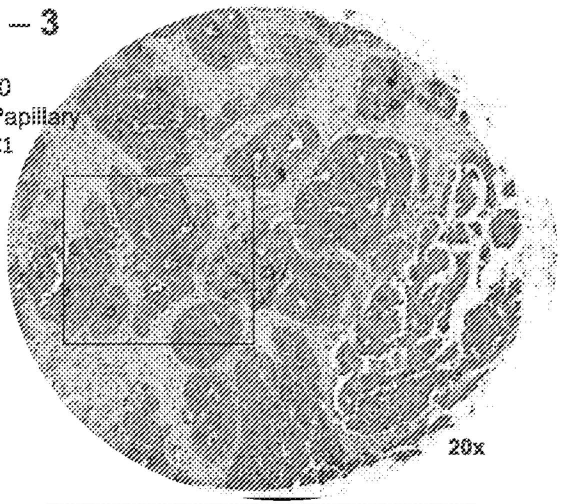


Figure 31A-31B



Score 2
Grade 3
T1aN0M0
Serous Papillary
Adenocarcinoma
Address C6

Fig. 31C



Score – 3
Grade 3
T2bN0M0
Serous Papillary
Address C1

Fig. 31D

Fig. 31E

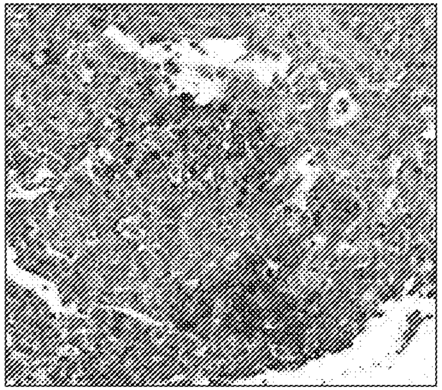


Fig. 31F

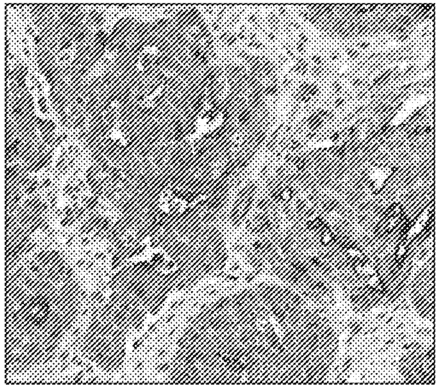


Figure 31C-31F

Pancreatic Cancer Array

Antibody: MN-hC2-scFv-Fc-Biotin 50ug/mL

Fig. 32A

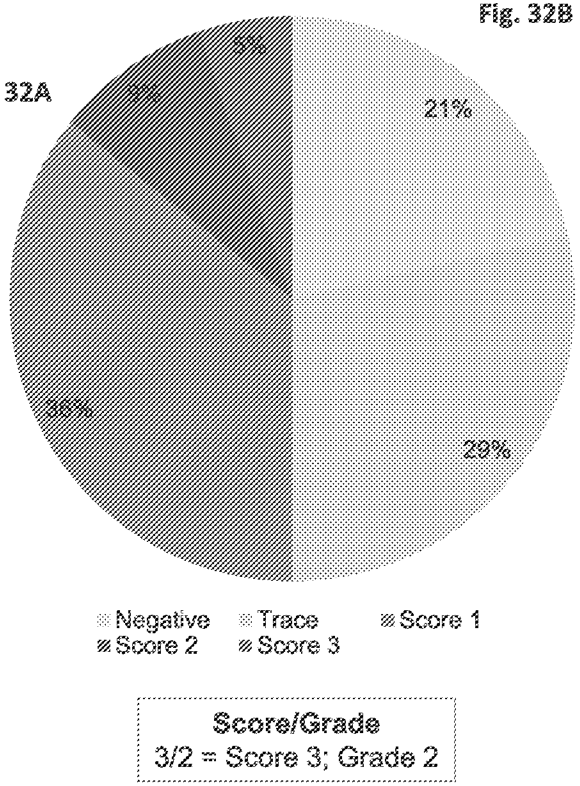


Fig. 32B

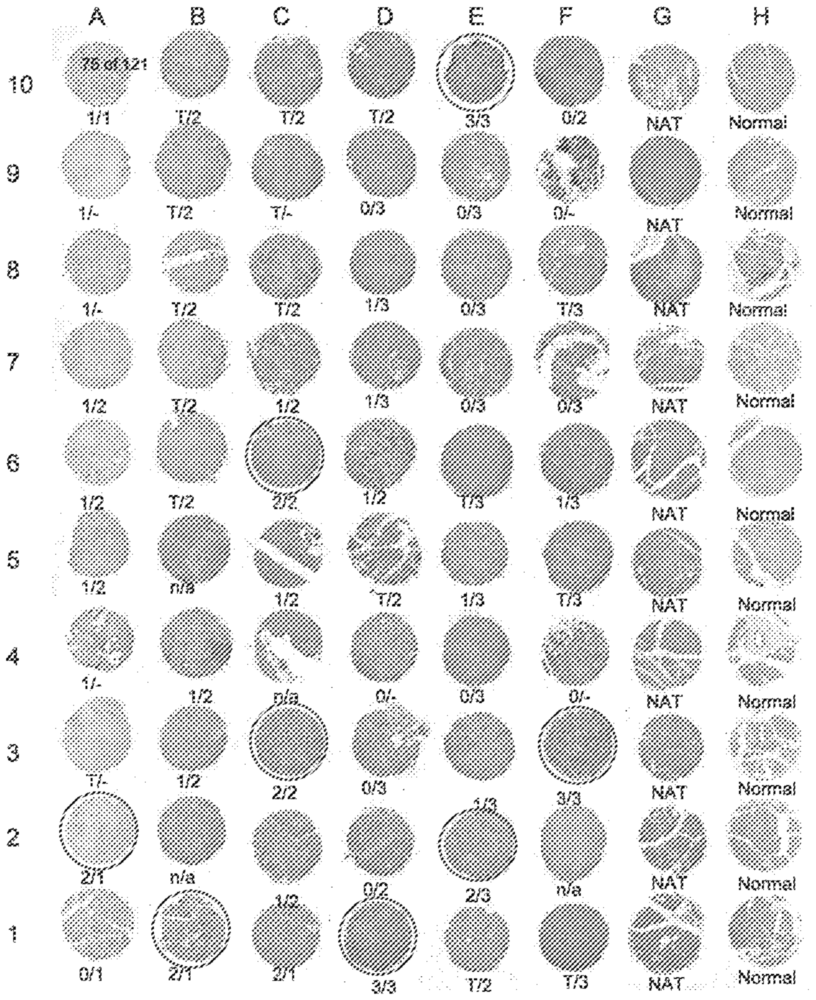
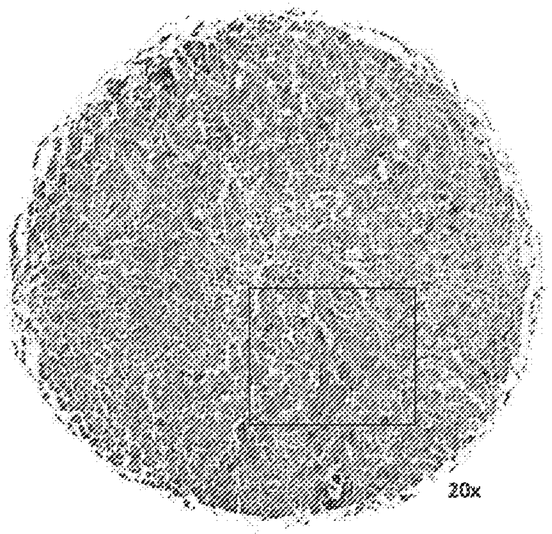


Figure 32A-32B

F3-Score 3
Grade 3
T2N1M0
Duct Adenocarcinoma

Fig. 32C



B1-Score 2
Grade 1
T3N0M0
Duct Adenocarcinoma

Fig. 32D

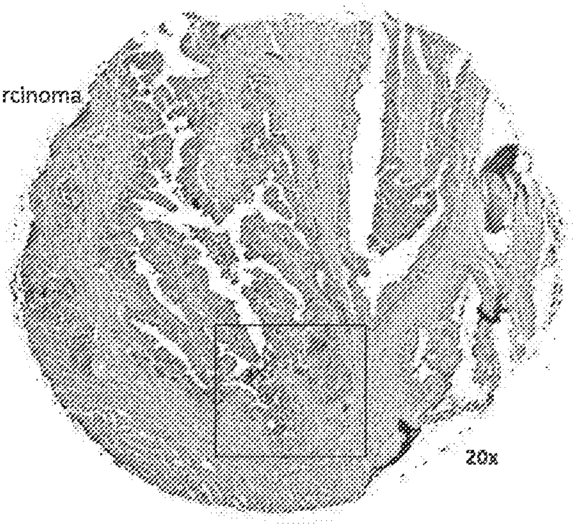


Fig. 32E

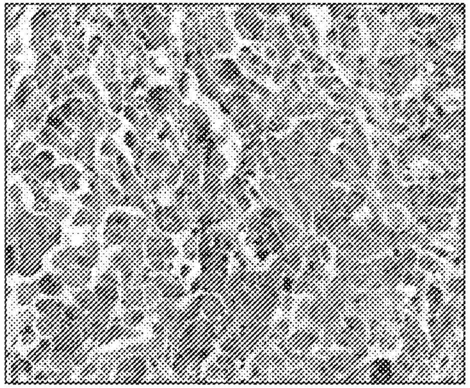


Fig. 32F

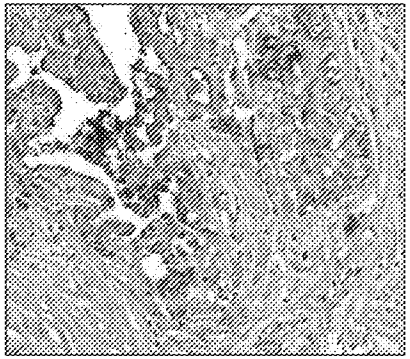


Figure 32C-32F

Fig. 33A

Lung Cancer Array

Antibody: MN-hC2-scFv-Fc-Biotin 50ug/mL

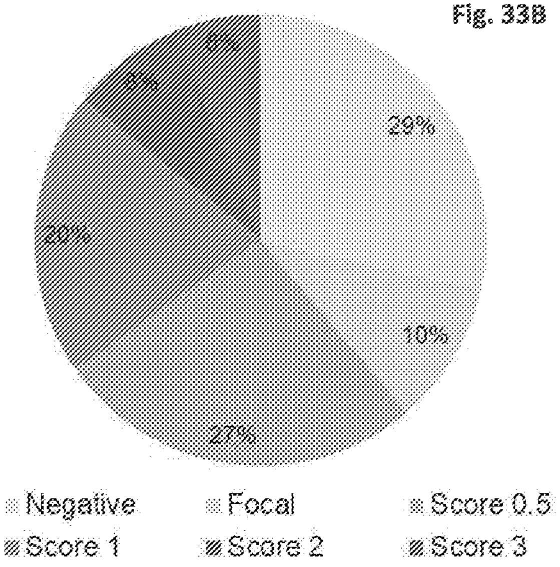


*Chart scores for Lung Adenocarcinoma

Score/Grade
3/2 = Score 3;Grade 2

Fig. 33B

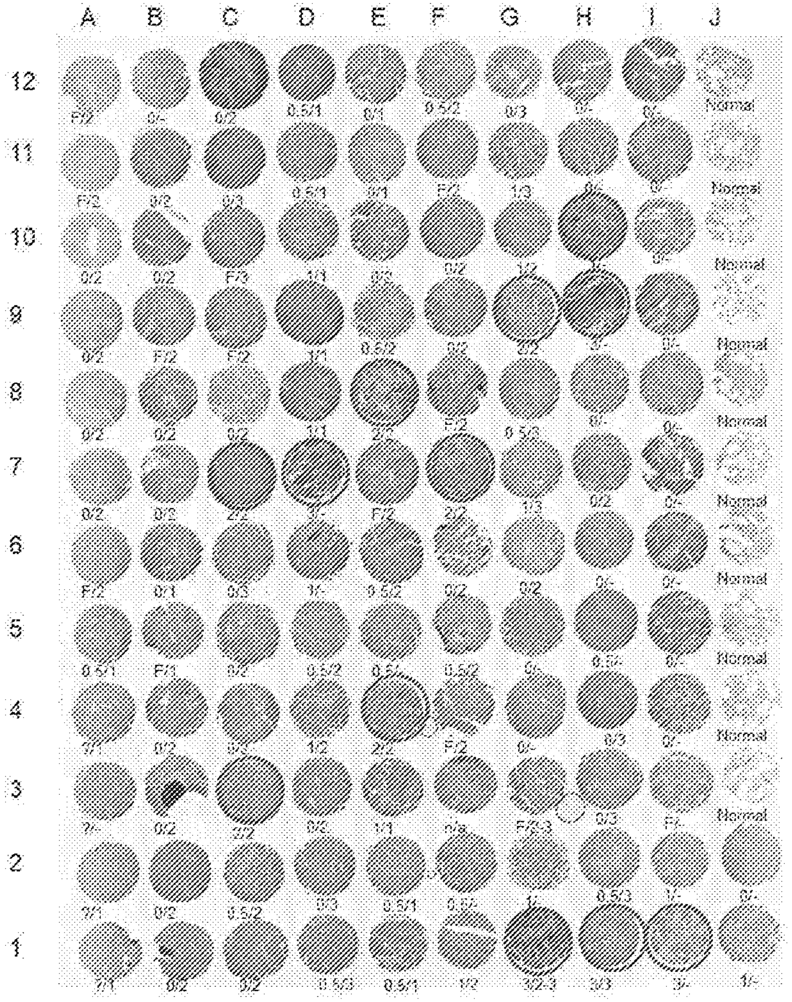
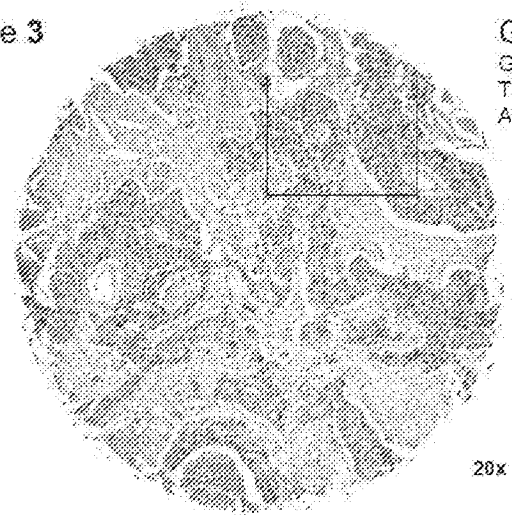


Figure 33A-33B

Lung Cancer Array; MN-hC2-scFv-Fc-Biotin [50ug/mL]

I1 - Score 3
Grade -
T2N1M0
Large Cell
Carcinoma

Fig. 33C



G1 – Score 3
Grade 2-3
T2N1M0
Adenocarcinoma

Fig. 33D

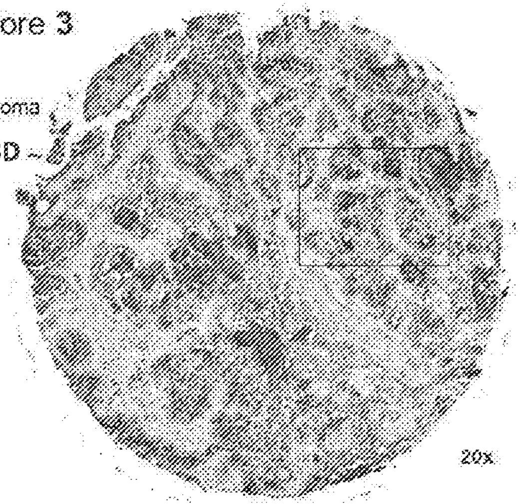


Fig. 33E

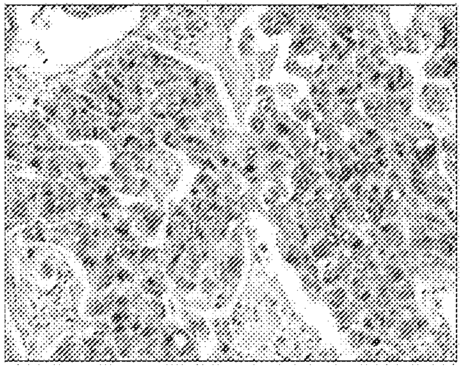


Fig. 33F

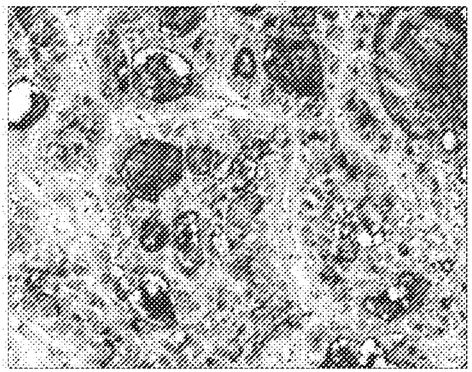


Figure 33C-33F

Humanized MNC2 does not bind to full-length MUC1 or MUC1* on healthy tissues.

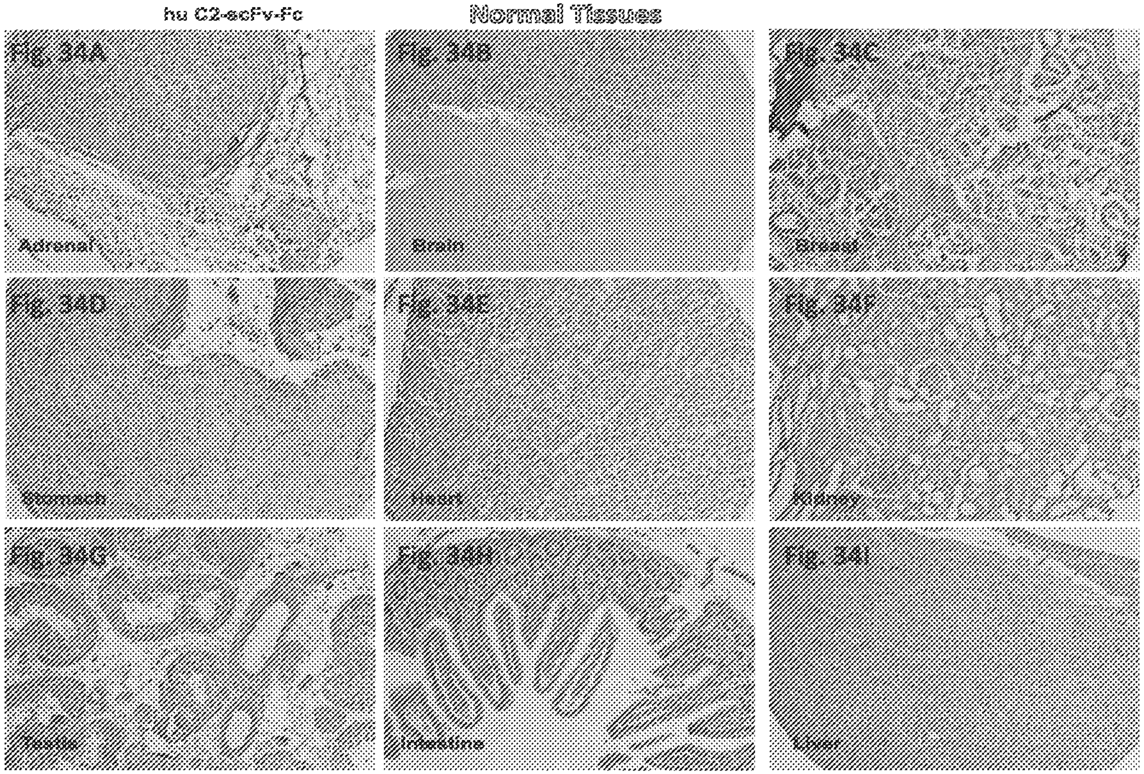


Figure 34A-34I

HCT-116 are a MUC1-negative colon cancer cell line; HCT-MUC1* is a stable cell line, pre-sorted to be 100% positive for MUC1*; HCT-MUC1-18 is a single cell clone of HCT's transfected with MUC1-full-length (43 TRs). HCT-MUC1-18 is resistant to MUC1 cleavage (~10% cleaved).

Fig. 35A

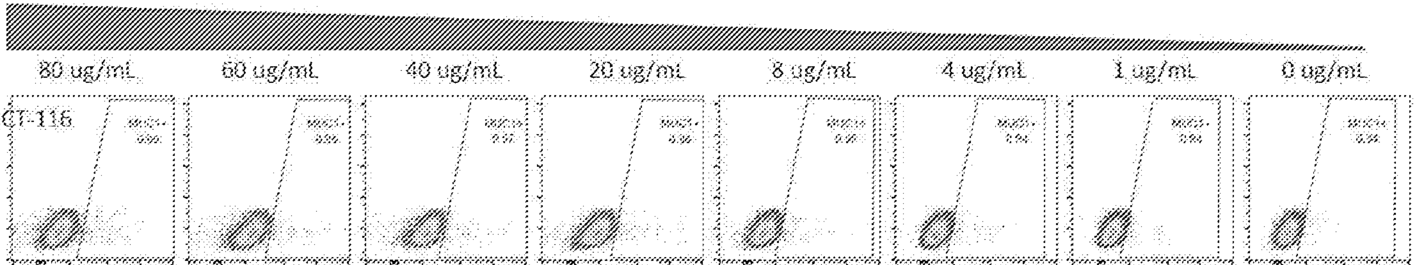


Fig. 35B

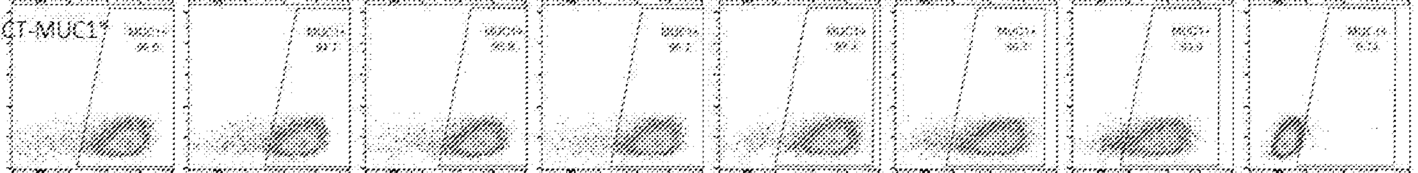


Fig. 35C

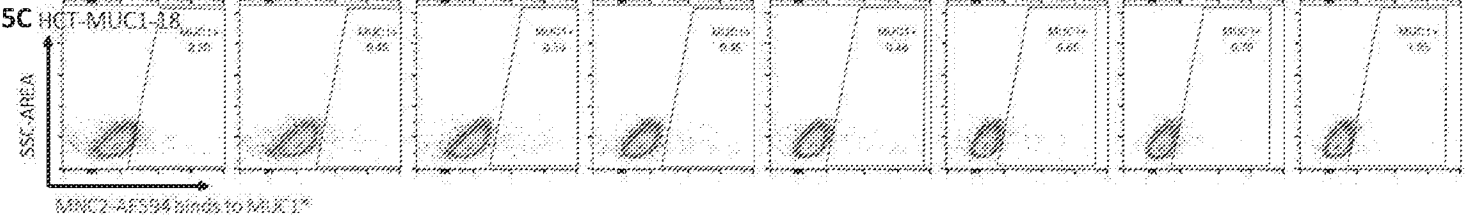


Fig. 35D

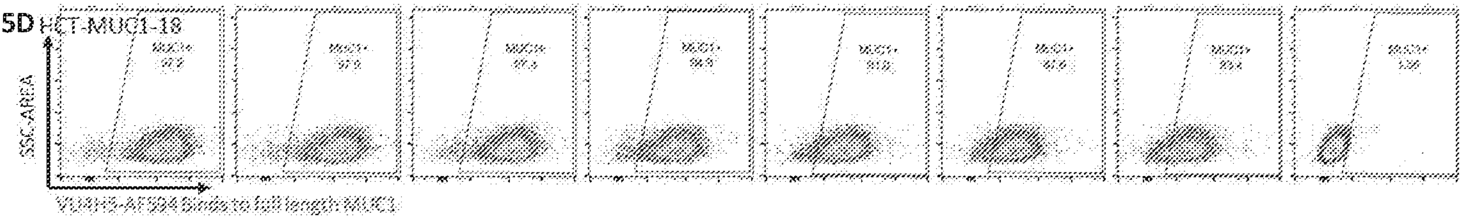


Figure 35A-35D

Fig. 36A

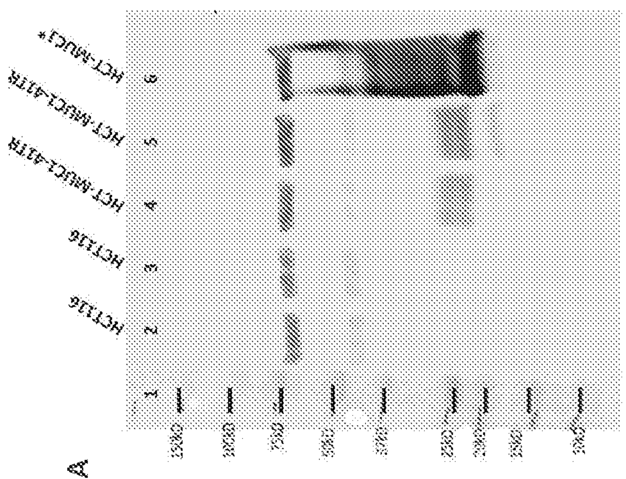


Fig. 36B

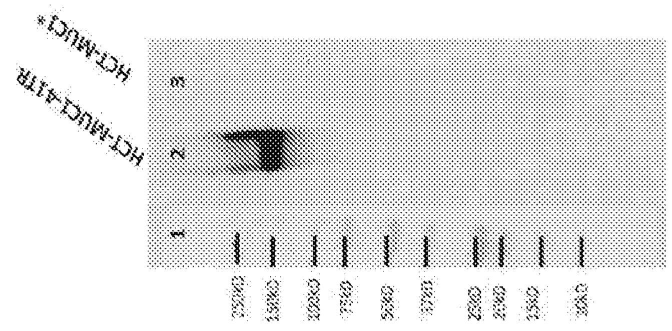


Fig. 36C

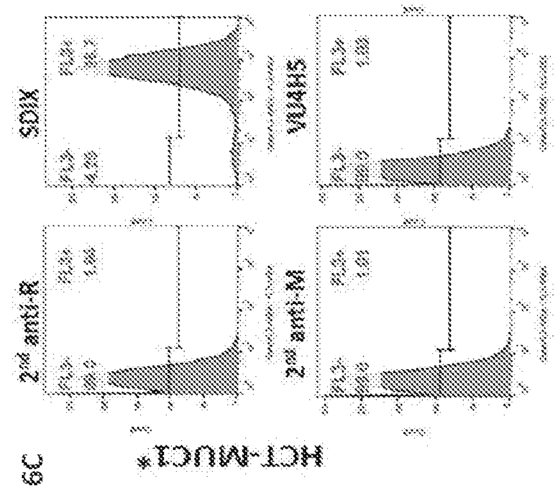


Fig. 36D

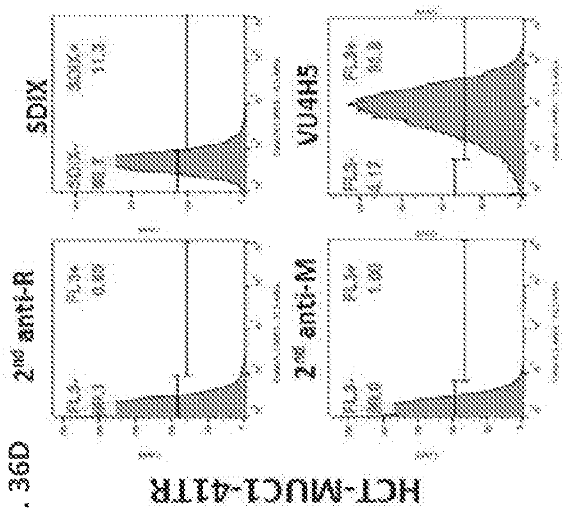


Figure 36A-36D

Cleavage releases tandem repeat domain; unmasks binding growth factor sites on MUC1*

Fig. 37A

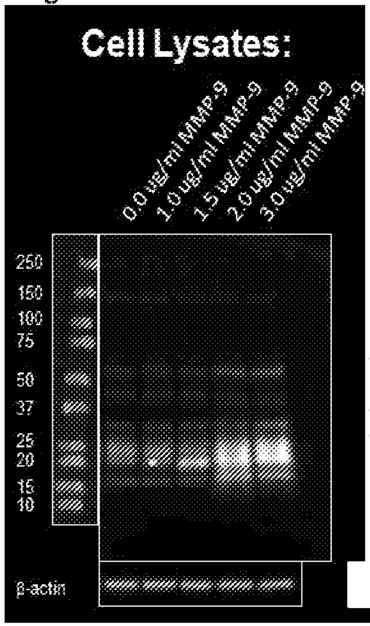


Fig. 37B

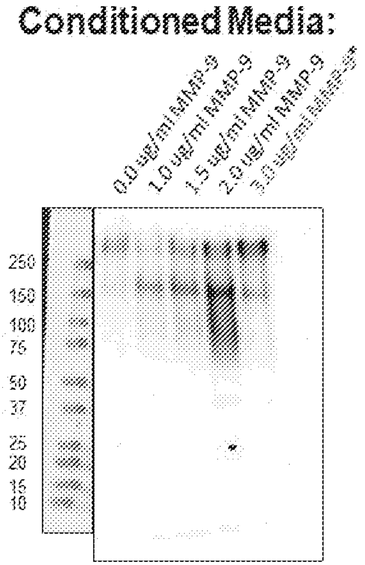


Fig. 37C

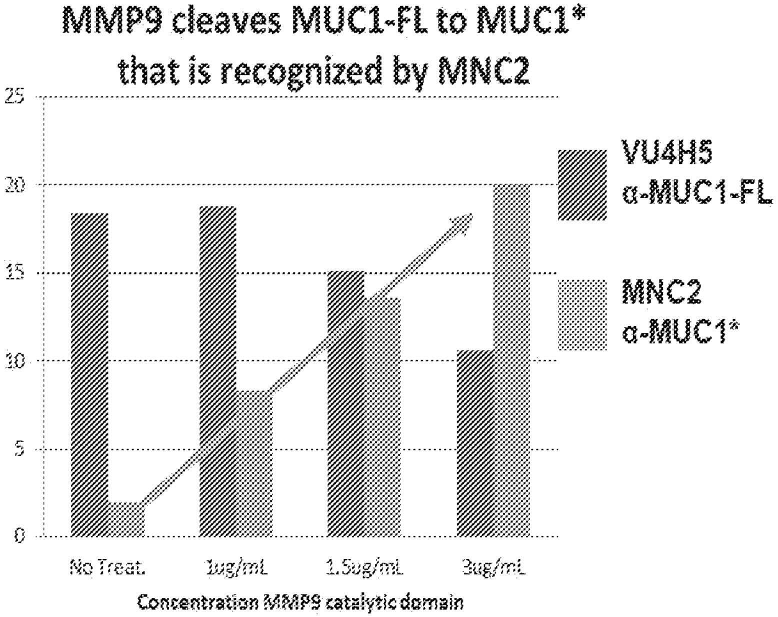


Figure 37A-37C

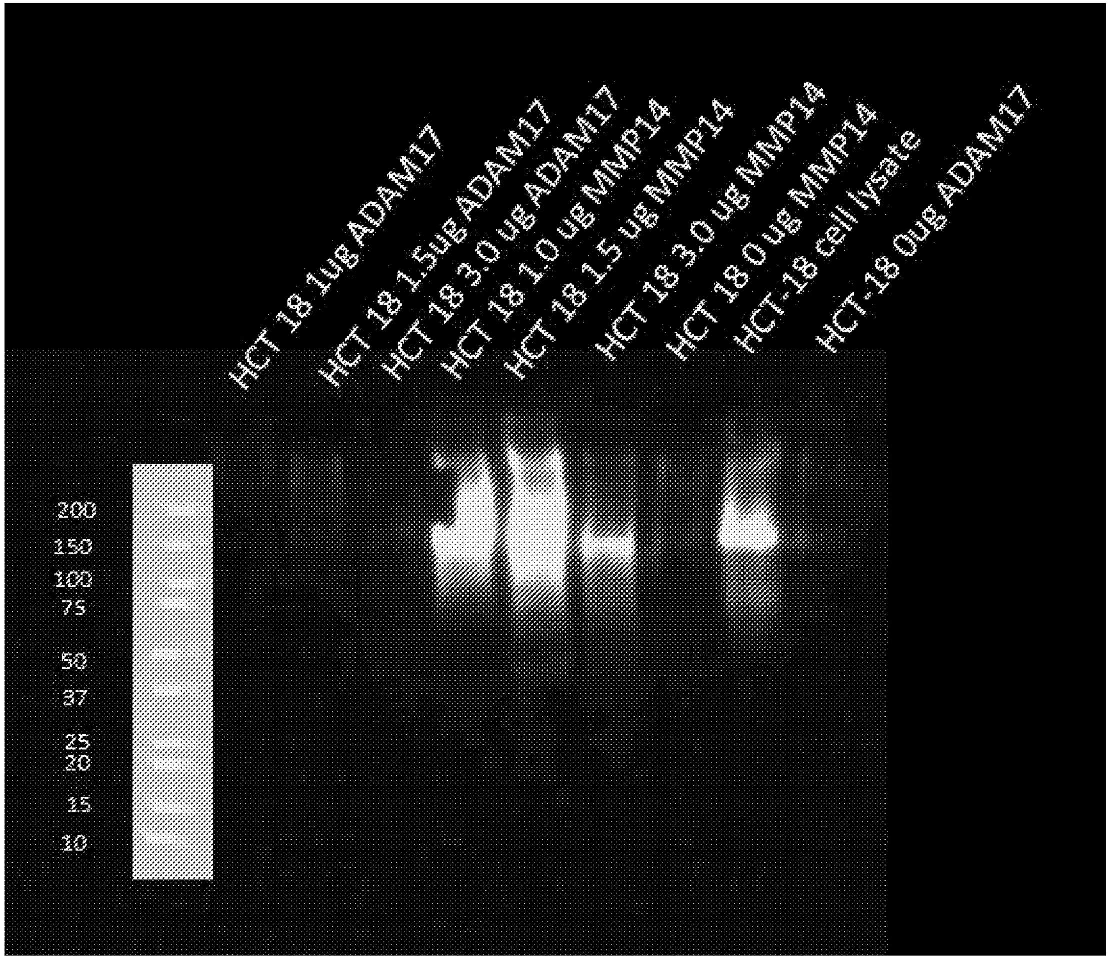

HCT 18 1ug ADAM17
HCT 18 1.5ug ADAM17
HCT 18 3.0 ug ADAM17
HCT 18 1.0 ug MMP14
HCT 18 1.5 ug MMP14
HCT 18 3.0 ug MMP14
HCT 18 0 ug MMP14
HCT-18 cell lysate
HCT-18 0ug ADAM17
200
150
100
75
50
37
25
20
15
10

Figure 38

Hematopoietic stem cells express a cleaved MUC1; recognized by SDIX polyclonal & mAb MNC3 but not mAbs MNE6 or MNC2

Fig. 39A

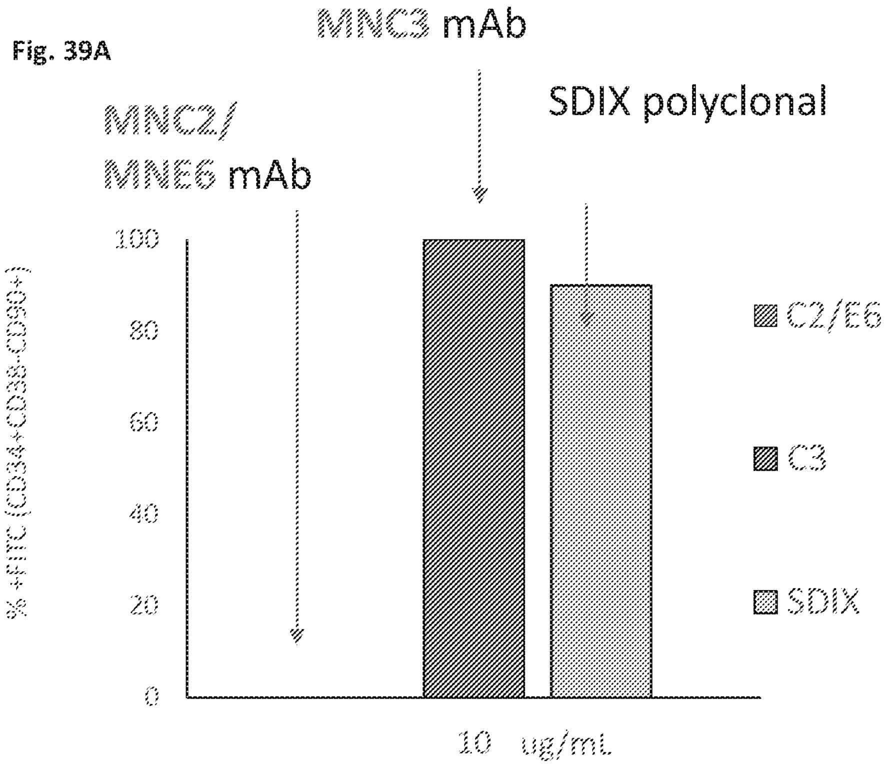


Fig. 39B

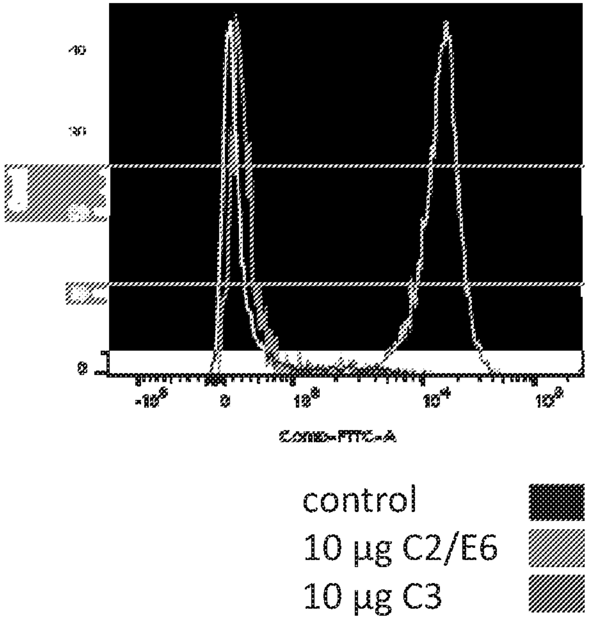


Figure 39A-39B

CD34+/CD38- HSCs are positive for MNC3 but negative for MNE6

Fig. 40A Total bone marrow cells

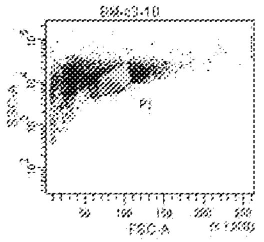


Fig. 40B

CD34+ cells

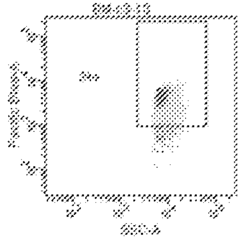


Fig. 40C

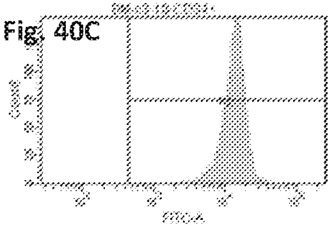


Fig. 40D

CD34+CD38-

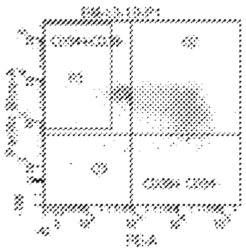


Fig. 40E

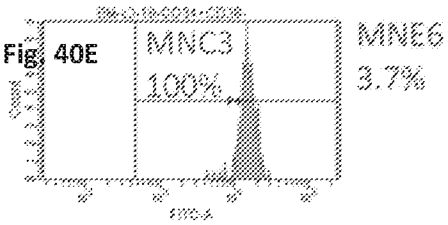


Fig. 40F

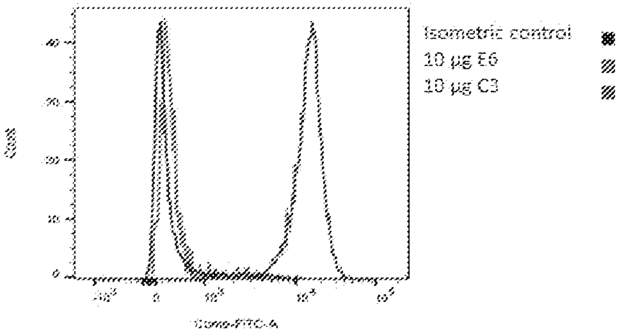


Fig. 40G

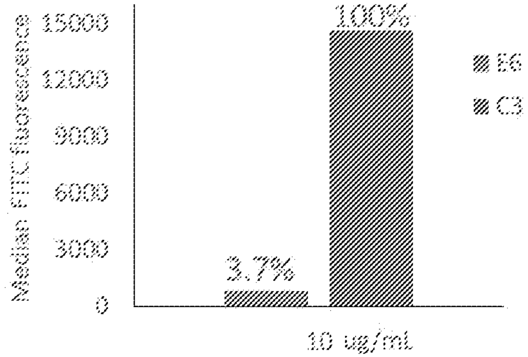


Figure 40A-40G

CD34+/CD38- HSCs stain positive for SDIX anti-MUC1* polyclonal, but negative for mAbs MNC2 and MNE6

Fig. 41A CD34⁺/CD38⁻/lo 5.62% of CD34+

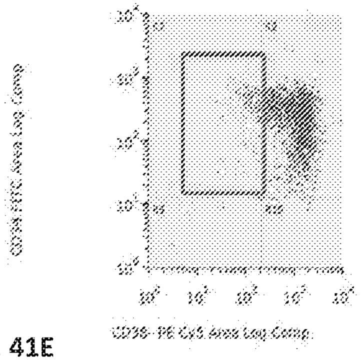


Fig. 41B CD34⁺/CD38⁻/lo 58% are SDIX pAb +

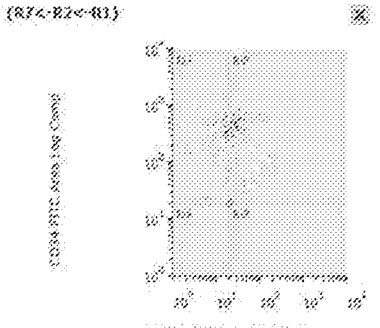


Fig. 41C CD34⁺/CD38⁻/lo 6.1% are MNE6 mAb +

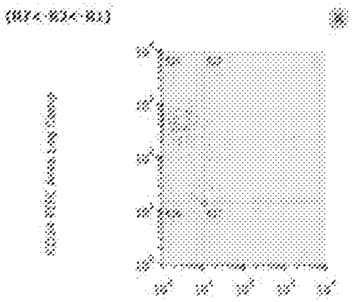


Fig. 41D CD34⁺/CD38⁻/lo 3.8% are MNc2 mAb +

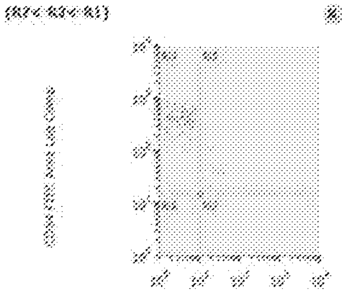
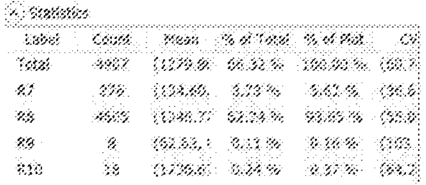


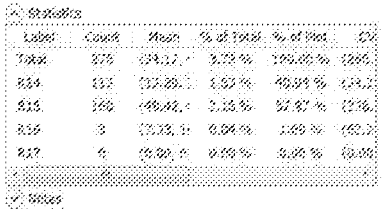
Fig. 41E



Statistics

Label	Count	Mean	% of Total	% of Plot	CV
Total	4907	(1279.0	66.32 %	100.00 %	(68.7
R7	276	(134.60,	3.73 %	5.62 %	(36.6
R8	4605	(1046.7	62.24 %	93.85 %	(55.0
R9	8	(62.53,	0.11 %	0.16 %	(103.
R10	18	(1736.6	0.24 %	0.37 %	(84.2

Fig. 41F

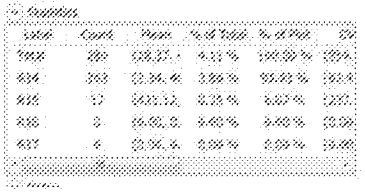


Statistics

Label	Count	Mean	% of Total	% of Plot	CV
Total	276	(29.17,	3.73 %	100.00 %	(266.
R14	135	[illegible]	1.82 %	48.91 %	[illegible]
R15	160	(48.42,	2.16 %	57.97 %	(236.
R16	3	(3.33, 1	0.04 %	1.09 %	(62.2
R17	0	[illegible]	0.00 %	0.00 %	(0.00

Slices

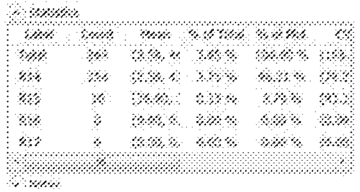
Fig. 41G



Statistics

Label	Count	Mean	% of Total	% of Plot	CV
Total	280	[illegible]	4.11 %	100.00 %	[illegible]
R34	263	[illegible]	3.86 %	93.93 %	[illegible]
R35	17	[illegible]	0.25 %	6.07 %	[illegible]
R36	0	[illegible]	0.00 %	0.00 %	(0.00
R37	0	[illegible]	0.00 %	0.00 %	(0.00

Fig. 41H



Statistics

Label	Count	Mean	% of Total	% of Plot	CV
Total	264	[illegible]	3.65 %	100.00 %	[illegible]
R34	254	[illegible]	3.51 %	96.21 %	[illegible]
R35	10	[illegible]	[illegible]	3.79 %	[illegible]
R36	0	[illegible]	0.00 %	0.00 %	(0.00
R37	0	[illegible]	0.00 %	0.00 %	(0.00

Figure 41A-41H

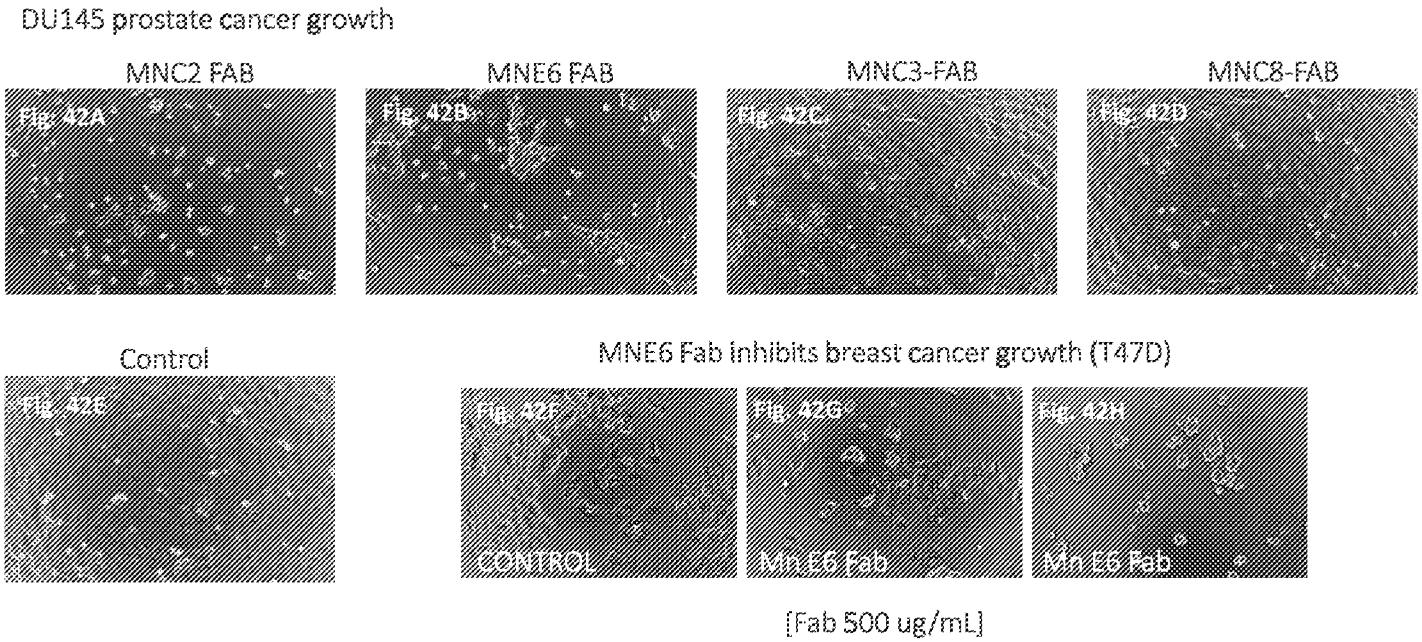


Figure 42A-42H

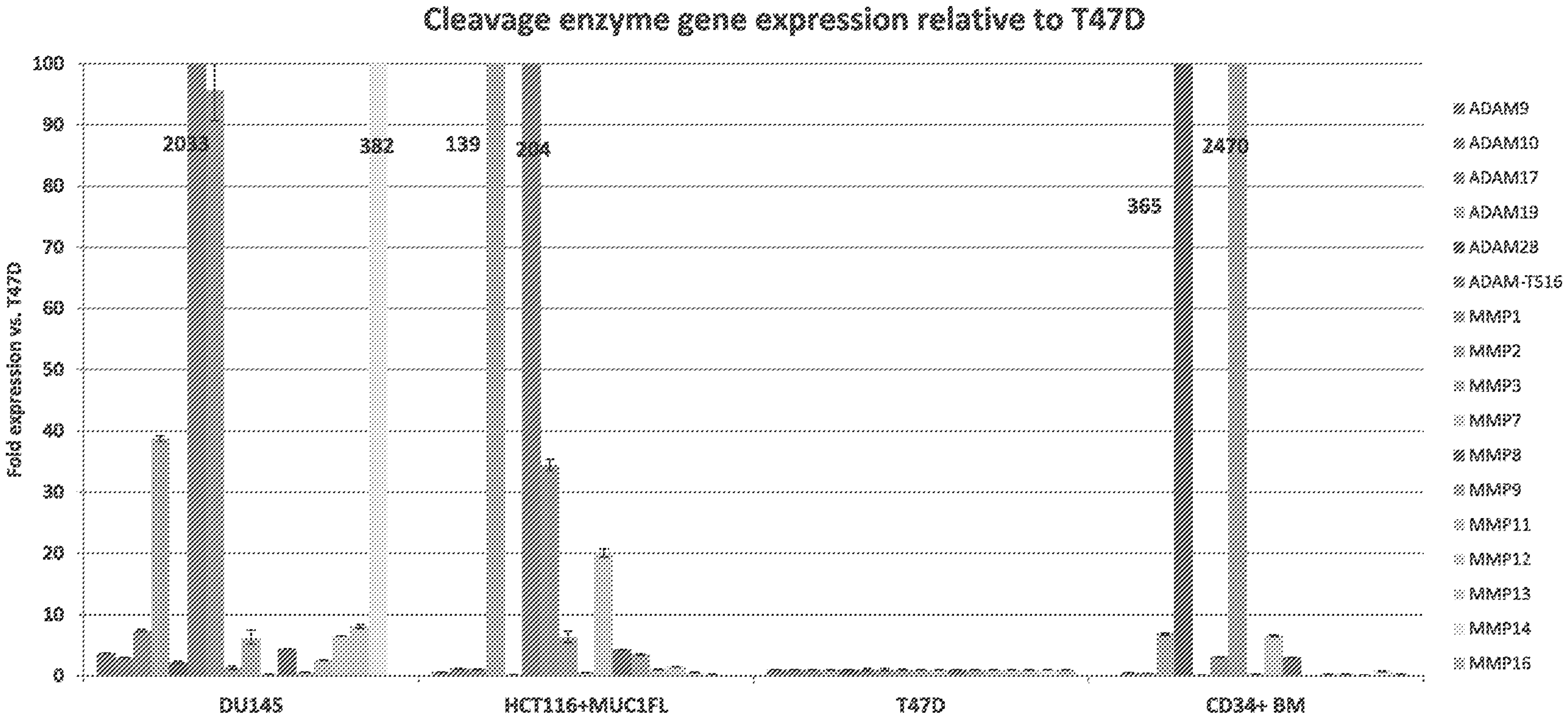

Cleavage enzyme gene expression relative to T47D
Fold expression vs. T47D
100
90
80
70
60
50
40
30
20
10
0
2033
382
139
204
365
2470
DU145
HCT116+MUC1FL
T47D
CD34+ BM
ADAM9
ADAM10
ADAM17
ADAM19
ADAM28
ADAM-TS16
MMP1
MMP2
MMP3
MMP7
MMP8
MMP9
MMP11
MMP12
MMP13
MMP14
MMP16

Figure 43

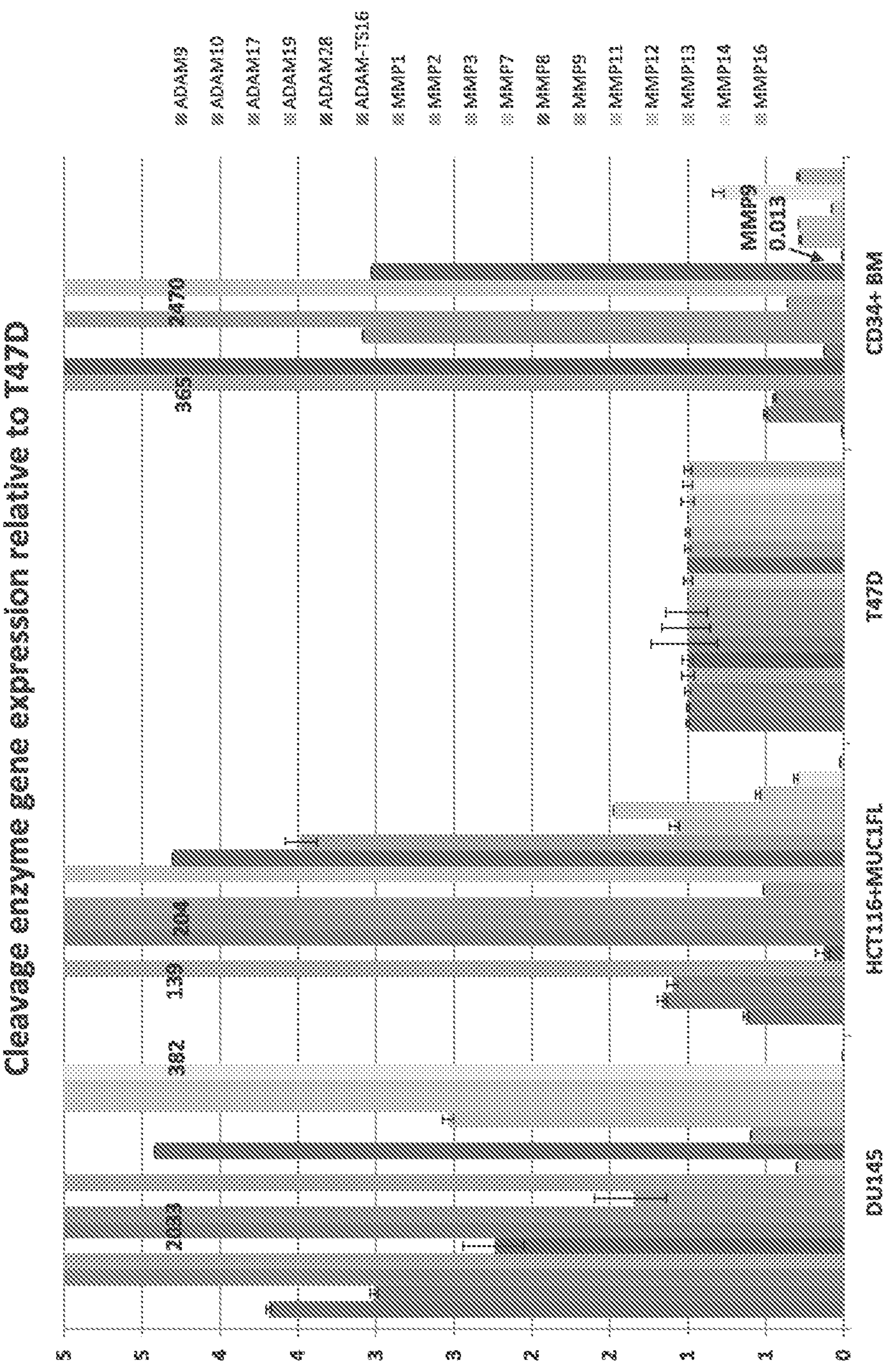

Cleavage enzyme gene expression relative to T47D
Fold expression vs. T47D
5
5
4
4
3
3
2
2
1
1
0
DU345
HCT116+MUC1FL
T47D
CD34+ BM
2033
382
139
104
365
2470
MMP9
0.013
ADAM9
ADAM10
ADAM17
ADAM19
ADAM28
ADAM-TS16
MMP1
MMP2
MMP3
MMP7
MMP8
MMP9
MMP11
MMP12
MMP13
MMP14
MMP16

Figure 44

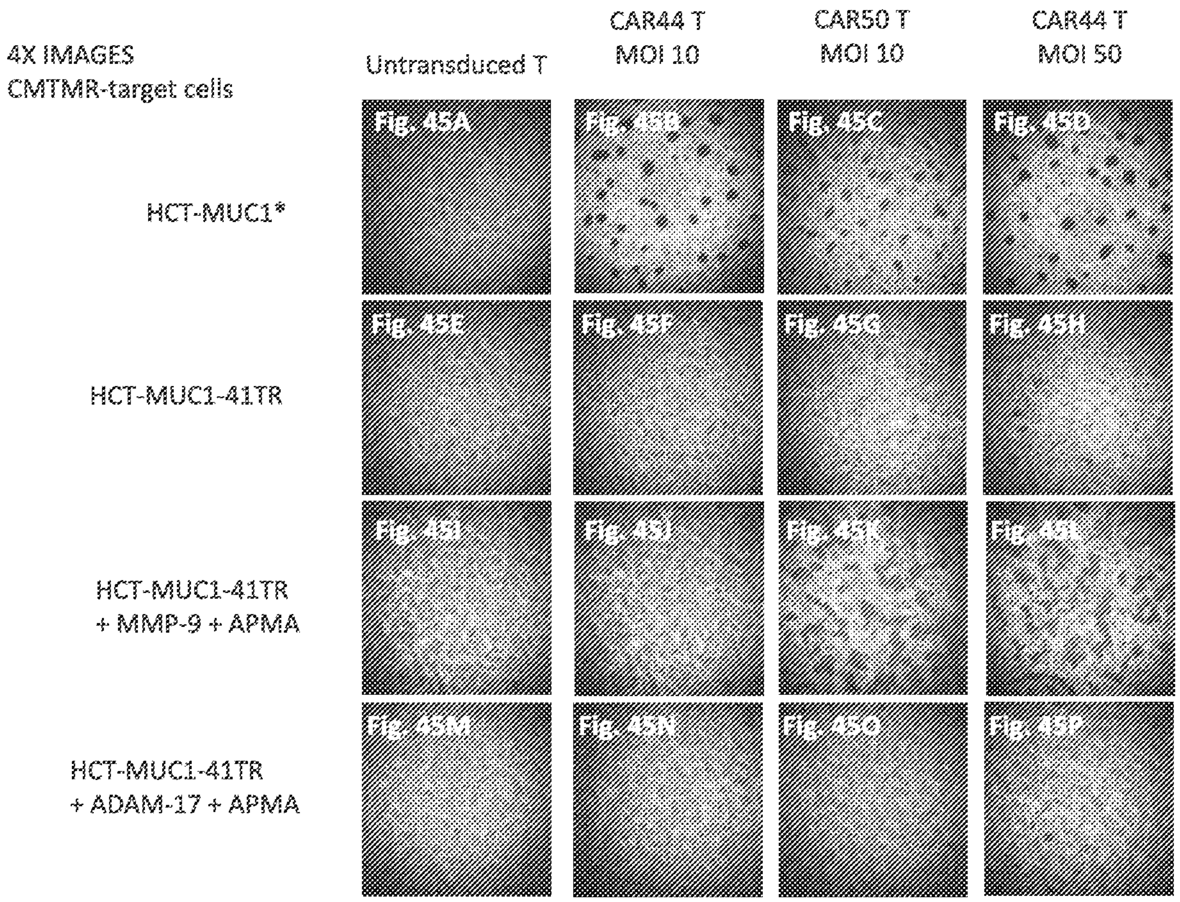


Figure 45A-45P

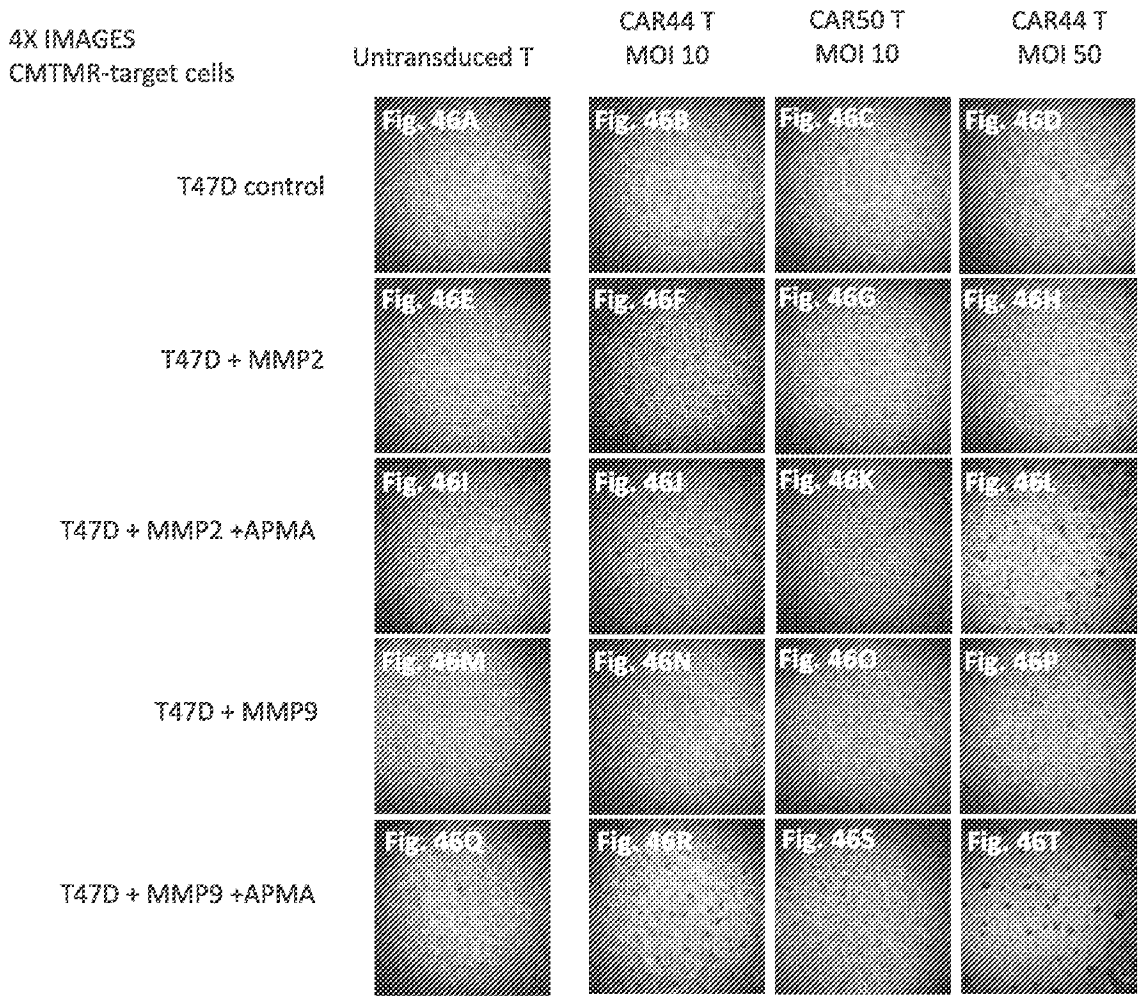


Figure 46A-46T

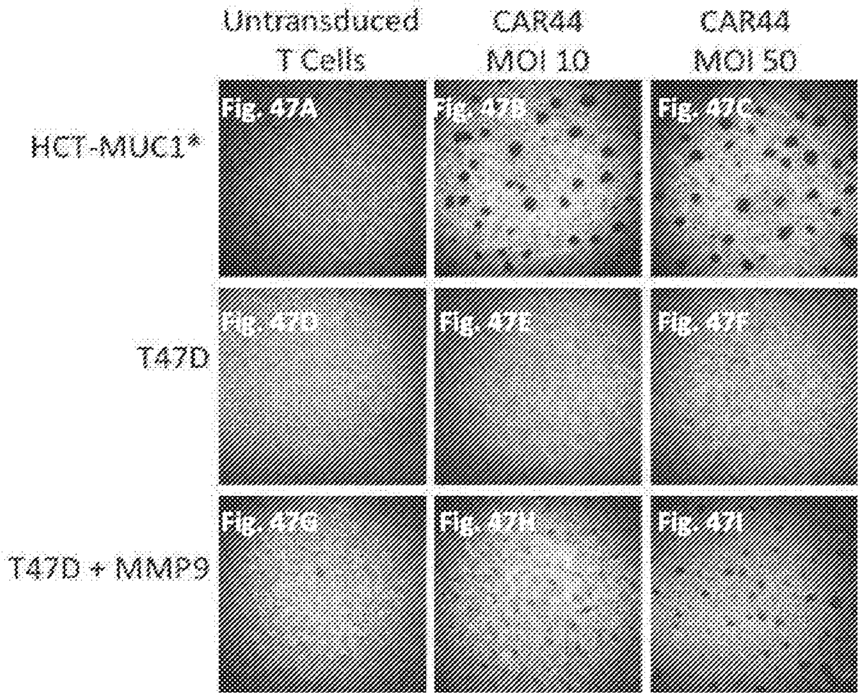


Figure 47A-47I

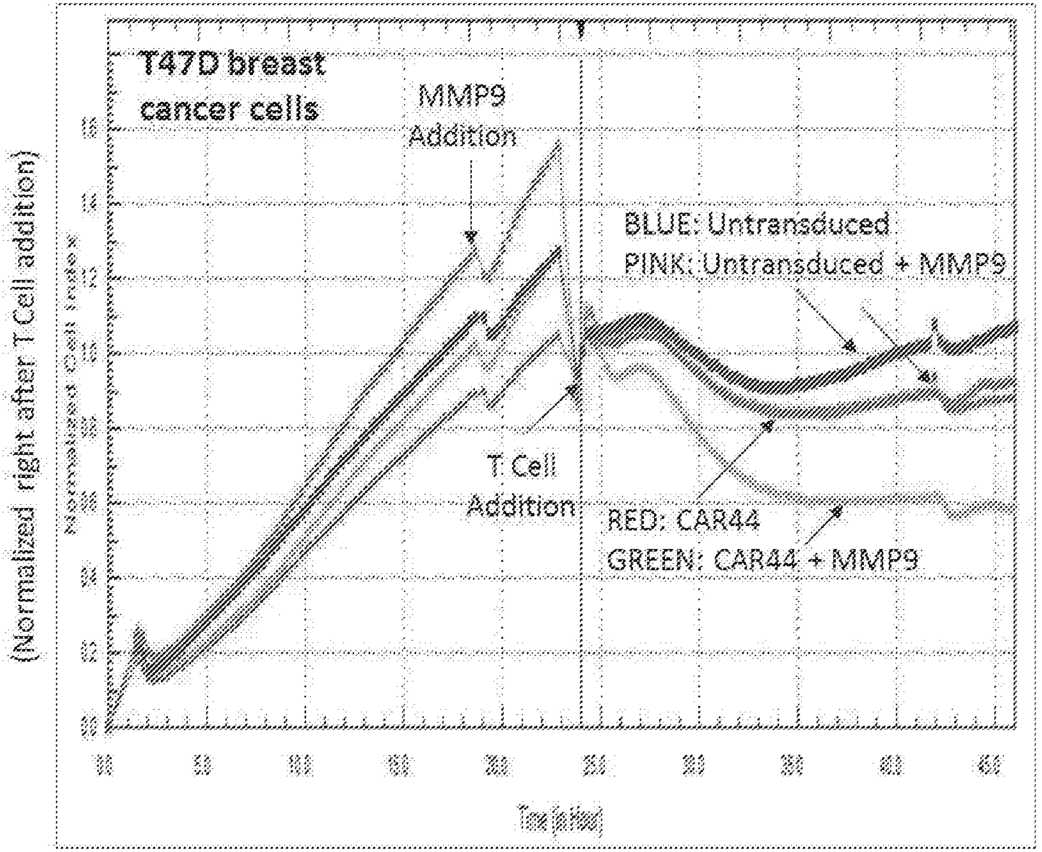

T47D breast cancer cells
MMP9 Addition
T Cell Addition
BLUE: Untransduced
PINK: Untransduced + MMP9
RED: CAR44
GREEN: CAR44 + MMP9
Normalized Cell Index
(Normalized right after T Cell addition)
Time (in Hour)

Figure 48

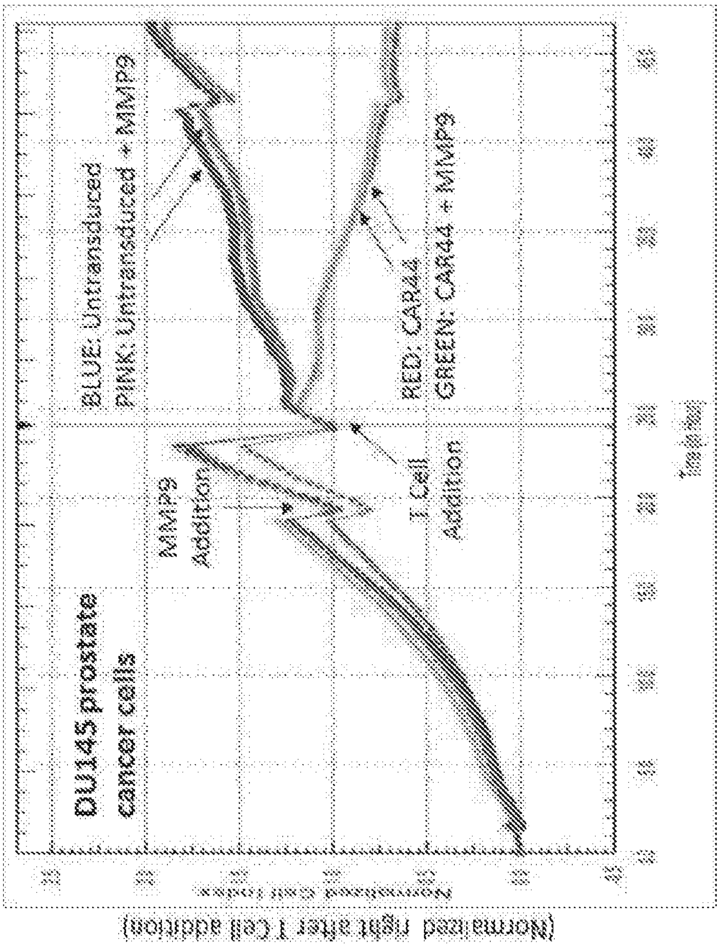

DU145 prostate cancer cells
BLUE: Untransduced
PINK: Untransduced + MMP9
RED: CAR44
GREEN: CAR44 + MMP9
MMP9 Addition
T Cell Addition
Normalized Cell Index
(Normalized right after T Cell addition)

Figure 49

PCR measurement of MUC1 expression in normal cells compared to T47D breast cancer cells and HCT-MUC1*, a colon cancer cell line transduced with MUC1*. Measurement was normalized to Hep. G2, MUC1 negative normal liver cells.

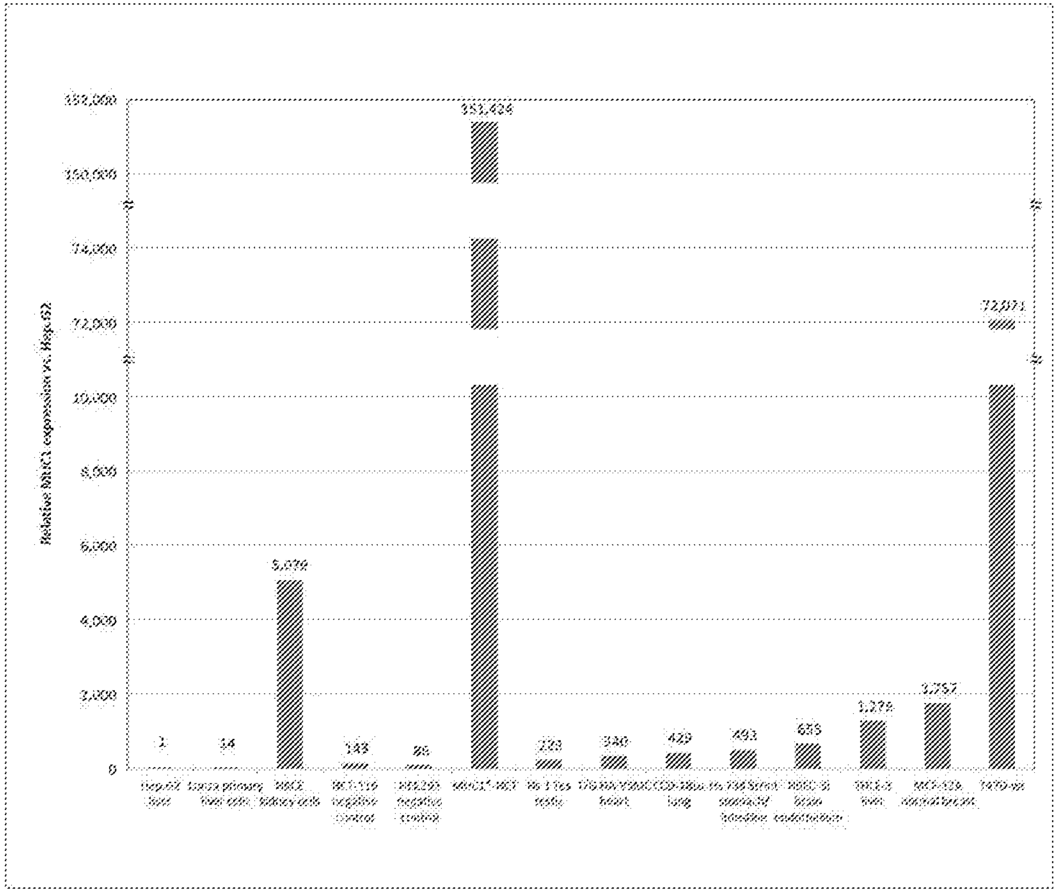


Figure 50

To assess CAR44 T cell activation in response to co-culture with target cells, IFN-g was measured in supernatant of CAR44 T cells in co-culture with normal cells, or cancer cells as a control. IFN-g was measured after 72 hours of co-culture. (A) CAR44 T cell to target cell ratio was 1:1; (B) CAR44 T cell to target cell ratio was 0.5:1.

Fig. 51A

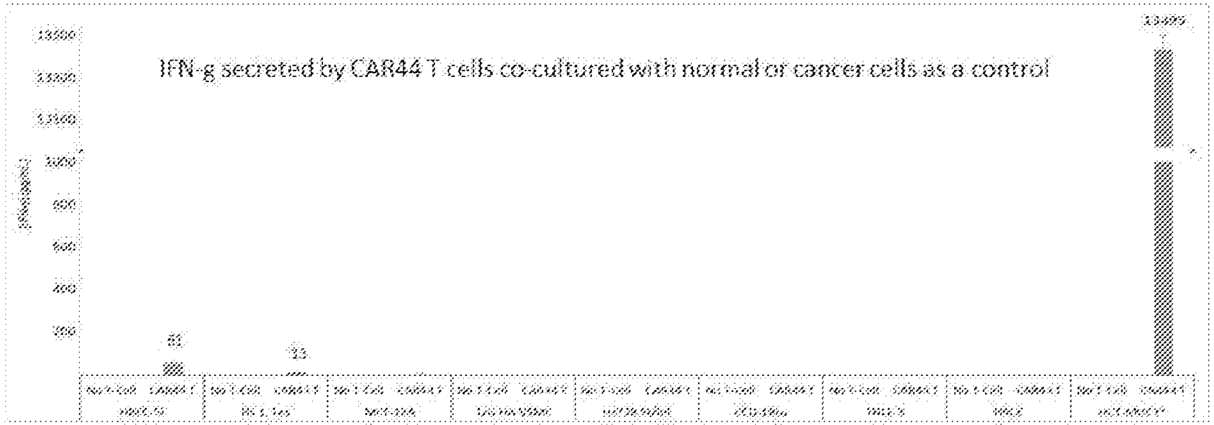


Fig. 51B

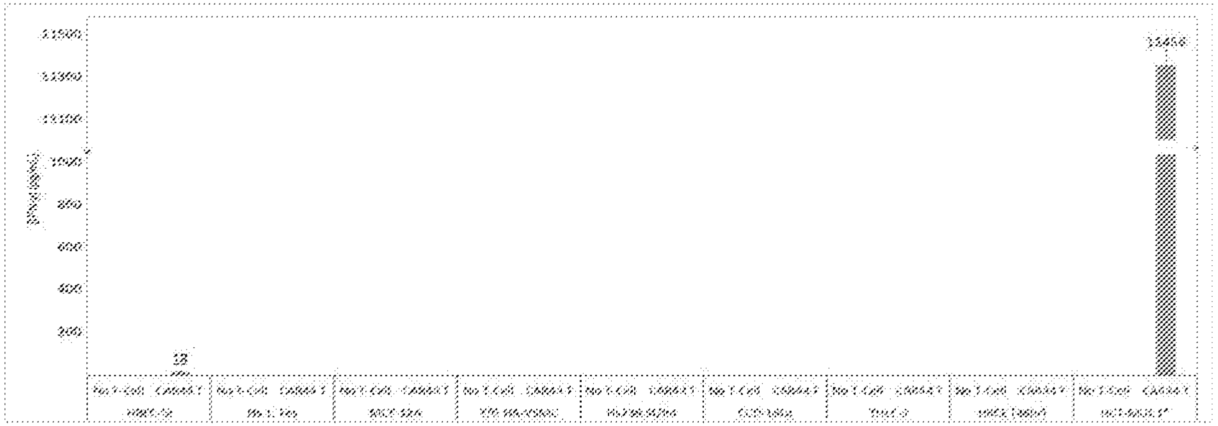


Figure 51A-51B

To assess CAR44 T cell activation in response to co-culture with target cells, IL-2 was measured in supernatant of CAR44 T cells in co-culture with normal cells, or cancer cells as a control. IL-2 was measured after 72 hours of co-culture. (A) CAR44 T cell to target cell ratio was 1:1; (B) CAR44 T cell to target cell ratio was 0.5:1.

Fig. 52A

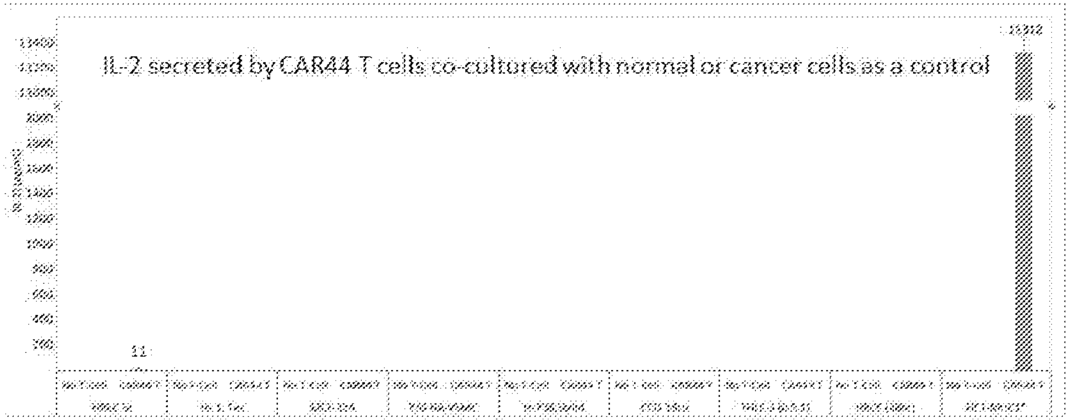


Fig. 52B

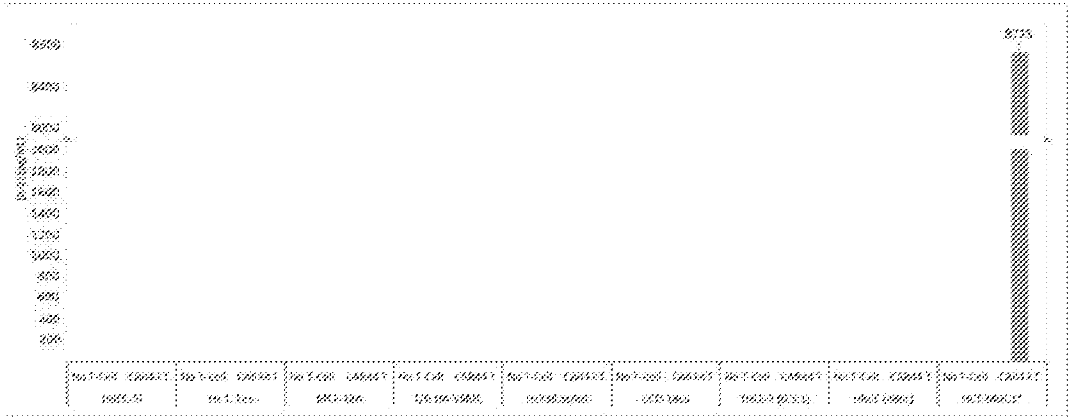
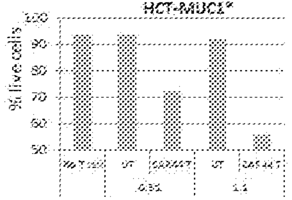


Figure 52A-52B

(1) Normal cells, or cancer cells as a control, were co-culture with no T cells, Untransduced T cells or with CAR44 T cells, at an E:T ratio of 1:1 or 0.5:1. Cells were then labeled with a cell death marker and analyzed by FACS. The CD3+ population (T cells) was eliminated from the cell count. A-F (2) & (3) Magnified photographs of normal cells in co-culture with Untransduced T cells or CAR44 T cells. FACS and magnified photographs were at 48 hours post addition of T cells.

Fig. 53A.1



UT | CAR44 T

Fig. 53A.2

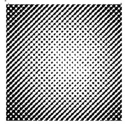


Fig. 53A.3

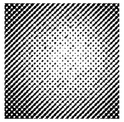
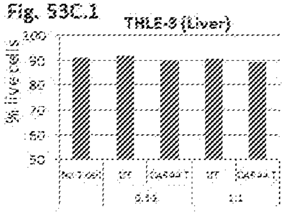


Fig. 53C.1



UT | CAR44 T

Fig. 53C.2

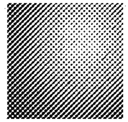


Fig. 53C.3

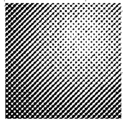
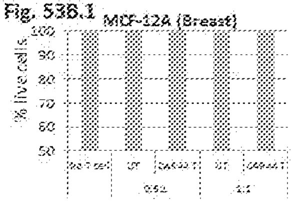


Fig. 53B.1



UT | CAR44 T

Fig. 53B.2

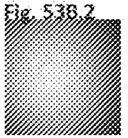


Fig. 53B.3

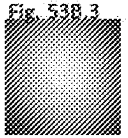
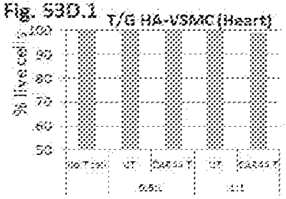


Fig. 53D.1



UT | CAR44 T

Fig. 53D.2

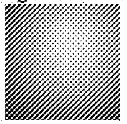


Fig. 53D.3

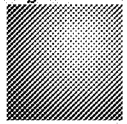
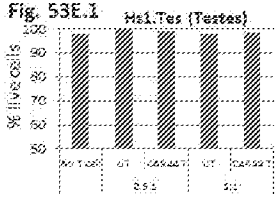


Fig. 53E.1



UT | CAR44 T

Fig. 53E.2

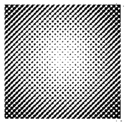


Fig. 53E.3

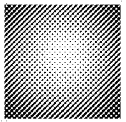
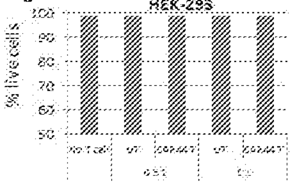


Fig. 53F.1



UT | CAR44 T

Fig. 53F.2

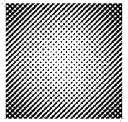


Fig. 53F.3

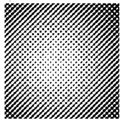
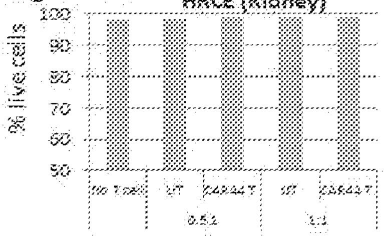


Figure 53A-53F

(1) Normal cells, or cancer cells as a control, were co-culture with no T cells, Untransduced T cells or with CAR44 T cells, at an E:T ratio of 1:1 or 0.5:1. Cells were then labeled with a cell death marker and analyzed by FACS. The CD3+ population (T cells) was eliminated from the cell count. G-J (2) & (3) Magnified photographs of normal cells in co-culture with Untransduced T cells or CAR44 T cells. FACS and magnified photographs were at 48 hours post addition of T cells.

Fig. 53G.1



UT | CAR44 T

Fig. 53G.2

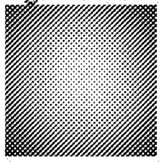


Fig. 53G.3

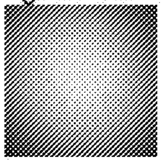
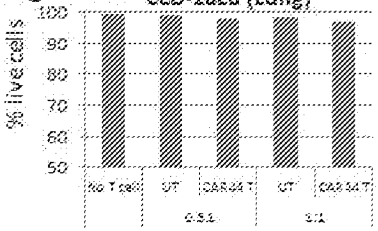


Fig. 53H.1



UT | CAR44 T

Fig. 53H.2

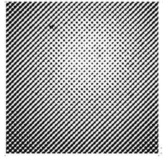


Fig. 53H.3

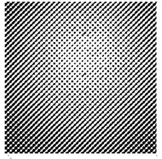
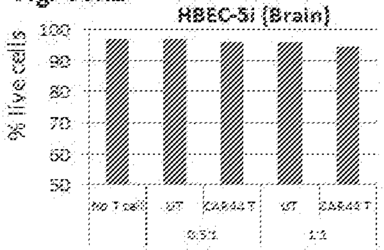


Fig. 53I.1



UT | CAR44 T

Fig. 53I.2

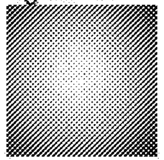


Fig. 53I.3

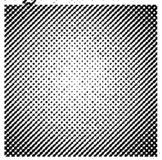
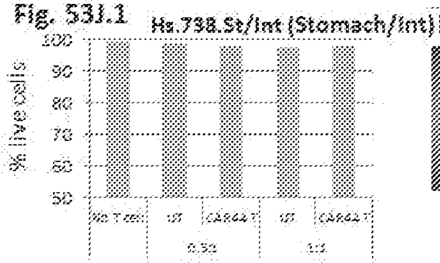


Fig. 53J.1



UT | CAR44 T

Fig. 53J.2

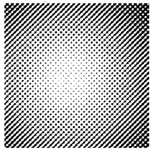


Fig. 53J.3

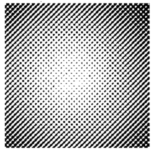


Figure 53G-53J

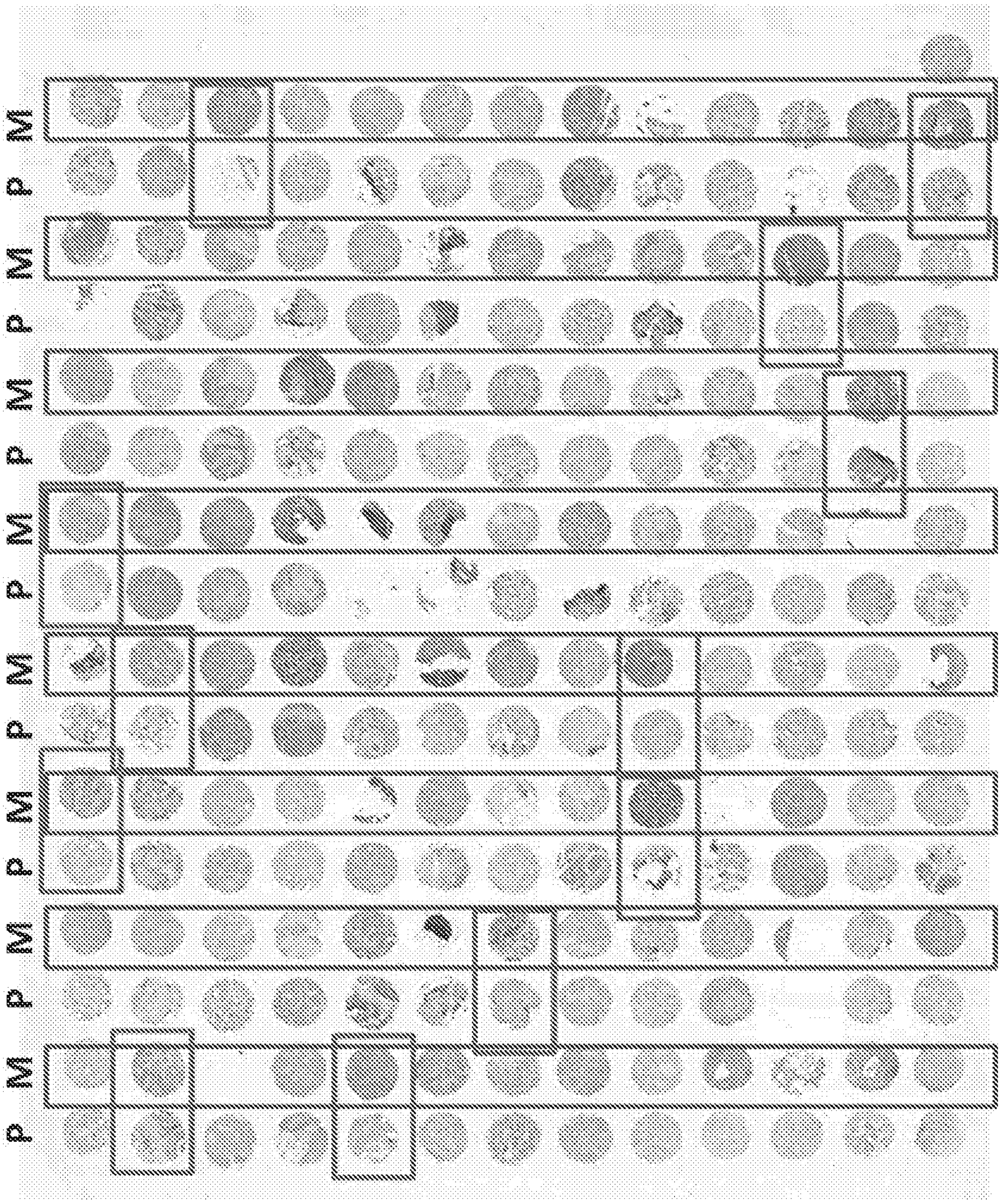


Figure 54

MUC1* positive prostate cancer cells co-cultured with huMNC2-MNCAR44 T cells

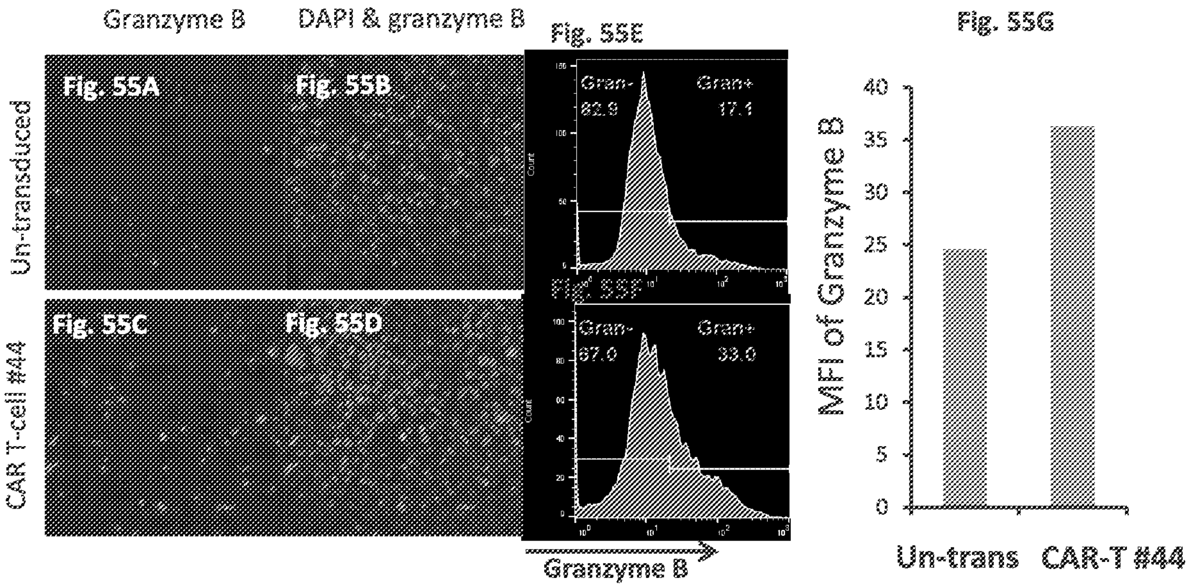


Fig. 55H

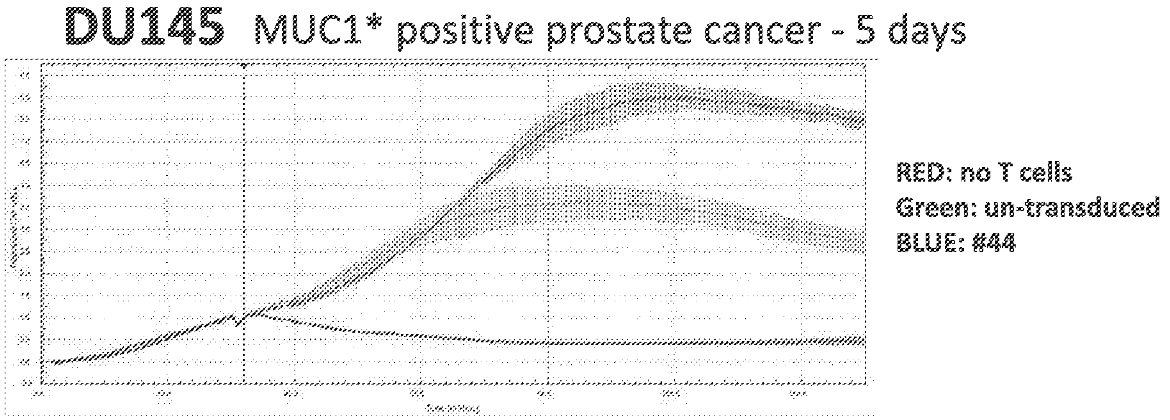
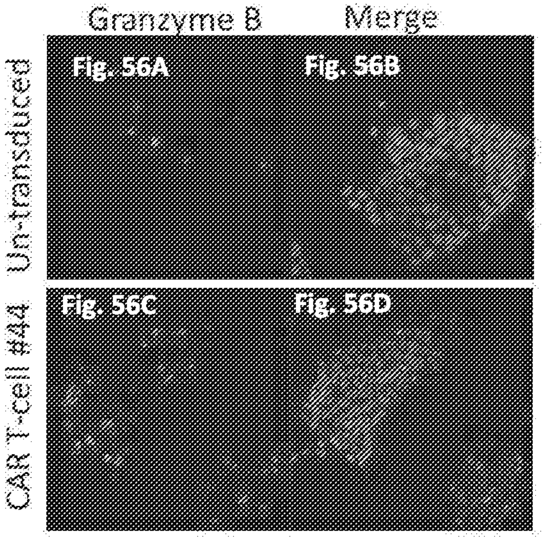


Figure 55A-55H

MUC1* positive pancreatic cancer cells co-cultured with huMNC2-MNCAR44 T cells



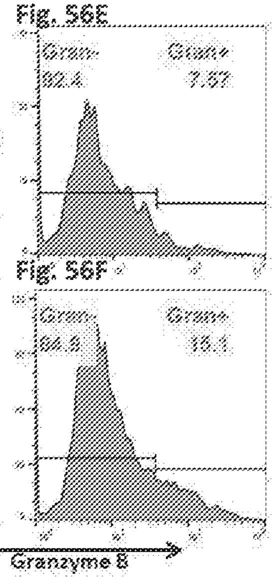


Fig. 56G

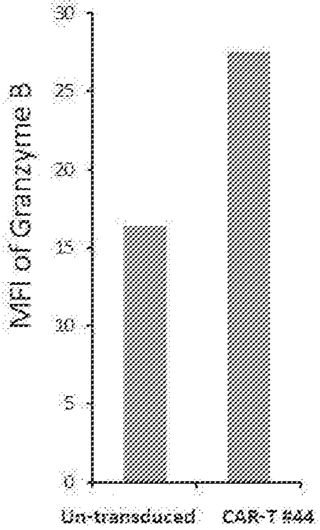


Fig. 56H

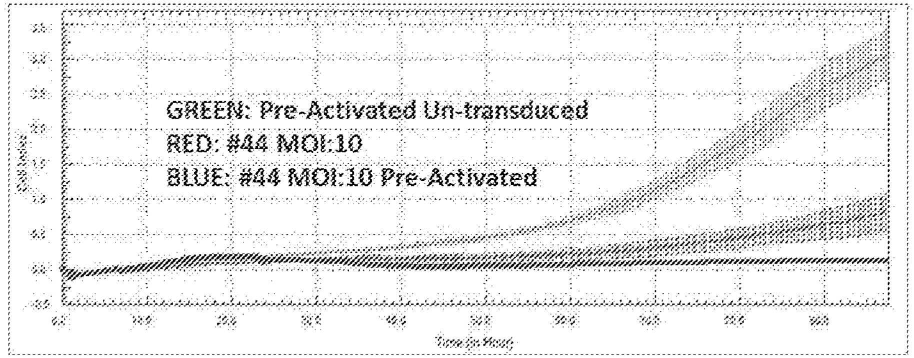


Figure 56A-56H

Fig. 57A

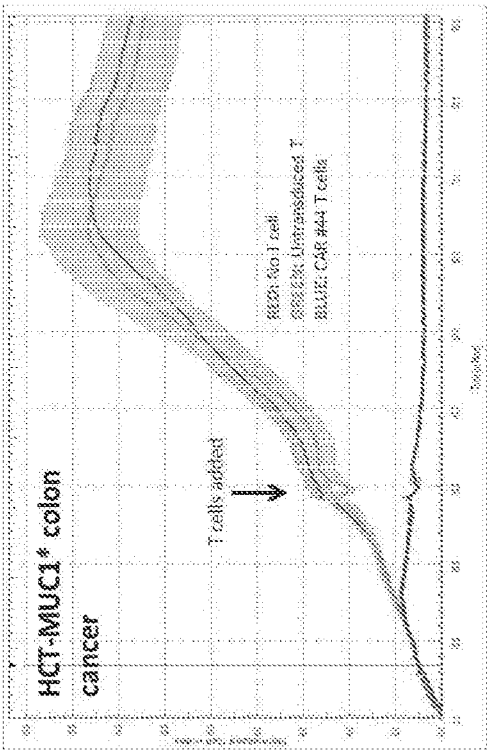


Fig. 57B

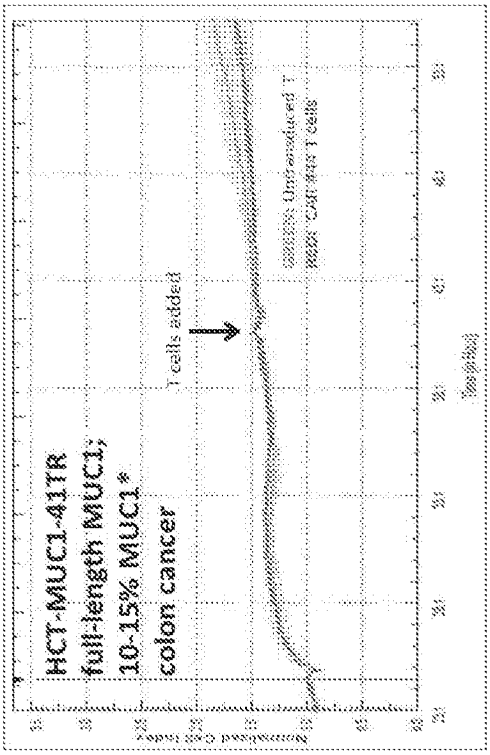


Fig. 57C

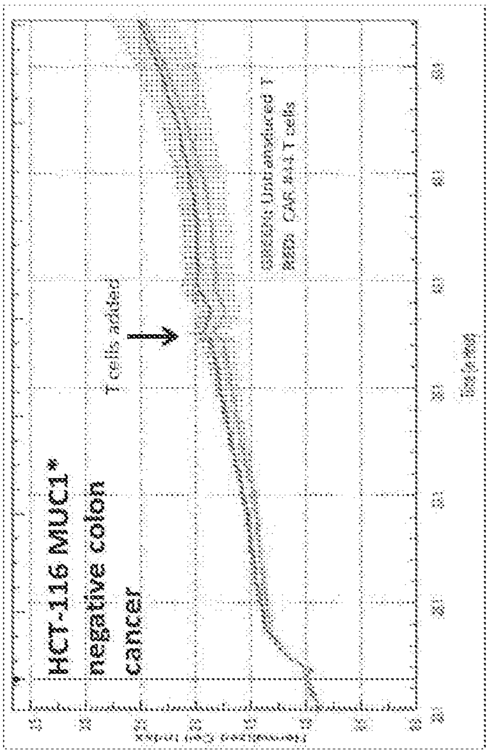


Figure 57A-57C

Single i.v. injection of huMNC2-CAR44 T cells wiped out MUC1* positive tumors

Fig. 58A

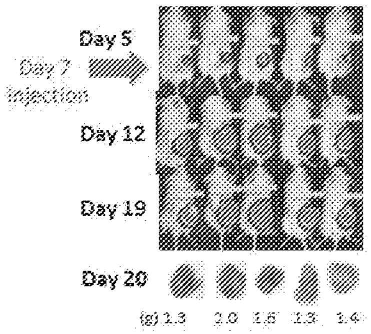


Fig. 58B

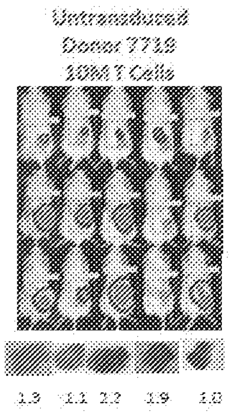


Fig. 58C

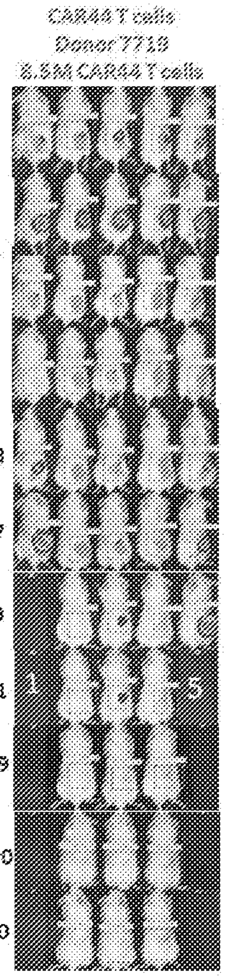


Fig. 58D

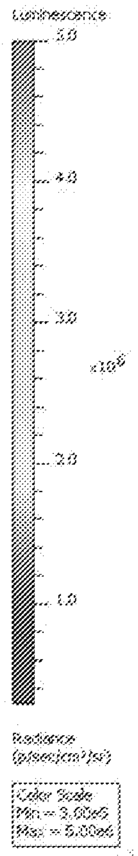


Fig. 58E

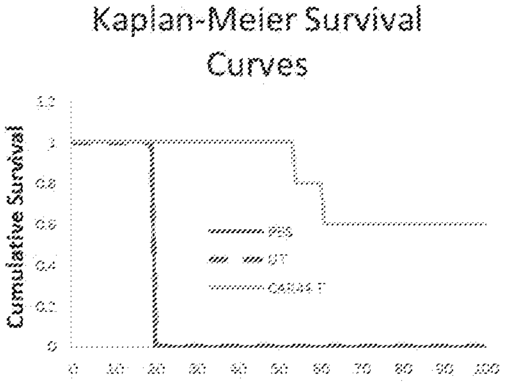


Fig. 58F

Blood FACS Data Starting CD4:CD8 was 43:51

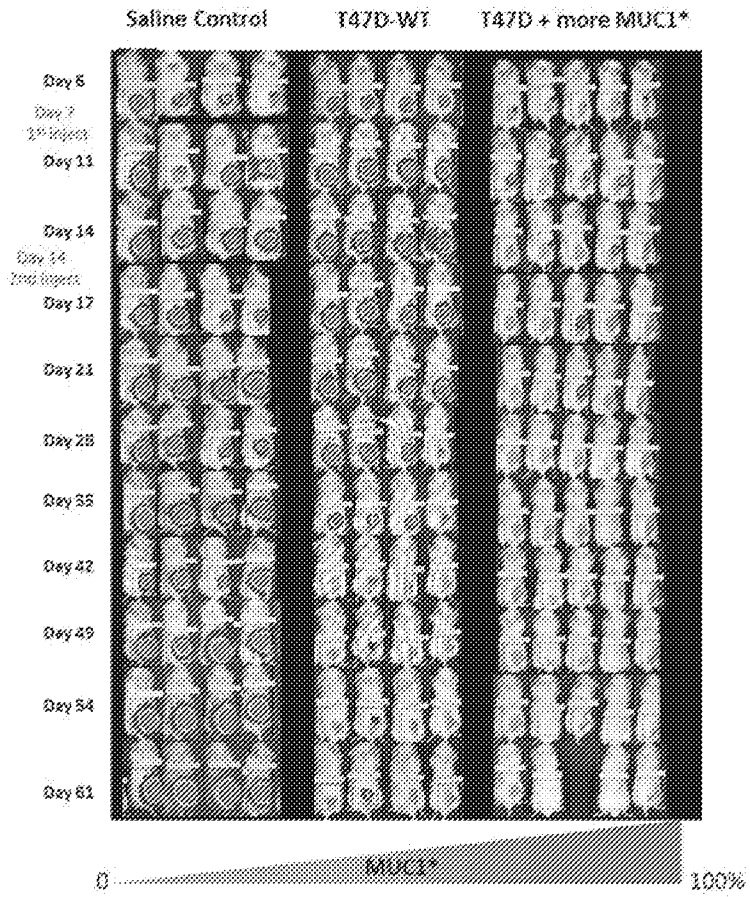
Color Code Death/Sacrifice Day: 20, 54, 61, 100							
UT 10 E6				CAR+ 1x 8.5 E6			
	Hu CD3+	CD8+	PD1		Hu CD3+	CD8+	PD1
1	0.5%	51.3%	6.3%	1	0.1%	75.0%	15.4%
2	0.1%	ND	ND	2	1.4%	75.0%	81.7%
3	4.3%	58.2%	0.8%	3	1.0%	66.7%	72.7%
4	0.9%	58.5%	7.3%	4	10.2%	93.7%	64.6%
5	1.4%	55.3%	12.9%	5	1.4%	66.7%	33.3%

Figure 58A-58F

huMNC2-CAR44 T kill human breast tumors (n > 300)

Killing increases as MUC1* expression increases; MUC1* expression increases with tumor stage & acquired resistance to chemo drugs

Fig. 59A **Fig. 59B** **Fig. 59C**


Saline Control T47D-WT T47D + more MUC1*

T47D-wt is a naturally occurring metastatic breast cancer cell line

T47D + more MUC1* is that same cell line but with 95% of the tumor cells engineered to express more MUC1*

Figures 59A-59C

huMNC2-CAR44 T cells kill breast tumors even if only a low percentage of tumor expresses high amounts of MUC1*

T47D human metastatic breast tumors where 30% of the tumor cells were engineered to express more MUC1* mimics mid stage tumors

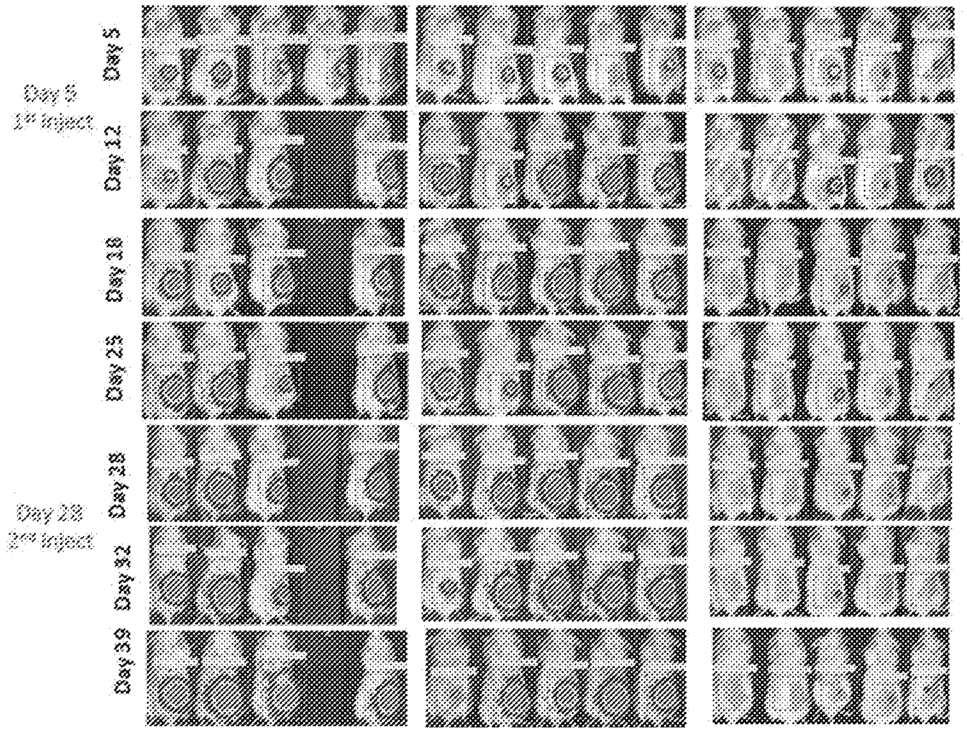


Fig. 60A Saline Control

Fig. 60B Untransduced T cells

Fig. 60C huMNC2-CAR44 T cells

Figures 60A-60C

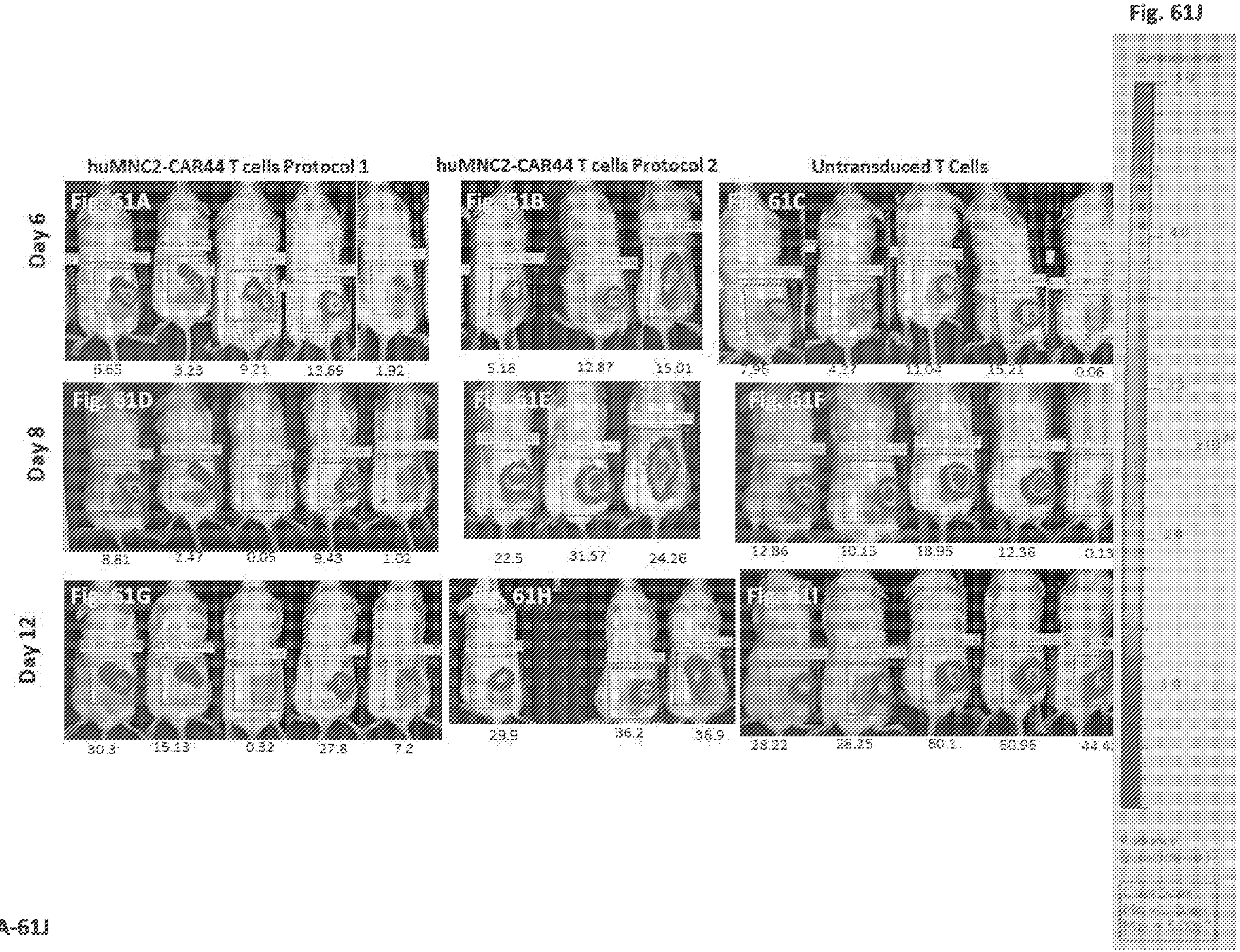
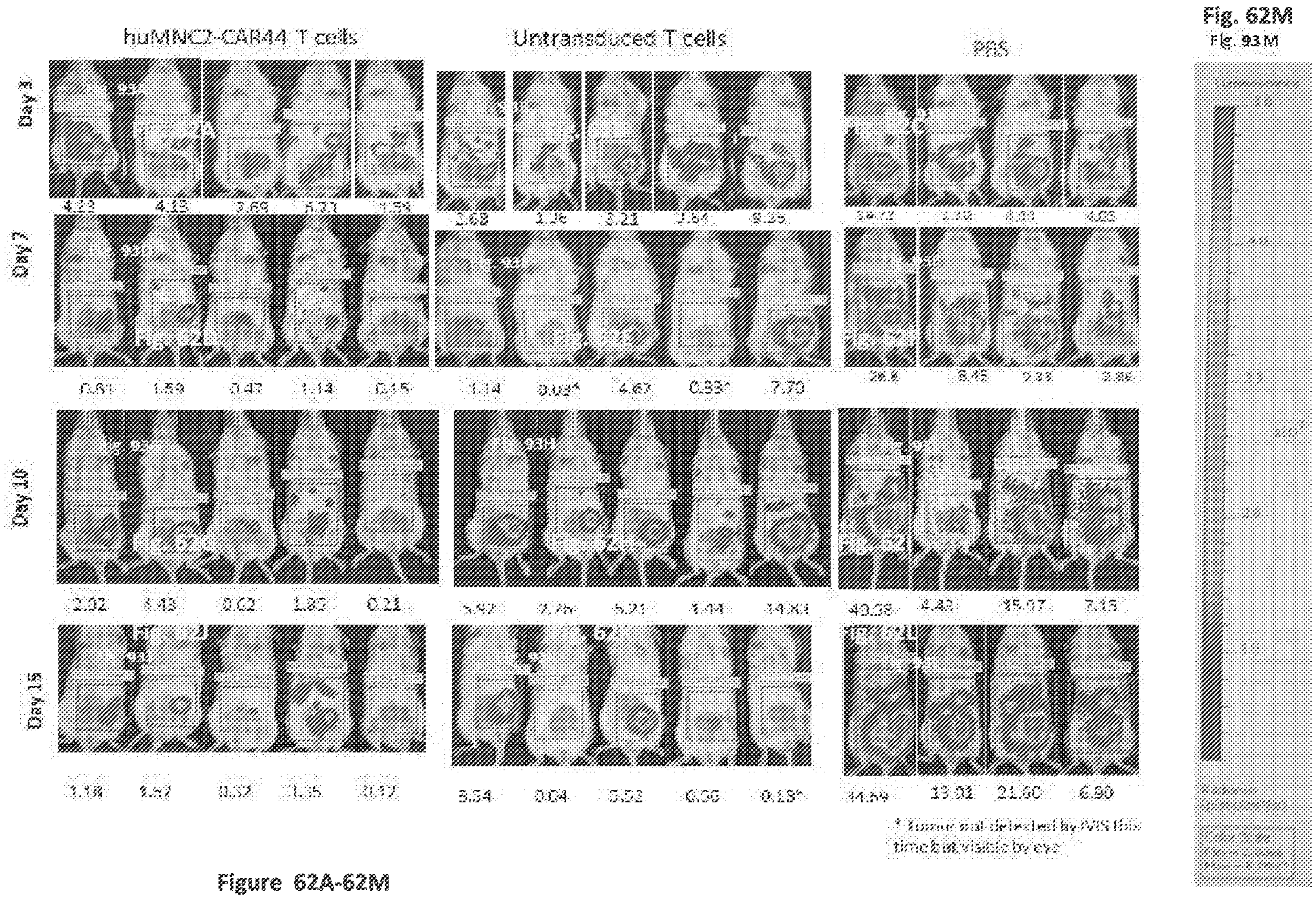


Figure 61A-61J



* Tumor not detected by IVIS this time but visible by eye

Figure 62A-62M

ELISA assay tests ability of monoclonal antibodies to bind to various peptides whose sequences are derived from the PSMGFR peptide

Fig. 63A

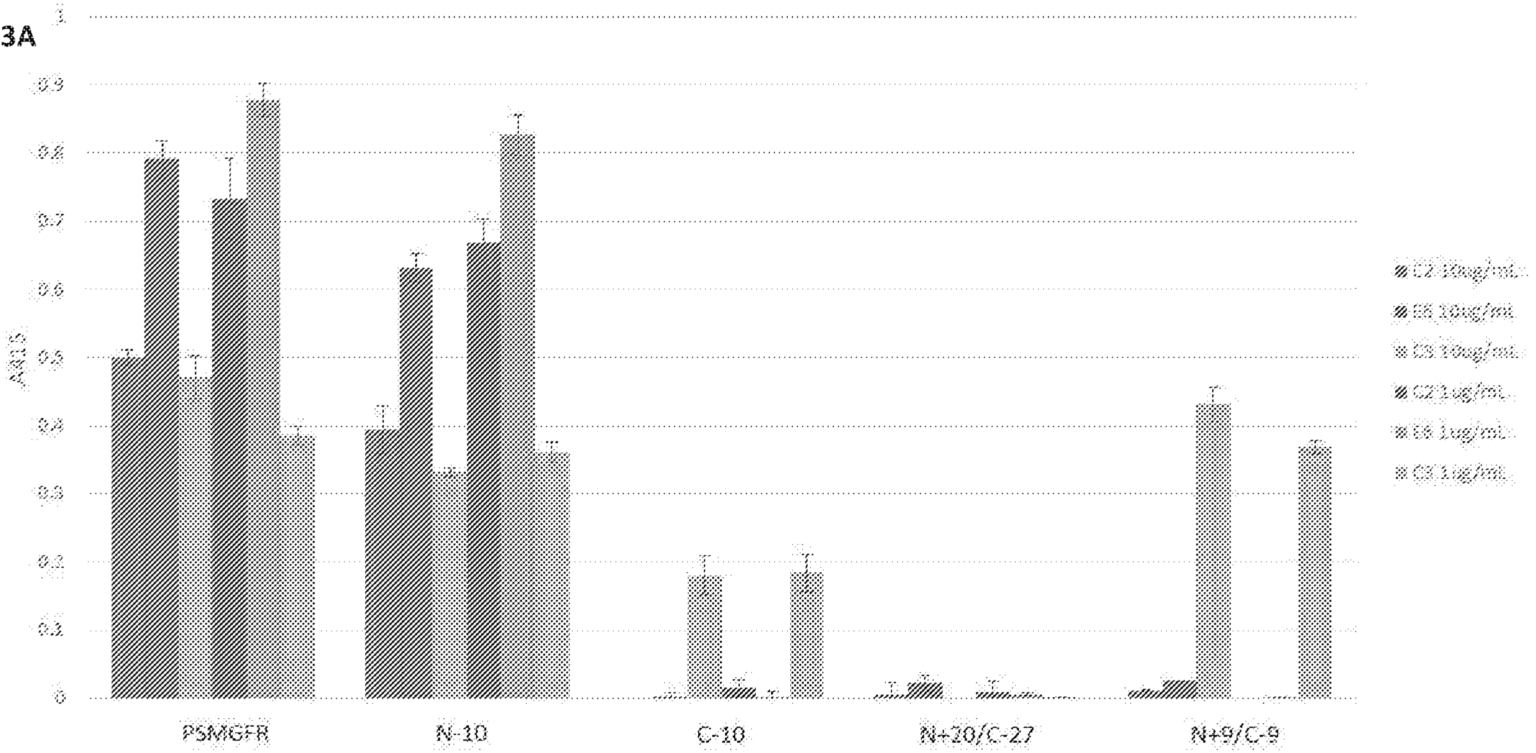


Fig. 63B

N+20/C-27	SNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTE
N+9/C-9	VQLTLAFREGTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVP
PSMGFR	GTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA
N-10	QFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA
C-10	GTINVHDVETQFNQYKTEAASRYNLTISDVSVSDV

Figure 63A-63B

Animals immunized with PSMGFR peptide; 1st selection: bind to PSMGFR; color indicates deductive cognate epitope

Fig. 64A

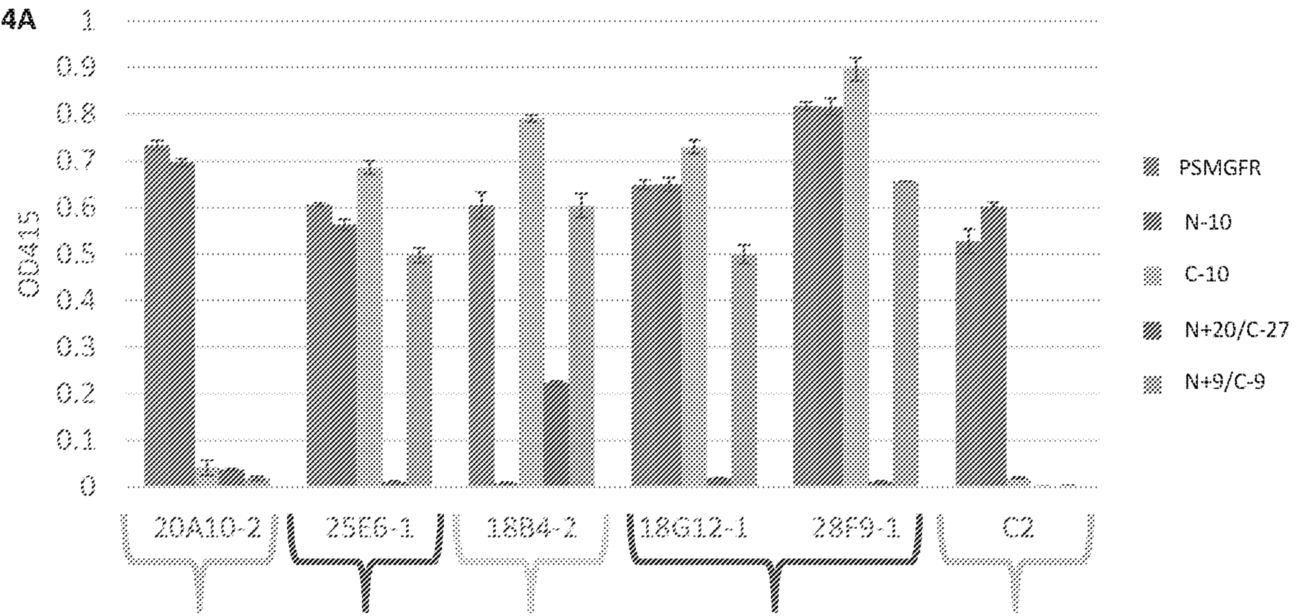


Fig. 64B

N+20/C-27 SNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTE

N+9/C-9 VQLTLAFREGTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVP

PSMGFR GTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA

N-10 QFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA

C-10 GTINVHDVETQFNQYKTEAASRYNLTISDVSVSDV

Figure 64A-64B

Animals immunized with N+20/C-27 peptide; 1st selection: binds to N+20/C-27; color indicates deductive cognate epitope

Fig. 65A

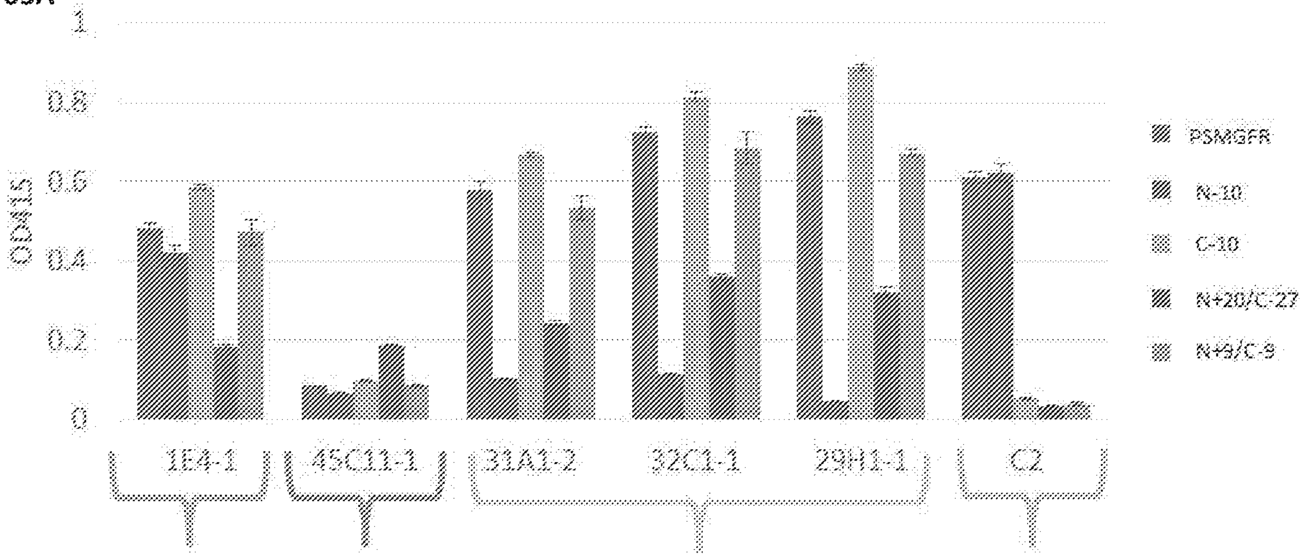


Fig. 65B

N+20/C-27 SNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTE

N+9/C-9 VQLTLAFREGTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVP

PSMGFR GTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA

N-10 QFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA

C-10 GTINVHDVETQFNQYKTEAASRYNLTISDVSVSDV

Figure 65A-65B

Animals immunized with 9+C-9 peptide; 1st selection: bind to 9+C-9; color indicates deductive cognate epitope

Fig. 66A

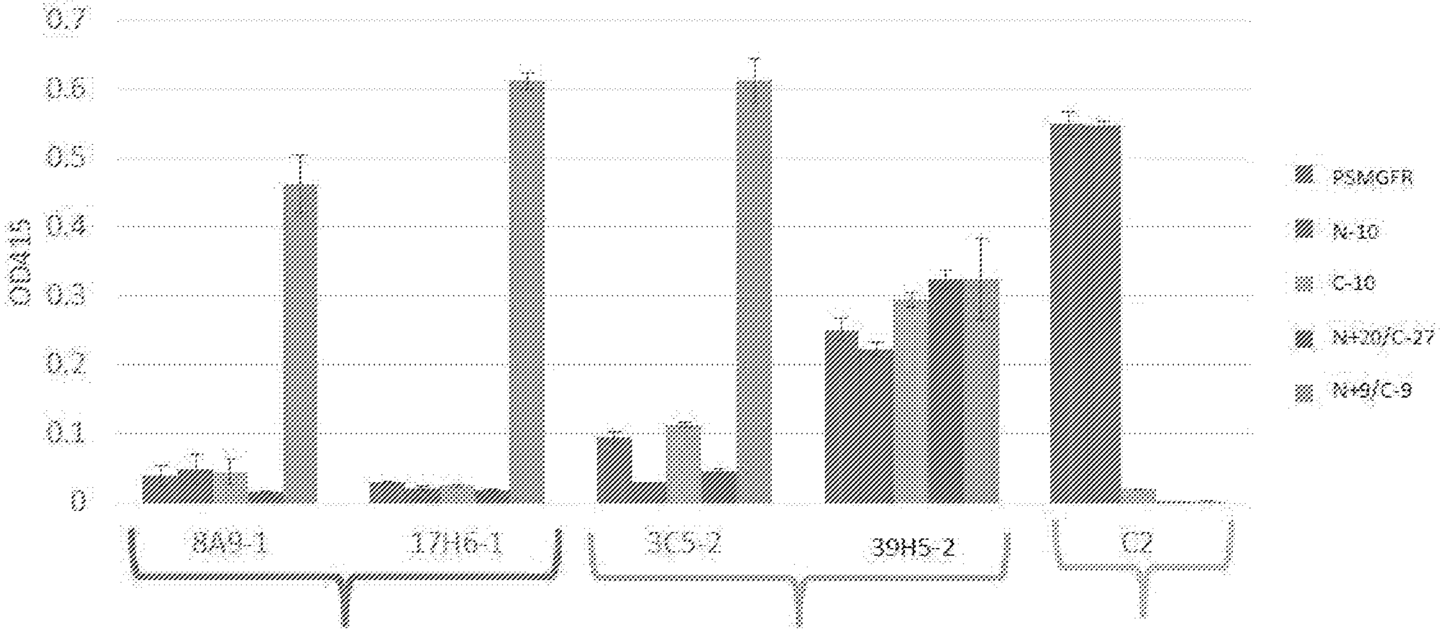


Fig. 66B

N+20/C-27 SNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTE

N+9/C-9 VQLTLAFREGTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVP

PSMGFR GTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA

N-10 QFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA

C-10 GTINVHDVETQFNQYKTEAASRYNLTISDVSVSDV

Figure 66A-66B

ELISA: PSMGFR antibodies – refined epitope mapping (all antibodies @10ug/mL)

Fig. 67A

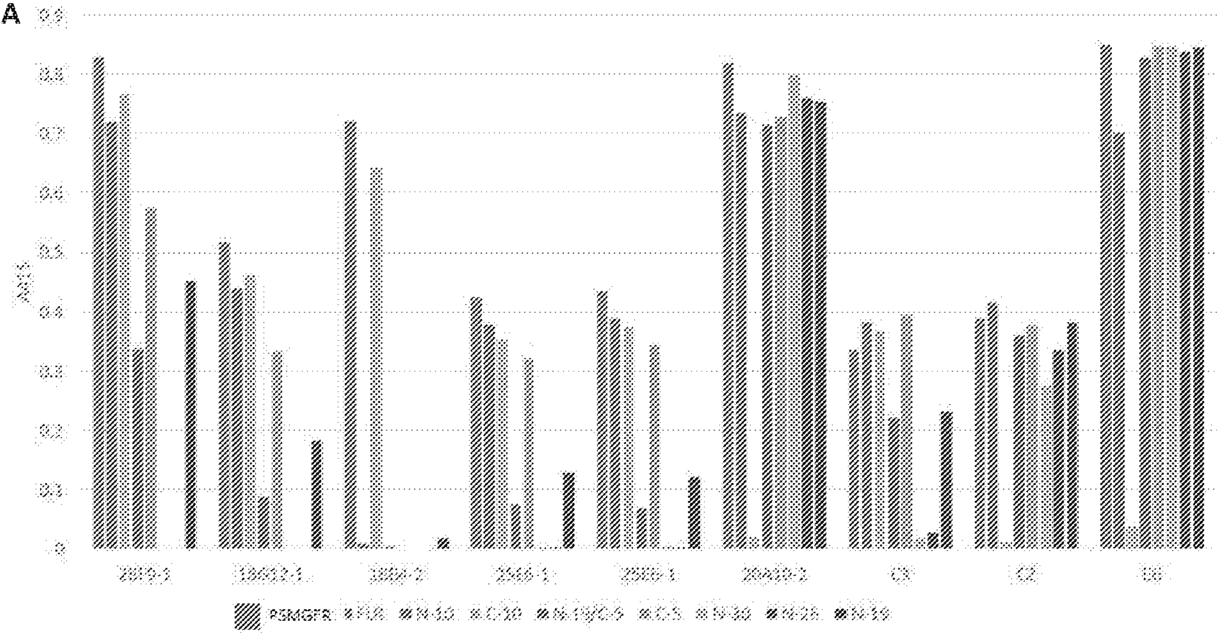


Fig. 67B

SNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA

Fig. 67C

N-19	ASRYNLTISDVSVSDVPFPFSAQSGA
N-26	ISDVSVSDVPFPFSAQSGA
N-30	SVSDVPFPFSAQSGA
N-10/C-5	QFNQYKTEAASRYNLTISDVSVSDVPFPFS-----
N-19/C-5	ASRYNLTISDVSVSDVPFPFS-----
PSMGFR	GTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA
N-10	QFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA
C-10	GTINVHDVETQFNQYKTEAASRYNLTISDVSVSDV----------

Fig. 67D

Refined epitope	
26F9-1	ASRYNLT
18G12-1	ASRYNLT
1E84-2	GTINVHDVET
25E6-1	ASRYNLT
20A10-2	FPFS
C3	ASRYNLT
C2	FPFS
E6	FPFS

Figure 67A-67D

ELISA: N+20/C-27 antibodies – refined epitope mapping (all antibodies @10ug/mL)

Fig. 68A

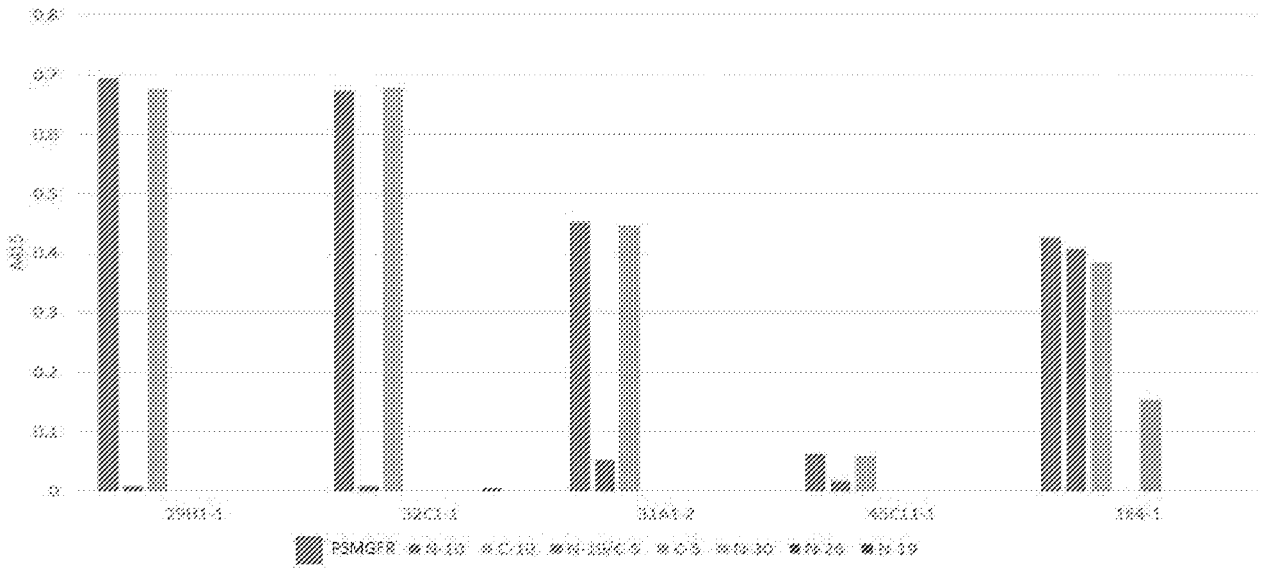


Fig. 68B

SNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA

Fig. 68C

N-19	ASRYNLTISDVSVSDVPFPFSAQSGA
N-26	ISDVSVSDVPFPFSAQSGA
N-30	SVSDVPFPFSAQSGA
C-5	QFNQYKTEAASRYNLTISDVSVSDVPFPFS
N-19 C-5	ASRYNLTISDVSVSDVPFPFS
PSMGFR	GTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA
N10	QFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA
C10	GTINVHDVETQFNQYKTEAASRYNLTISDVSVSDV

Fig. 68D

Refined Epitope	
29H1-1	GTINVHDVET
32C1-1	GTINVHDVET
31A1-2	GTINVHDVET
45C11-1	SNIKFRPGSVV
1E4-1	QFNQYKTEA

Figure 68A-68D

ELISA: N+9/C-9 antibodies – refined epitope mapping (all antibodies @10ug/mL)

Fig. 69A

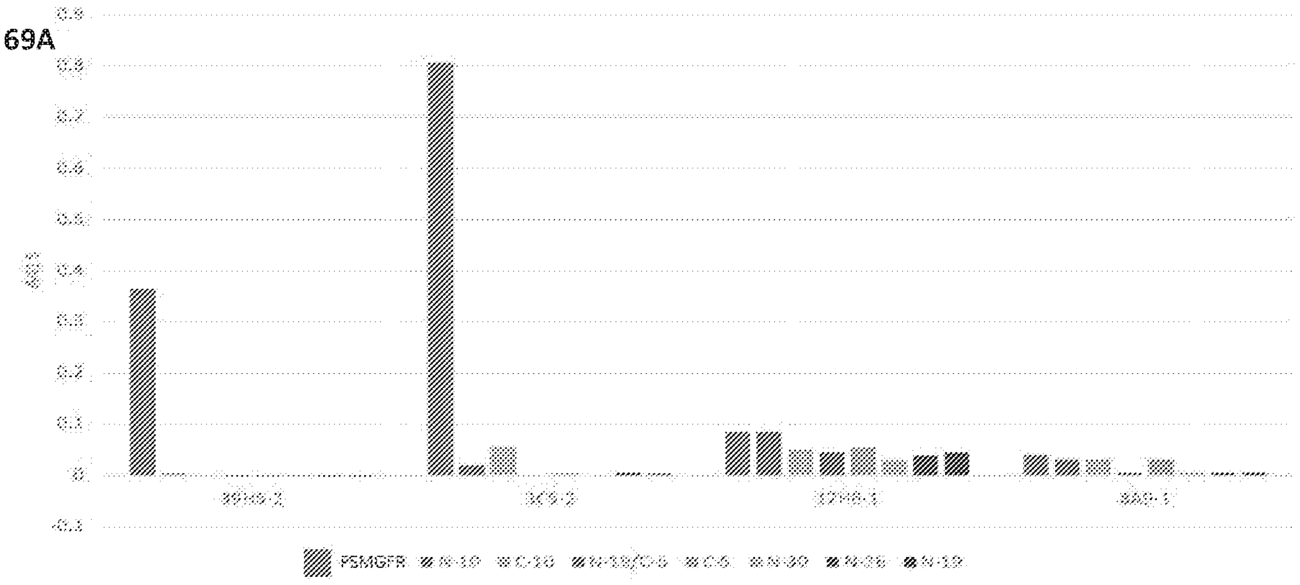


Fig. 69B

SNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA

Fig. 69C

N-19	ASRYNLTISDVSVSDVPFPFSAQSGA
N-26	ISDVSVSDVPFPFSAQSGA
N-30	SVSDVPFPFSAQSGA
N-10/C-5	QFNQYKTEAASRYNLTISDVSVSDVPFPFS-----
N-19/C-5	ASRYNLTISDVSVSDVPFPFS-----
PSMGFR	GTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA
N-10	QFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA
C-10	GTINVHDVETQFNQYKTEAASRYNLTISDVSVSDV----------

Fig. 69D

Refined Epitope	
39H5-2	GTINVHDVET
3C5-2	GTINVHDVET
17H6-1	VQLTLAFRE
8A9-1	VQLTLAFRE

Figure 69A-69D

ELISA displacement assay tests ability of antibodies of the invention to displace NME7$_{AB}$ from binding to PSMGFR peptide.

Figure 70A

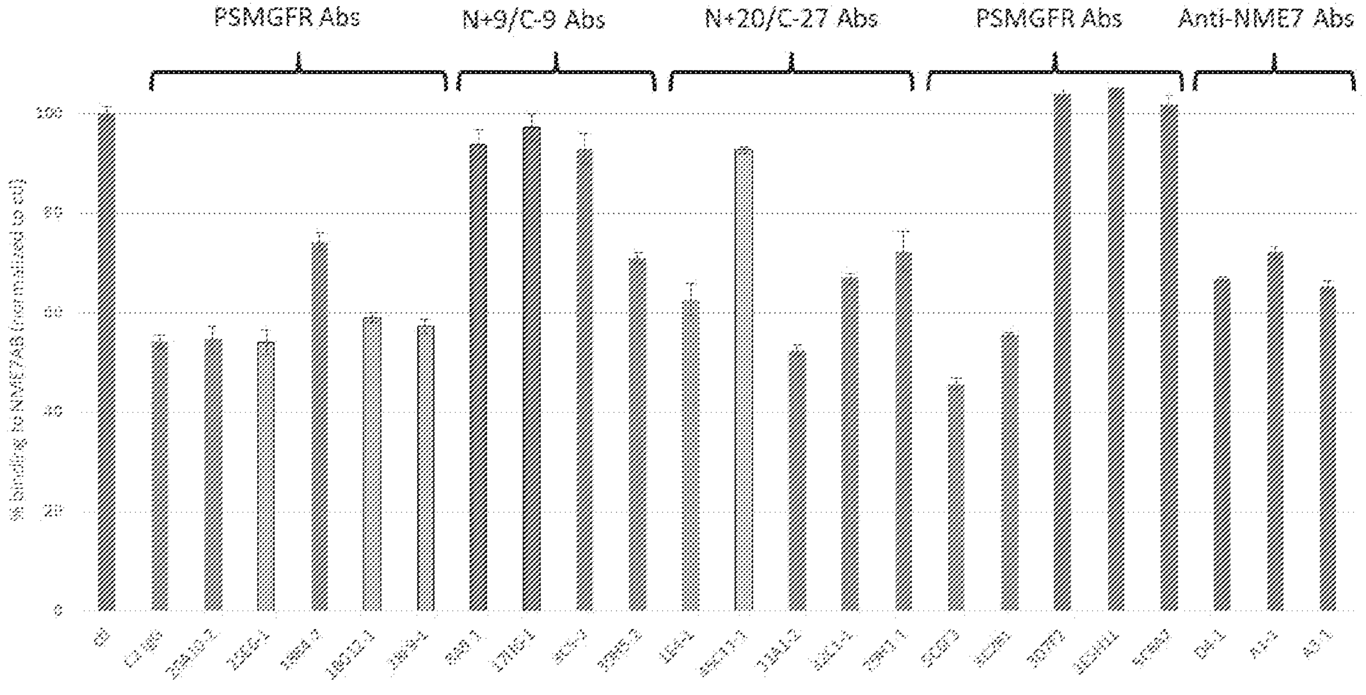
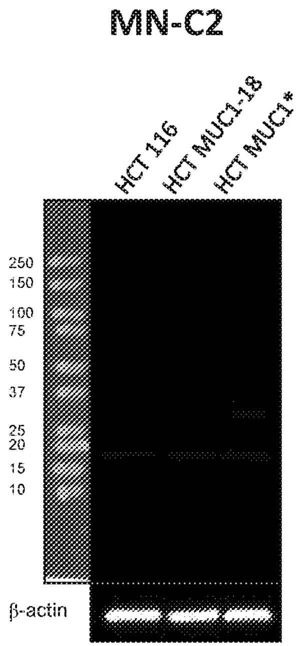


Figure 70B

SNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA

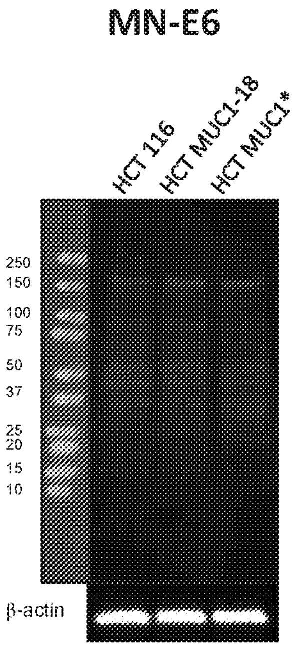
Figure 70A-70B

Fig. 71A



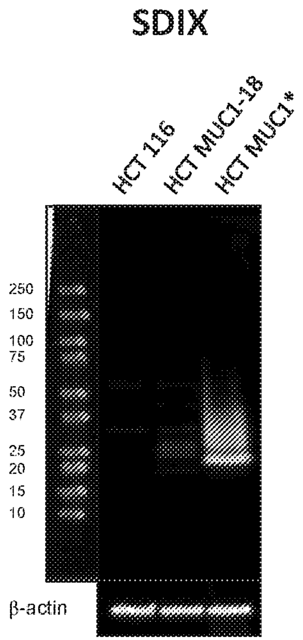
Stock Concentration: 1.85 mg/mL
Dilution Tested: 1:500
Exposure: 5 min
Reagent: ECL

Fig. 71B



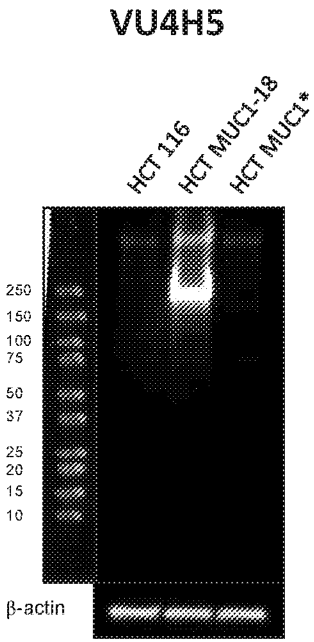
Stock Concentration: 1.859mg/mL
Dilution Tested: 1:500
Exposure: 5 min
Reagent: ECL

Fig. 71C



Stock Concentration: 1mg/mL
Dilution : 1:1000
Exposure: 2 min
Reagent: ECL

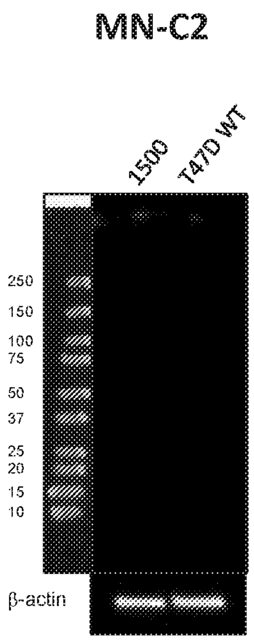
Fig. 71D



Stock Concentration: 200 μg/mL
Dilution : 1:200
Exposure: 5 min
Reagent: ECL

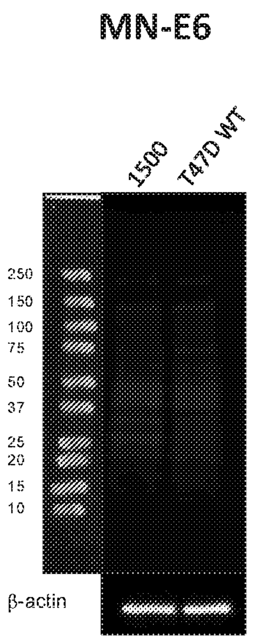
Figure 71A-71D

Fig. 71E



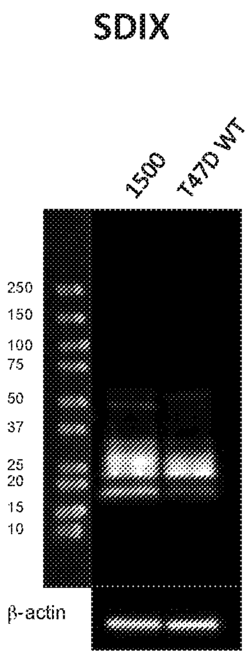
Stock Concentration: 1.85 mg/mL
Dilution Tested: 1:500
Exposure: 5 min
Reagent: ECL

Fig. 71F



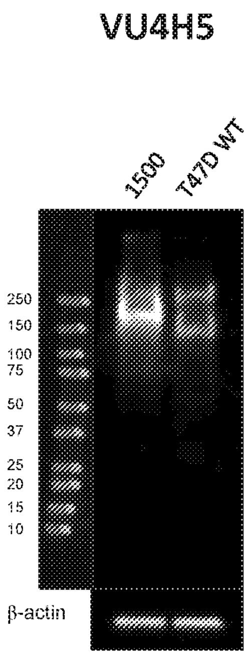
Stock Concentration: 1.89 mg/mL
Dilution Tested: 1:500
Exposure: 5 min
Reagent: ECL

Fig. 71G



Stock Concentration: 1mg/mL
Dilution : 1:1000
Exposure: 5 min
Reagent: ECL

Fig. 71H



Stock Concentration: 200 ug/mL
Dilution : 1:200
Exposure: 5 min
Reagent: ECL

Figure 71E-71H

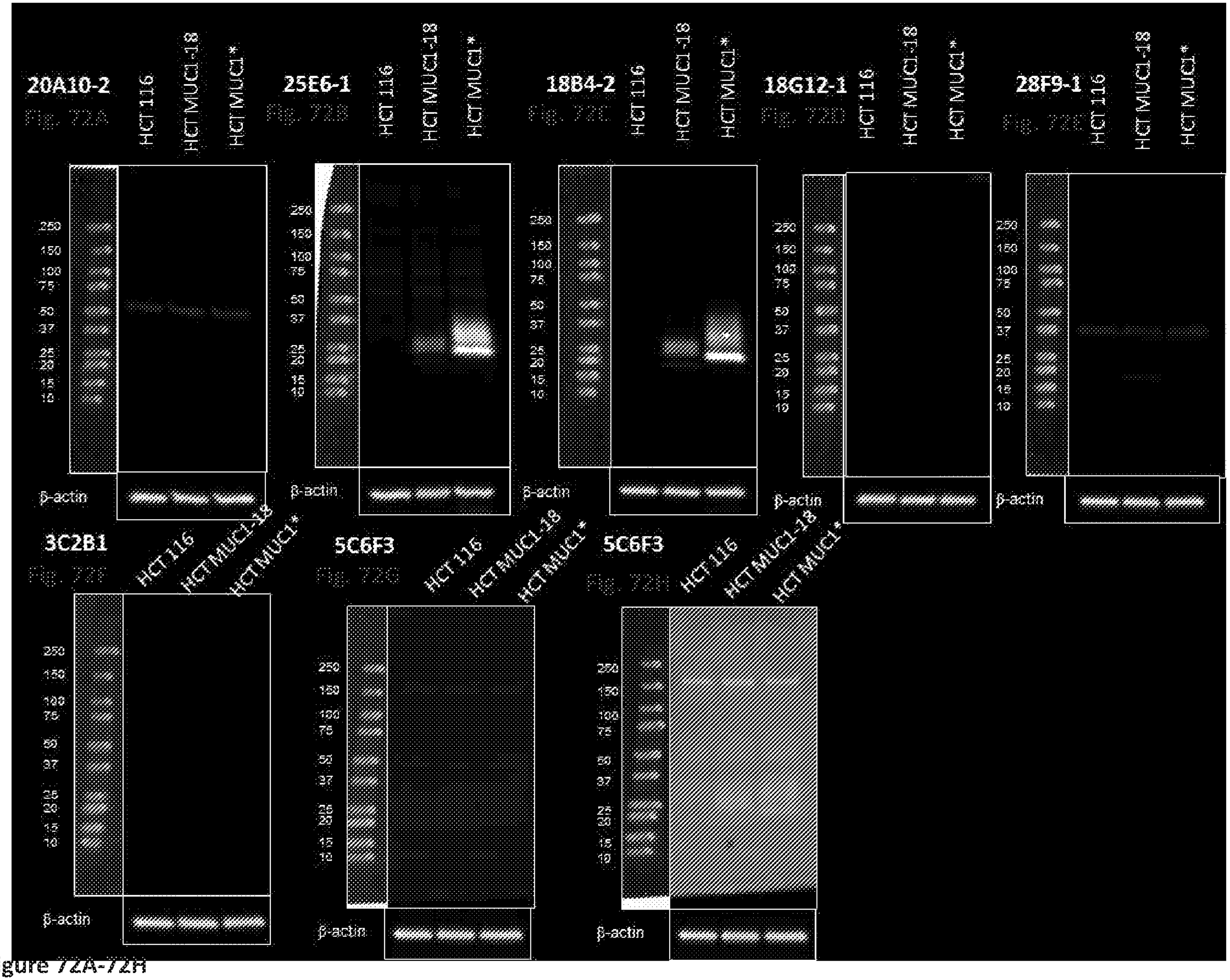
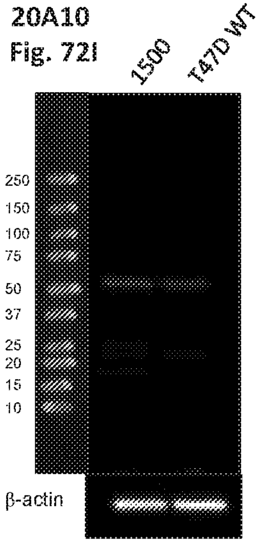
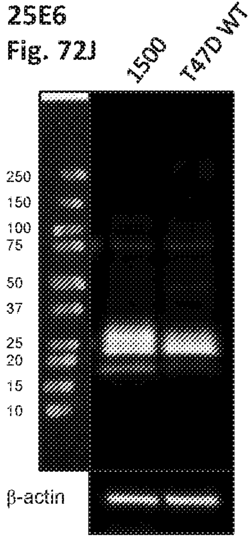


Figure 72A-72H

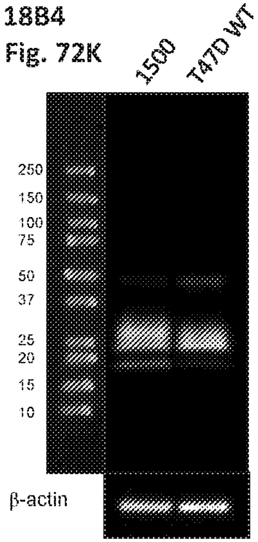
20A10
Fig. 72I



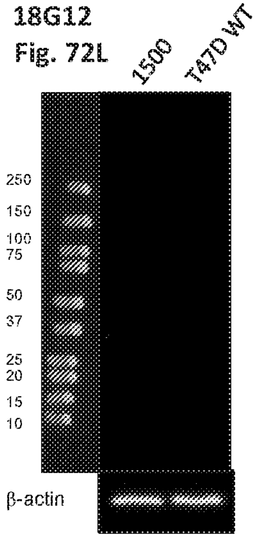
25E6
Fig. 72J



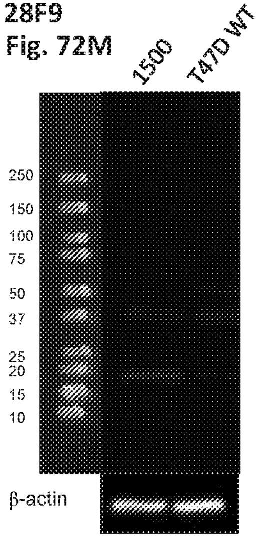
18B4
Fig. 72K



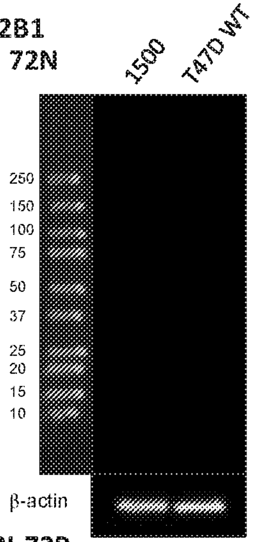
18G12
Fig. 72L



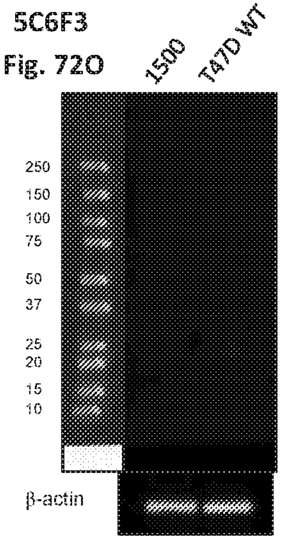
28F9
Fig. 72M



3C2B1
Fig. 72N



5C6F3
Fig. 72O



5C6F3
Fig. 72P

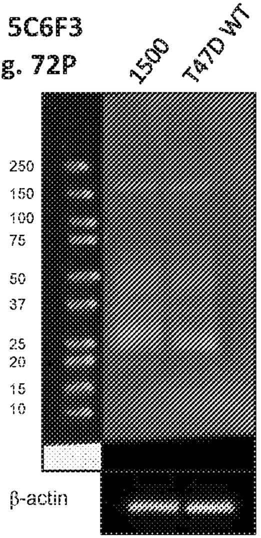


Figure 72I-72P

Fig. 73A

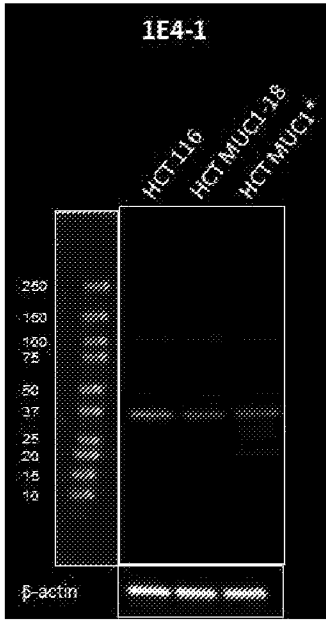


Fig. 73B

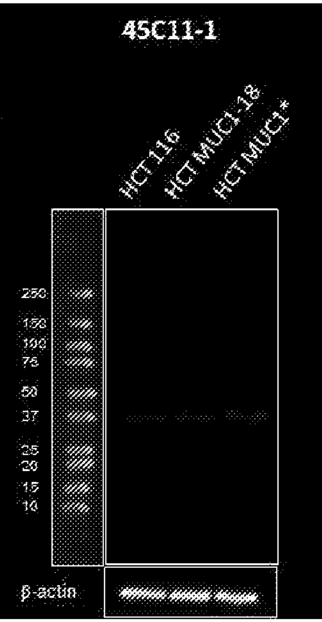


Fig. 73C

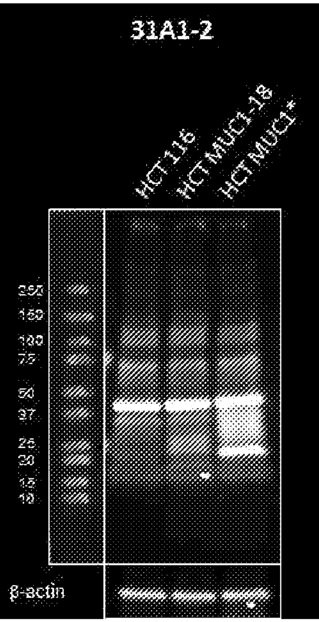


Fig. 73D

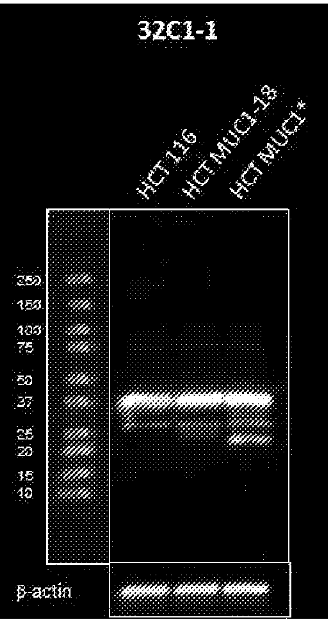


Fig. 73E

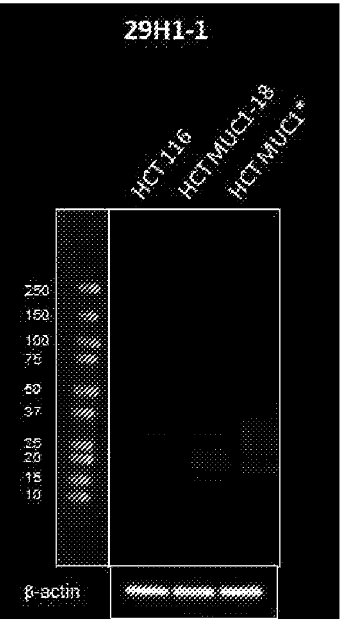


Figure 73A-73E

Fig. 73F

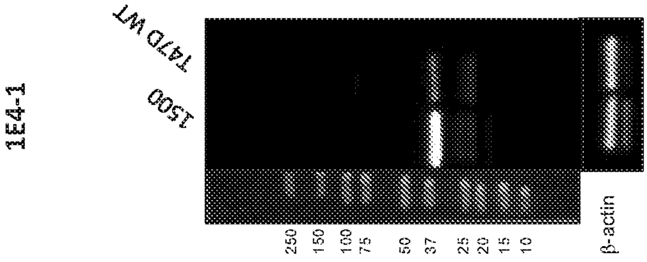


Fig. 73G

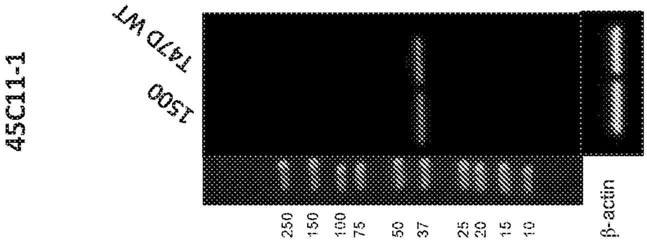


Fig. 73H

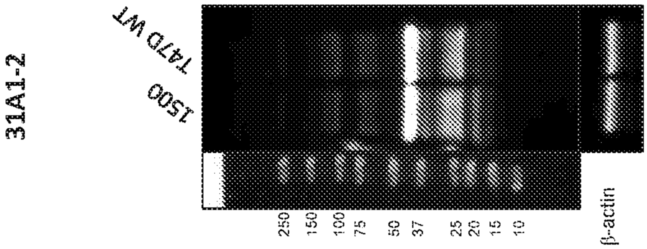


Fig. 73I

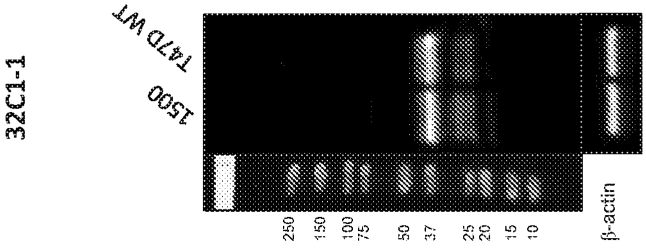


Fig. 73J

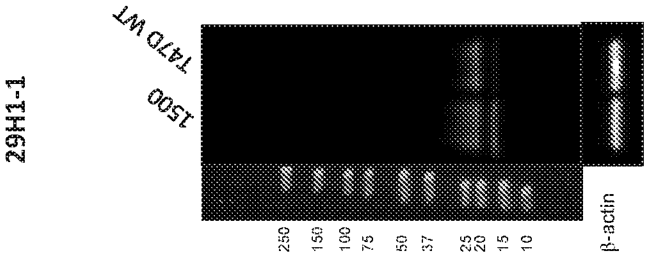


Figure 73F-73J

Fig. 74A

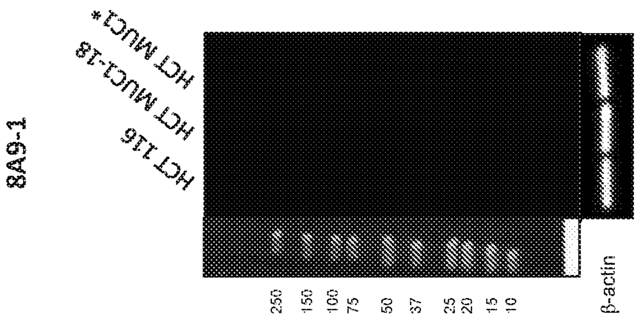


Fig. 74B

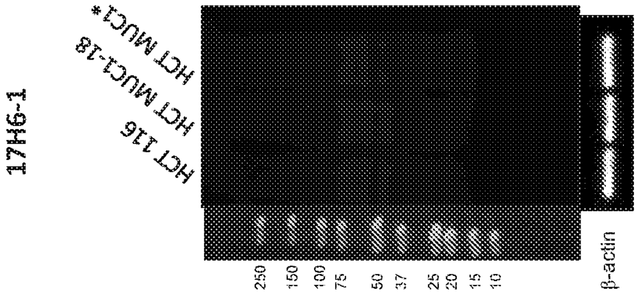


Fig. 74C

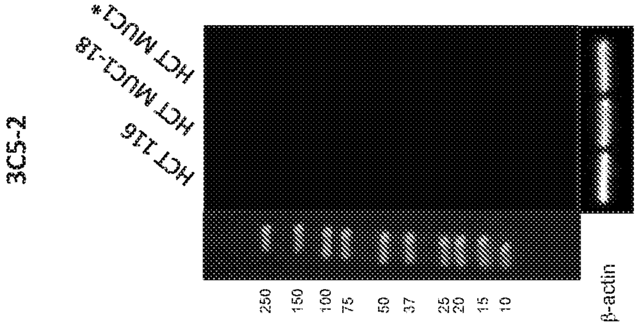


Fig. 74D

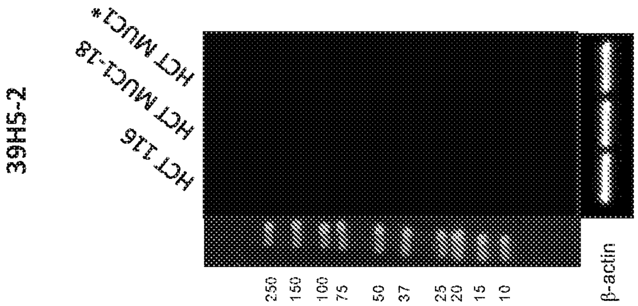


Figure 74A-74D

Fig. 74E

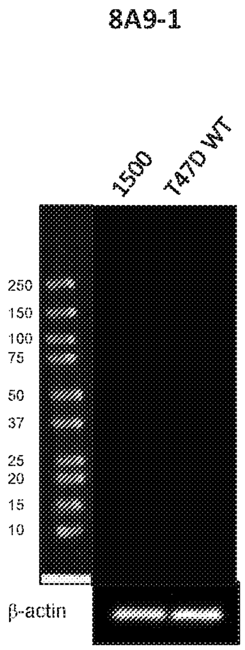


Fig. 74F

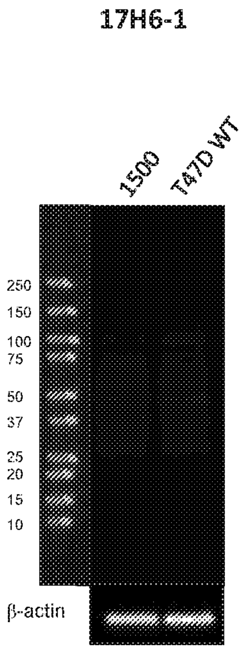


Fig. 74G

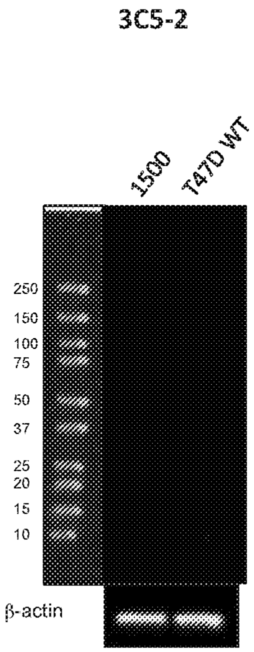


Fig. 74H

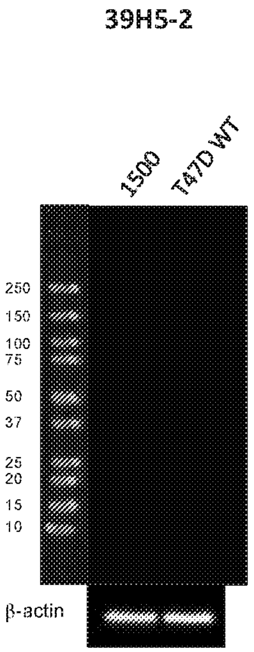


Figure 74E-74H

N-SHIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA-C

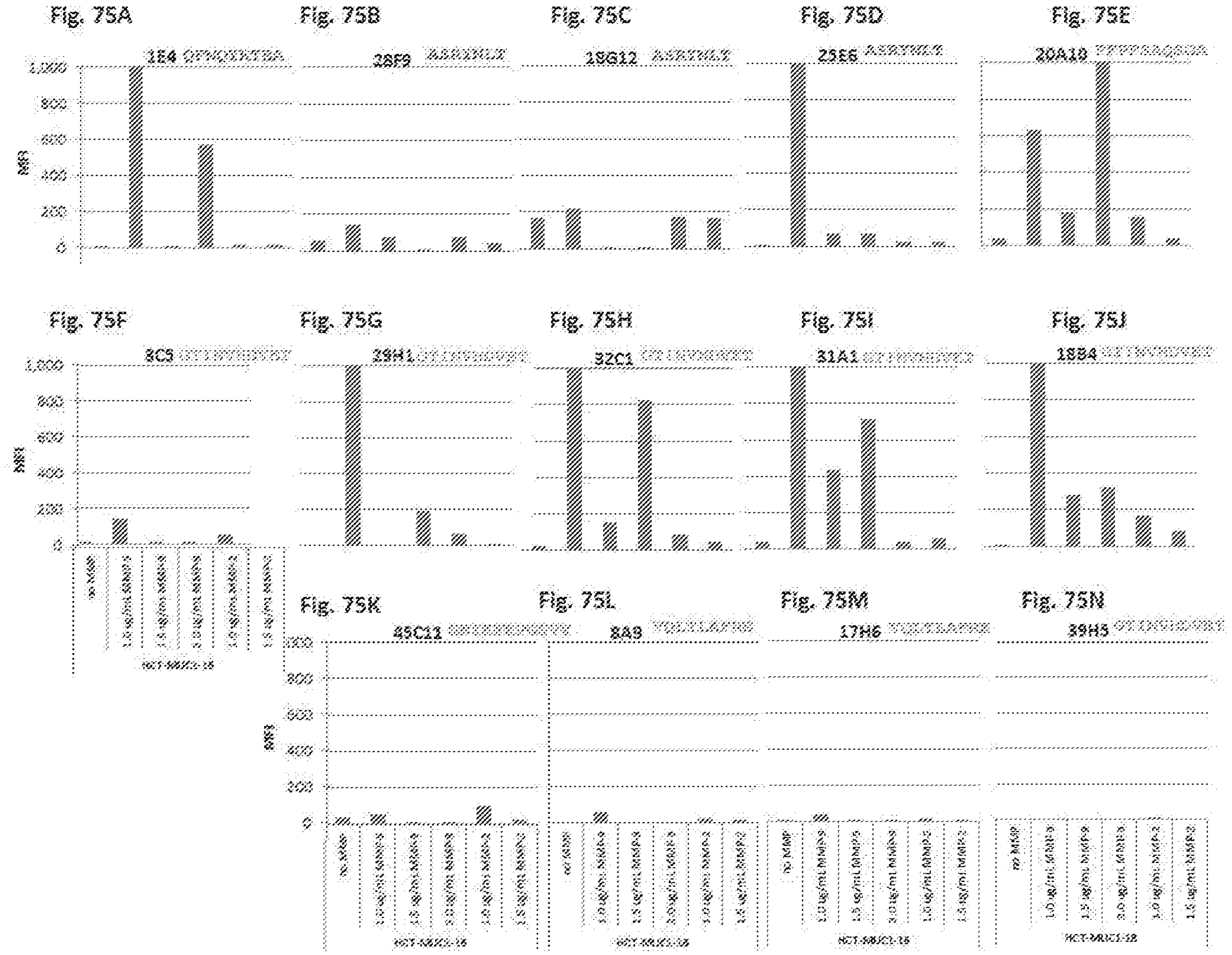


Figure 75A-75N

N- SNIKFRPGSVV VQLTLAFRE GTINVHDVET QFNQYKTEA ASRYNLT ISDVSVSDV PFPFSAQSGA -C

Fig. 75O

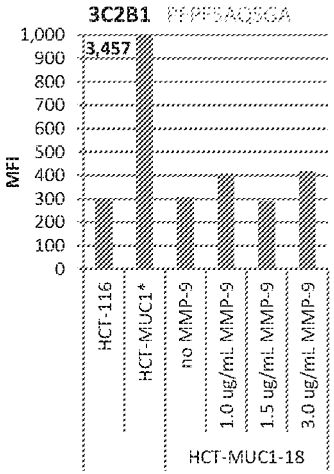


Fig. 75P

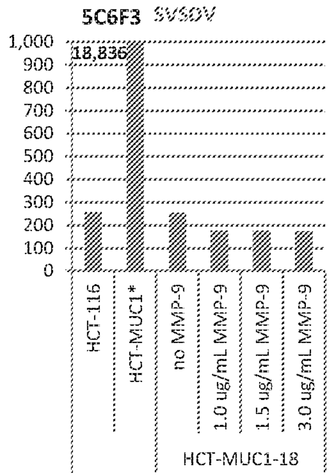


Figure 75O-75P

FACS: Reference antibodies per cell line

Fig. 76A

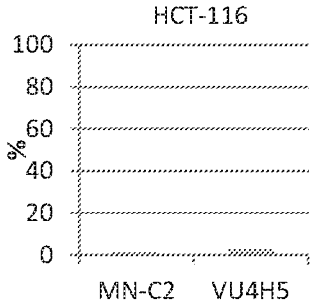


Fig. 76B

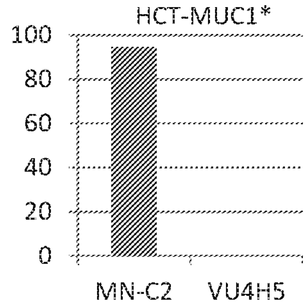


Fig. 76C

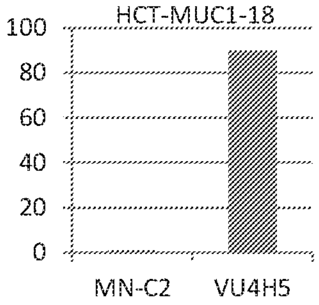


Fig. 76D

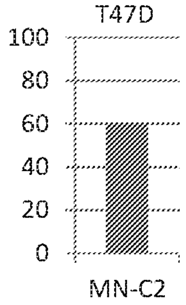


Fig. 76E

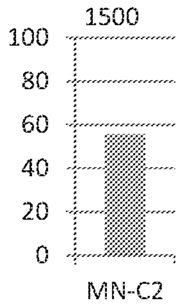


Fig. 76F

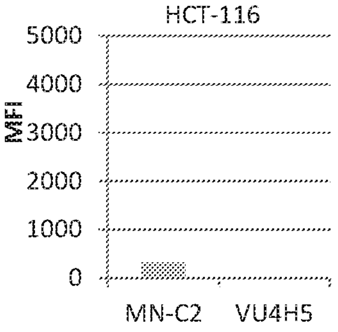


Fig. 76G

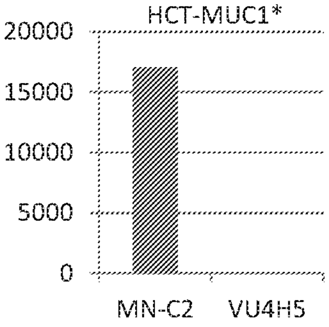


Fig. 76H

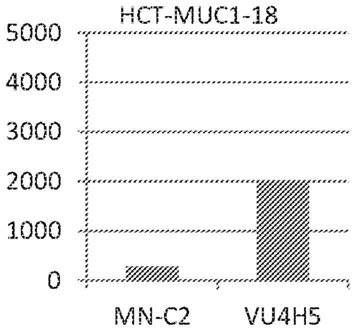


Fig. 76I

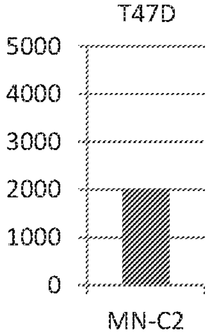


Fig. 76J

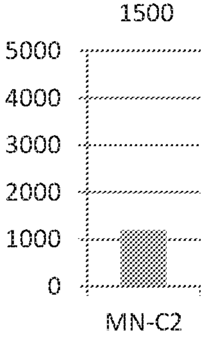


Figure 76A-76J

FACS: Reference antibodies per cell line

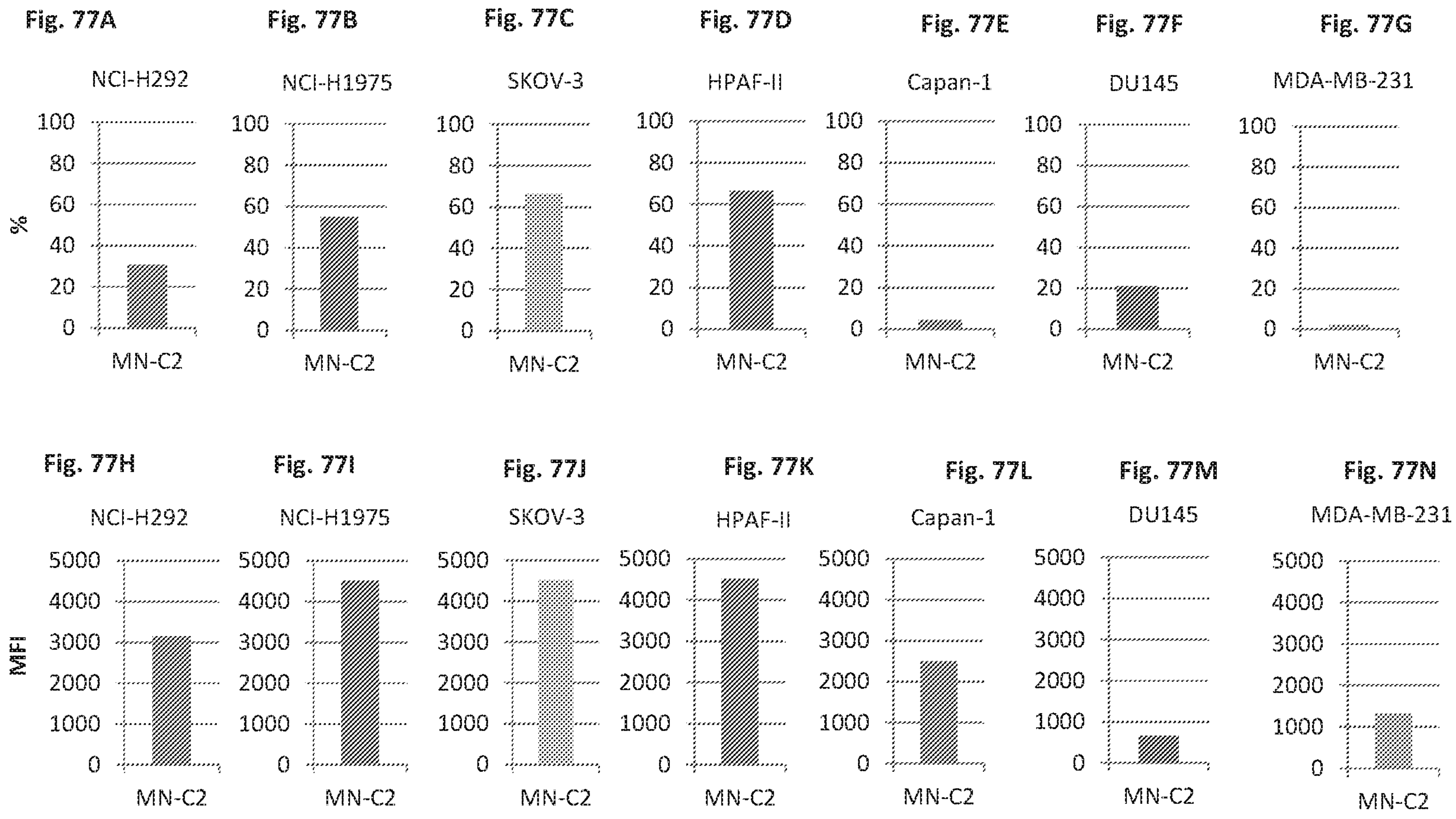


Fig. 77A Fig. 77B Fig. 77C Fig. 77D Fig. 77E Fig. 77F Fig. 77G

Fig. 77H Fig. 77I Fig. 77J Fig. 77K Fig. 77L Fig. 77M Fig. 77N

Figure 77A-77N

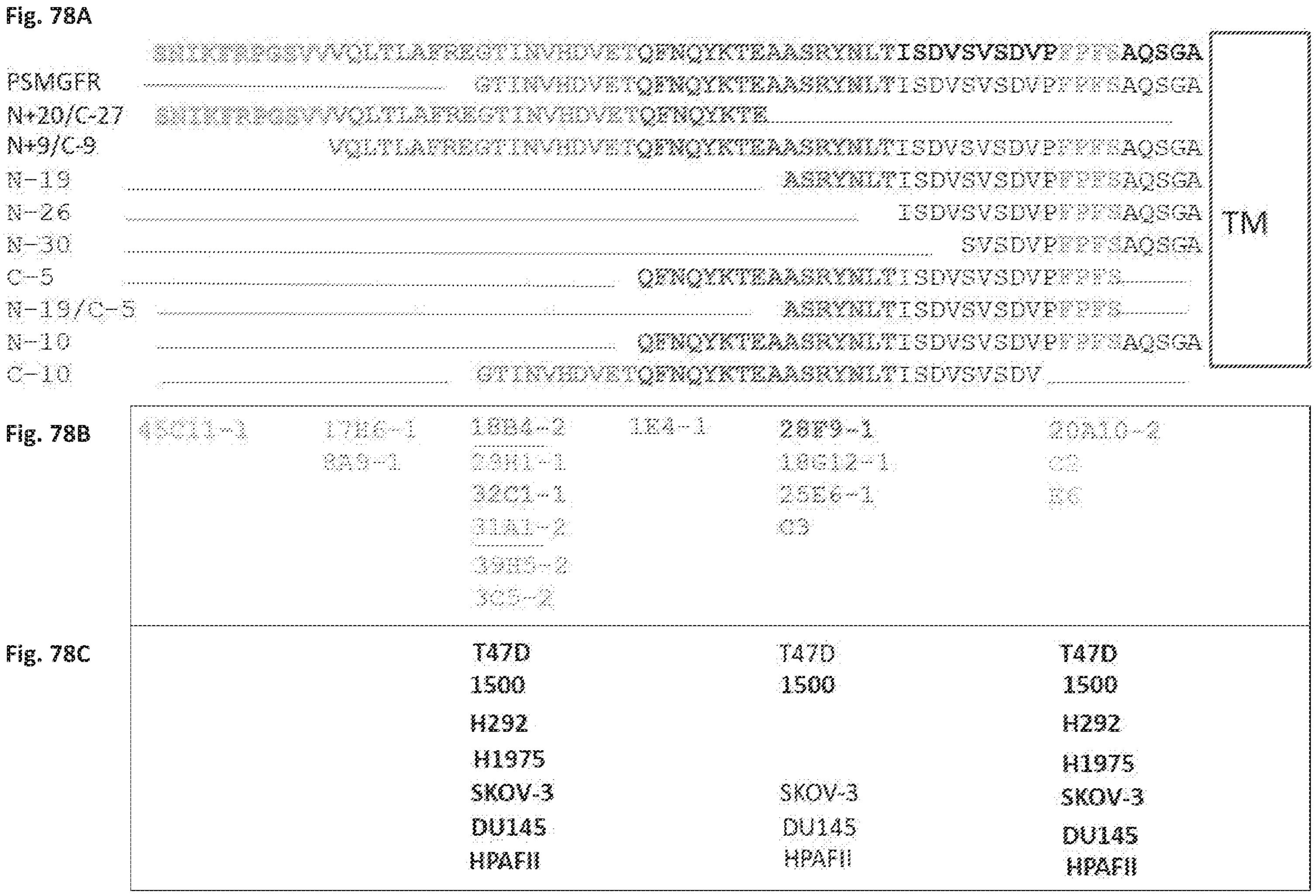


Figure 78A-78C

FACS Analyses: Binding of antibodies to T47D breast cancer cells

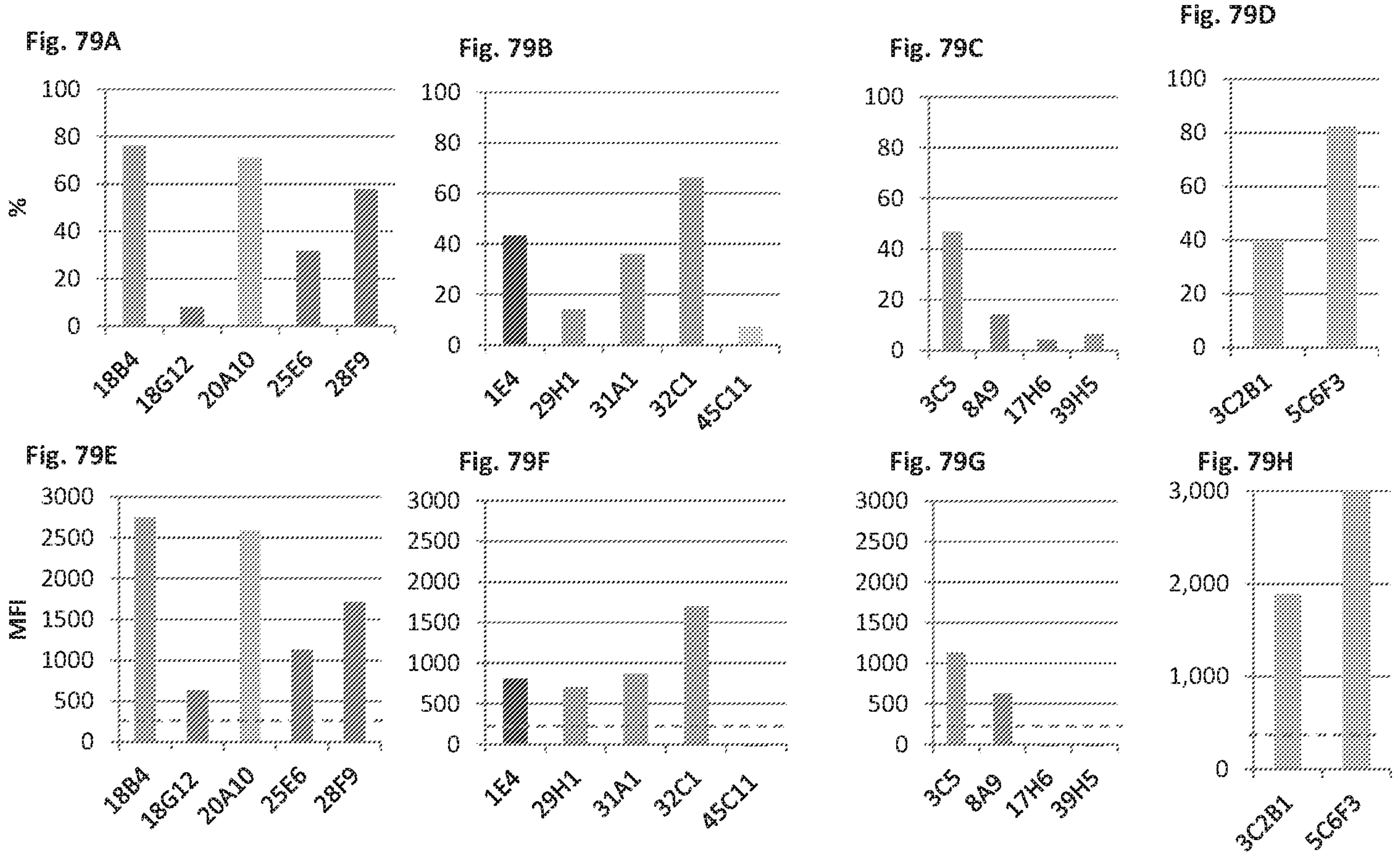


Fig. 79I

SNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA

Figure 79A-79I

FACS Analyses: Binding of antibodies to 1500 breast cancer cells

Fig. 80A

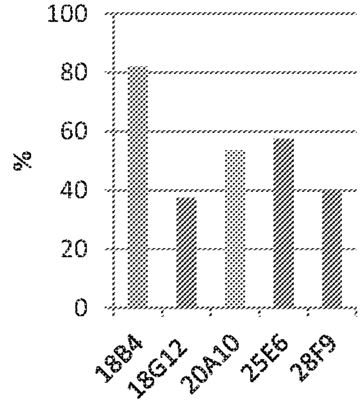


Fig. 80B

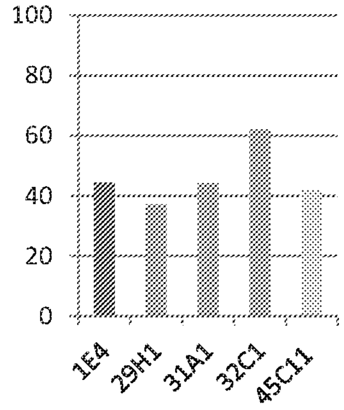


Fig. 80C

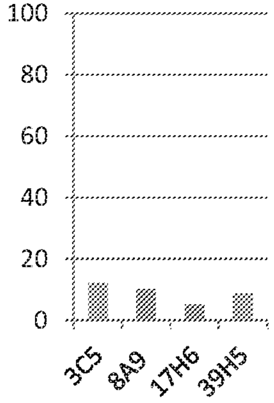


Fig. 80D

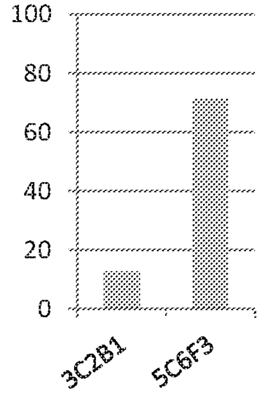


Fig. 80E

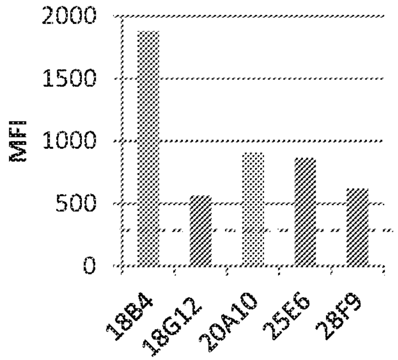


Fig. 80F

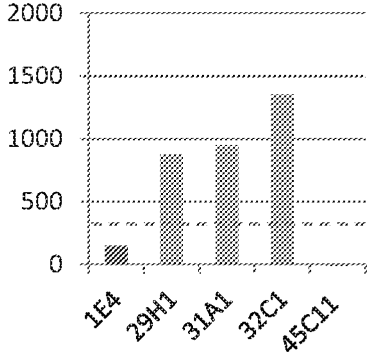


Fig. 80G

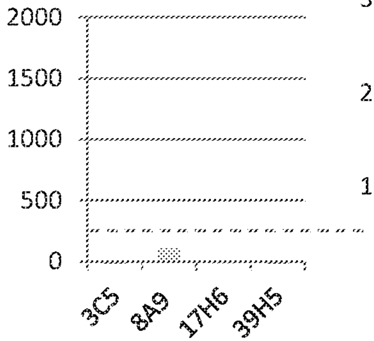


Fig. 80H

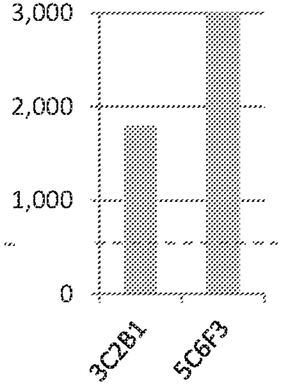


Fig. 80I

SNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTEAASRYNLT**ISDVSVSDVP**FPFS**AQSGA**

Figure 80A-80I

FACS Analyses: Binding of antibodies to NCI-H292 lung cancer cells

Fig. 81A

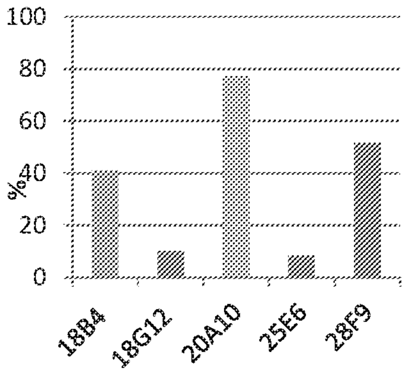


Fig. 81B

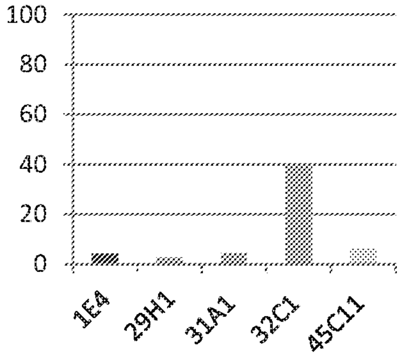


Fig. 81C

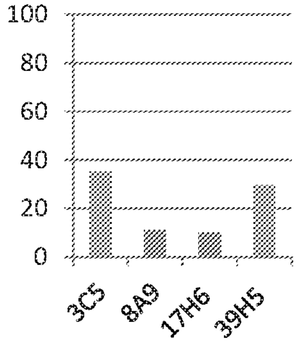


Fig. 81D

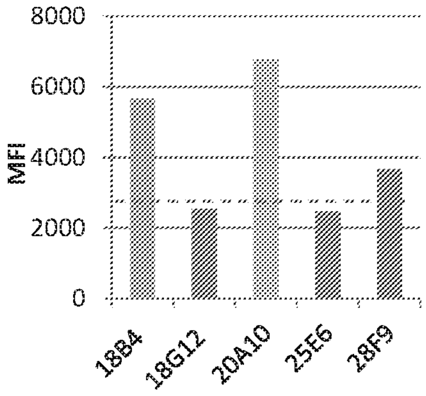


Fig. 81E

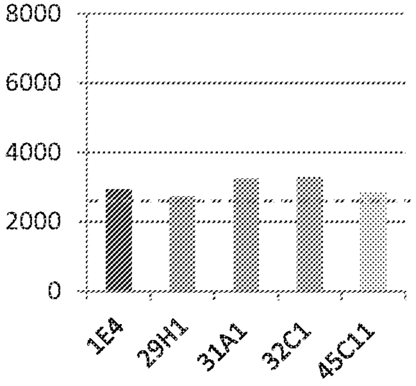


Fig. 81F

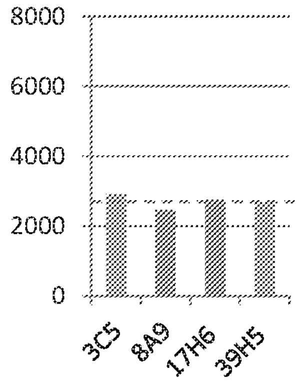


Fig. 81G

SNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA

Figure 81A-81G

FACS Analyses: Binding of antibodies to NCI-H1975 lung cancer cells

Fig. 82A

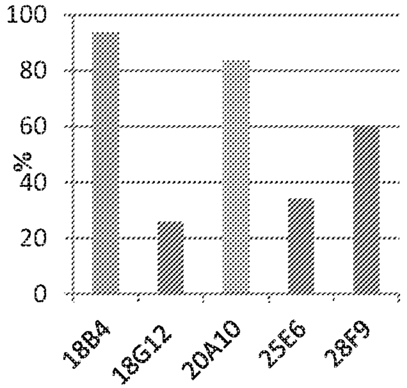


Fig. 82B

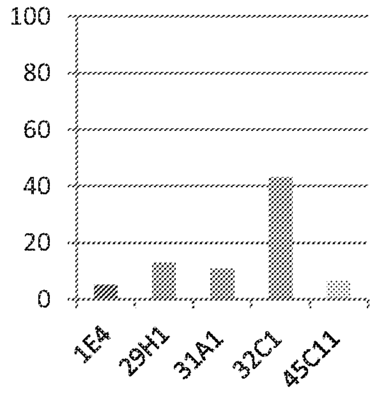


Fig. 82C

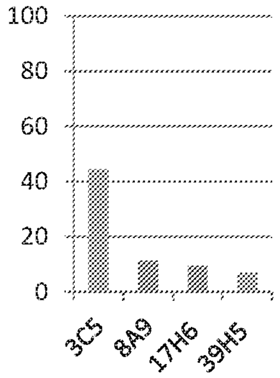


Fig. 82D

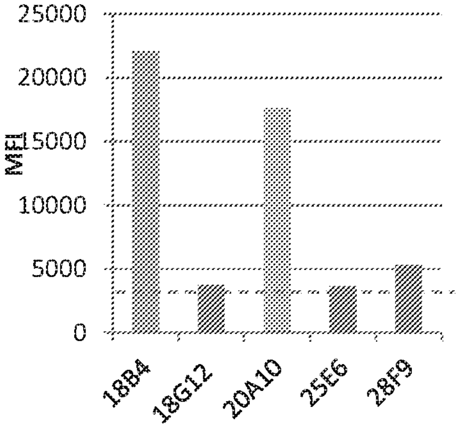


Fig. 82E

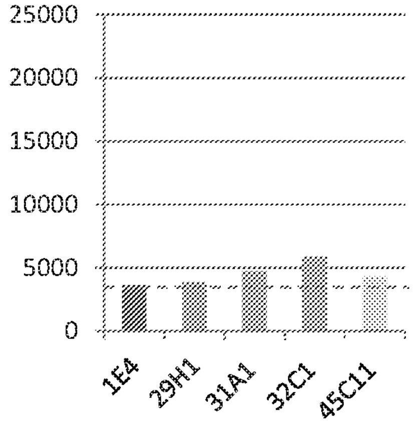


Fig. 82F

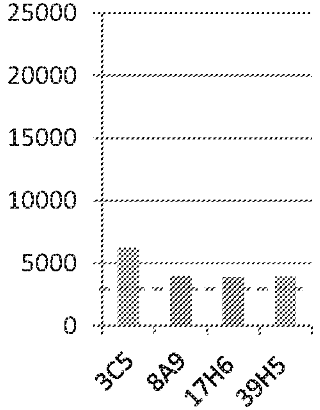


Fig. 82G

SNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA

Figure 82A-82G

FACS Analyses: Binding of antibodies to SKOV-3 ovarian cancer cells

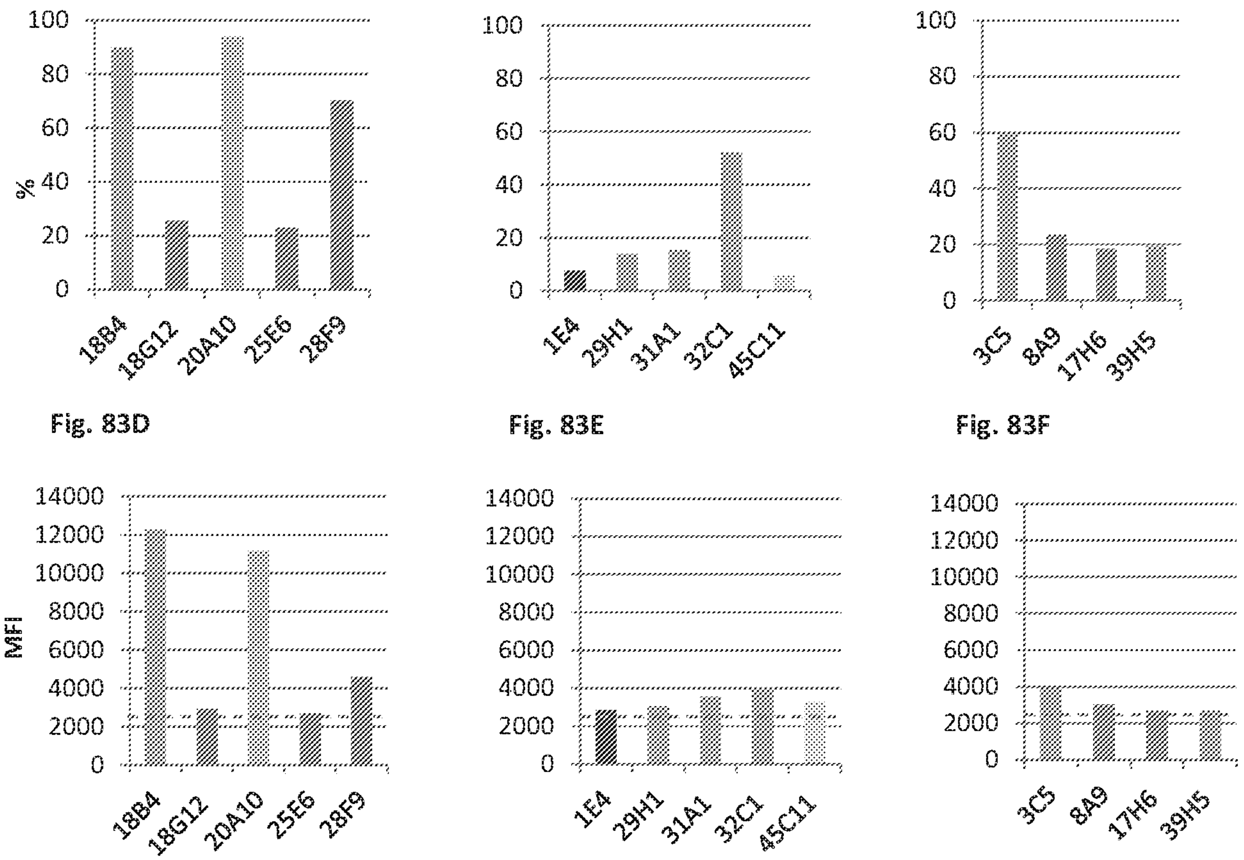


Fig. 83A

Fig. 83B

Fig. 83C

Fig. 83D

Fig. 83E

Fig. 83F

Fig. 83G

SNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA

Figure 83A-83G

FACS Analyses: Binding of antibodies to DU145 prostate cancer cells

Fig. 84A

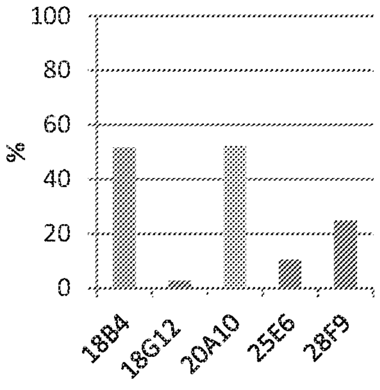


Fig. 84B

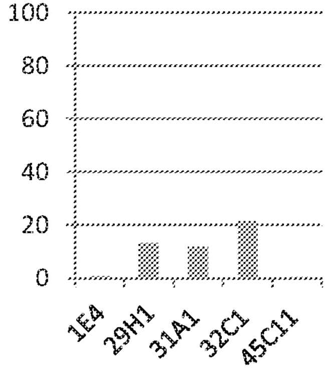


Fig. 84C

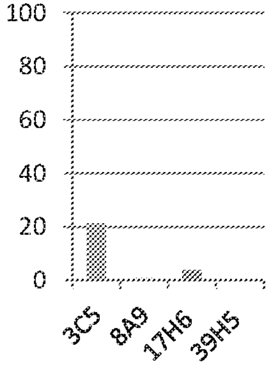


Fig. 84D

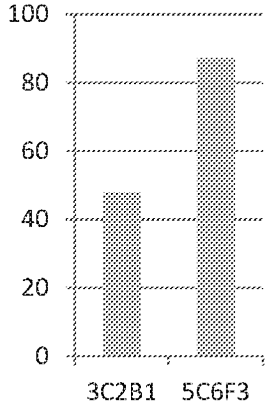


Fig. 84E

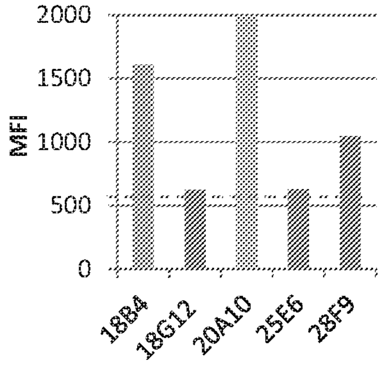


Fig. 84F

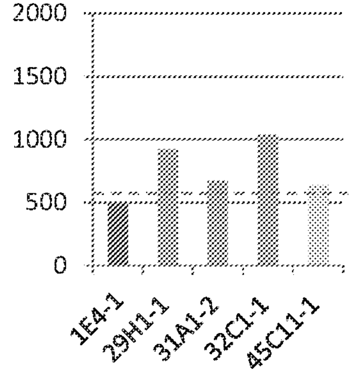


Fig. 84G

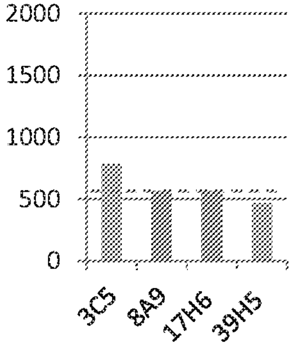


Fig. 84H

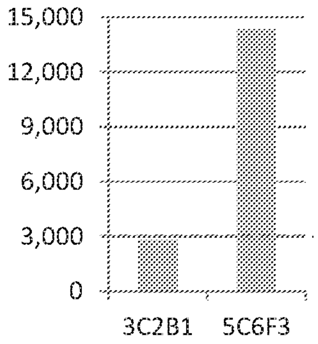


Fig. 84I

SNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA

Figure 84A-84I

FACS Analyses: Binding of antibodies to HPAF-II pancreatic cancer cells

Fig. 85A Fig. 85B Fig. 85C

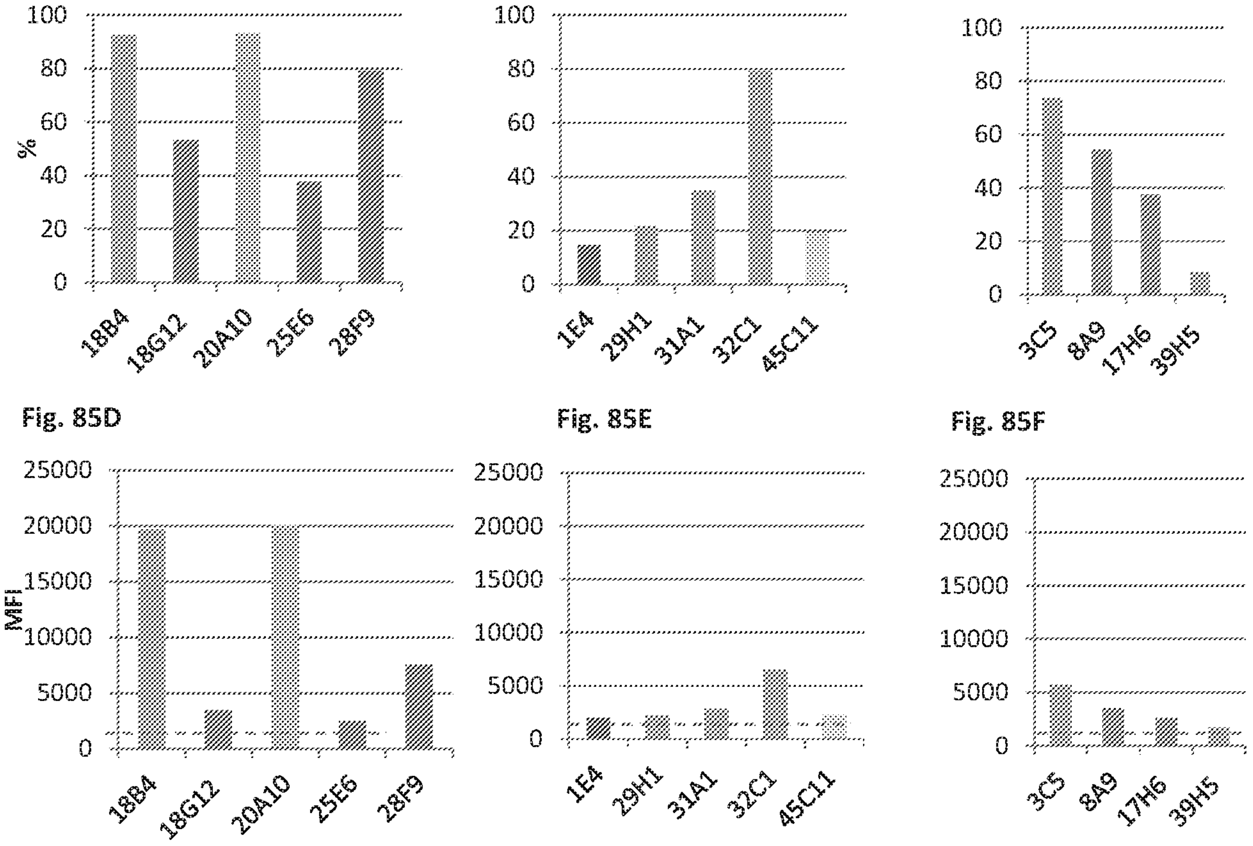


Fig. 85G

SNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA

Figure 85A-85G

FACS Analyses: Binding of antibodies to Capan-1 pancreatic cancer cells

Fig. 86A

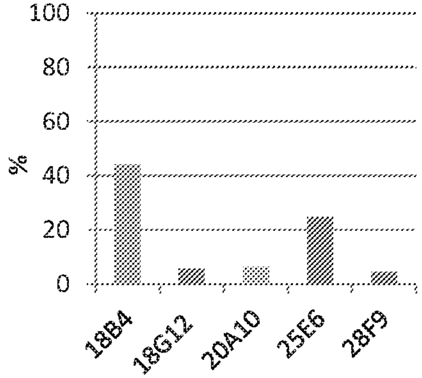


Fig. 86B

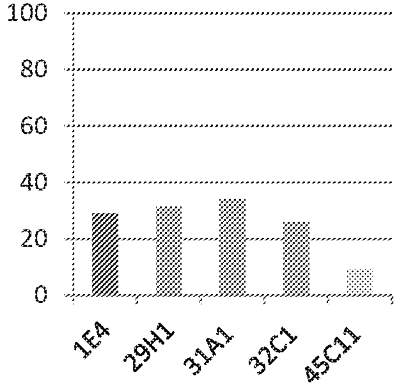


Fig. 86C

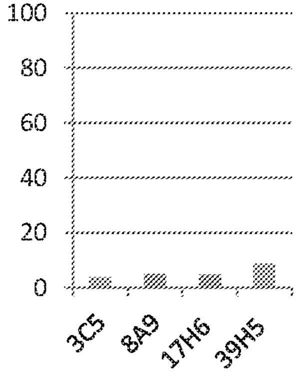


Fig. 86D

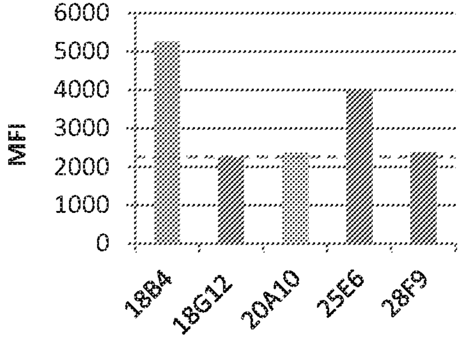


Fig. 86E

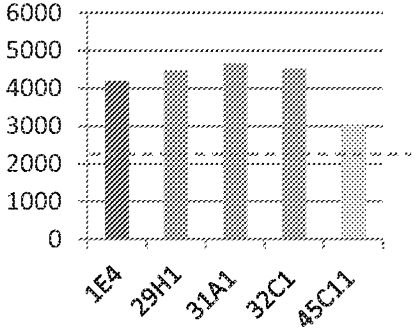


Fig. 86F

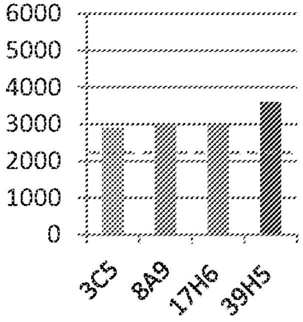


Fig. 86G

SNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA

Figure 86A-86G

FACS Analyses: Binding of antibodies to MDA-MB-231 breast cancer cells

Fig. 87A

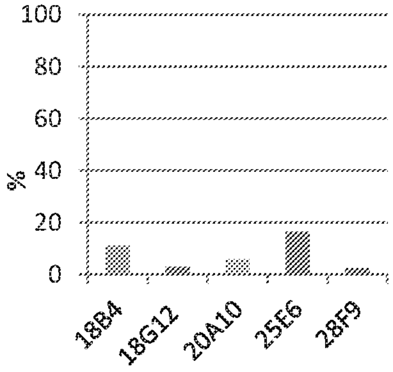


Fig. 87B

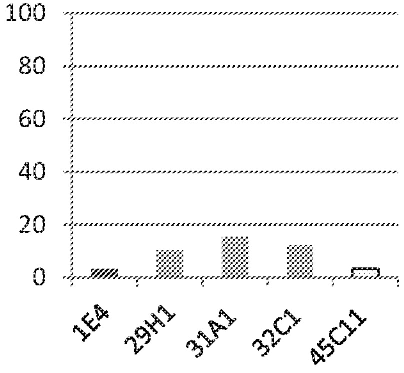


Fig. 87C

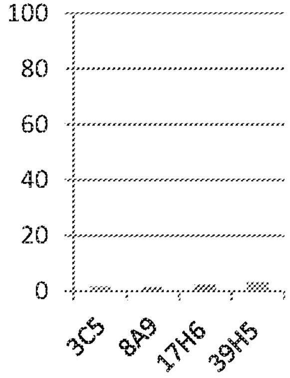


Fig. 87D

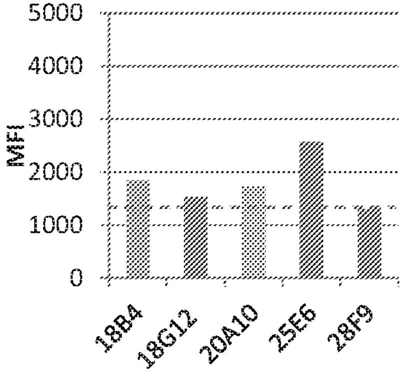


Fig. 87E

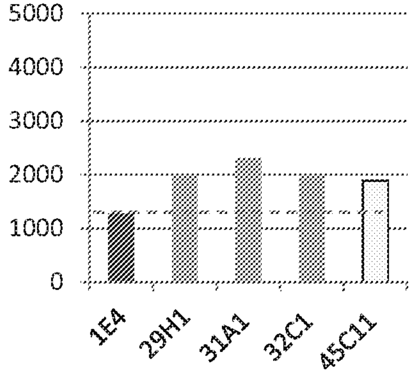


Fig. 87F

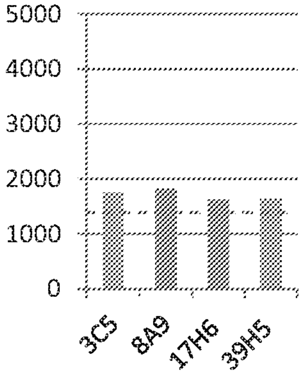


Fig. 87G

SNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTEAASRYNLTISDVSVSDVPFPFSAQSGA

Figure 87A-87G

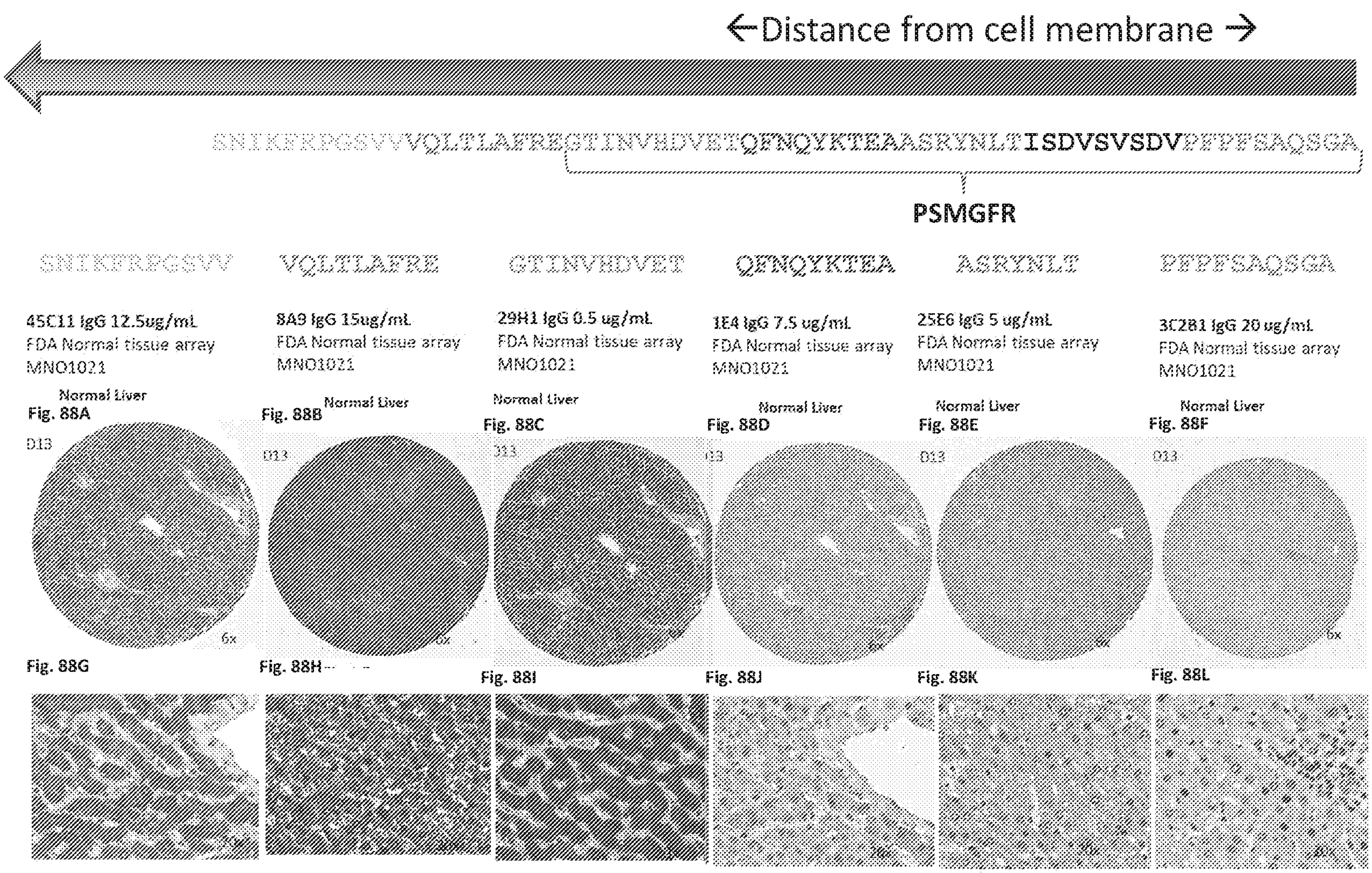
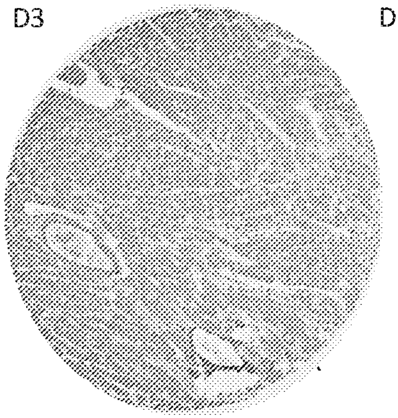


Figure 88A-88L

IHC of critical organs organized by antibody epitope: Antibodies that bind to N-10 but not C-10: epitope comprises all or part of FPFS or FPFS is critical for antibody binding

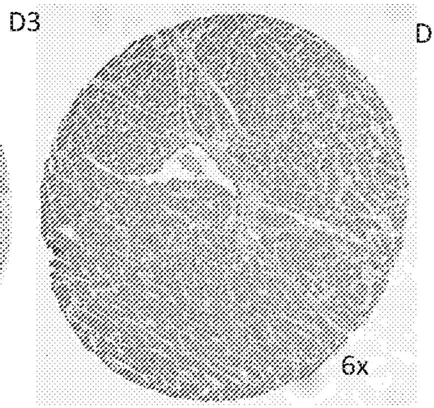
huMNC2-scFv 50 ug/mL
FDA Normal tissue array
MN88021

Normal Heart
Fig. 89A



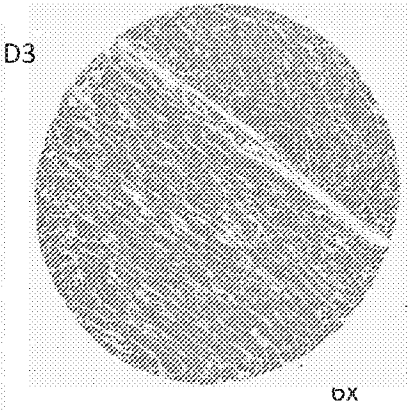
Mn-E6 IgG 2.50 ug/mL
FDA Normal tissue array
MN88021

Normal Heart
Fig. 89B



20A10 IgG 0.25 ug/mL
FDA Normal tissue array
MN88021

Normal Heart
Fig. 89C



3C2B1 IgG 20 ug/mL
FDA Normal tissue array
MN88021

Normal Heart
Fig. 89D

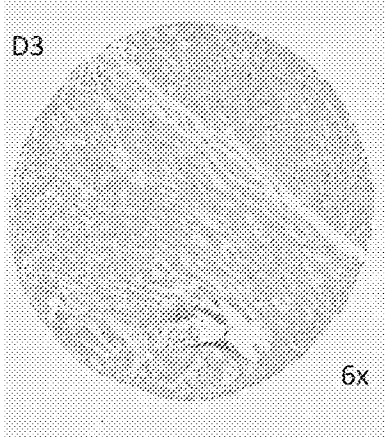


Fig. 89E

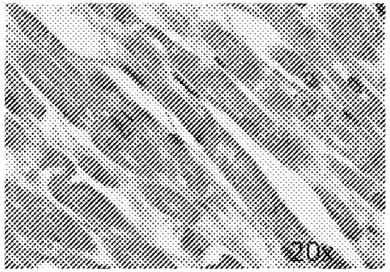


Fig. 89F

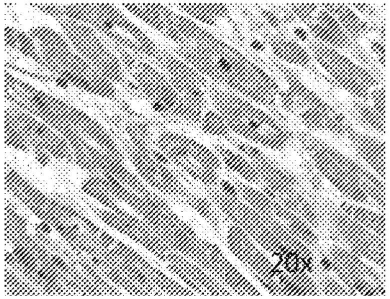


Fig. 89G

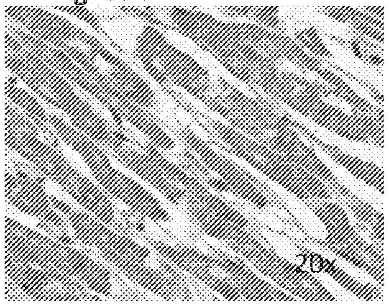


Fig. 89H

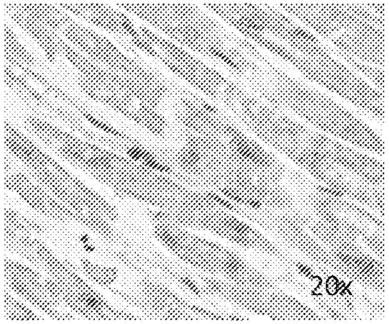


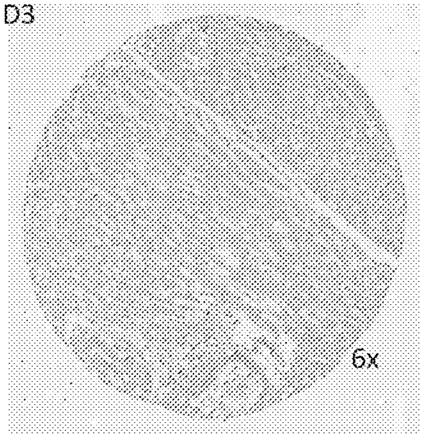
Figure 89A-89H

IHC of critical organs organized by antibody epitope: Antibodies that bind to N-10 but also bind C-10: epitope comprises all or part of ASRYNLT

MNC3 IgG 5 ug/mL
FDA Normal tissue array
MN88021

25E6 IgG 5 ug/mL
FDA Normal tissue array
MN88021

Normal Heart
Fig. 90A



Normal Heart
Fig. 90B

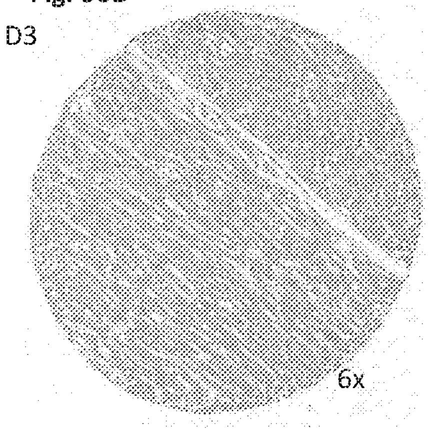


Fig. 90C

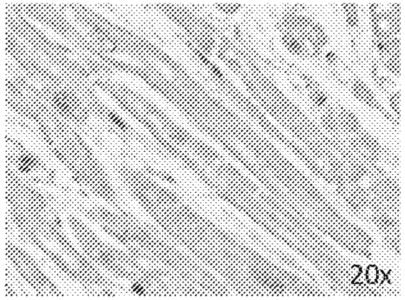


Fig. 90D

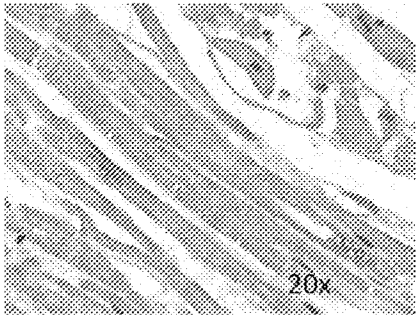


Figure 90A-90D

IHC of critical organs organized by antibody epitope: Antibodies that bind to N-10 but also bind C-10: epitope comprises all or part of QFNQYKTEA

1E4 IgG 7.5 ug/mL
FDA Normal tissue array
MN88021

Normal Heart
Fig. 91A

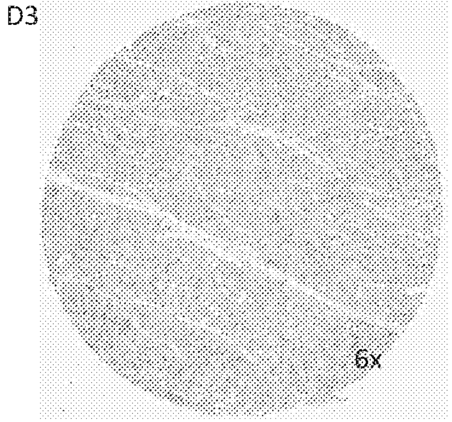


Fig. 91B

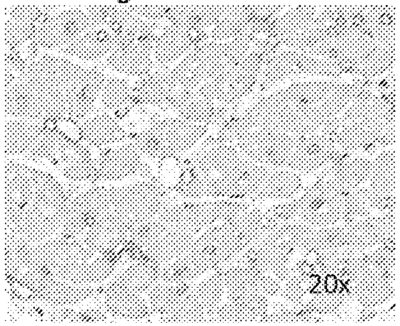
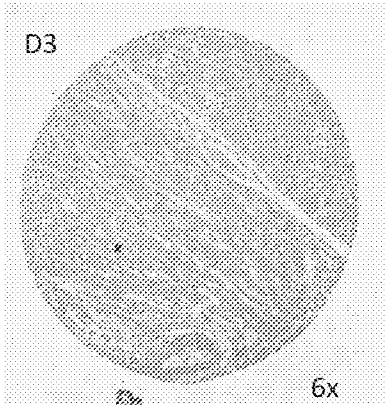


Figure 91A-91B

IHC of critical organs organized by antibody epitope: Antibodies that cannot bind to bind to N-10 but can bind to C-10: epitope comprises all or part of GTINVHDVET

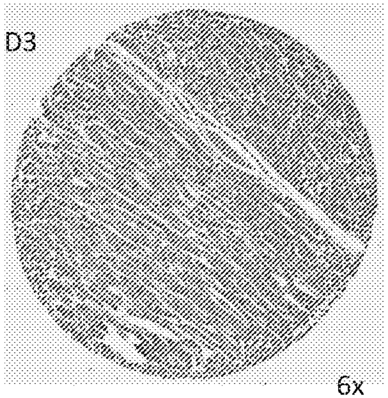
18B4 IgG 10ug/mL
FDA Normal tissue array
MN88021

Normal Heart
Fig. 92A



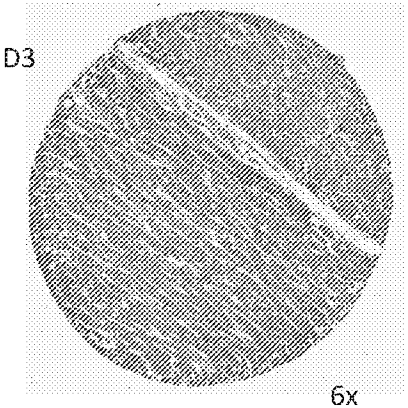
31A1 IgG 0.5 ug/mL
FDA Normal tissue array
MN88021

Normal Heart
Fig. 92B



32C1 IgG 0.25 ug/mL
FDA Normal tissue array
MN88021

Normal Heart
Fig. 92C



29H1 IgG 0.5 ug/mL
FDA Normal tissue array
MN88021

Normal Heart
Fig. 92D

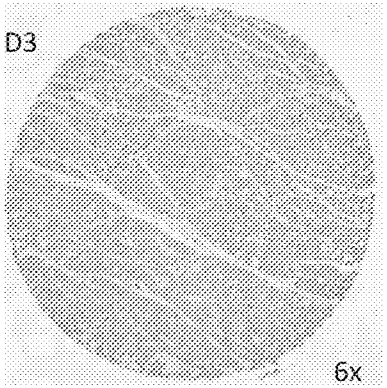


Fig. 92E

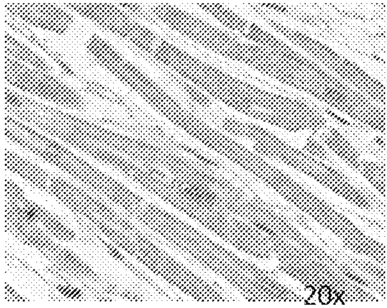


Fig. 92F

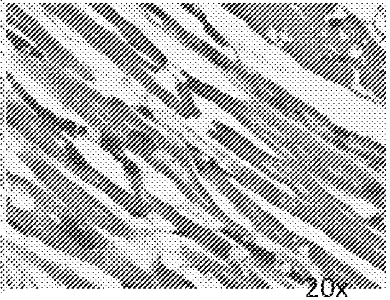


Fig. 92G

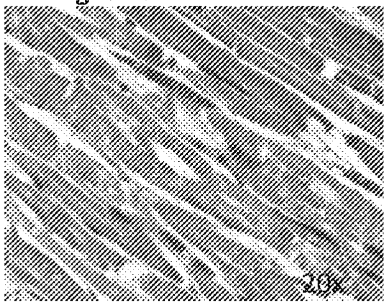


Fig. 92H

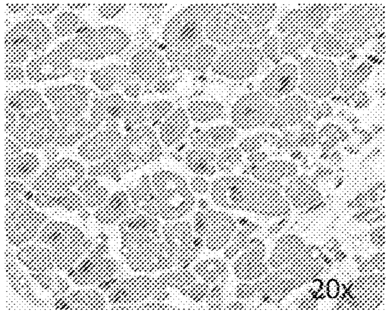
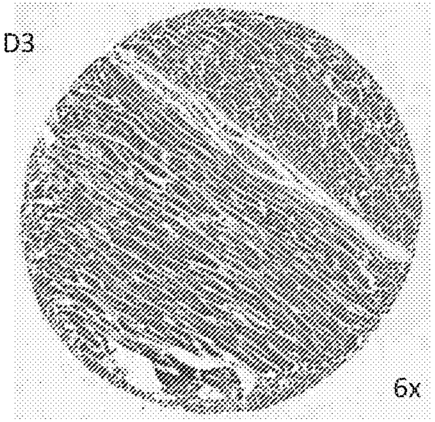


Figure 92A-92H

IHC of critical organs organized by antibody epitope: Antibodies that bind to sequences that are outside of, and N-terminal to, the PSMGFR (MUC1* extra cellular domain) sequence: epitope comprises all or part of VQLTLAFRE

8A9 IgG 15ug/mL
FDA Normal tissue array
MN88021
Normal Heart
Fig. 93A



17H6 IgG 30 ug/mL
FDA Normal tissue array
MN88021
Normal Heart
Fig. 93B

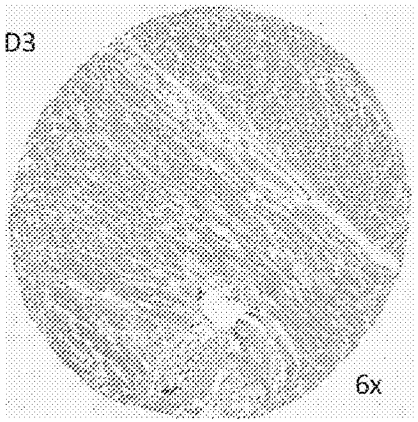


Fig. 93C

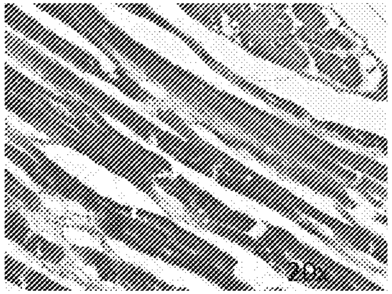


Fig. 93D

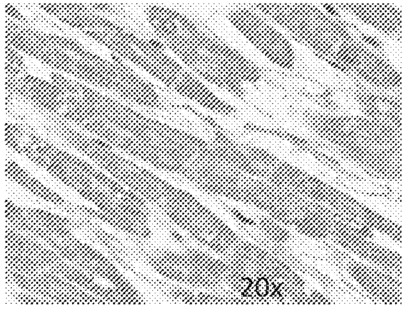


Figure 93A-93D

IHC of critical organs organized by antibody epitope: Antibodies that bind to sequences that are outside of, and N-terminal to, the PSMGFR (MUC1* extra cellular domain) sequence: epitope comprises all or part of SNIKFRPGSVV

45C11 IgG 12.5ug/mL
FDA Normal tissue array
MN88021

Normal Heart
Fig. 94A

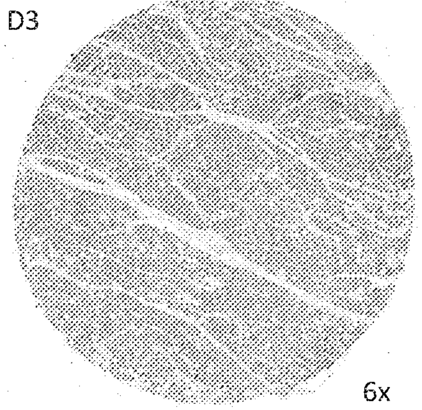


Fig. 94B

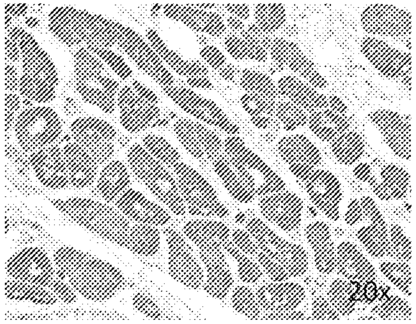
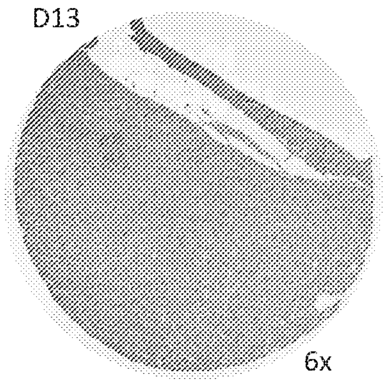


Figure 94A-94B

IHC of critical organs organized by antibody epitope: Antibodies that bind to N-10 but not C-10: epitope comprises all or part of FPFS or FPFS is critical for antibody binding

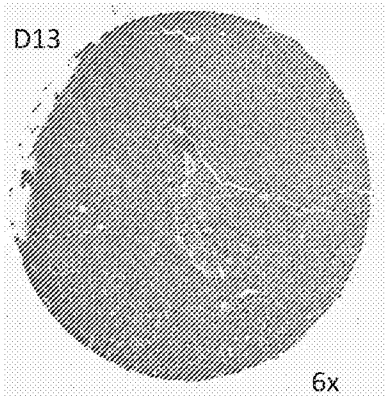
huMNC2-scFv 50 ug/mL
FDA Normal tissue array
MN88021

Normal Liver
Fig. 95A



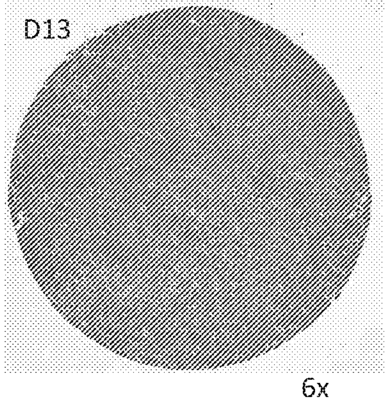
MNE6 IgG 2.50 ug/mL
FDA Normal tissue array
MN88021

Normal Liver
Fig. 95B



20A10 IgG 0.25 ug/mL
FDA Normal tissue array
MN88021

Normal Liver
Fig. 95C



3C2B1 IgG 20 ug/mL
FDA Normal tissue array
MN88021

Normal Liver
Fig. 95D

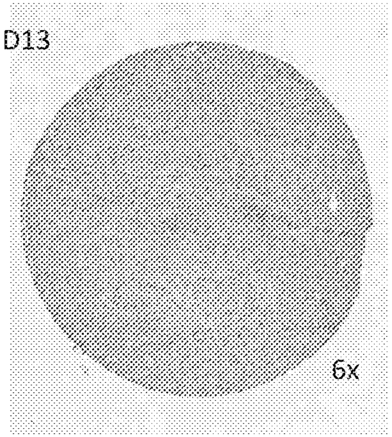


Fig. 95E

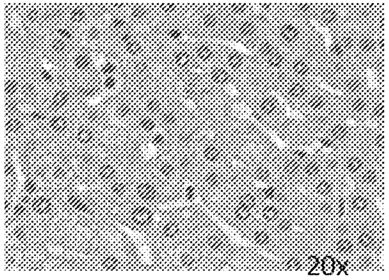


Fig. 95F

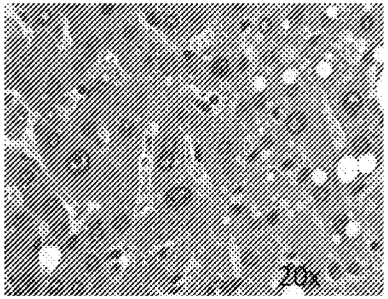


Fig. 95G

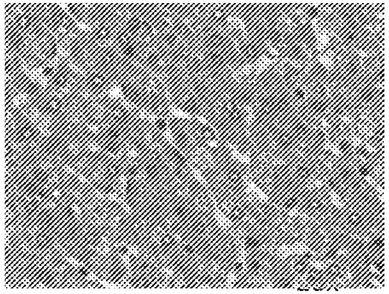


Fig. 95H

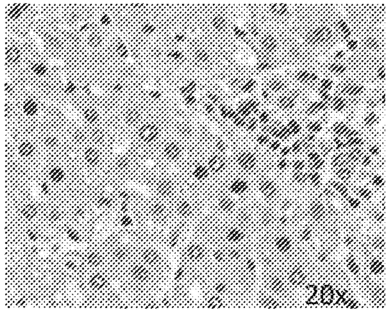


Figure 95A-95H

IHC of critical organs organized by antibody epitope: Antibodies that bind to N-10 but also bind C-10: epitope comprises all or part of ASRYNLT

MNC3 IgG 5 ug/mL
FDA Normal tissue array
MN88021

Normal Liver
Fig. 96A

25E6 IgG 5 ug/mL
FDA Normal tissue array
MN88021

Normal Liver
Fig. 96B

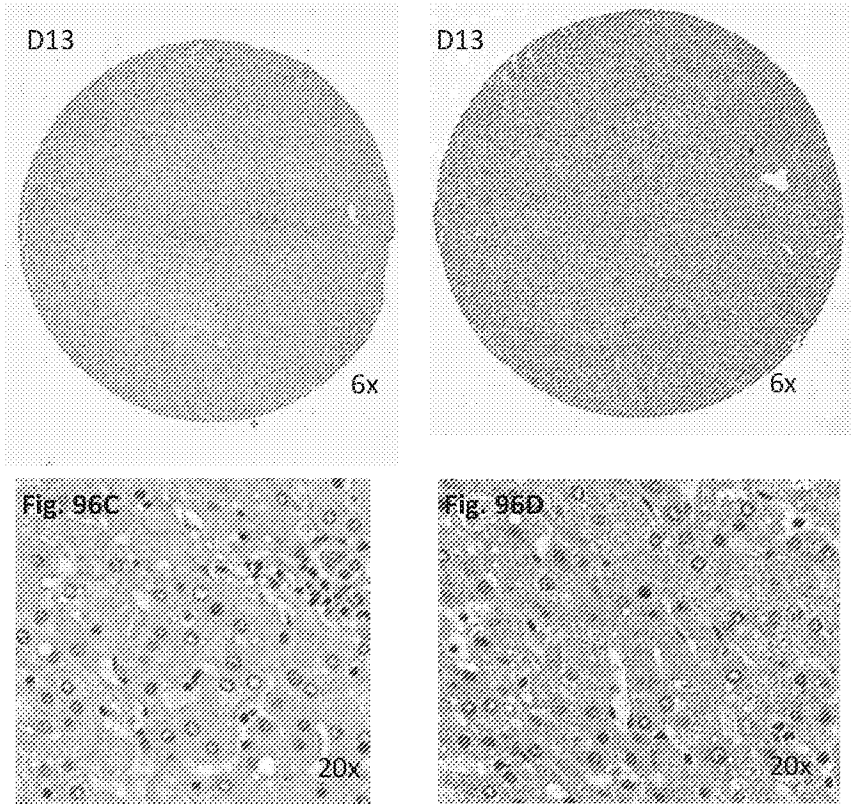


Figure 96A-96D

IHC of critical organs organized by antibody epitope: Antibodies that bind to N-10 but also bind C-10: epitope comprises all or part of QFNQYKTEA

1E4 IgG 7.5 ug/mL
FDA Normal tissue array
MN88021

Normal Liver

Fig. 97A

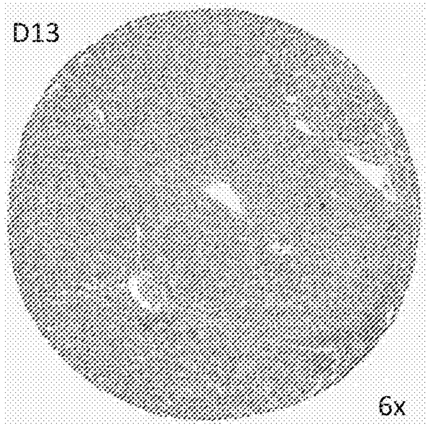


Fig. 97B

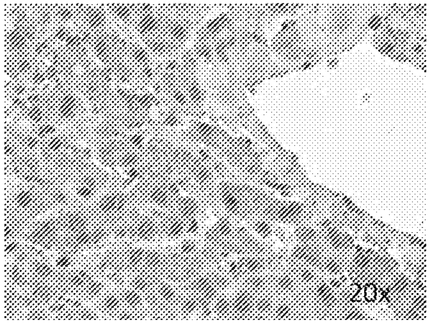


Figure 97A-97B

IHC of critical organs organized by antibody epitope: Antibodies that cannot bind to bind to N-10 but can bind to C-10: epitope comprises all or part of GTINVHDVET

18B4 IgG 10ug/mL
FDA Normal tissue array
MN88021

Normal Liver
Fig. 98A

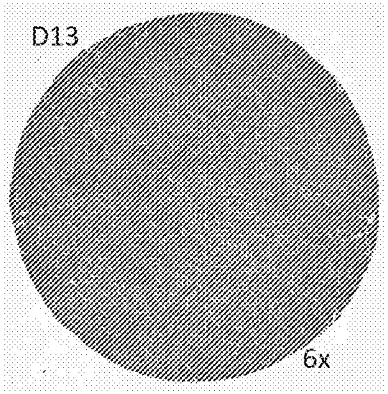
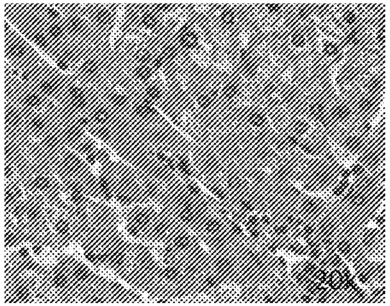


Fig. 98E



31A1 IgG 0.5 ug/mL
FDA Normal tissue array
MN88021

Normal Liver
Fig. 98B

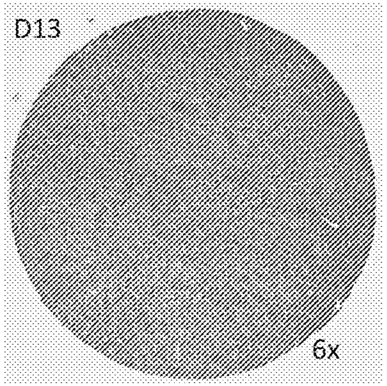
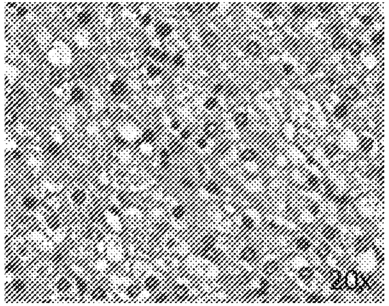


Fig. 98F



32C1 IgG 0.25 ug/mL
FDA Normal tissue array
MN88021

Normal Liver
Fig. 98C

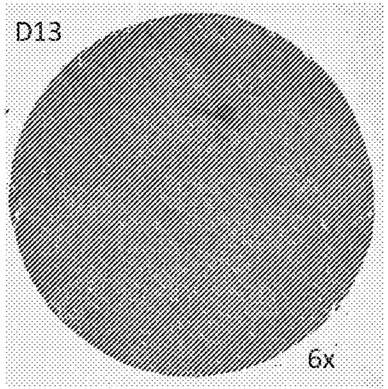
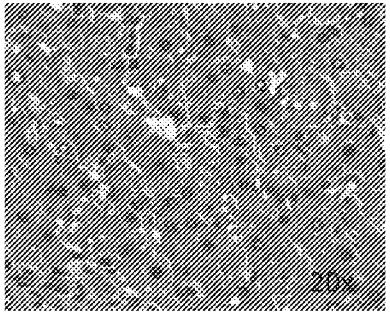


Fig. 98G



29H1 IgG 0.5 ug/mL
FDA Normal tissue array
MN88021

Normal Liver
Fig. 98D

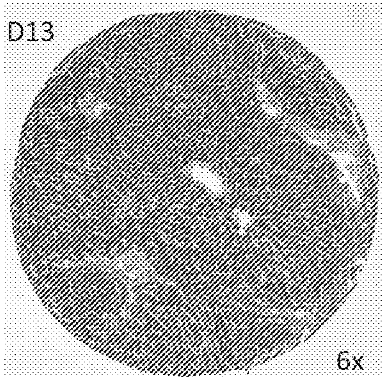


Fig. 98H

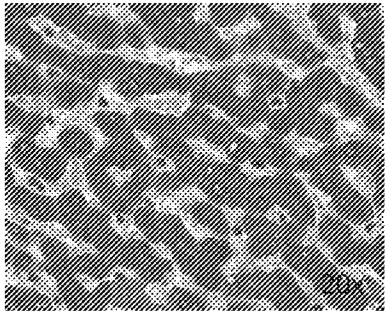
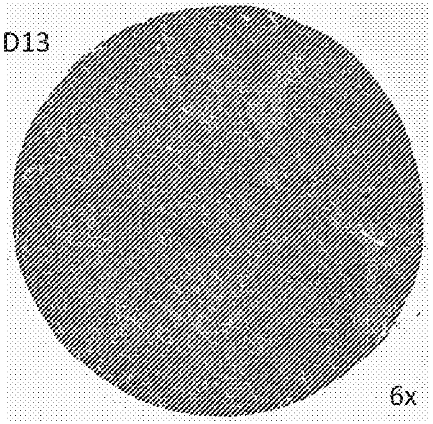


Figure 98A-98H

IHC of critical organs organized by antibody epitope: Antibodies that bind to sequences that are outside of, and N-terminal to, the PSMGFR (MUC1* extra cellular domain) sequence: epitope comprises all or part of VQLTLAFRE

8A9 IgG 15ug/mL
FDA Normal tissue array
MN88021

Normal Liver
Fig. 99A



17H6 IgG 30 ug/mL
FDA Normal tissue array
MN88021

Normal Liver
Fig. 99B

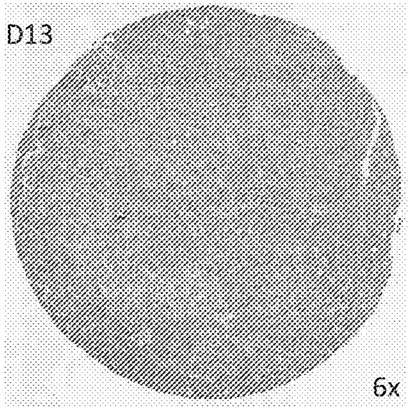


Fig. 99C

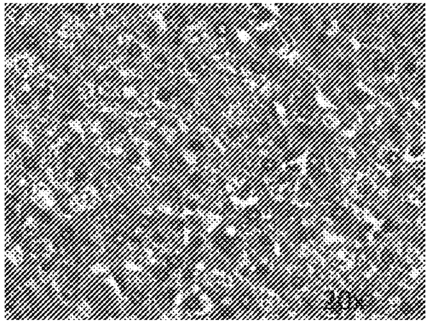


Fig. 99D

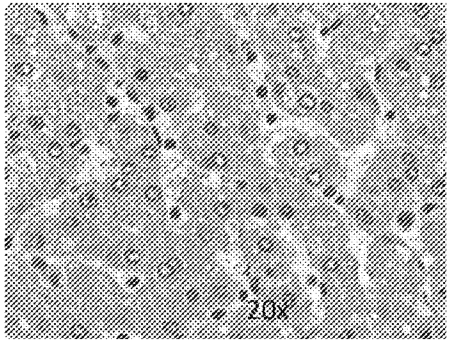


Figure 99A-99D

IHC of critical organs organized by antibody epitope: Antibodies that bind to sequences that are outside of, and N-terminal to, the PSMGFR (MUC1* extra cellular domain) sequence: epitope comprises all or part of SNIKFRPGSVV

45C11 IgG 12.5ug/mL
FDA Normal tissue array
MN88021

Normal Liver
Fig. 100A

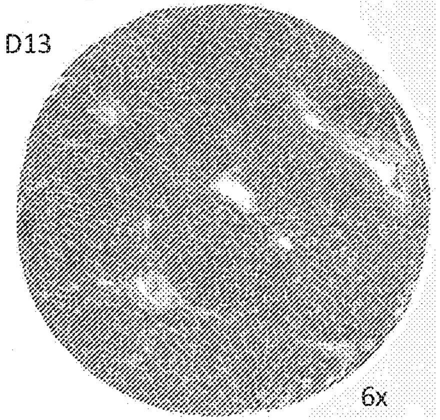


Fig. 100B

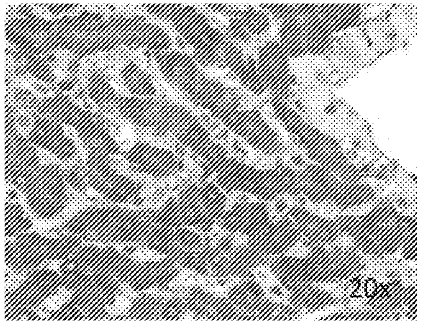
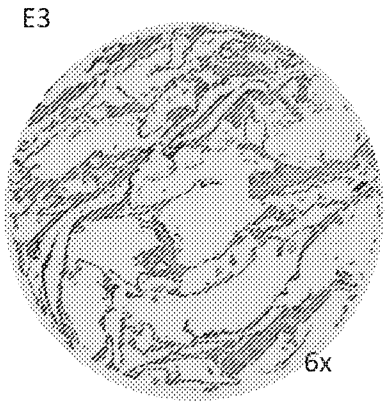


Figure 100A-100B

IHC of critical organs organized by antibody epitope: Antibodies that bind to N-10 but not C-10: epitope comprises all or part of FPFS or FPFS is critical for antibody binding

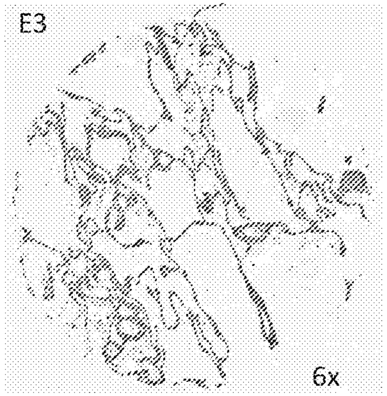
huMNC2-scFv 50 ug/mL
FDA Normal tissue array
MN88021

Normal Lung
Fig. 101A



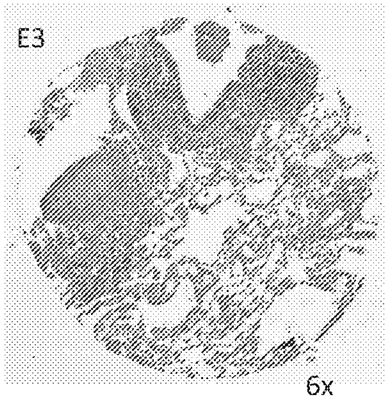
MNE6 IgG 2.50 ug/mL
FDA Normal tissue array
MN88021

Normal Lung
Fig. 101B



20A10 IgG 0.25 ug/mL
FDA Normal tissue array
MN88021

Normal Lung
Fig. 101C



3C2B1 IgG 20 ug/mL
FDA Normal tissue array
MN88021

Normal Lung
Fig. 101D

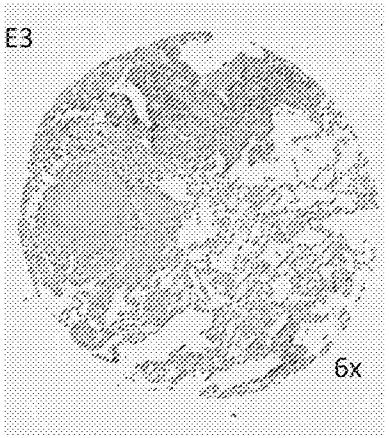


Fig. 101E

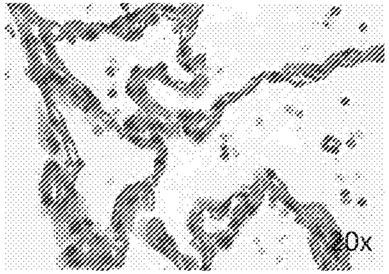


Fig. 101F

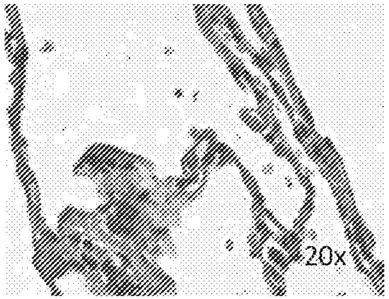


Fig. 101G

Fig. 101H

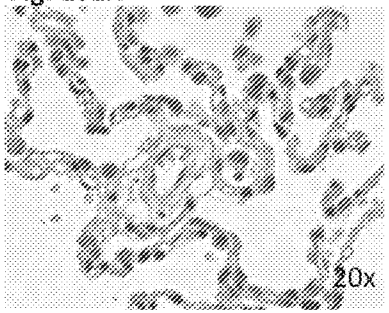


Figure 101A-101H

IHC of critical organs organized by antibody epitope: Antibodies that bind to N-10 but also bind C-10: epitope comprises all or part of ASRYNLT

MNC3 IgG 5 ug/mL
FDA Normal tissue array
MN88021
Normal Lung
Fig. 102A

25E6 IgG 5 ug/mL
FDA Normal tissue array
MN88021
Normal Lung
Fig. 102B

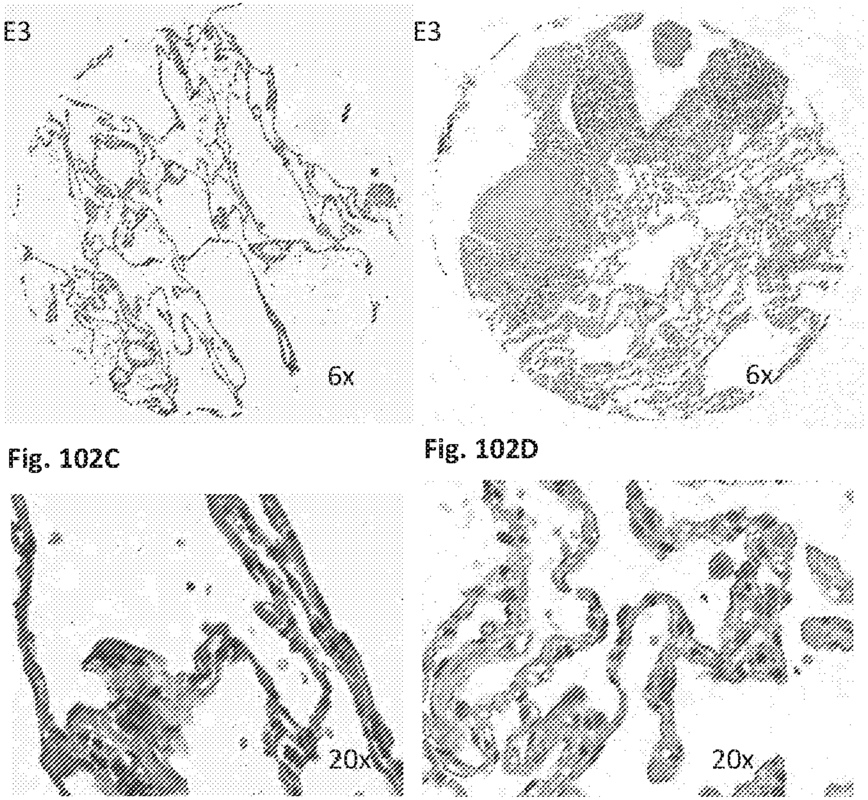


Fig. 102C

Fig. 102D

Figure 102A-102D

IHC of critical organs organized by antibody epitope: Antibodies that bind to N-10 but also bind C-10: epitope comprises all or part of QFNQYKTEA

1E4 IgG 7.5 ug/mL
FDA Normal tissue array
MN88021

Normal Lung
Fig. 103A

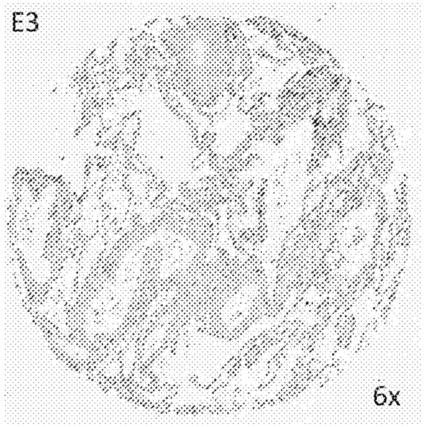


Fig. 103B

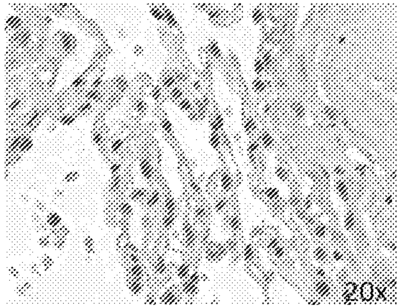
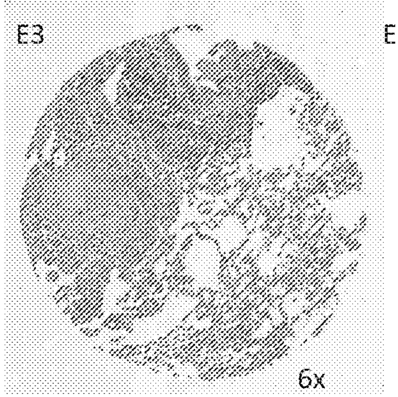


Figure 103A-103B

IHC of critical organs organized by antibody epitope: Antibodies that cannot bind to bind to N-10 but can bind to C-10: epitope comprises all or part of GTINVHDVET

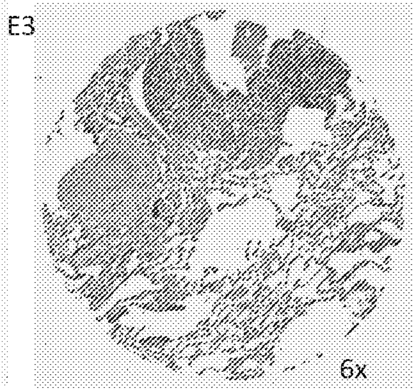
18B4 IgG 10ug/mL
FDA Normal tissue array
MN88021
Normal Lung

Fig. 104A



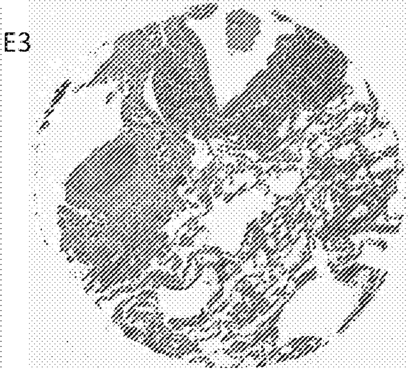
31A1 IgG 0.5 ug/mL
FDA Normal tissue array
MN88021
Normal Lung

Fig. 104B



32C1 IgG 0.25 ug/mL
FDA Normal tissue array
MN88021
Normal Lung

Fig. 104C



29H1 IgG 0.5 ug/mL
FDA Normal tissue array
MN88021
Normal Lung

Fig. 104D

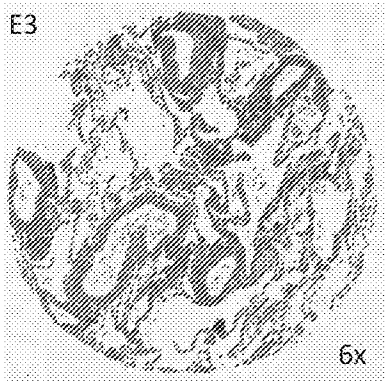


Fig. 104E

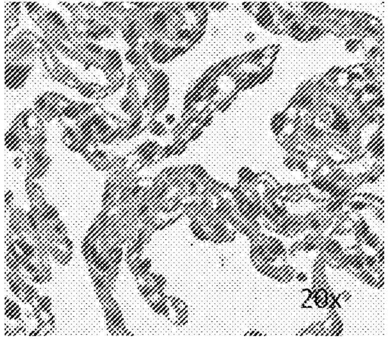


Fig. 104F

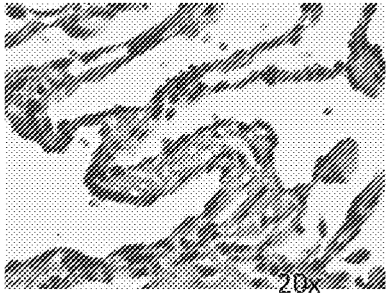


Fig. 104G

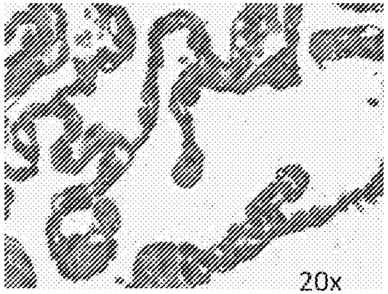


Fig. 104H

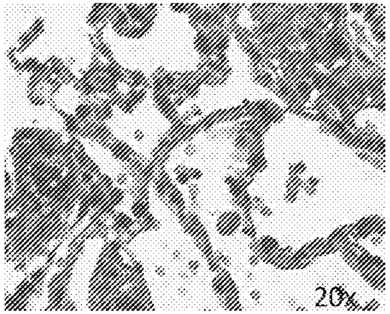
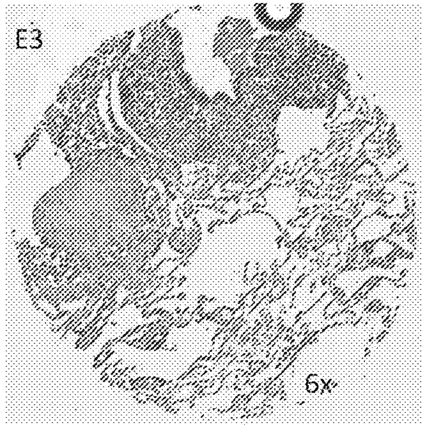


Figure 104A-104H

IHC of critical organs organized by antibody epitope: Antibodies that bind to sequences that are outside of, and N-terminal to, the PSMGFR (MUC1* extra cellular domain) sequence: epitope comprises all or part of VQLTLAFRE

8A9 IgG 15ug/mL
FDA Normal tissue array
MN88021

Normal Lung
Fig. 105A



17H6 IgG 30 ug/mL
FDA Normal tissue array
MN88021

Normal Lung
Fig. 105B

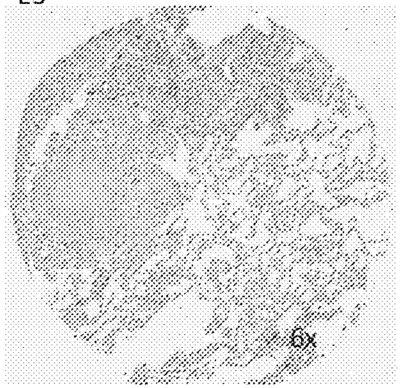


Fig. 105C

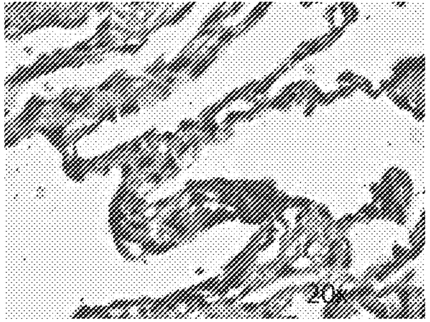


Fig. 105D

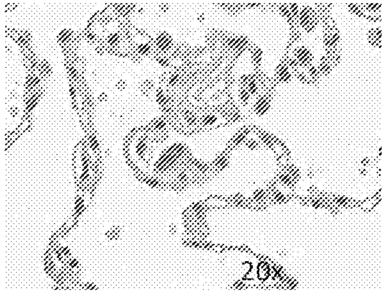


Figure 105A-105D

IHC of critical organs organized by antibody epitope: Antibodies that bind to sequences that are outside of, and N-terminal to, the PSMGFR (MUC1* extra cellular domain) sequence: epitope comprises all or part of SNIKFRPGSVV

45C11 IgG 12.5ug/mL
FDA Normal tissue array
MN88021

Normal Lung
Fig. 106A

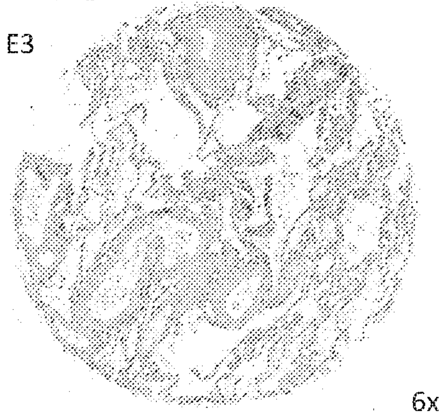


Fig. 106B

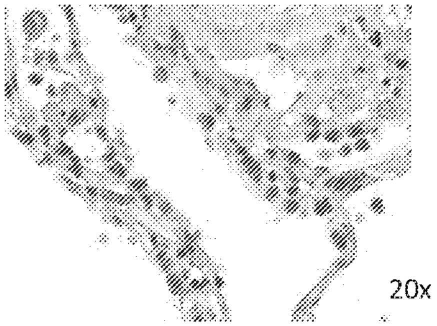
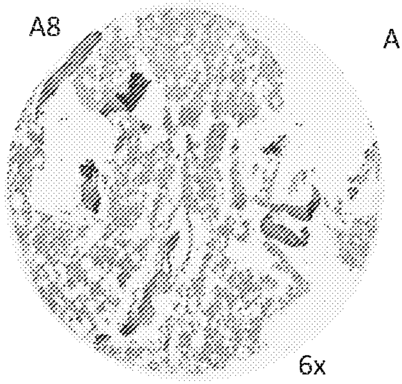


Figure 106A-106B

IHC of critical organs organized by antibody epitope: Antibodies that bind to N-10 but not C-10: epitope comprises all or part of FPFS or FPFS is critical for antibody binding

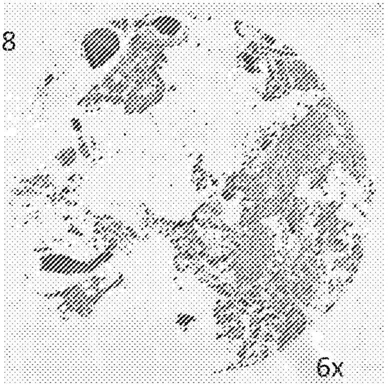
huMNC2-scFv 50 ug/mL
FDA Normal tissue array
MN88021

Normal Bone Marrow
Fig. 107A



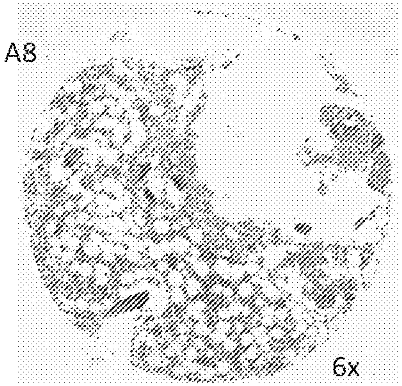
MNE6 IgG 2.50 ug/mL
FDA Normal tissue array
MN88021

Normal Bone Marrow
Fig. 107B



20A10 IgG 0.25 ug/mL
FDA Normal tissue array
MN88021

Normal Bone Marrow
Fig. 107C



3C2B1 IgG 20 ug/mL
FDA Normal tissue array
MN88021

Normal Bone Marrow
Fig. 107D

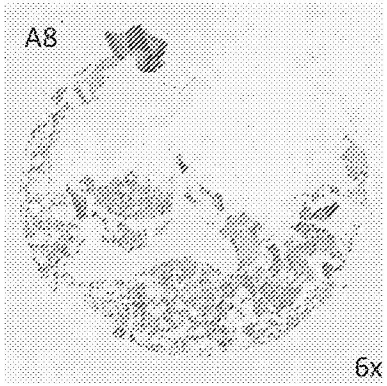


Fig. 107E

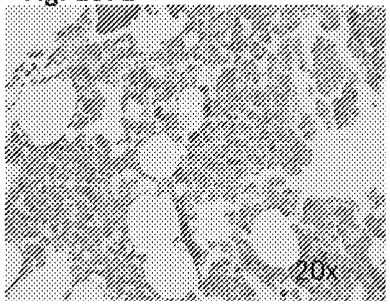


Fig. 107F

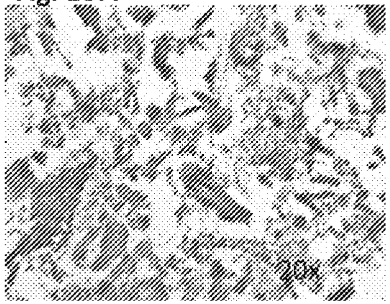


Fig. 107G

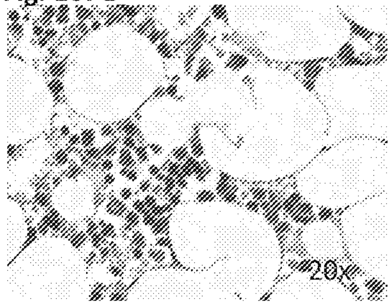


Fig. 107H

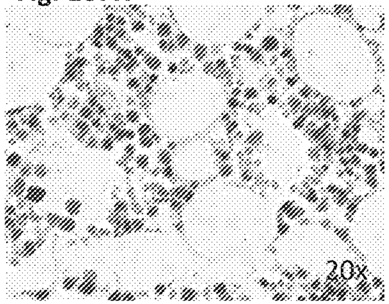


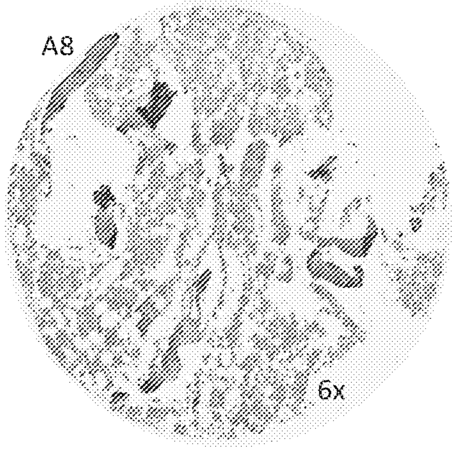
Figure 107A-107H

IHC of critical organs organized by antibody epitope: Antibodies that bind to N-10 but also bind C-10: epitope comprises all or part of ASRYNLT

MNC3 IgG 5 ug/mL
FDA Normal tissue array
MN88021

25E6 IgG 5 ug/mL
FDA Normal tissue array
MN88021

Normal Bone Marrow
Fig. 108A



Normal Bone Marrow
Fig. 108B

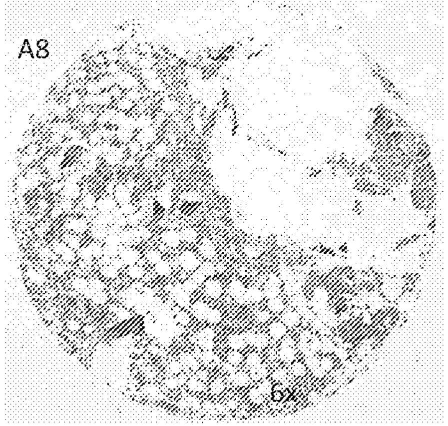


Fig. 108C

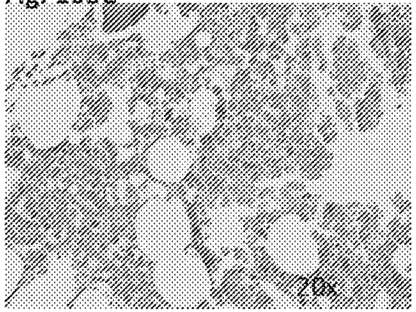


Fig. 108D

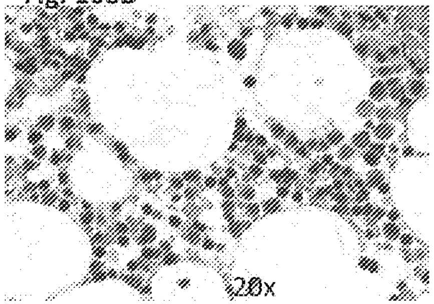


Figure 108A-108D

IHC of critical organs organized by antibody epitope: Antibodies that bind to N-10 but also bind C-10: epitope comprises all or part of QFNQYKTEA

1E4 IgG 7.5 ug/mL
FDA Normal tissue array
MN88021
Normal Bone Marrow

Fig. 109A

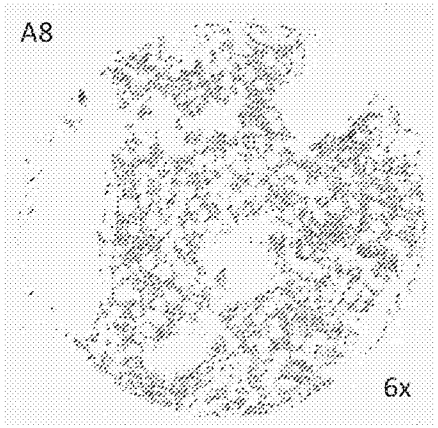


Fig. 109B

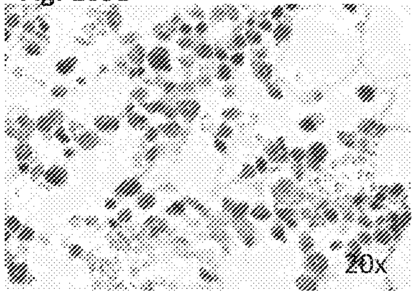


Figure 109A-109B

IHC of critical organs organized by antibody epitope: Antibodies that cannot bind to bind to N-10 but can bind to C-10: epitope comprises all or part of GTINVHDVET

18B4 IgG 10ug/mL
FDA Normal tissue array
MN88021
Normal Bone Marrow

31A1 IgG 0.5 ug/mL
FDA Normal tissue array
MN88021
Normal Bone Marrow

32C1 IgG 0.25 ug/mL
FDA Normal tissue array
MN88021
Normal Bone Marrow

29H1 IgG 0.5 ug/mL
FDA Normal tissue array
MN88021
Normal Bone Marrow

Fig. 110A

Fig. 110B

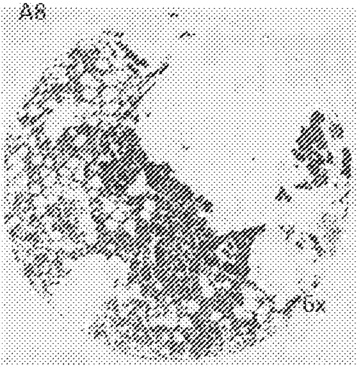


Fig. 110C

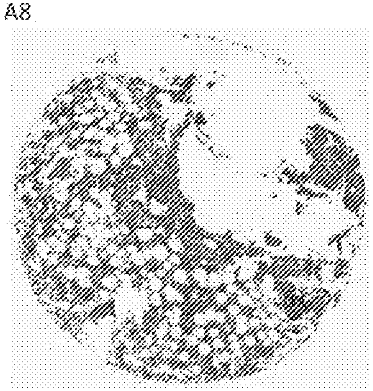


Fig. 110D

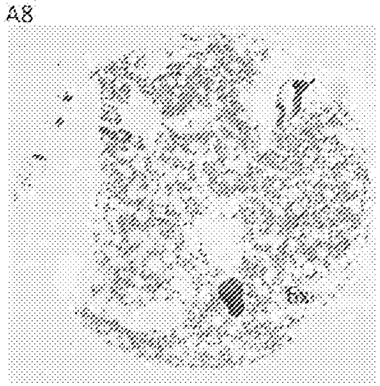


Fig. 110E

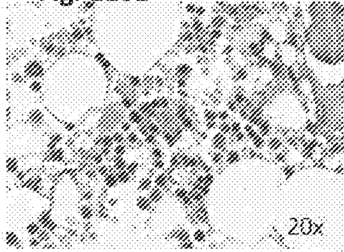


Fig. 110F

Fig. 110G

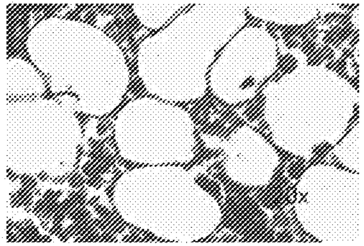


Fig. 110H

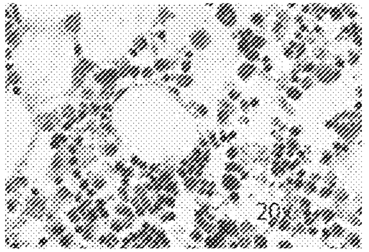


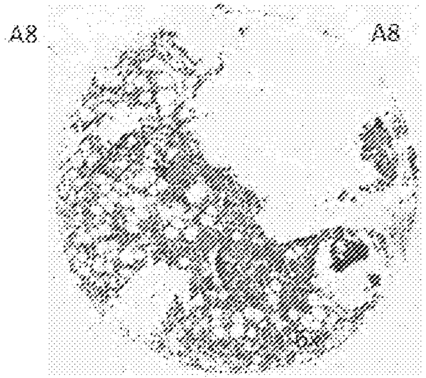
Figure 110A-110H

IHC of critical organs organized by antibody epitope: Antibodies that bind to sequences that are outside of, and N-terminal to, the PSMGFR (MUC1* extra cellular domain) sequence: epitope comprises all or part of VQLTLAFRE

8A9 IgG 15ug/mL
FDA Normal tissue array
MN88021

17H6 IgG 30 ug/mL
FDA Normal tissue array
MN88021

Normal Bone Marrow
Fig. 111A



Normal Bone Marrow
Fig. 111B

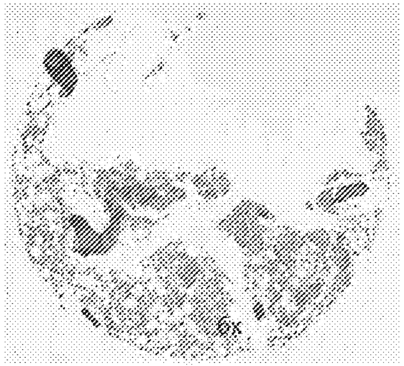


Fig. 111C

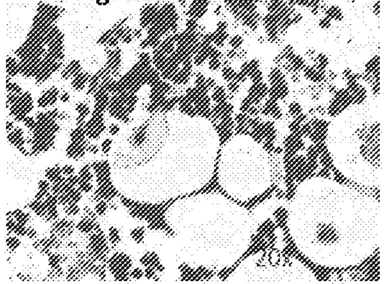


Fig. 111D

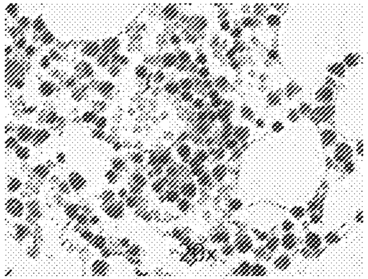


Figure 111A-111D

IHC of critical organs organized by antibody epitope: Antibodies that bind to sequences that are outside of, and N-terminal to, the PSMGFR (MUC1* extra cellular domain) sequence: epitope comprises all or part of SNIKFRPGSVV

45C11 IgG 12.5ug/mL
FDA Normal tissue array
MN88021

Normal Bone Marrow
Fig. 112A

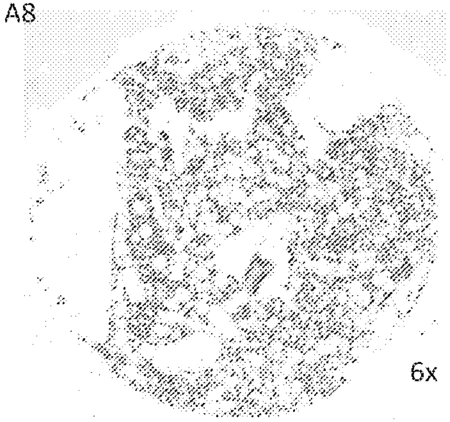


Fig. 112B

Figure 112A-112B

PSMGFR-antibody 20A10 IgG 0.25 ug/mL

FDA Normal tissue array MNO1021

Fig. 113A

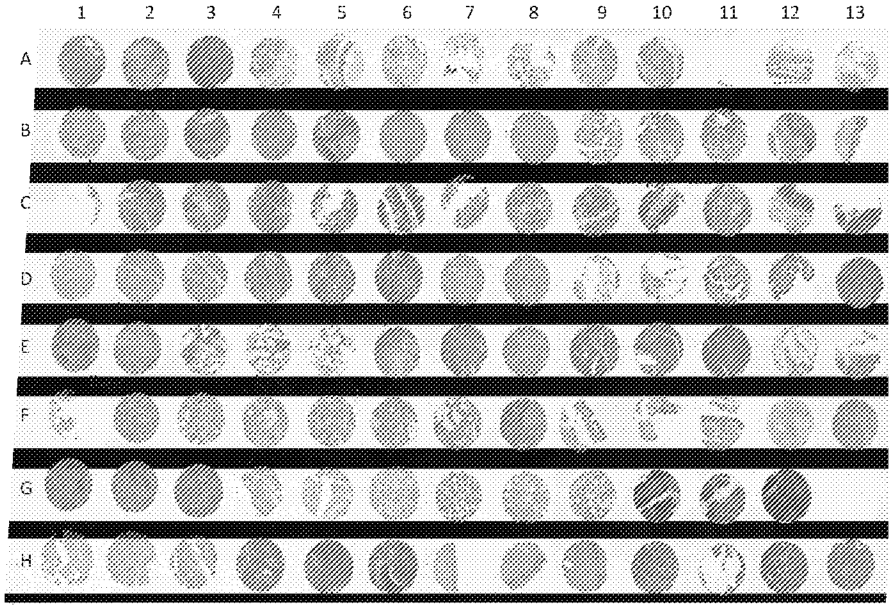


Fig. 113B

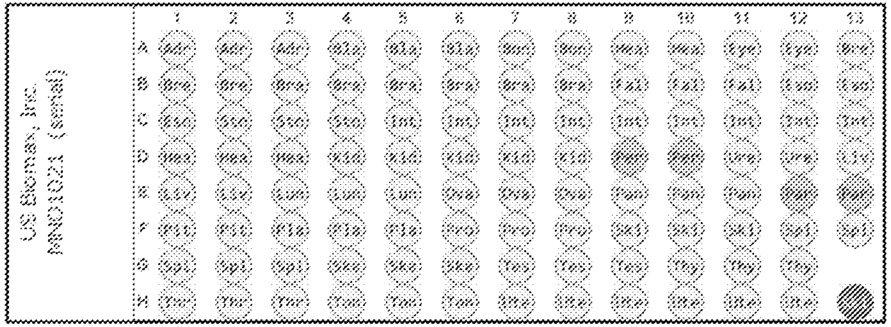


Fig. 113C

Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis	Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis
A1	F	31	Adrenal gland	Normal	E1	M	59	Liver	Normal
A2	M	51	Adrenal gland	Normal	E2	F	27	Liver	Normal
A3	M	53	Adrenal gland	Normal	E3	M	72	Lung	Normal
A4	M	75	Bladder, urinary	Normal	E4	F	55	Lung	Normal
A5	M	72	Bladder, urinary	Normal	E5	M	43	Lung	Normal
A6	M	52	Bladder, urinary	Normal	E6	F	47	Ovary	Normal
A7	M	53	Bone, bone marrow	Normal	E7	F	46	Ovary	Normal
A8	M	43	Bone, bone marrow	Normal	E8	F	40	Ovary	Normal
A9	F	44	Head and neck, salivary gland	Normal	E9	M	42	Pancreas	Normal
A10	M	18	Head and neck, salivary gland	Normal	E10	F	26	Pancreas	Normal
A11	M	55	Eye	Normal	E11	F	59	Pancreas	Normal
A12	M	50	Eye	Normal	E12	M	17	Parathyroid	Adenoma
A13	F	35	Breast	Normal	E13	M	72	Parathyroid	Adenoma
B1	F	38	Breast	Normal	F1	F	3	Pituitary gland	Normal
B2	F	33	Breast	Normal	F2	F		Pituitary gland	Normal
B3	M	58	Brain, cerebellum	Normal	F3	F	32	Placenta	Normal
B4	M	65	Brain, cerebellum	Normal	F4	F	30	Placenta	Normal
B5	F		Brain, cerebellum	Normal	F5	F	27	Placenta	Normal
B6	M	58	Brain, cerebral cortex	Normal	F6	M	64	Prostate	Normal
B7	M	65	Brain, cerebral cortex	Normal	F7	M	65	Prostate	Normal
B8	F		Brain, cerebral cortex	Normal	F8	M	65	Prostate	Normal
B9	F	42	Fallopian tube	Normal	F9	F	32	Skin	Normal
B10	F	32	Fallopian tube	Normal	F10	F	68	Skin	Normal
B11	F	24	Fallopian tube	Normal	F11	M	28	Skin	Normal
B12	M	45	Esophagus	Normal	F12	M	47	Spinal cord	Normal
B13	F	68	Esophagus	Normal	F13	M	58	Spinal cord	Normal
C1	M	54	Esophagus	Normal	G1	M	27	Spleen	Normal
C2	M	45	Stomach	Normal	G2	M	60	Spleen	Normal
C3	M	49	Stomach	Normal	G3	M	31	Spleen	Normal
C4	M	77	Stomach	Normal	G4	F	60	Skeletal muscle	Normal
C5	M	45	intestine, small intestine	Normal	G5	F	49	Skeletal muscle	Normal
C6	F	75	Intestine, small intestine	Normal	G6	M	70	Skeletal muscle	Normal
C7	F	75	Intestine, small intestine	Normal	G7	M	43	Testis	Normal
C8	M	2	Intestine, colon	Normal	G8	M	30	Testis	Normal
C9	M	48	Intestine, colon	Normal	G9	M	77	Testis	Normal
C10	M	74	Intestine, colon	Normal	G10	M	15	Thymus	Normal
C11	F	47	Intestine, rectum	Normal	G11	M	28	Thymus	Normal
C12	F	75	Intestine, rectum	Normal	G12	F	9	Thymus	Normal
C13	M	66	Intestine, rectum	Normal	G13	-	-	-	-
D1	M	58	Heart	Normal	H1	F	28	Thyroid	Normal
D2	M	46	Heart	Normal	H2	F	37	Thyroid	Normal
D3	F	34	Heart	Normal	H3	F	51	Thyroid	Normal
D4	F	52	Kidney, cortex	Normal	H4	M	46	Tonsil	Normal
D5	M	23	Kidney, cortex	Normal	H5	M	37	Tonsil	Normal
D6	M	63	Kidney, cortex	Normal	H6	M	13	Tonsil	Normal
D7	F	52	Kidney, medulla	Normal	H7	F	38	Uterus, cervl1	Normal
D8	M	23	Kidney, medulla	Normal	H8	F	35	Uterus, cervl1	Normal
D9	M	59	Peripheral nerve	Schwannoma	H9	F	44	Uterus, cervl1	Normal
D10	F	29	Peripheral nerve	Schwannoma	H10	F	38	Uterus, endometrium	Normal
D11	F	44	Ureter	Normal	H11	F	41	Uterus, endometrium	Normal
D12	F	42	Ureter	Normal	H12	F	46	Uterus, endometrium	Normal
D13	F	57	Liver	Normal	H13	M	58	Skin	Malignant melanoma (tissue marker)

Figure 113A-113C

PSMGFR-antibody 20A10 IgG 0.25 ug/mL

FDA Normal tissue array MNO1021

Fig. 114A
Normal Adrenal Gland

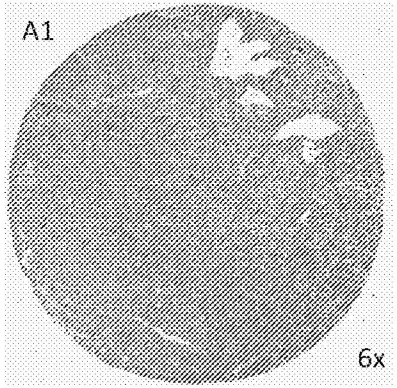


Fig. 114B
Normal Breast

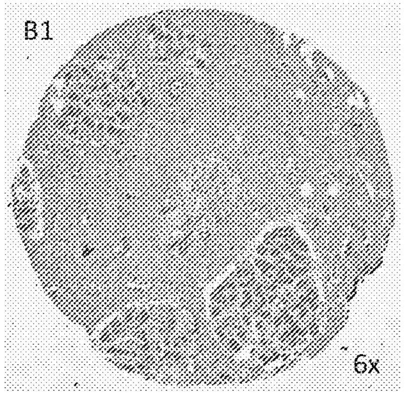


Fig. 114C
Normal Fallopian Tubes

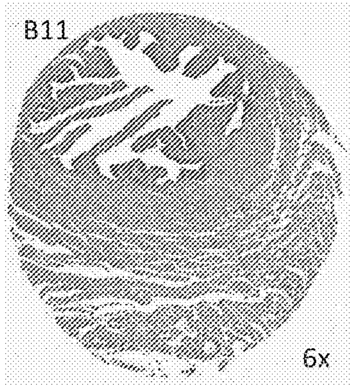


Fig. 114D
Normal Kidney

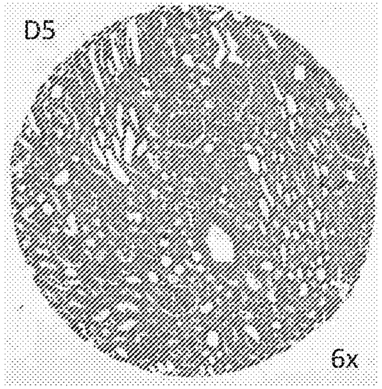


Fig. 114E

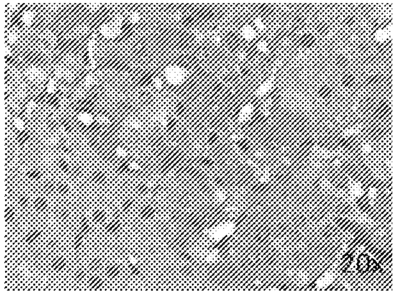


Fig. 114F

Fig. 114G

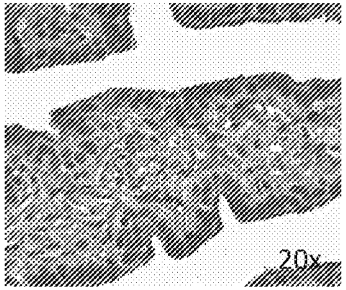


Fig. 114H

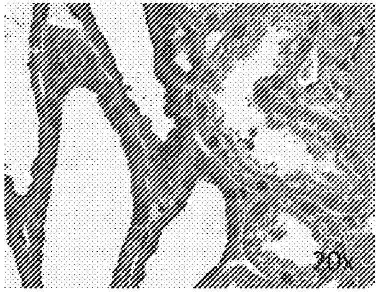


Figure 114A-114H

PSMGFR-antibody 20A10 IgG 0.25 ug/mL

FDA Normal tissue array MNO1021

Fig. 114I
Normal Heart

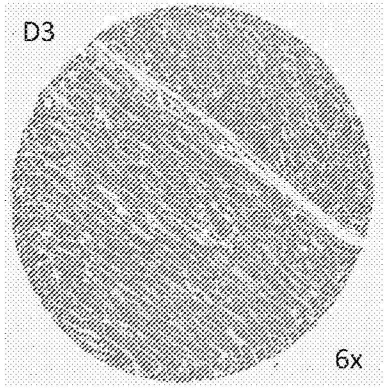


Fig. 114J
Normal Liver

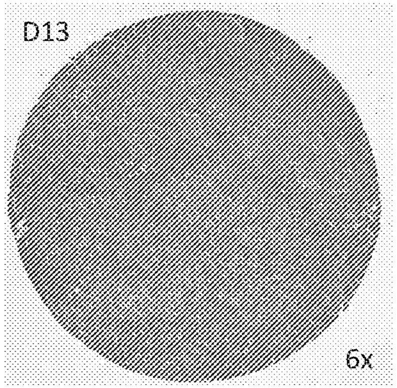


Fig. 114K
Normal Lung

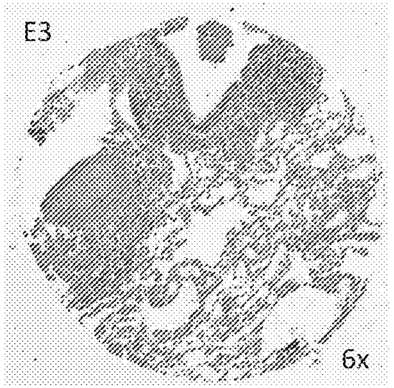


Fig. 114L
Normal Ureter

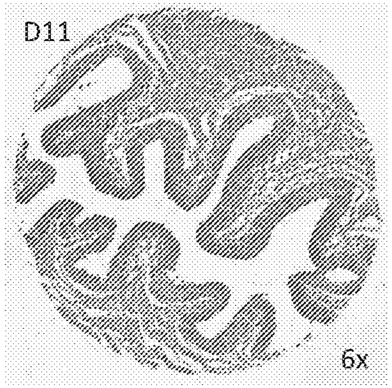


Fig. 114M

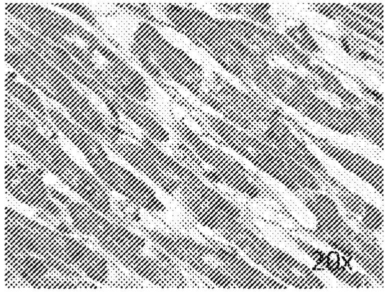


Fig. 114N

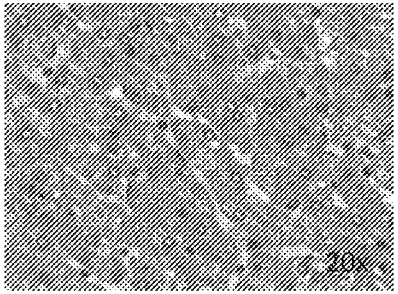


Fig. 114O

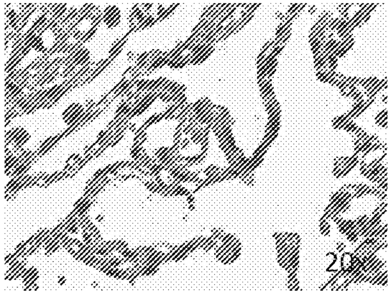


Fig. 114P

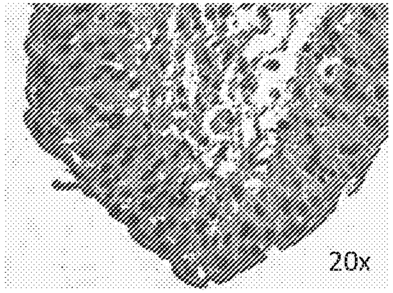


Figure 114I-114P

PSMGFR-antibody 20A10 IgG 0.25 ug/mL

FDA Normal tissue array MNO1021

Fig. 114Q
Normal Heart

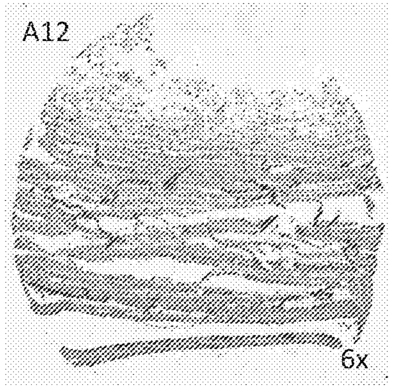


Fig. 114R
Normal Liver

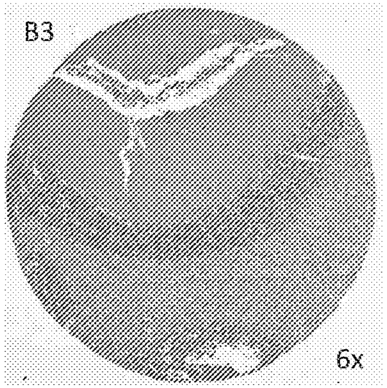


Fig. 114S
Normal Lung

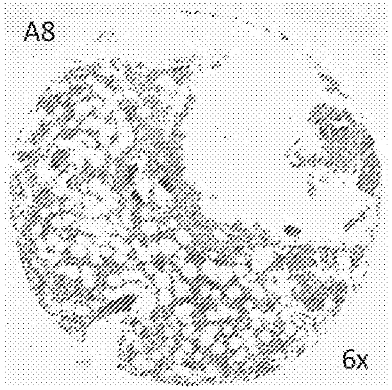


Fig. 114T
Normal Ureter

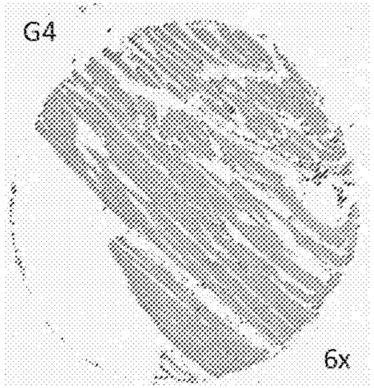


Fig. 114U

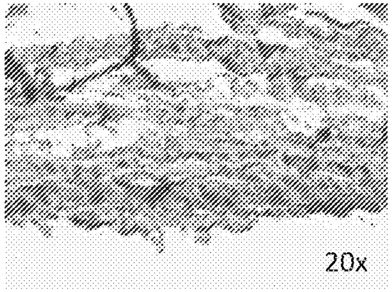


Fig. 114V

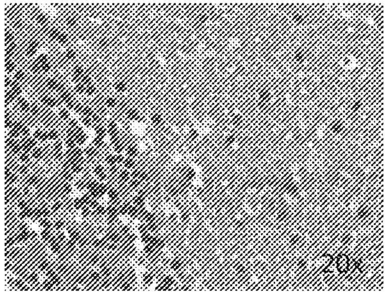


Fig. 114W

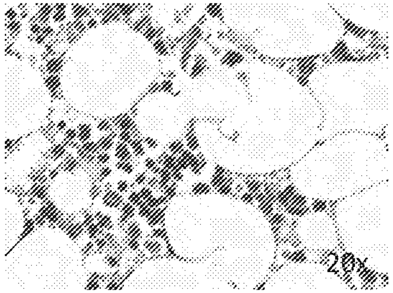


Fig. 114X

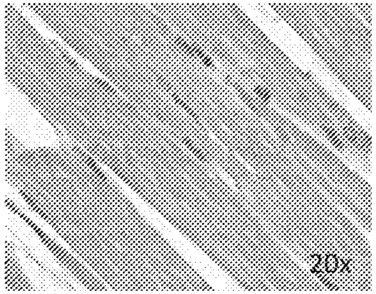


Figure 114Q-114X

PSMGFR-antibody 20A10 IgG 0.25 ug/mL

Breast cancer tissue array BR1141

Fig. 115A

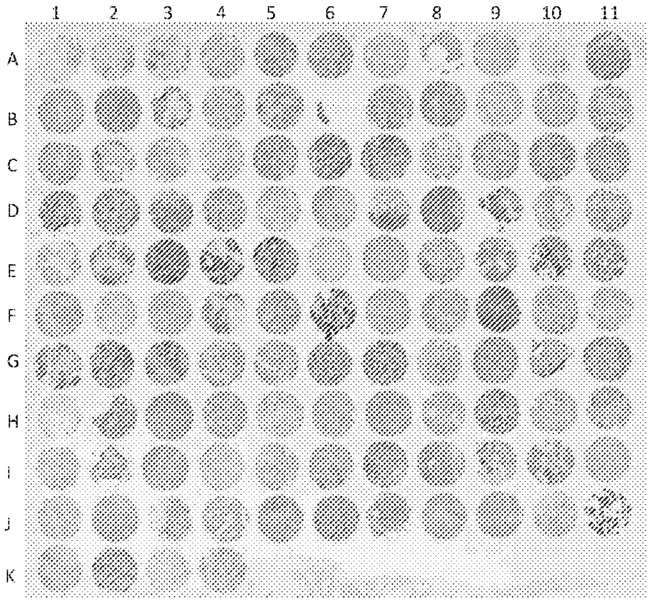


Fig. 115B

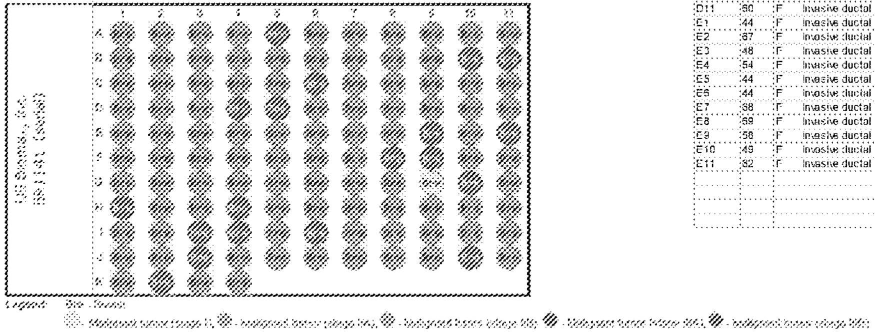


Fig. 115C

Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type
A1	45	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A2	38	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A3	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A4	41	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A5	70	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
A6	46	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
A7	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
A8	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A9	68	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
A10	62	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
A11	50	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B1	43	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B2	63	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
B3	57	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
B4	77	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B5	56	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B6	46	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B7	48	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B8	40	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B9	53	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B10	54	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
B11	47	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
C1	48	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
C2	48	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
C3	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C4	41	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C5	56	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C6	41	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
C7	41	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C8	60	F	Invasive ductal carcinoma	T2N1M0	*	IIB	Malignant
C9	40	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C10	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
C11	57	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D1	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D2	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D3	48	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
D4	46	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
D5	52	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
D6	51	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D7	62	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D8	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D9	43	F	Invasive ductal carcinoma	T2N1M0	1	IIB	Malignant
D10	44	F	Invasive ductal carcinoma	T2N0M0	*	IIA	Malignant
D11	60	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E1	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E2	67	F	Invasive ductal carcinoma	T2N0M0	3	IIA	Malignant
E3	48	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E4	54	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
E5	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E6	44	F	Invasive ductal carcinoma	T2N0M0	*	IIA	Malignant
E7	38	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E8	69	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E9	58	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
E10	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E11	32	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
F1	52	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F2	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F3	53	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F4	64	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
F5	63	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F6	69	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
F7	43	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F8	45	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
F9	82	F	Invasive ductal carcinoma	T3N1M0	*	IIIA	Malignant
F10	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
F11	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G1	45	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G2	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G3	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G4	45	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
G5	45	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G6	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G7	53	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G8	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
G9	38	F	Invasive ductal carcinoma	T1N0M0	2	I	Malignant
G10	46	F	Invasive ductal carcinoma	T4N1M0	2	IIIB	Malignant
G11	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H1	49	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
H2	63	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
H3	52	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
H4	50	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
H5	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H6	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H7	47	F	Invasive ductal carcinoma	T2N0M0	3	IIA	Malignant
H8	48	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H9	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H10	51	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H11	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I1	45	F	Invasive ductal carcinoma	T2N1M0	*	IIB	Malignant
I2	68	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I3	79	F	Invasive ductal carcinoma	T4N1M0	2	IIIB	Malignant
I4	56	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
I5	54	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I6	42	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
I7	38	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I8	62	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I9	39	F	Invasive ductal carcinoma	T2N0M0	1	IIA	Malignant
I10	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I11	57	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
J1	73	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
J2	66	F	Invasive ductal carcinoma	T2N0M0	3	IIA	Malignant
J3	45	F	Invasive ductal carcinoma	T2N2M0	3	IIIA	Malignant
J4	44	F	Invasive ductal carcinoma	T2N1M0	3	IIB	Malignant
J5	46	F	Medullary carcinoma	T3N0M0	-	IIB	Malignant
J6	52	F	Medullary carcinoma	T2N0M0	-	IIA	Malignant
J7	56	F	Medullary carcinoma	T2N0M0	-	IIA	Malignant
J8	42	F	Medullary carcinoma	T2N0M0	-	IIA	Malignant
J9	41	F	Medullary carcinoma	T2N1M0	-	IIB	Malignant
J10	53	F	Mucinous carcinoma	T3N1M0	-	IIIA	Malignant
J11	57	F	Medullary carcinoma	T3N0M0	*	IIB	Malignant
K1	45	F	Invasive lobular carcinoma	T2N0M0	-	IIA	Malignant
K2	48	F	Invasive apocrine carcinor	T3N1M0	-	IIIA	Malignant
K3	48	F	Invasive apocrine carcinor	T2N0M0	*	IIA	Malignant
K4	48	F	Invasive micropapillary ca	T2N1M0	-	IIB	Malignant

Figure 115A-115C

PSMGFR-antibody 20A10 IgG 0.25 ug/mL

Breast cancer tissue array BR1141

Fig. 116A

Position: A4
Cell Type: Invasive Ductal Carcinoma
Tumor Grade: 2
TNM: T2N0M0

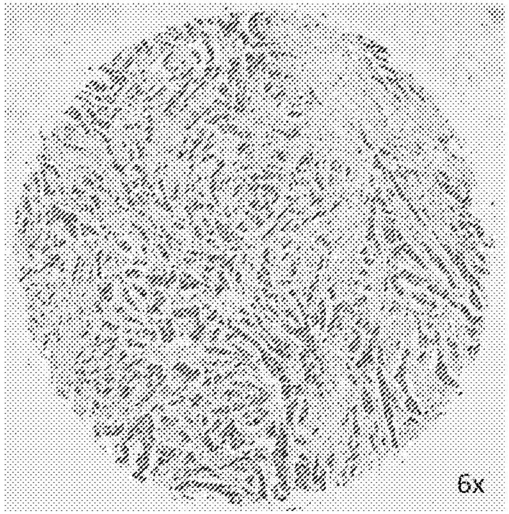


Fig. 116B

Position: A11
Cell Type: Invasive Ductal Carcinoma
Tumor Grade: 2
TNM: T2N0M0

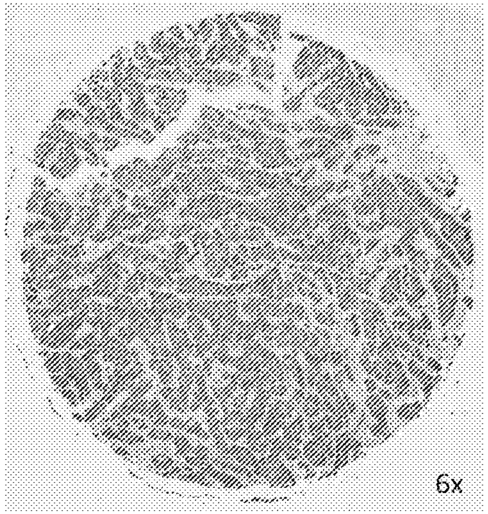


Fig. 116C

Position: G11
Cell Type: Invasive Ductal Carcinoma
Tumor Grade: 2
TNM: T2N0M0

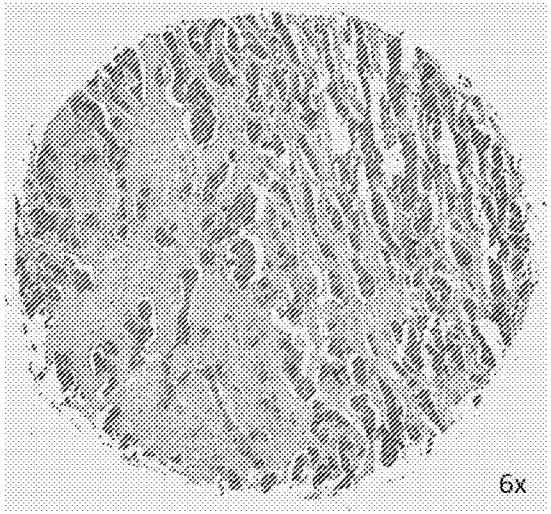


Fig. 116D

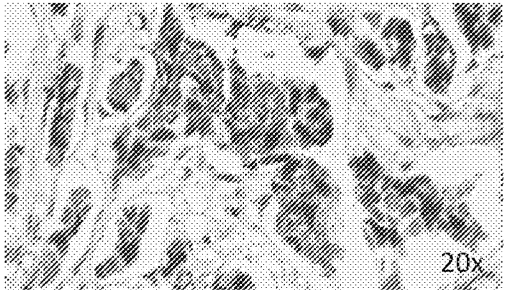


Fig. 116E

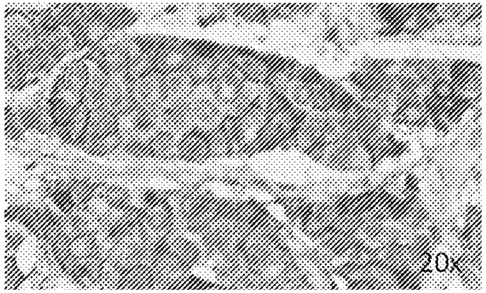


Fig. 116F

Fig. 116A – 116F

PSMGFR-antibody 20A10 IgG 0.25 ug/mL

Pancreatic cancer tissue array PA805c

Fig. 117A

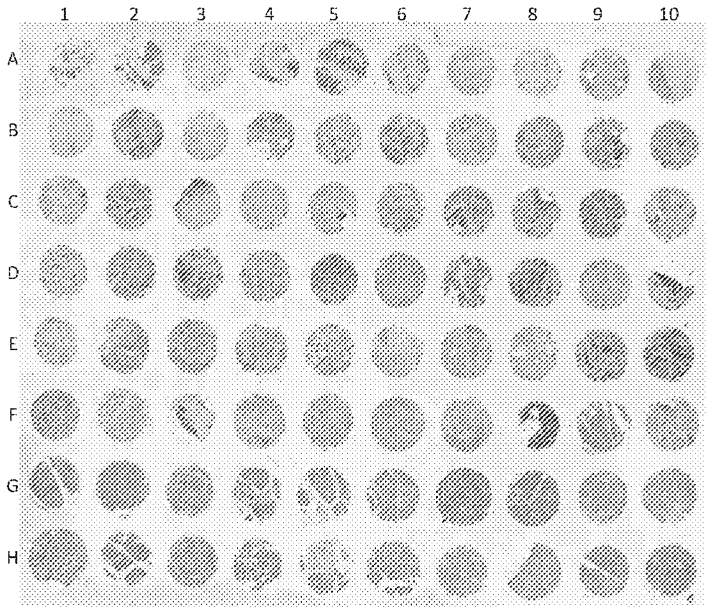


Fig. 117B

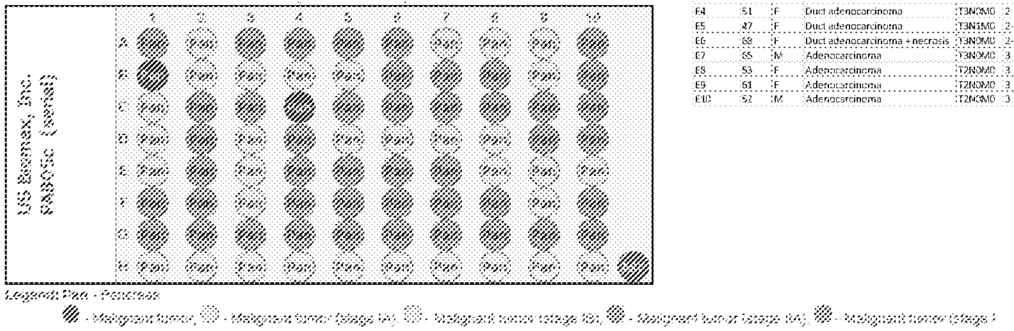


Fig. 117C

Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type	Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type
A1	42	F	Duct adenocarcinoma	T3N0M0	2	IIA	Malignant	F1	51	M	Adenocarcinoma	T3N0M0	3	IIA	Malignant
A2	47	M	Duct adenocarcinoma	T2N0M0	1	IB	Malignant	F2	23	F	Adenocarcinoma	T3N0M0	3	IIA	Malignant
A3	51	F	Duct adenocarcinoma	T3N0M0	1	IIA	Malignant	F3	55	F	Adenocarcinoma	T2N0M0	3	IB	Malignant
A4	56	M	Duct adenocarcinoma	T2N1M0	1	IIB	Malignant	F4	61	M	Adenocarcinoma	T3N0M0	3	IIA	Malignant
A5	58	M	Mucinous adenocarcinoma	T3N0M0	1	IIA	Malignant	F5	62	F	Adenocarcinoma	T3N0M0	3	IIA	Malignant
A6	60	M	Duct adenocarcinoma	T3N0M0	1	IIA	Malignant	F6	64	M	Adenocarcinoma	T3N0M0	3	IIA	Malignant
A7	61	M	Duct adenocarcinoma	T2N0M0	*	IB	Malignant	F7	62	M	Adenocarcinoma	T3N0M0	3	IIA	Malignant
A8	56	F	Duct adenocarcinoma	T2N0M0	1	IB	Malignant	F8	66	F	Adenocarcinoma	T2N1M0	3	IIB	Malignant
A9	42	M	Duct adenocarcinoma	T2N0M0	1	IB	Malignant	F9	40	M	Acinic cell carcinoma	T1N0M0	-	IA	Malignant
A10	51	M	Duct adenocarcinoma	T3N1M0	3	IIB	Malignant	F10	62	M	Squamous cell carcinoma	T3N0M0	2--3	IIA	Malignant
B1	66	M	Adenocarcinoma	T2N0M1	*	IV	Malignant	G1	52	M	Adjacent normal pancreas tissue	-	-	-	NAT
B2	80	M	Duct adenocarcinoma	T2N0M0	1	IB	Malignant	G2	51	F	Adjacent normal pancreas tissue	-	-	-	NAT
B3	64	F	Duct adenocarcinoma	T2N0M0	2	IB	Malignant	G3	51	M	Adjacent normal pancreas tissue	-	-	-	NAT
B4	77	M	Duct adenocarcinoma	T1N0M0	2	IA	Malignant	G4	48	F	Adjacent normal pancreas tissue	-	-	-	NAT
B5	58	M	Adenocarcinoma	T2N0M0	1--2	IB	Malignant	G5	56	F	Adjacent normal pancreas tissue	-	-	-	NAT
B6	54	F	Duct adenocarcinoma	T3N0M0	2	IIA	Malignant	G6	75	M	Adjacent normal pancreas tissue	-	-	-	NAT
B7	51	F	Duct adenocarcinoma	T3N0M0	1	IIA	Malignant	G7	60	M	Adjacent normal pancreas tissue	-	-	-	NAT
B8	44	M	Duct adenocarcinoma	T3N0M0	2	IIA	Malignant	G8	52	M	Adjacent normal pancreas tissue	-	-	-	NAT
B9	54	M	Duct adenocarcinoma	T2N0M0	2	IB	Malignant	G9	38	M	Adjacent normal pancreas tissue	-	-	-	NAT
B10	40	M	Duct adenocarcinoma	T2N1M0	2	IIB	Malignant	G10	60	F	Adjacent normal pancreas tissue	-	-	-	NAT
C1	54	M	Duct adenocarcinoma	T2N0M0	2	IB	Malignant	H1	49	F	Pancreas tissue	-	-	-	Normal
C2	56	F	Mucinous adenocarcinoma	T3N1M0	2	IIB	Malignant	H2	40	M	Pancreas tissue	-	-	-	Normal
C3	44	M	Mucinous adenocarcinoma	T3N1M0	2	IIB	Malignant	H3	47	M	Pancreas tissue	-	-	-	Normal
C4	62	F	Duct adenocarcinoma	T3N1M1	2	IV	Malignant	H4	25	M	Pancreas tissue	-	-	-	Normal
C5	58	F	Duct adenocarcinoma	T3N1M0	2	IIB	Malignant	H5	42	M	Pancreas tissue	-	-	-	Normal
C6	54	M	Papillary adenocarcinoma	T3N0M0	2	IIA	Malignant	H6	29	M	Pancreas tissue	-	-	-	Normal
C7	60	M	Duct adenocarcinoma	T3N0M0	2	IIA	Malignant	H7	50	M	Head of pancreas tissue	-	-	-	Normal
C8	59	M	Duct adenocarcinoma	T3N0M0	2	IIA	Malignant	H8	39	F	Pancreas tissue	-	-	-	Normal
C9	56	M	Duct adenocarcinoma	T3N1M0	2	IIB	Malignant	H9	35	M	Pancreas tissue	-	-	-	Normal
C10	67	F	Duct adenocarcinoma	T3N1M0	2	IIB	Malignant	H10	21	F	Pancreas tissue	-	*	-	Normal
D1	60	M	Duct adenocarcinoma	T2N0M0	1	IB	Malignant								
D2	48	F	Duct adenocarcinoma	T3N0M0	2	IIA	Malignant								
D3	53	M	Duct adenocarcinoma	T2N0M0	2	IB	Malignant								
D4	64	M	Duct adenocarcinoma	T3N0M0	2	IIA	Malignant								
D5	71	F	Duct adenocarcinoma	T2N0M0	2--3	IB	Malignant								
D6	44	F	Duct adenocarcinoma	T2N0M0	2--3	IB	Malignant								
D7	46	F	Papillary adenocarcinoma	T2N0M0	2	IB	Malignant								
D8	68	F	Mucinous adenocarcinoma	T2N0M0	3	IB	Malignant								
D9	57	M	Duct adenocarcinoma	T3N0M0	*	IIA	Malignant								
D10	60	M	Adenocarcinoma	T2N1M0	3	IIB	Malignant								
E1	56	M	Adenocarcinoma	T2N0M0	2	IB	Malignant								
E2	41	M	Duct adenocarcinoma	T3N0M0	2--3	IIA	Malignant								
E3	56	M	Duct adenocarcinoma	T2N0M0	2--3	IB	Malignant								
E4	51	F	Duct adenocarcinoma	T3N0M0	2--3	IIA	Malignant								
E5	47	F	Duct adenocarcinoma	T3N1M0	2--3	IIB	Malignant								
E6	68	F	Duct adenocarcinoma + necrosis	T3N0M0	2--3	IIA	Malignant								
E7	65	M	Adenocarcinoma	T3N0M0	3	IIA	Malignant								
E8	53	F	Adenocarcinoma	T2N0M0	3	IB	Malignant								
E9	61	F	Adenocarcinoma	T2N0M0	3	IB	Malignant								
E10	52	M	Adenocarcinoma	T2N0M0	3	IB	Malignant								

Figure 117A-117C

PSMGFR-antibody 20A10 IgG 0.25 ug/mL

Pancreatic cancer tissue array PA805c

Fig. 118A

Position: D7

Cell Type: Papillary Adenocarcinoma

Tumor Grade: 2

TNM: T2N0M0

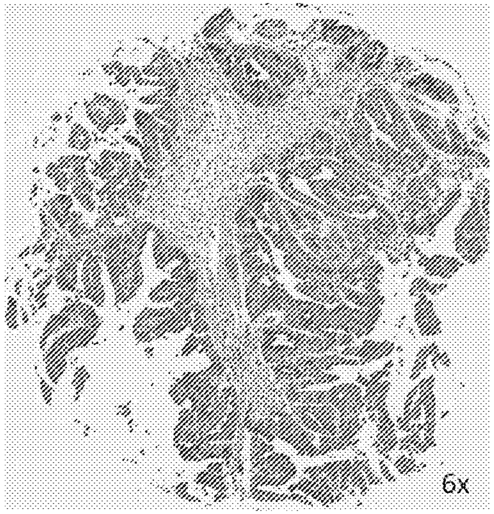


Fig. 118B

Position: E5

Cell Type: Ductal Carcinoma

Tumor Grade: 2-3

TNM: T3N1M0

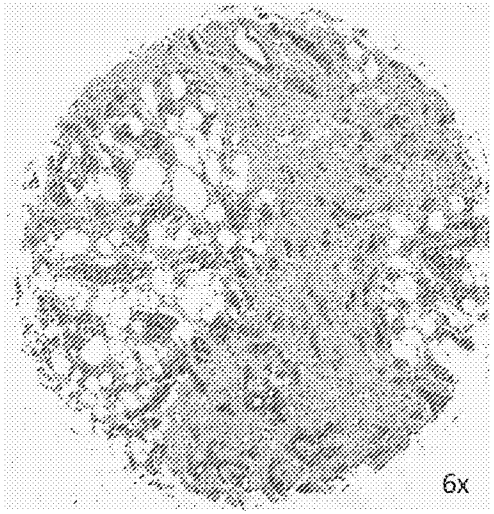


Fig. 118C

Position: F1

Cell Type: Adenocarcinoma

Tumor Grade: 3

TNM: T3N0M0

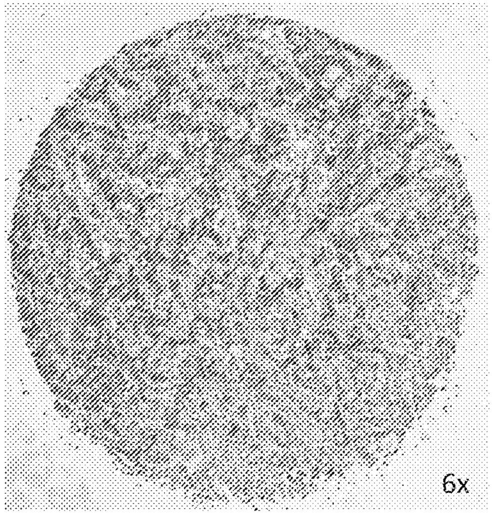


Fig. 118D

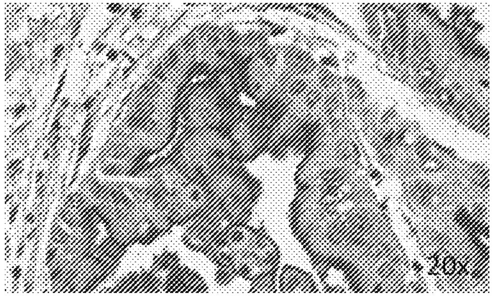


Fig. 118E

Fig. 118F

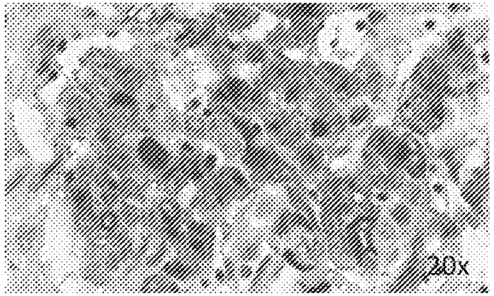


Fig. 118A–118F

PSMGFR-antibody 20A10 IgG 0.25 ug/mL

Esophageal cancer tissue array BC001113a

Fig. 119A

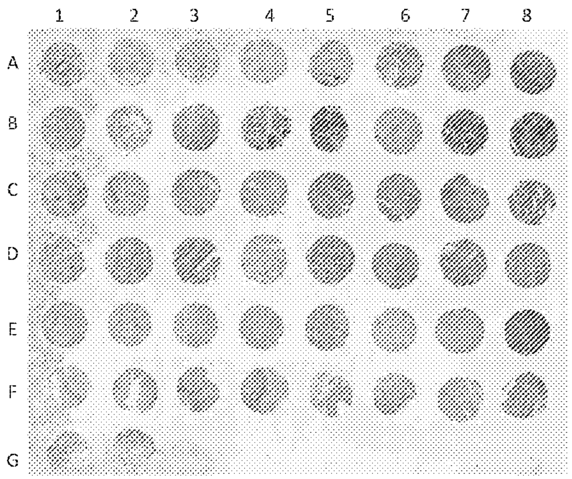


Fig. 119B

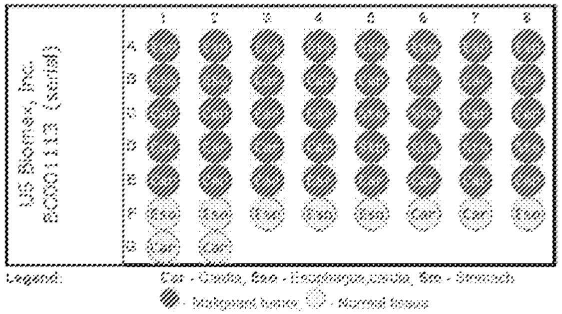


Fig. 119C

Position	Age	Sex	Organ	Pathology diagnosis	TNM	Grade	Type
A1	72	M	Esophagus	Adenocarcinoma	T3N1M0	2	Malignant
A2	33	F	Esophagus	Adenocarcinoma	T3N0M0	2--3	Malignant
A3	61	M	Esophagus	Adenocarcinoma	T3N0M0	2	Malignant
A4	71	M	Esophagus	Adenocarcinoma	T3N0M0	2--3	Malignant
A5	68	M	Esophagus	Adenocarcinoma	T3N0M0	3	Malignant
A6	58	F	Esophagus	Adenocarcinoma	T4N0M0	3	Malignant
A7	51	F	Esophagus	Adenocarcinoma	T3N0M0	3	Malignant
A8	65	M	Esophagus	Adenocarcinoma	T4N1M0	3	Malignant
B1	63	M	Esophagus	Adenocarcinoma	T3N0M0	3	Malignant
B2	61	M	Esophagus	Adenocarcinoma	T3N0M0	3	Malignant
B3	36	M	Cardia	Adenocarcinoma	T3N0M0	1	Malignant
B4	55	F	Cardia	Adenocarcinoma	T3N0M0	1	Malignant
B5	67	M	Cardia	Adenocarcinoma	T2N0M0	1	Malignant
B6	60	F	Cardia	Adenocarcinoma	T3N0M0	1	Malignant
B7	69	M	Cardia	Adenocarcinoma	T3N0M0	1	Malignant
B8	43	M	Cardia	Adenocarcinoma	T2N0M0	1	Malignant
C1	63	F	Cardia	Adenocarcinoma	T3N0M0	1	Malignant
C2	54	F	Cardia	Adenocarcinoma	T3N0M0	1--2	Malignant
C3	30	F	Cardia	Adenocarcinoma	T2N0M0	3	Malignant
C4	61	M	Cardia	Adenocarcinoma	T4N1M0	2	Malignant
C5	62	M	Cardia	Adenocarcinoma	T4N1M0	2	Malignant
C6	65	M	Cardia	Adenocarcinoma	T3N0M0	3	Malignant
C7	72	M	Cardia	Adenocarcinoma	T3N0M0	3	Malignant
C8	74	M	Cardia	Adenocarcinoma	T3N0M0	2	Malignant
D1	55	M	Cardia	Adenocarcinoma	T3N0M0	2	Malignant
D2	70	M	Cardia	Adenocarcinoma	T4N2M0	2	Malignant
D3	50	M	Cardia	Adenocarcinoma	T3N0M0	2	Malignant
D4	64	M	Cardia	Adenocarcinoma	T2N0M0	2	Malignant
D5	54	F	Cardia	Adenocarcinoma	T3N0M0	3	Malignant
D6	59	M	Cardia	Adenocarcinoma	T3N0M0	3	Malignant
D7	72	M	Cardia	Adenocarcinoma	T3N0M0	2	Malignant
D8	60	M	Cardia	Adenocarcinoma	T3N0M0	3	Malignant
E1	64	M	Cardia	Adenocarcinoma	T3N1M0	3	Malignant
E2	42	M	Cardia	Adenocarcinoma	T4N1M0	3	Malignant
E3	73	M	Cardia	Adenocarcinoma	T3N3M0	3	Malignant
E4	41	M	Cardia	Adenocarcinoma	T3N0M0	3	Malignant
E5	63	F	Cardia	Adenocarcinoma	T2N0M0	3	Malignant
E6	64	F	Cardia	Adenocarcinoma	T3N0M0	3	Malignant
E7	37	F	Cardia	Adenocarcinoma	T4BN0M0	3	Malignant
E8	51	F	Cardia	Adenocarcinoma	T4BN0M0	3	Malignant
F1	64	F	Esophagus	Adjacent normal	-	-	NAT
F2	59	M	Esophagus	Adjacent normal	-	-	NAT
F3	67	M	Esophagus	Adjacent normal	-	-	NAT
F4	43	M	Esophagus	Cancer adjacent	-	-	AT
F5	72	M	Esophagus	Cancer adjacent	-	-	AT
F6	53	M	Cardia	Adjacent normal, chronic inflammation	-	-	Inflammation
F7	61	M	Cardia	Adjacent normal, chronic inflammation	-	-	Inflammation
F8	62	M	Cardia	Adjacent normal, chronic inflammation	-	-	Inflammation
G1	58	M	Cardia	Adjacent normal	-	-	NAT
G2	66	M	Cardia	Adjacent normal, chronic inflammation	-	-	Inflammation

Figure 119A-119C

PSMGFR-antibody 20A10 IgG 0.25 ug/mL

Esophageal cancer tissue array BC001113a

Fig. 120A
Position: A1
Cell Type: Adenocarcinoma
Tumor Grade: 2
TNM: T3N1M0

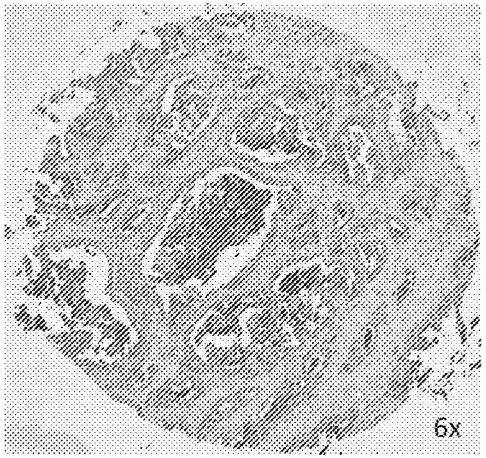


Fig. 120B
Position: A7
Cell Type: Adenocarcinoma
Tumor Grade: 3
TNM: T3N0M0

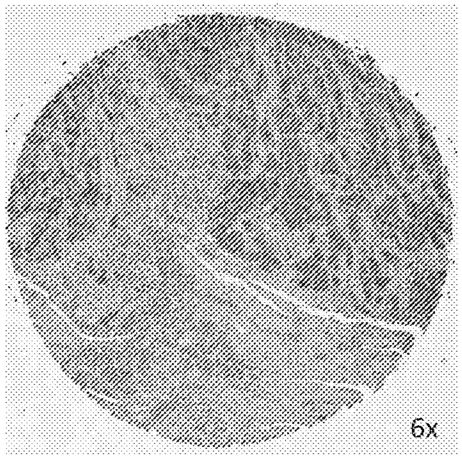


Fig. 120C
Position: A8
Cell Type: Adenocarcinoma
Tumor Grade: 3
TNM: T4N1M0

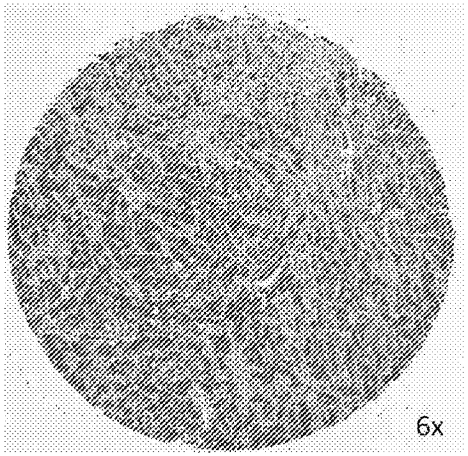


Fig. 120D

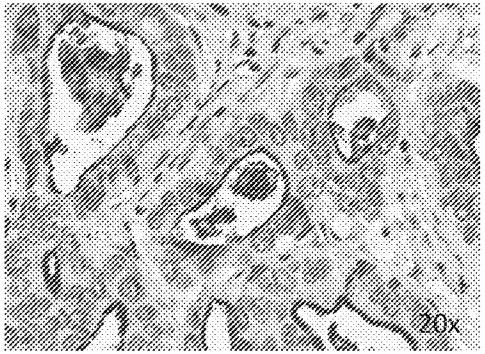


Fig. 120E

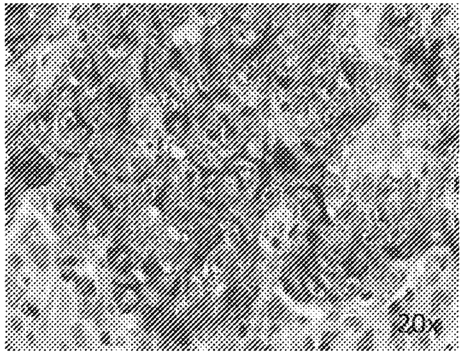


Fig. 120F

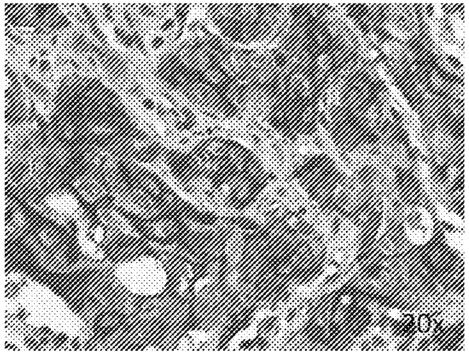


Fig. 120A – 120F

PSMGFR-antibody 3C2B1 20 ug/mL

FDA Normal tissue array MNO1021

Fig. 121A

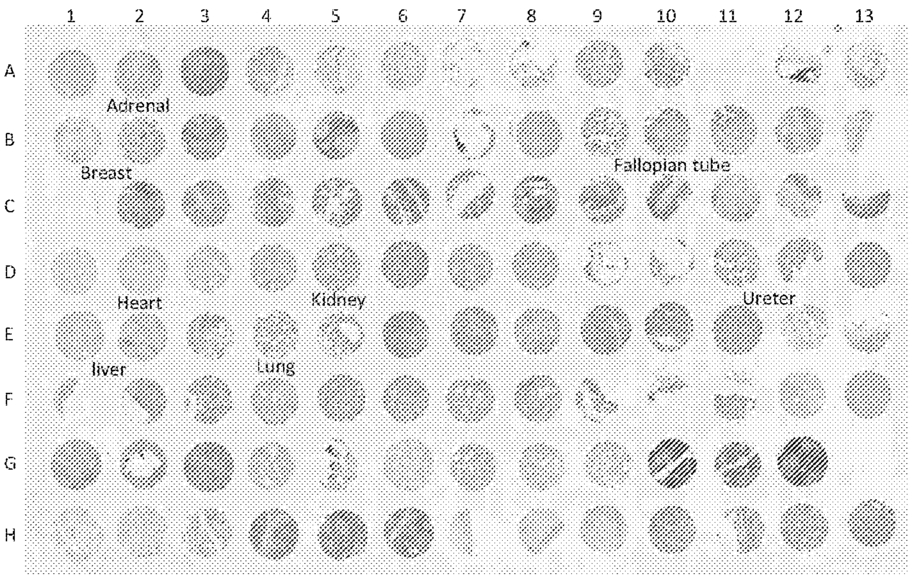


Fig. 121B

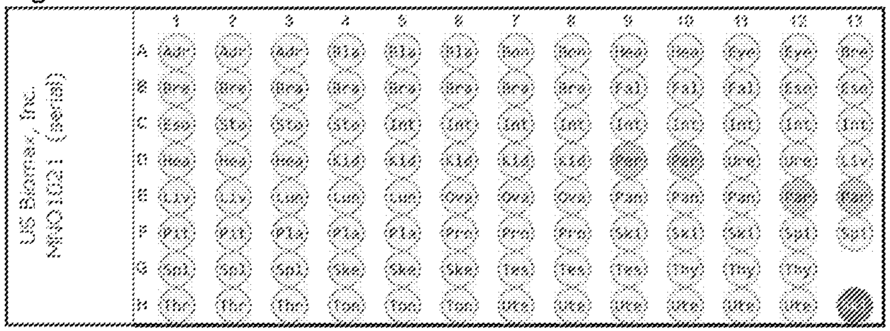


Fig. 121C

Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis	Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis
A1	F	31	Adrenal gland	Normal	E1	M	59	Liver	Normal
A2	M	51	Adrenal gland	Normal	E2	F	27	Liver	Normal
A3	M	53	Adrenal gland	Normal	E3	M	72	Lung	Normal
A4	M	75	Bladder, urinary	Normal	E4	F	55	Lung	Normal
A5	M	72	Bladder, urinary	Normal	E5	M	43	Lung	Normal
A6	M	52	Bladder, urinary	Normal	E6	F	47	Ovary	Normal
A7	M	53	Bone, bone marrow	Normal	E7	F	46	Ovary	Normal
A8	M	43	Bone, bone marrow	Normal	E8	F	40	Ovary	Normal
A9	F	44	Head &neck, salivary gland	Normal	E9	M	42	Pancreas	Normal
A10	M	18	Head &neck, salivary gland	Normal	E10	F	28	Pancreas	Normal
A11	M	55	Eye	Normal	E11	F	59	Pancreas	Normal
A12	M	50	Eye	Normal	E12	M	17	Parathyroid	Adenoma
A13	F	35	Breast	Normal	E13	M	72	Parathyroid	Adenoma
B1	F	38	Breast	Normal	F1	F	3	Pituitary gland	Normal
B2	F	33	Breast	Normal	F2	F		Pituitary gland	Normal
B3	M	58	Brain, cerebellum	Normal	F3	F	32	Placenta	Normal
B4	M	65	Brain, cerebellum	Normal	F4	F	30	Placenta	Normal
B5	F		Brain, cerebellum	Normal	F5	F	27	Placenta	Normal
B6	M	58	Brain, cerebral cortex	Normal	F6	M	64	Prostate	Normal
B7	M	65	Brain, cerebral cortex	Normal	F7	M	65	Prostate	Normal
B8	F		Brain, cerebral cortex	Normal	F8	M	65	Prostate	Normal
B9	F	42	Fallopian tube	Normal	F9	F	32	Skin	Normal
B10	F	32	Fallopian tube	Normal	F10	F	68	Skin	Normal
B11	F	24	Fallopian tube	Normal	F11	M	28	Skin	Normal
B12	M	45	Esophagus	Normal	F12	M	47	Spinal cord	Normal
B13	F	68	Esophagus	Normal	F13	M	58	Spinal cord	Normal
C1	M	54	Esophagus	Normal	G1	M	27	Spleen	Normal
C2	M	45	Stomach	Normal	G2	M	60	Spleen	Normal
C3	M	49	Stomach	Normal	G3	M	31	Spleen	Normal
C4	M	77	Stomach	Normal	G4	F	60	Skeletal muscle	Normal
C5	M	45	Intestine, small intestine	Normal	G5	F	49	Skeletal muscle	Normal
C6	F	75	Intestine, small intestine	Normal	G6	M	70	Skeletal muscle	Normal
C7	F	75	Intestine, small intestine	Normal	G7	M	43	Testis	Normal
C8	M	2	Intestine, colon	Normal	G8	M	30	Testis	Normal
C9	M	48	Intestine, colon	Normal	G9	M	77	Testis	Normal
C10	M	74	Intestine, colon	Normal	G10	M	15	Thymus	Normal
C11	F	47	Intestine, rectum	Normal	G11	M	28	Thymus	Normal
C12	F	75	Intestine, rectum	Normal	G12	F	9	Thymus	Normal
C13	M	66	Intestine, rectum	Normal	G13	-	-	-	-
D1	M	58	Heart	Normal	H1	F	28	Thyroid	Normal
D2	M	46	Heart	Normal	H2	F	37	Thyroid	Normal
D3	F	34	Heart	Normal	H3	F	51	Thyroid	Normal
D4	F	52	Kidney, cortex	Normal	H4	M	46	Tonsil	Normal
D5	M	23	Kidney, cortex	Normal	H5	M	37	Tonsil	Normal
D6	M	63	Kidney, cortex	Normal	H6	M	13	Tonsil	Normal
D7	F	52	Kidney, medulla	Normal	H7	F	38	Uterus, cervl1	Normal
D8	M	23	Kidney, medulla	Normal	H8	F	35	Uterus, cervl1	Normal
D9	M	59	Peripheral nerve	Schwannoma	H9	F	44	Uterus, cervl1	Normal
D10	F	29	Peripheral nerve	Schwannoma	H10	F	38	Uterus, endometrium	Normal
D11	F	44	Ureter	Normal	H11	F	41	Uterus, endometrium	Normal
D12	F	42	Ureter	Normal	H12	F	46	Uterus, endometrium	Normal
D13	F	57	Liver	Normal	H13	M	58	Skin	Malignant melanoma (tissue marker)

Figure 121A-121C

PSMGFR-antibody 3C2B1 IgG 20 ug/mL

FDA Normal tissue array MNO1021

Fig. 122A
Normal Adrenal Gland

A1

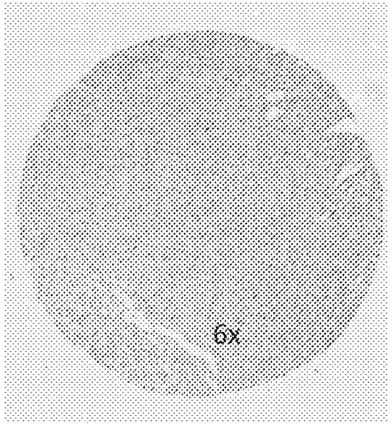


Fig. 122B
Normal Breast

B2

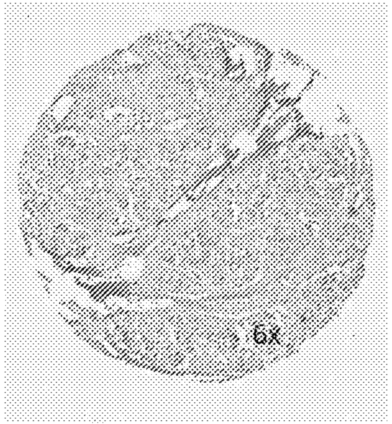


Fig. 122C
Normal Fallopian Tubes

B10

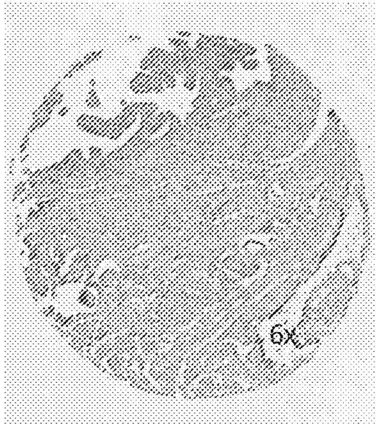


Fig. 122D
Normal Kidney

D5

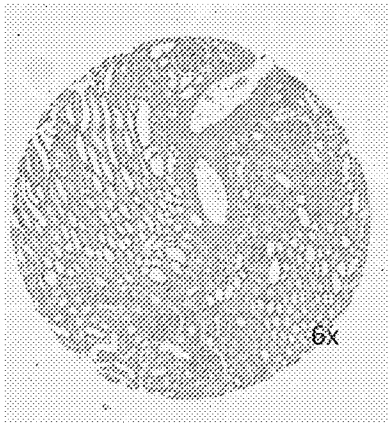


Fig. 122E

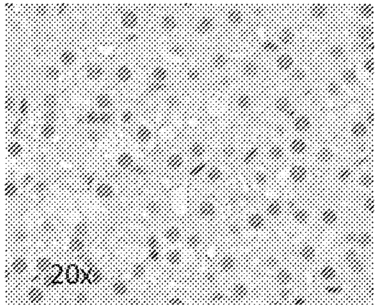


Fig. 122F

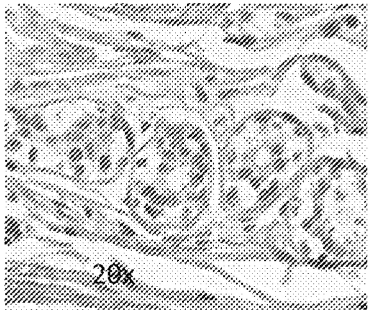


Fig. 122G

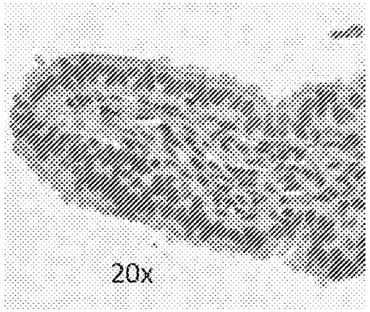


Fig. 122H

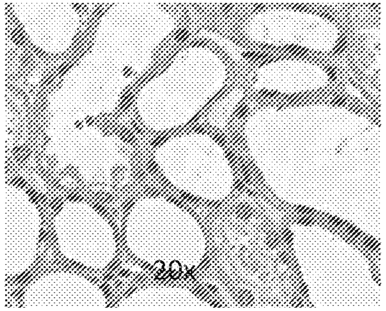


Figure 122A-122H

PSMGFR-antibody 3C2B1 IgG 20 ug/mL
FDA Normal tissue array MNO1021

Fig. 122I
Normal Heart

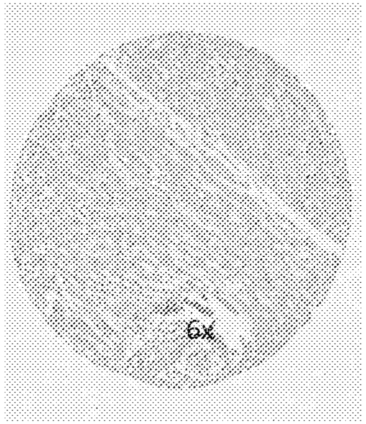


Fig. 122J
Normal Liver

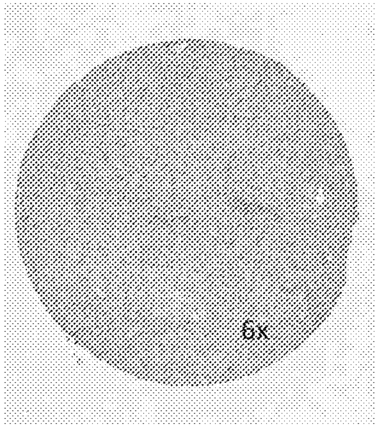


Fig. 122K
Normal Lung

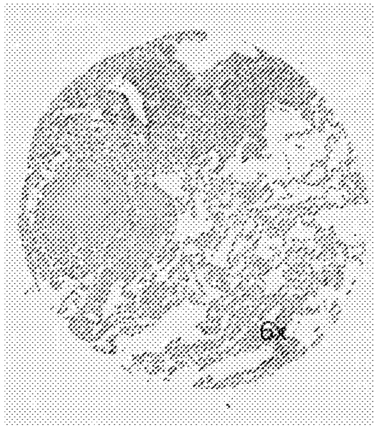


Fig. 122L
Normal Ureter

Fig. 122M

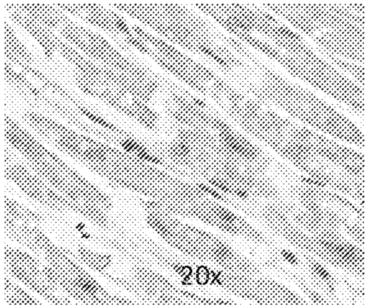


Fig. 122N

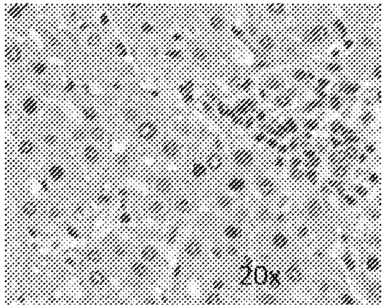


Fig. 122O

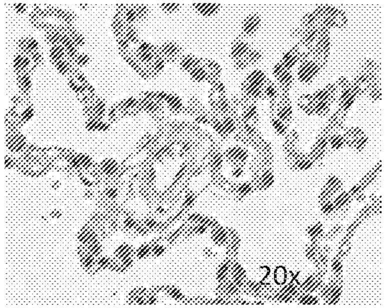


Fig. 122P

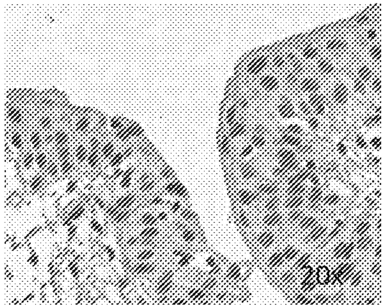


Figure 122I-122P

PSMGFR-antibody 3C2B1 IgG 20 ug/mL

FDA Normal tissue array MNO1021

Fig. 122Q
Normal eye

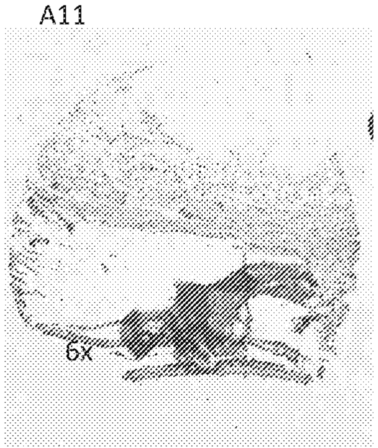


Fig. 122R
Normal Cerebral cortex

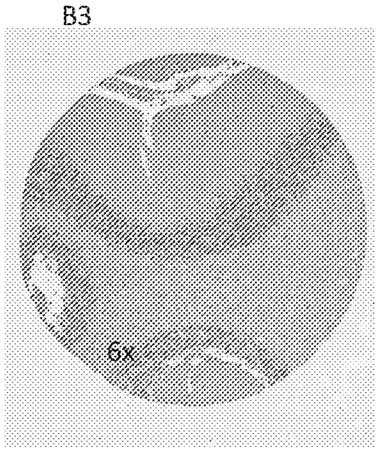


Fig. 122S
Normal Bone marrow

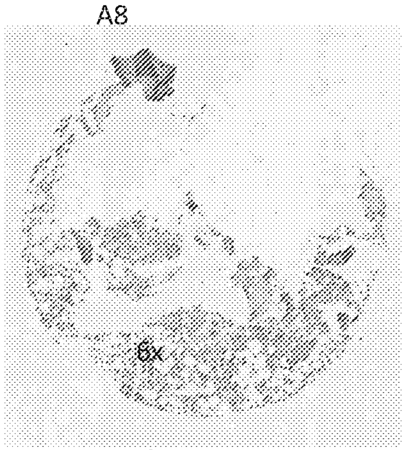


Fig. 122T
Normal Skeletal muscle

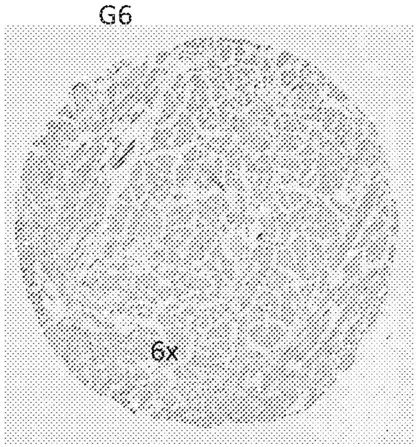


Fig. 122U

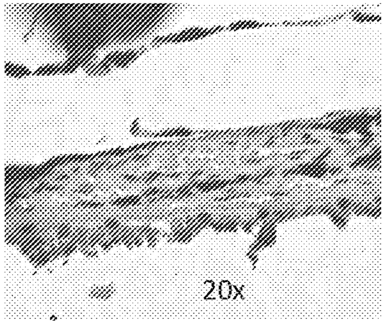


Fig. 122V

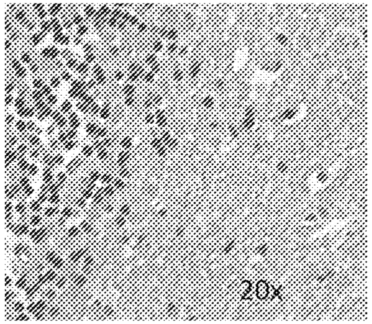


Fig. 122W

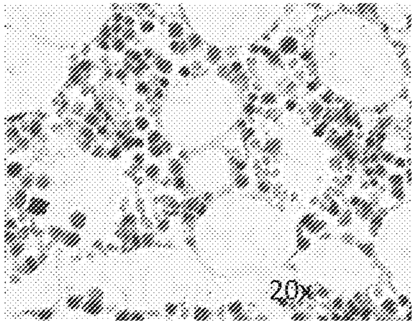


Fig. 122X

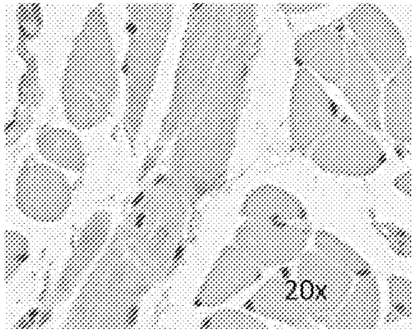


Figure 122Q-122X

PSMGFR-antibody 3C2B1 IgG 20 ug/mL

Pancreatic cancer tissue array PA1003

Fig. 123A

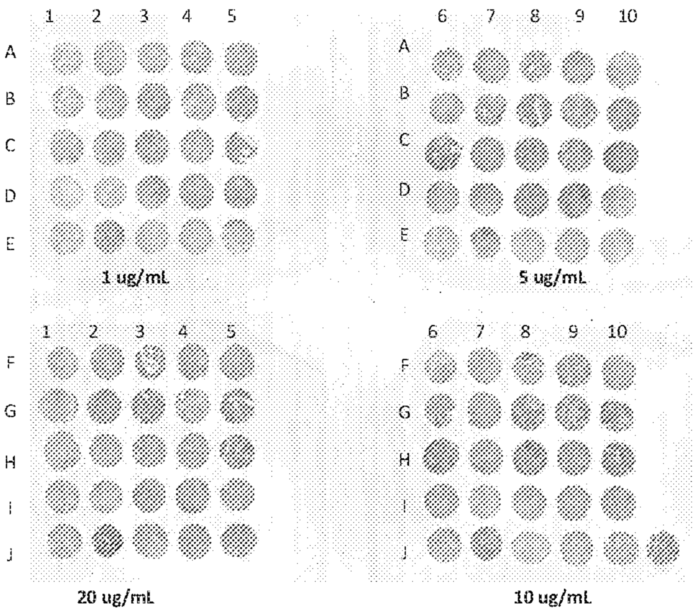


Fig. 123B

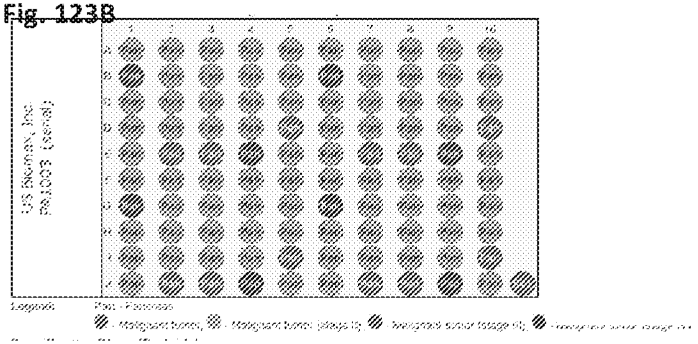


Fig. 123C

Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type	Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type
A1	38	F	Adenocarcinoma	T3N0M0	2	II	malignant	F1	38	F	Adenocarcinoma	T3N0M0	2	II	malignant
A2	44	M	Adenocarcinoma	T3N0M0	2	II	malignant	F2	44	M	Adenocarcinoma	T3N0M0	2	II	malignant
A3	59	M	Adenocarcinoma	T3N0M0	2	II	malignant	F3	59	M	Adenocarcinoma	T3N0M0	2	II	malignant
A4	65	M	Adenocarcinoma	T3N0M0	2	II	malignant	F4	65	M	Adenocarcinoma	T3N0M0	2	II	malignant
A5	53	M	Adenocarcinoma	T3N0M0	2	II	malignant	F5	53	M	Adenocarcinoma	T3N0M0	2	II	malignant
A6	39	F	Adenocarcinoma	T3N0M0	2	II	malignant	F6	39	F	Adenocarcinoma	T3N0M0	2	II	malignant
A7	44	M	Adenocarcinoma	T3N0M0	2	II	malignant	F7	44	M	Adenocarcinoma	T3N0M0	2	II	malignant
A8	59	M	Adenocarcinoma	T3N0M0	2	II	malignant	F8	59	M	Adenocarcinoma	T3N0M0	2	II	malignant
A9	65	M	Adenocarcinoma	T3N0M0	2	II	malignant	F9	65	M	Adenocarcinoma	T3N0M0	-	II	malignant
A10	53	M	Adenocarcinoma	T3N0M0	2	II	malignant	F10	53	M	Adenocarcinoma	T3N0M0	2	II	malignant
B1	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant	G1	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant
B2	52	M	Adenocarcinoma	T3N0M0	1	II	malignant	G2	52	M	Adenocarcinoma	T3N0M0	1	II	malignant
B3	57	M	Adenocarcinoma	T3N0M0	2	II	malignant	G3	57	M	Adenocarcinoma	T3N0M0	2	II	malignant
B4	34	M	Adenocarcinoma	T3N0M0	2	II	malignant	G4	34	M	Adenocarcinoma	T3N0M0	2	II	malignant
B5	72	F	Adenocarcinoma	T3N0M0	2	II	malignant	G5	72	F	Adenocarcinoma	T3N0M0	1	II	malignant
B6	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant	G6	42	M	Adenocarcinoma	T2N0M1	-	IV	malignant
B7	52	M	Adenocarcinoma	T3N0M0	2	II	malignant	G7	52	M	Adenocarcinoma	T3N0M0	2	II	malignant
B8	57	M	Adenocarcinoma	T3N0M0	2	II	malignant	G8	57	M	Adenocarcinoma	T3N0M0	2	II	malignant
B9	34	M	Adenocarcinoma	T3N0M0	1	II	malignant	G9	34	M	Adenocarcinoma	T3N0M0	2	II	malignant
B10	72	F	Adenocarcinoma	T3N0M0	2	II	malignant	G10	72	F	Adenocarcinoma	T3N0M0	2	II	malignant
C1	47	M	Adenocarcinoma	T3N0M0	1	II	malignant	H1	47	M	Adenocarcinoma	T3N0M0	1	II	malignant
C2	64	F	Adenocarcinoma	T3N0M0	1	II	malignant	H2	64	F	Adenocarcinoma	T3N0M0	-	II	malignant
C3	51	M	Adenocarcinoma	T3N0M0	2	II	malignant	H3	51	M	Adenocarcinoma	T3N0M0	2	II	malignant
C4	68	F	Adenocarcinoma	T3N0M0	2	II	malignant	H4	68	F	Adenocarcinoma	T3N0M0	3	II	malignant
C5	41	M	Adenocarcinoma	T3N0M0	-	II	malignant	H5	41	M	Adenocarcinoma	T3N0M0	2	II	malignant
C6	47	M	Adenocarcinoma	T3N0M0	1	II	malignant	H6	47	M	Adenocarcinoma	T3N0M0	1	II	malignant
C7	64	F	Adenocarcinoma	T3N0M0	2	II	malignant	H7	64	F	Adenocarcinoma	T3N0M0	2	II	malignant
C8	51	M	Adenocarcinoma	T3N0M0	2	II	malignant	H8	51	M	Adenocarcinoma	T3N0M0	-	II	malignant
C9	68	F	Adenocarcinoma	T3N0M0	2	II	malignant	H9	68	F	Adenocarcinoma	T3N0M0	2	II	malignant
C10	41	M	Adenocarcinoma	T3N0M0	2	II	malignant	H10	41	M	Adenocarcinoma	T3N0M0	2	II	malignant
D1	58	F	Adenocarcinoma	T3N0M0	2	II	malignant	I1	58	F	Adenocarcinoma	T3N0M0	2	II	malignant
D2	41	F	Adenocarcinoma	T3N0M0	3	II	malignant	I2	41	F	Adenocarcinoma	T3N0M0	3	II	malignant
D3	72	F	Adenocarcinoma	T3N0M0	3	II	malignant	I3	72	F	Adenocarcinoma	T3N0M0	3	II	malignant
D4	59	M	Adenocarcinoma	T3N0M0	3	II	malignant	I4	59	M	Adenocarcinoma	T3N0M0	3	II	malignant
D5	50	M	Adenocarcinoma	T3N1M0	3	III	malignant	I5	50	M	Adenocarcinoma	T3N1M0	3	III	malignant
D6	58	F	Adenocarcinoma	T3N0M0	2	II	malignant	I6	58	F	Adenocarcinoma	T3N0M0	2	II	malignant
D7	41	F	Adenocarcinoma	T3N0M0	3	II	malignant	I7	41	F	Adenocarcinoma	T3N0M0	2	II	malignant
D8	72	F	Adenocarcinoma	T3N0M0	3	II	malignant	I8	72	F	Adenocarcinoma	T3N0M0	3	II	malignant
D9	59	M	Adenocarcinoma	T3N0M0	3	II	malignant	I9	59	M	Adenocarcinoma	T3N0M0	3	II	malignant
D10	50	M	Adenocarcinoma	T3N1M0	3	III	malignant	I10	50	M	Adenocarcinoma	T3N1M0	3	III	malignant
E1	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant	J1	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant
E2	60	M	Adenocarcinoma	T3N1M0	2--3	III	malignant	J2	60	M	Adenocarcinoma	T3N1M0	2--3	III	malignant
E3	56	M	Adenocarcinoma	T2N1M0	3	III	malignant	J3	56	M	Adenocarcinoma	T2N1M0	3	III	malignant
E4	60	F	Adenocarcinoma	T2N1M1	3	IV	malignant	J4	60	F	Adenocarcinoma	T2N1M1	2	IV	malignant
E5	66	F	Adenocarcinoma	T3N0M0	-	II	malignant	J5	66	F	Adenocarcinoma	T3N0M0	3	II	malignant
E6	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant	J6	53	F	Adenocarcinoma	T3N0M0	3	II	malignant
E7	60	M	Adenocarcinoma	T3N1M0	2	III	malignant	J7	60	M	Adenocarcinoma	T3N1M0	3	III	malignant
E8	56	M	Adenocarcinoma	T2N1M0	3	III	malignant	J8	56	M	Adenocarcinoma	T2N1M0	3	III	malignant
E9	60	F	Adenocarcinoma	T2N1M1	3	IV	malignant	J9	60	F	Adenocarcinoma	T2N1M1	-	IV	malignant
E10	66	F	Adenocarcinoma	T3N0M0	3	II	malignant	J10	66	F	Adenocarcinoma	T3N0M0	3	II	malignant

Figure 123A-123C

PSMGFR-antibody 3C2B1 IgG 20 ug/mL

Pancreatic cancer tissue array PA1003

Fig. 124A

Position: A2
Cell Type: Adenocarcinoma
Tumor Grade: 2
TNM: T3N0M0

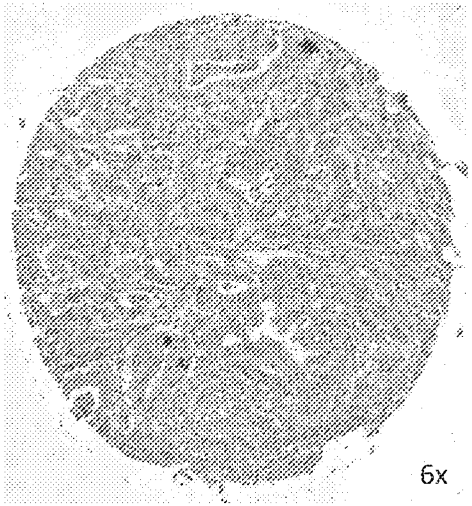


Fig. 124B

Position: B2
Cell Type: Adenocarcinoma
Tumor Grade: 2
TNM: T3N0M0

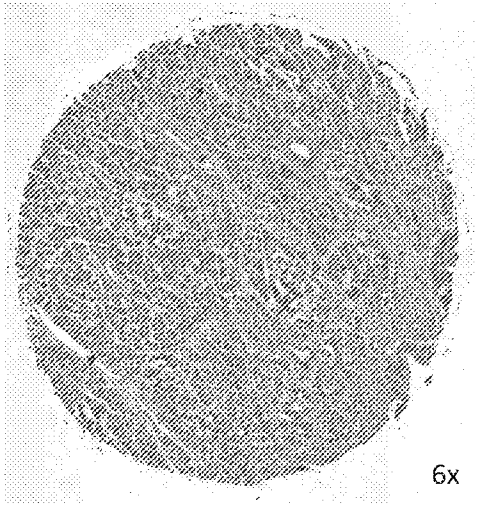


Fig. 124C

Position: C2
Cell Type: Adenocarcinoma
Tumor Grade: 2
TNM: T3N0M0

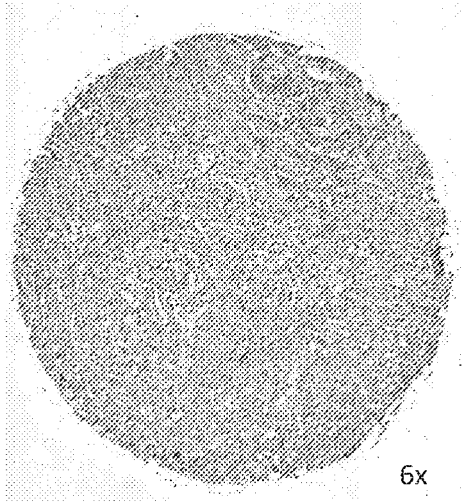


Fig. 124D

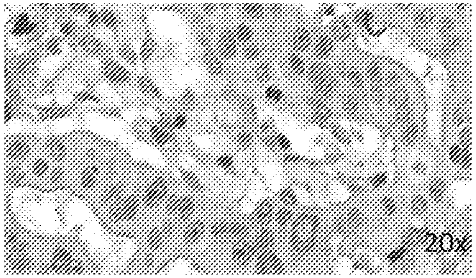


Fig. 124E

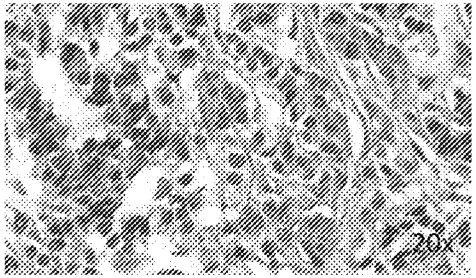


Fig. 124F

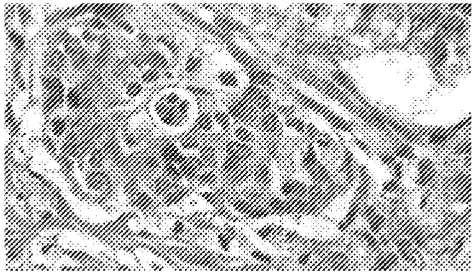


Fig. 124D–124F

PSMGFR-antibody 3C2B1 20 ug/mL

Breast cancer tissue array BR1141a

Fig. 125A

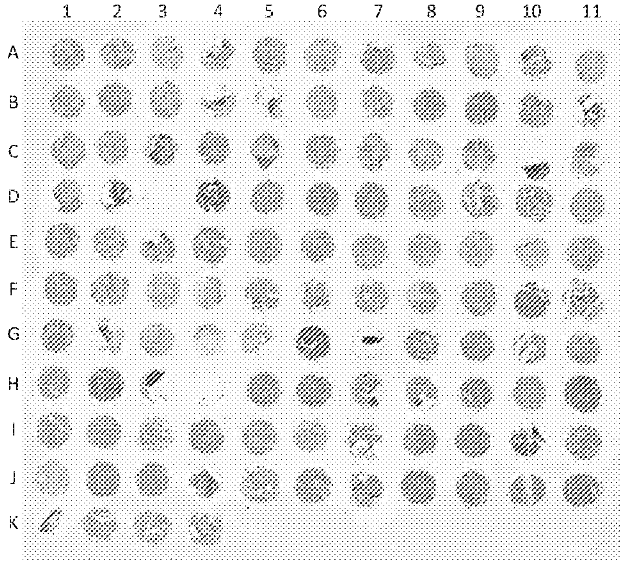


Fig. 125B

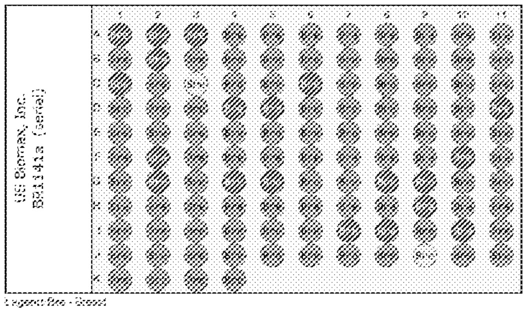


Fig. 125C

Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type	Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type
A1	50	F	Invasive carcinoma	-	2	-	Malignant	F1	43	F	invasive carcinoma	T2N0M0	2	IIA	Malignant
A2	54	F	Invasive carcinoma	T3N2M0	1	IIIA	Malignant	F2	57	F	invasive carcinoma	T3N1M0	3	IIIA	Malignant
A3	42	F	Invasive carcinoma	T2N2M0	2	IIIA	Malignant	F3	62	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
A4	40	F	Invasive carcinoma	T2N1M0	2	IIB	Malignant	F4	48	F	invasive carcinoma	T2N0M0	2	IIA	Malignant
A5	41	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant	F5	45	F	invasive carcinoma	T2N0M0	2	IIA	Malignant
A6	41	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant	F6	47	F	invasive carcinoma	T2N0M0	2	IIA	Malignant
A7	72	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant	F7	50	F	invasive carcinoma	T2N1M0	2	IIB	Malignant
A8	45	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant	F8	48	F	invasive carcinoma	T2N0M0	2	IIA	Malignant
A9	41	F	Invasive carcinoma	T3N0M0	1	IIB	Malignant	F9	42	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
A10	43	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant	F10	50	F	invasive carcinoma	T3N1M0	3	IIIA	Malignant
A11	45	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant	F11	32	F	invasive carcinoma	T2N1M0	3	IIB	Malignant
B1	42	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant	G1	47	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
B2	45	F	Invasive carcinoma	T2N2M0	2	IIIA	Malignant	G2	42	F	invasive carcinoma	T2N2M0	2	IIIA	Malignant
B3	38	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant	G3	54	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant
B4	46	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant	G4	56	F	Invasive carcinoma	T3N1M0	2	IIIA	Malignant
B5	45	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant	G5	45	F	Invasive carcinoma	T2N2M0	2	IIIA	Malignant
B6	45	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant	G6	48	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant
B7	55	F	Invasive carcinoma	T2N1M0	1	IIB	Malignant	G7	50	F	Invasive carcinoma	T1N1M0	3	IIA	Malignant
B8	50	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant	G8	45	F	Invasive carcinoma	T2N3M0	2	IIIC	Malignant
B9	63	F	Invasive carcinoma	T2N1M0	2	IIB	Malignant	G9	42	F	Invasive carcinoma	T3N2M0	3	IIIA	Malignant
B10	56	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant	G10	36	F	Invasive carcinoma	T2N0M0	3	IIA	Malignant
B11	50	F	Invasive carcinoma	T2N0M0	1	IIA	Malignant	G11	44	F	Invasive carcinoma	T2N0M0	3	IIA	Malignant
C1	40	F	Invasive carcinoma	T2N2M0	2	IIIA	Malignant	H1	47	F	invasive carcinoma	T2N1M0	3	IIB	Malignant
C2	42	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant	H2	50	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
C3	61	F	Invasive carcinoma	T1N0M0	2	IA	Malignant	H3	52	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
C4	43	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant	H4	35	F	invasive carcinoma	T2N0M0	2	IIA	Malignant
C5	53	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant	H5	30	F	invasive carcinoma	T2N1M0	3	IIB	Malignant
C6	41	F	Invasive carcinoma	T3N2M0	2	IIIA	Malignant	H6	46	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
C7	56	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant	H7	44	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
C8	41	F	Invasive carcinoma	T2N0M0	1	IIA	Malignant	H8	43	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
C9	46	F	Invasive carcinoma	T2N1M0	1	IIB	Malignant	H9	48	F	invasive carcinoma	T4N2M0	3	IIIB	Malignant
C10	33	F	Invasive carcinoma	T2N0M0	1	IIA	Malignant	H10	42	F	invasive carcinoma	T2N1M0	3	IIB	Malignant
C11	45	F	Invasive carcinoma	T2N1M0	2	IIB	Malignant	H11	43	F	invasive carcinoma	T1N1M0	3	IIA	Malignant
D1	48	F	Invasive carcinoma	T3N0M0	2	IIB	Malignant	I1	72	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
D2	46	F	Invasive carcinoma	T2N0M0	*	IIA	Malignant	I2	68	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
D3	52	F	Invasive carcinoma	T2N1M0	2	IIB	Malignant	I3	56	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
D4	45	F	Invasive carcinoma	T2N2aM0	2	IIIA	Malignant	I4	72	F	Invasive carcinoma	T2N1M0	3	IIB	Malignant
D5	48	F	Invasive carcinoma	T2N2M0	2	IIIA	Malignant	I5	45	F	Invasive carcinoma	T3N0M0	3	IIB	Malignant
D6	62	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant	I6	33	F	Invasive carcinoma	T3N0M0	3	IIB	Malignant
D7	50	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant	I7	62	F	Invasive carcinoma	T3N1M0	3	IIIA	Malignant
D8	44	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant	I8	49	F	Invasive carcinoma	T4N0M0	3	IIIB	Malignant
D9	41	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant	I9	44	F	Invasive carcinoma	T2N0M0	3	IIA	Malignant
D10	42	F	Invasive carcinoma	T2N1M0	2	IIB	Malignant	I10	51	F	Invasive carcinoma	T3N2M0	3	IIIA	Malignant
D11	42	F	Invasive carcinoma	T2N2M0	2	IIIA	Malignant	I11	45	F	Invasive carcinoma	T3M0N0	3	IIB	Malignant
E1	52	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant	J1	77	F	Invasive carcinoma	T2N0M0	3	IIA	Malignant
E2	45	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant	J2	47	F	carcinoma	T2N0M0		IIA	Malignant
E3	44	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant	J3	59	F	carcinoma	T2N0M0		IIA	Malignant
E4	59	F	Invasive carcinoma	T2N0M0	3	IIA	Malignant	J4	50	F	carcinoma	T2N0M0	-	IIA	Malignant
E5	36	F	Invasive carcinoma	T2N0M0	3	IIA	Malignant	J5	55	F	carcinoma	T2N1M0	-	IIB	Malignant
E6	48	F	Invasive carcinoma	T2N0M0	3	IIA	Malignant	J6	46	F	carcinoma	T2N0M0	-	IIA	Malignant
E7	42	F	Invasive carcinoma	T2N0M0	3	IIA	Malignant	J7	46	F	carcinoma	T2N0M0	-	IIA	Malignant
E8	59	F	Invasive carcinoma	T2N0M0	3	IIA	Malignant	J8	63	F	carcinoma	T2N0M0	-	IIA	Malignant
E9	46	F	Invasive carcinoma	T2N0M0	3	IIA	Malignant	J9	38	F	carcinoma	T1N0M0	-	IA	Malignant
E10	63	F	Invasive carcinoma	T2N0M0	3	IIA	Malignant	J10	56	F	carcinoma	T2N0M0	-	IIA	Malignant
E11	64	F	Invasive carcinoma	T2N1M0	2	IIB	Malignant	J11	42	F	carcinoma	T2N0M0	-	IIA	Malignant
								K1	42	F	invasive carcinoma	T2N0M0	2	IIA	Malignant
								K2	48	F	invasive carcinoma	T2N0M0	2	IIA	Malignant
								K3	50	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
								K4	48	F	invasive papillary carcinoma	T2N1M0	-	IIB	Malignant

Figure 125A-125C

PSMGFR-antibody 3C2B1 20 ug/mL

Breast cancer tissue array BR1141a

Fig. 126A

Position: C6
Cell Type: Invasive carcinoma
Tumor Grade: 2
TNM: T3N2M0

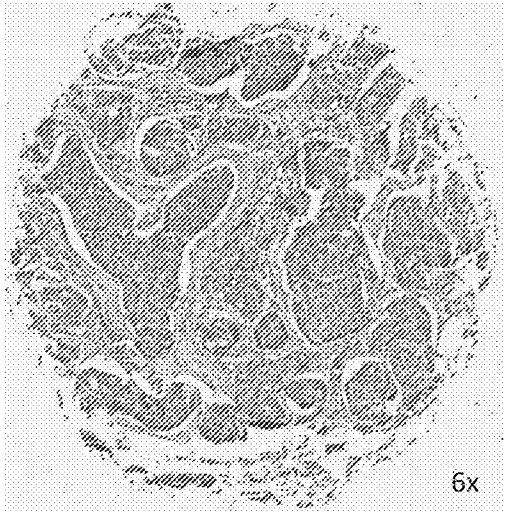


Fig. 126B

Position: D6
Cell Type: Invasive carcinoma
Tumor Grade: 2
TNM: T2N0M0

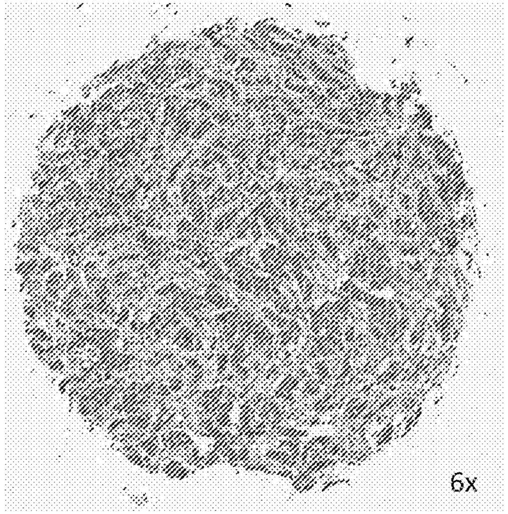


Fig. 126C

Position: E1
Cell Type: Invasive carcinoma
Tumor Grade: 2
TNM: T2N0M0

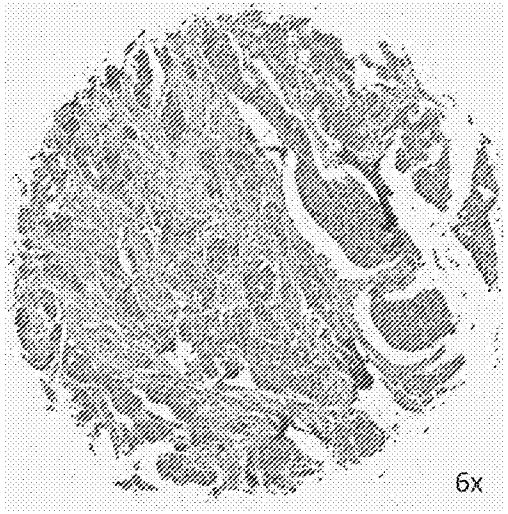


Fig. 126D

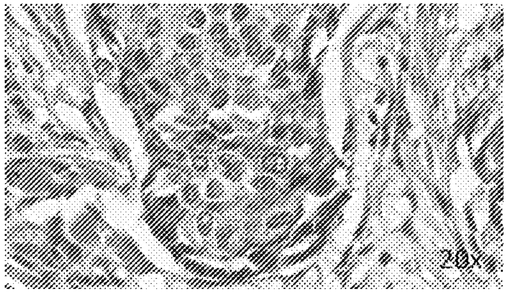


Fig. 126E

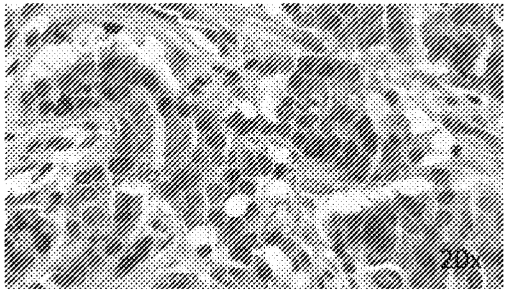


Fig. 126F

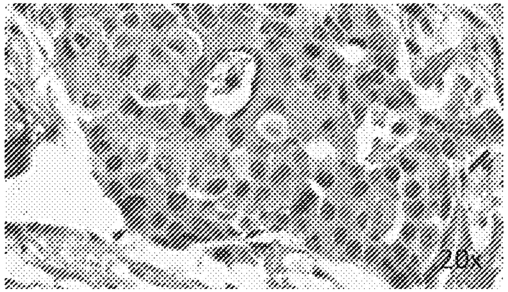


Fig. 126A–126F

PSMGFR-antibody 5C6F3 1 ug/mL

FDA Normal tissue array MNO1021

Fig. 127A

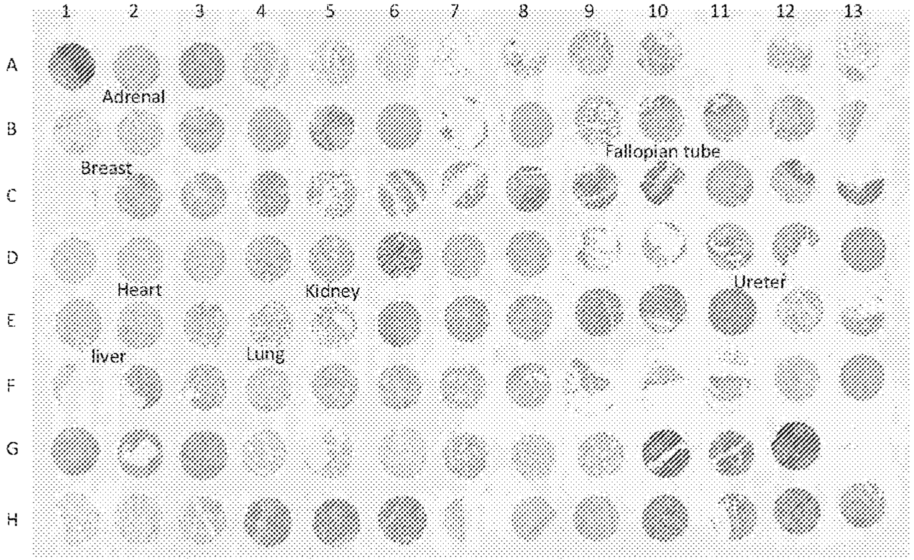


Fig. 127B

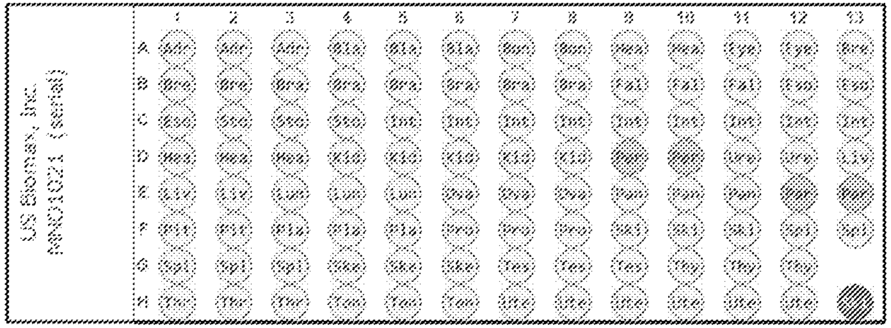


Figure 127A-127C

Fig. 127C

Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis	Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis
A1	F	31	Adrenal gland	Normal	E1	M	59	Liver	Normal
A2	M	51	Adrenal gland	Normal	E2	F	27	Liver	Normal
A3	M	53	Adrenal gland	Normal	E3	M	72	Lung	Normal
A4	M	75	Bladder, urinary	Normal	E4	F	55	Lung	Normal
A5	M	72	Bladder, urinary	Normal	E5	M	43	Lung	Normal
A6	M	52	Bladder, urinary	Normal	E6	F	47	Ovary	Normal
A7	M	53	Bone, bone marrow	Normal	E7	F	46	Ovary	Normal
A8	M	43	Bone, bone marrow	Normal	E8	F	40	Ovary	Normal
A9	F	44	Head and neck, salivary gland	Normal	E9	M	42	Pancreas	Normal
A10	M	18	Head and neck, salivary gland	Normal	E10	F	26	Pancreas	Normal
A11	M	55	Eye	Normal	E11	F	59	Pancreas	Normal
A12	M	50	Eye	Normal	E12	M	17	Parathyroid	Adenoma
A13	F	35	Breast	Normal	E13	M	72	Parathyroid	Adenoma
B1	F	36	Breast	Normal	F1	F	3	Pituitary gland	Normal
B2	F	33	Breast	Normal	F2	F		Pituitary gland	Normal
B3	M	58	Brain, cerebellum	Normal	F3	F	32	Placenta	Normal
B4	M	65	Brain, cerebellum	Normal	F4	F	30	Placenta	Normal
B5	F		Brain, cerebellum	Normal	F5	F	27	Placenta	Normal
B6	M	58	Brain, cerebral cortex	Normal	F6	M	64	Prostate	Normal
B7	M	65	Brain, cerebral cortex	Normal	F7	M	65	Prostate	Normal
B8	F		Brain, cerebral cortex	Normal	F8	M	65	Prostate	Normal
B9	F	42	Fallopian tube	Normal	F9	F	32	Skin	Normal
B10	F	32	Fallopian tube	Normal	F10	F	68	Skin	Normal
B11	F	24	Fallopian tube	Normal	F11	M	28	Skin	Normal
B12	M	45	Esophagus	Normal	F12	M	47	Spinal cord	Normal
B13	F	68	Esophagus	Normal	F13	M	58	Spinal cord	Normal
C1	M	54	Esophagus	Normal	G1	M	27	Spleen	Normal
C2	M	45	Stomach	Normal	G2	M	60	Spleen	Normal
C3	M	49	Stomach	Normal	G3	M	31	Spleen	Normal
C4	M	77	Stomach	Normal	G4	F	60	Skeletal muscle	Normal
C5	M	45	Intestine, small intestine	Normal	G5	F	49	Skeletal muscle	Normal
C6	F	75	Intestine, small intestine	Normal	G6	M	70	Skeletal muscle	Normal
C7	F	75	Intestine, small intestine	Normal	G7	M	43	Testis	Normal
C8	M	2	Intestine, colon	Normal	G8	M	30	Testis	Normal
C9	M	46	Intestine, colon	Normal	G9	M	77	Testis	Normal
C10	M	74	Intestine, colon	Normal	G10	M	15	Thymus	Normal
C11	F	47	Intestine, rectum	Normal	G11	M	28	Thymus	Normal
C12	F	75	Intestine, rectum	Normal	G12	F	9	Thymus	Normal
C13	M	66	Intestine, rectum	Normal	G13	-	-	-	-
D1	M	58	Heart	Normal	H1	F	26	Thyroid	Normal
D2	M	48	Heart	Normal	H2	F	37	Thyroid	Normal
D3	F	34	Heart	Normal	H3	F	51	Thyroid	Normal
D4	F	52	Kidney, cortex	Normal	H4	M	46	Tonsil	Normal
D5	M	23	Kidney, cortex	Normal	H5	M	37	Tonsil	Normal
D6	M	63	Kidney, cortex	Normal	H6	M	13	Tonsil	Normal
D7	F	52	Kidney, medulla	Normal	H7	F	38	Uterus, cervl85	Normal
D8	M	23	Kidney, medulla	Normal	H8	F	35	Uterus, cervl85	Normal
D9	M	59	Peripheral nerve	Schwannoma	H9	F	44	Uterus, cervl85	Normal
D10	F	29	Peripheral nerve	Schwannoma	H10	F	38	Uterus, endometrium	Normal
D11	F	44	Ureter	Normal	H11	F	41	Uterus, endometrium	Normal
D12	F	42	Ureter	Normal	H12	F	46	Uterus, endometrium	Normal
D13	F	57	Liver	Normal	H13	M	58	Skin	Malignant melanoma (tissue marker)

PSMGFR-antibody 5C6F3 1 ug/mL
FDA Normal tissue array MNO1021

Fig. 128A
Normal Adrenal Gland

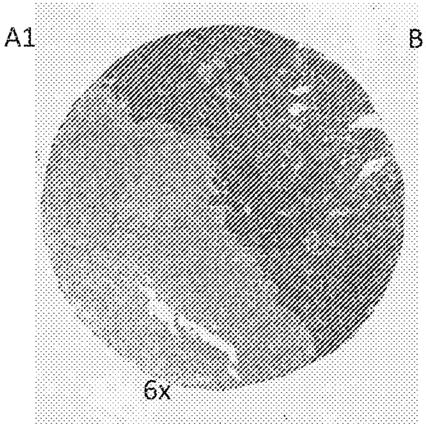


Fig. 128B
Normal Breast

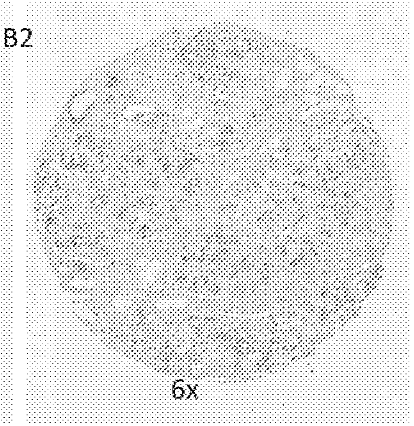


Fig. 128C
Normal Fallopian Tubes

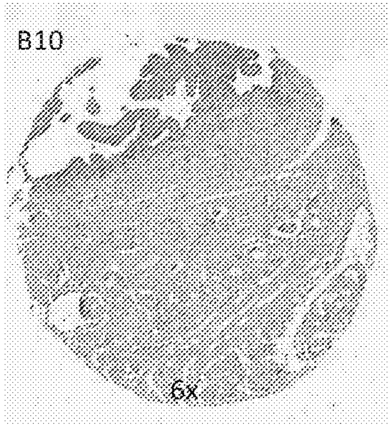


Fig. 128D
Normal Kidney

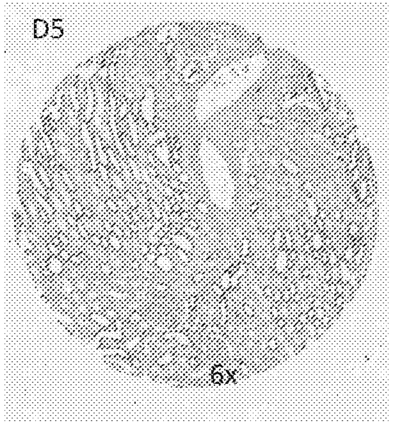


Fig. 128E

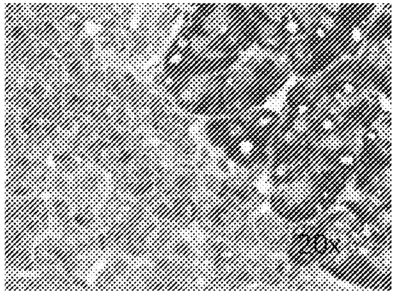


Fig. 128F

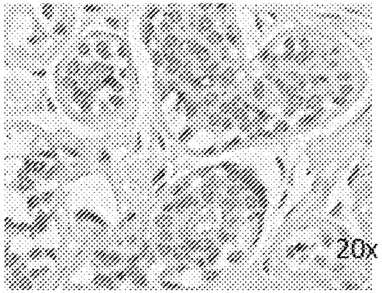


Fig. 128G

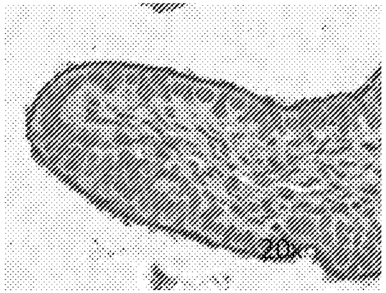


Fig. 128H

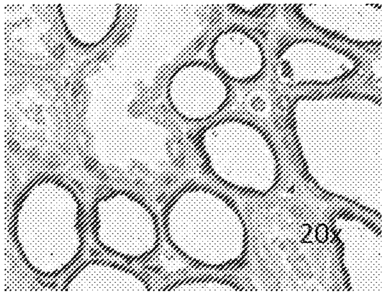


Figure 128A-128H

PSMGFR-antibody 5C6F3 1 ug/mL

FDA Normal tissue array MNO1021

Fig. 128I
Normal Heart

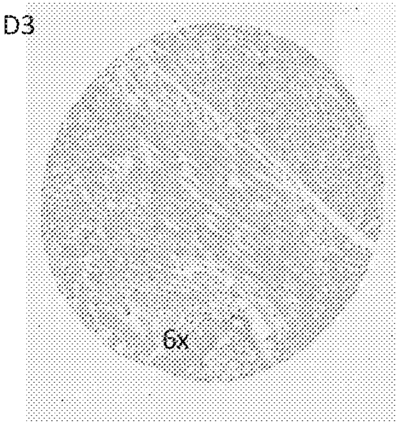


Fig. 128J
Normal Liver

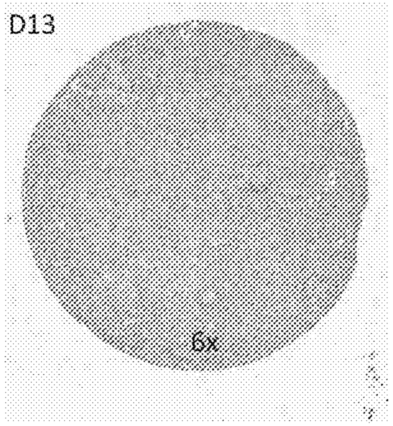


Fig. 128K
Normal Lung

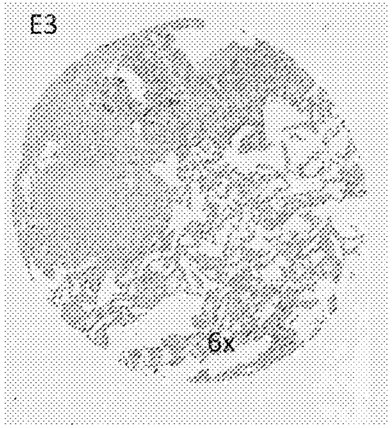


Fig. 128L
Normal Ureter

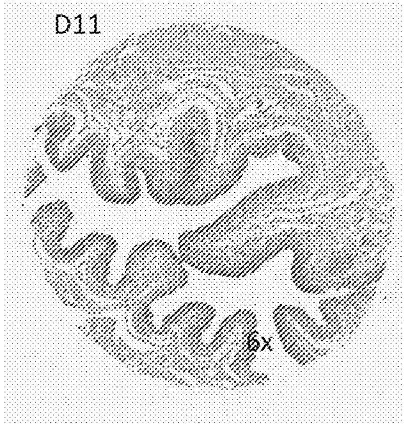


Fig. 128M

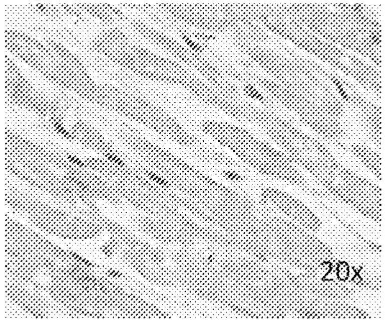


Fig. 128N

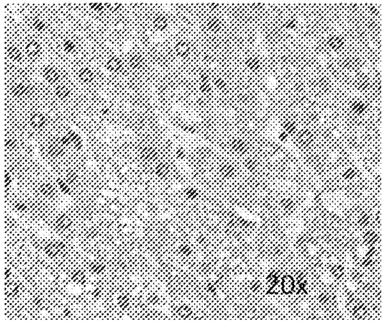


Fig. 128O

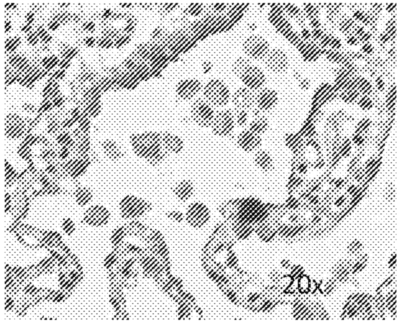


Fig. 128P

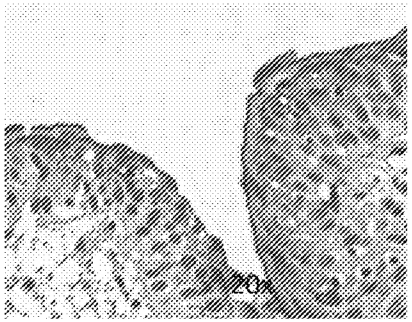


Figure 128I-128P

PSMGFR-antibody 5C6F3 1 ug/mL

FDA Normal tissue array MNO1021

Fig. 128Q
Normal eye

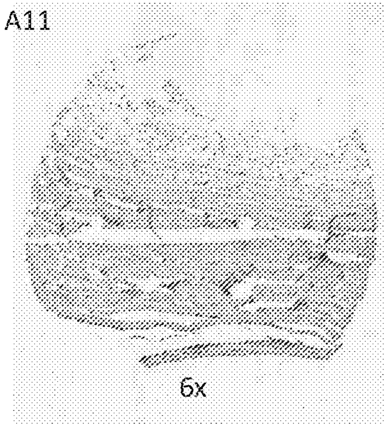


Fig. 128R
Normal Cerebral cortex

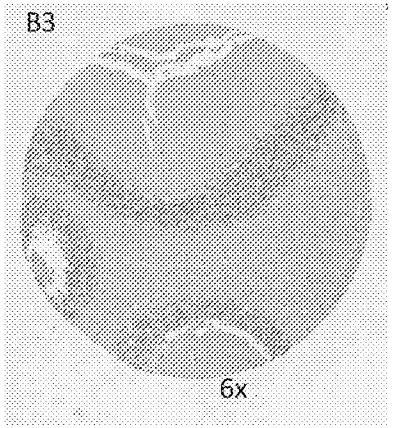


Fig. 128S
Normal Bone marrow

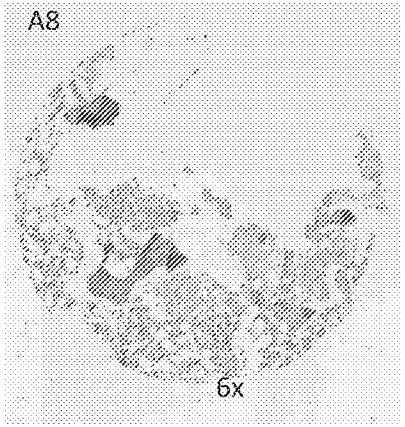


Fig. 128T
Normal Skeletal muscle

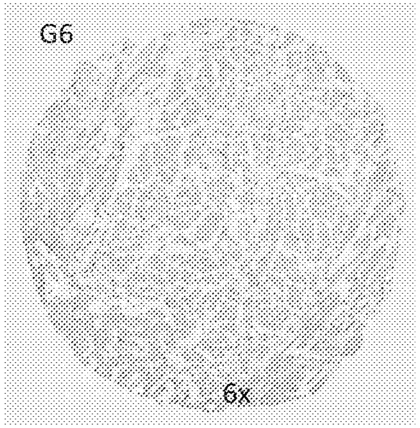


Fig. 128U

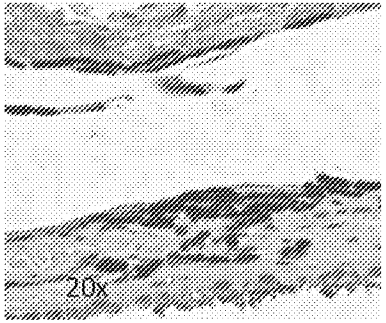


Fig. 128V

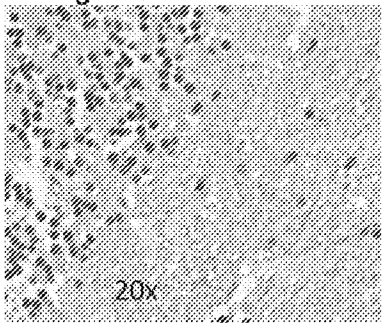


Fig. 128W

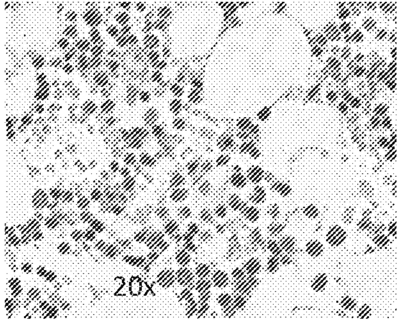


Fig. 128X

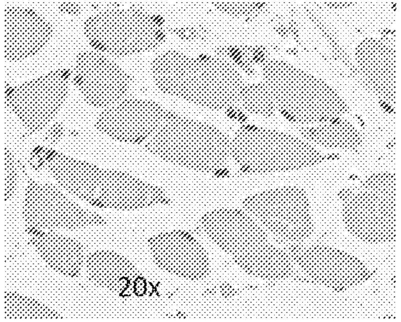


Figure 128Q-128X

PSMGFR-antibody 5C6F3 1 - 20 ug/mL

Pancreatic cancer tissue array PA1003

Fig. 129A

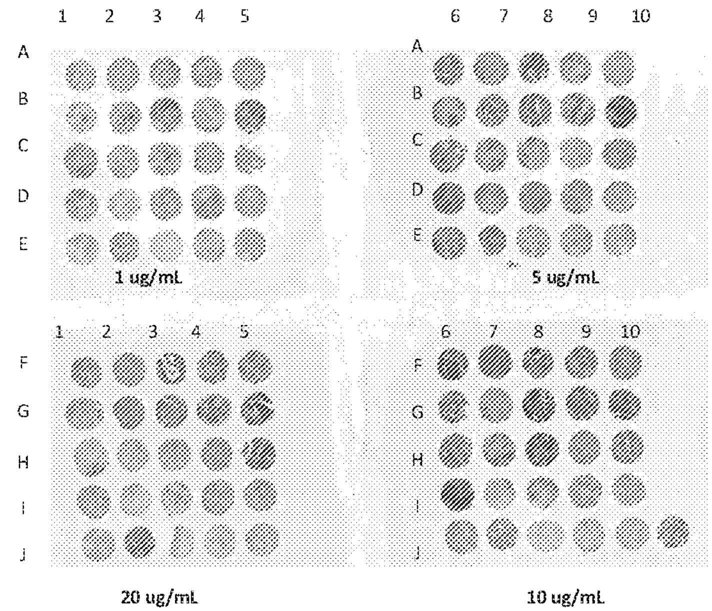


Fig. 129B

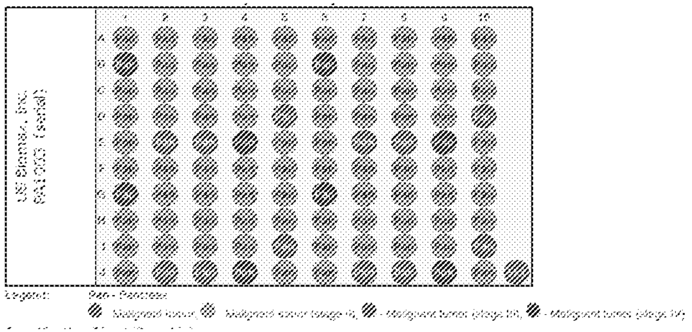


Fig. 129C

Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type		Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type
A1	39	F	Adenocarcinoma	T3N0M0	2	II	malignant		F1	39	F	Adenocarcinoma	T3N0M0	2	II	malignant
A2	44	M	Adenocarcinoma	T3N0M0	2	II	malignant		F2	44	M	Adenocarcinoma	T3N0M0	2	II	malignant
A3	59	M	Adenocarcinoma	T3N0M0	2	II	malignant		F3	59	M	Adenocarcinoma	T3N0M0	2	II	malignant
A4	65	M	Adenocarcinoma	T3N0M0	2	II	malignant		F4	65	M	Adenocarcinoma	T3N0M0	2	II	malignant
A5	53	M	Adenocarcinoma	T3N0M0	2	II	malignant		F5	53	M	Adenocarcinoma	T3N0M0	2	II	malignant
A6	39	F	Adenocarcinoma	T3N0M0	2	II	malignant		F6	39	F	Adenocarcinoma	T3N0M0	2	II	malignant
A7	44	M	Adenocarcinoma	T3N0M0	2	II	malignant		F7	44	M	Adenocarcinoma	T3N0M0	2	II	malignant
A8	59	M	Adenocarcinoma	T3N0M0	2	II	malignant		F8	59	M	Adenocarcinoma	T3N0M0	2	II	malignant
A9	65	M	Adenocarcinoma	T3N0M0	2	II	malignant		F9	65	M	Adenocarcinoma	T3N0M0	-	II	malignant
A10	53	M	Adenocarcinoma	T3N0M0	2	II	malignant		F10	53	M	Adenocarcinoma	T3N0M0	2	II	malignant
B1	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant		G1	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant
B2	52	M	Adenocarcinoma	T3N0M0	1	II	malignant		G2	52	M	Adenocarcinoma	T3N0M0	1	II	malignant
B3	57	M	Adenocarcinoma	T3N0M0	2	II	malignant		G3	57	M	Adenocarcinoma	T3N0M0	2	II	malignant
B4	34	M	Adenocarcinoma	T3N0M0	2	II	malignant		G4	34	M	Adenocarcinoma	T3N0M0	2	II	malignant
B5	72	F	Adenocarcinoma	T3N0M0	2	II	malignant		G5	72	F	Adenocarcinoma	T3N0M0	1	II	malignant
B6	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant		G6	42	M	Adenocarcinoma	T2N0M1	-	IV	malignant
B7	52	M	Adenocarcinoma	T3N0M0	2	II	malignant		G7	52	M	Adenocarcinoma	T3N0M0	2	II	malignant
B8	57	M	Adenocarcinoma	T3N0M0	2	II	malignant		G8	57	M	Adenocarcinoma	T3N0M0	2	II	malignant
B9	34	M	Adenocarcinoma	T3N0M0	1	II	malignant		G9	34	M	Adenocarcinoma	T3N0M0	2	II	malignant
B10	72	F	Adenocarcinoma	T3N0M0	2	II	malignant		G10	72	F	Adenocarcinoma	T3N0M0	2	II	malignant
C1	47	M	Adenocarcinoma	T3N0M0	1	II	malignant		H1	47	M	Adenocarcinoma	T3N0M0	1	II	malignant
C2	64	F	Adenocarcinoma	T3N0M0	1	II	malignant		H2	64	F	Adenocarcinoma	T3N0M0	-	II	malignant
C3	51	M	Adenocarcinoma	T3N0M0	2	II	malignant		H3	51	M	Adenocarcinoma	T3N0M0	2	II	malignant
C4	68	F	Adenocarcinoma	T3N0M0	2	II	malignant		H4	68	F	Adenocarcinoma	T3N0M0	3	II	malignant
C5	41	M	Adenocarcinoma	T3N0M0	-	II	malignant		H5	41	M	Adenocarcinoma	T3N0M0	2	II	malignant
C6	47	M	Adenocarcinoma	T3N0M0	1	II	malignant		H6	47	M	Adenocarcinoma	T3N0M0	1	II	malignant
C7	64	F	Adenocarcinoma	T3N0M0	2	II	malignant		H7	64	F	Adenocarcinoma	T3N0M0	2	II	malignant
C8	51	M	Adenocarcinoma	T3N0M0	2	II	malignant		H8	51	M	Adenocarcinoma	T3N0M0	-	II	malignant
C9	68	F	Adenocarcinoma	T3N0M0	2	II	malignant		H9	68	F	Adenocarcinoma	T3N0M0	2	II	malignant
C10	41	M	Adenocarcinoma	T3N0M0	2	II	malignant		H10	41	M	Adenocarcinoma	T3N0M0	2	II	malignant
D1	58	F	Adenocarcinoma	T3N0M0	2	II	malignant		I1	58	F	Adenocarcinoma	T3N0M0	2	II	malignant
D2	41	F	Adenocarcinoma	T3N0M0	3	II	malignant		I2	41	F	Adenocarcinoma	T3N0M0	3	II	malignant
D3	72	F	Adenocarcinoma	T3N0M0	3	II	malignant		I3	72	F	Adenocarcinoma	T3N0M0	3	II	malignant
D4	59	M	Adenocarcinoma	T3N0M0	3	II	malignant		I4	59	M	Adenocarcinoma	T3N0M0	3	II	malignant
D5	50	M	Adenocarcinoma	T3N1M0	3	III	malignant		I5	50	M	Adenocarcinoma	T3N1M0	3	III	malignant
D6	58	F	Adenocarcinoma	T3N0M0	2	II	malignant		I6	58	F	Adenocarcinoma	T3N0M0	2	II	malignant
D7	41	F	Adenocarcinoma	T3N0M0	3	II	malignant		I7	41	F	Adenocarcinoma	T3N0M0	2	II	malignant
D8	72	F	Adenocarcinoma	T3N0M0	3	II	malignant		I8	72	F	Adenocarcinoma	T3N0M0	3	II	malignant
D9	59	M	Adenocarcinoma	T3N0M0	3	II	malignant		I9	59	M	Adenocarcinoma	T3N0M0	3	II	malignant
D10	50	M	Adenocarcinoma	T3N1M0	3	III	malignant		I10	50	M	Adenocarcinoma	T3N1M0	3	III	malignant
E1	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant		J1	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant
E2	60	M	Adenocarcinoma	T3N1M0	2--3	III	malignant		J2	60	M	Adenocarcinoma	T3N1M0	2--3	III	malignant
E3	56	M	Adenocarcinoma	T2N1M0	3	III	malignant		J3	56	M	Adenocarcinoma	T2N1M0	3	III	malignant
E4	60	F	Adenocarcinoma	T2N1M1	3	IV	malignant		J4	60	F	Adenocarcinoma	T2N1M1	2	IV	malignant
E5	66	F	Adenocarcinoma	T3N0M0	-	II	malignant		J5	66	F	Adenocarcinoma	T3N0M0	3	II	malignant
E6	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant		J6	53	F	Adenocarcinoma	T3N0M0	3	II	malignant
E7	60	M	Adenocarcinoma	T3N1M0	2	III	malignant		J7	60	M	Adenocarcinoma	T3N1M0	3	III	malignant
E8	56	M	Adenocarcinoma	T2N1M0	3	III	malignant		J8	56	M	Adenocarcinoma	T2N1M0	3	III	malignant
E9	60	F	Adenocarcinoma	T2N1M1	3	IV	malignant		J9	60	F	Adenocarcinoma	T2N1M1	-	IV	malignant
E10	66	F	Adenocarcinoma	T3N0M0	3	II	malignant		J10	66	F	Adenocarcinoma	T3N0M0	3	II	malignant

Figure 129A-129C

PSMGFR-antibody 5C6F3 1 ug/mL

Pancreatic cancer tissue array PA1003

Fig. 130D

Position: A2
Cell Type: Adenocarcinoma
Tumor Grade: 2
TNM: T3N0M0

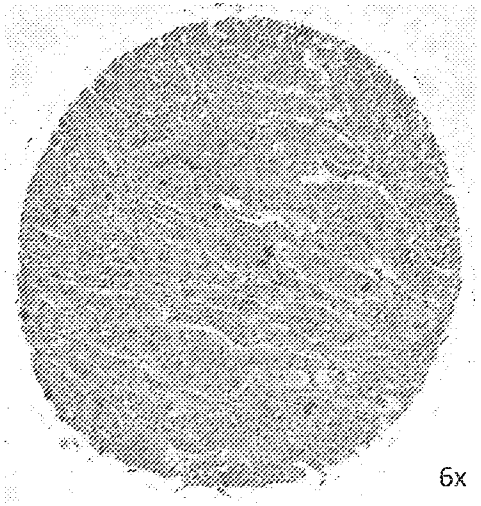


Fig. 130E

Position: B2
Cell Type: Adenocarcinoma
Tumor Grade: 2
TNM: T3N0M0

Fig. 130F

Position: C2
Cell Type: Adenocarcinoma
Tumor Grade: 2
TNM: T3N0M0

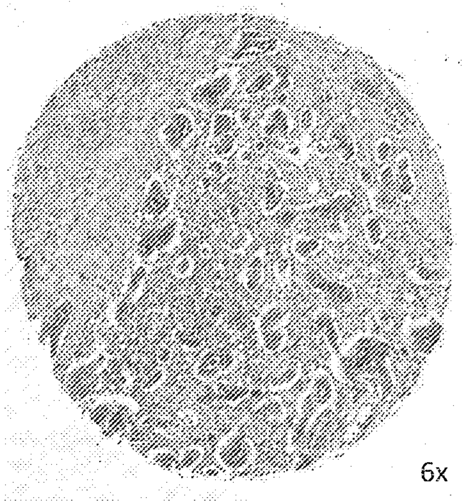


Fig. 130D

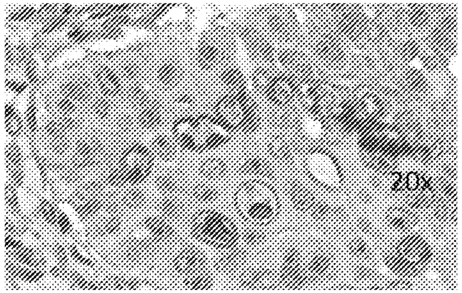


Fig. 130E

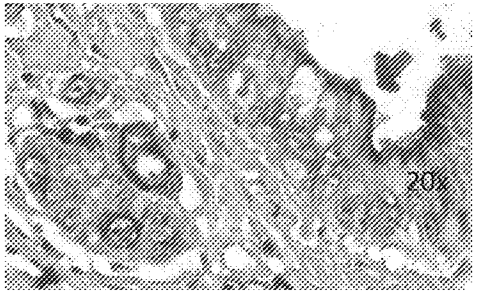


Fig. 130F

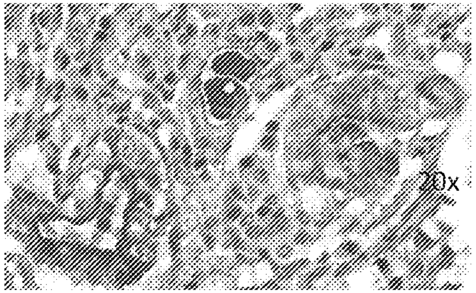


Fig. 130A–130F

PSMGFR-antibody 5C6F3 1 ug/mL

Breast cancer tissue array BR1141a

Fig. 131A

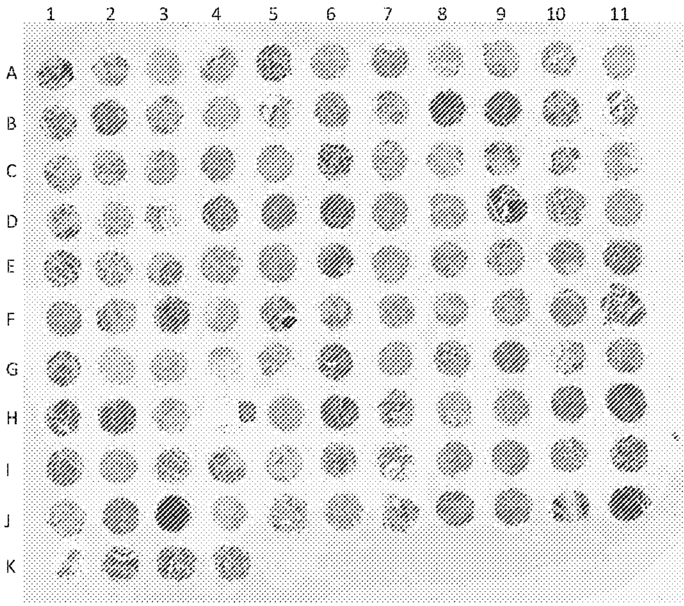


Fig. 131B

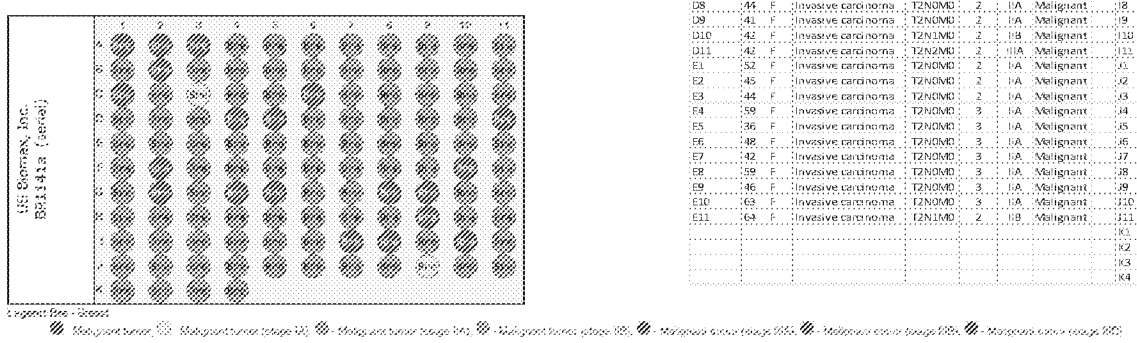


Fig. 131C

Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type
A1	50	F	Invasive carcinoma	-	2	-	Malignant
A2	54	F	Invasive carcinoma	T3N2M0	1	IIIA	Malignant
A3	42	F	Invasive carcinoma	T2N2M0	2	IIIA	Malignant
A4	40	F	Invasive carcinoma	T2N1M0	2	IIB	Malignant
A5	41	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant
A6	41	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant
A7	72	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant
A8	45	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant
A9	41	F	Invasive carcinoma	T3N0M0	1	IIB	Malignant
A10	43	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant
A11	45	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant
B1	42	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant
B2	45	F	Invasive carcinoma	T2N2M0	2	IIIA	Malignant
B3	38	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant
B4	46	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant
B5	45	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant
B6	45	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant
B7	55	F	Invasive carcinoma	T2N1M0	1	IIB	Malignant
B8	50	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant
B9	63	F	Invasive carcinoma	T2N1M0	2	IIB	Malignant
B10	56	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant
B11	50	F	Invasive carcinoma	T2N0M0	1	IIA	Malignant
C1	40	F	Invasive carcinoma	T2N2M0	2	IIIA	Malignant
C2	42	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant
C3	61	F	Invasive carcinoma	T1N0M0	2	IA	Malignant
C4	48	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant
C5	53	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant
C6	41	F	Invasive carcinoma	T3N2M0	2	IIIA	Malignant
C7	56	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant
C8	41	F	Invasive carcinoma	T2N0M0	1	IIA	Malignant
C9	46	F	Invasive carcinoma	T2N1M0	1	IIB	Malignant
C10	33	F	Invasive carcinoma	T2N0M0	1	IIA	Malignant
C11	45	F	Invasive carcinoma	T2N1M0	2	IIB	Malignant
D1	48	F	Invasive carcinoma	T3N0M0	2	IIB	Malignant
D2	46	F	Invasive carcinoma	T2N0M0	*	IIA	Malignant
D3	52	F	Invasive carcinoma	T2N1M0	2	IIB	Malignant
D4	45	F	Invasive carcinoma	T2N2aM0	2	IIIA	Malignant
D5	48	F	Invasive carcinoma	T2N2M0	2	IIIA	Malignant
D6	62	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant
D7	50	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant
D8	44	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant
D9	41	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant
D10	42	F	Invasive carcinoma	T2N1M0	2	IIB	Malignant
D11	42	F	Invasive carcinoma	T2N2M0	2	IIIA	Malignant
E1	52	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant
E2	45	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant
E3	44	F	Invasive carcinoma	T2N0M0	2	IIA	Malignant
E4	59	F	Invasive carcinoma	T2N0M0	3	IIA	Malignant
E5	36	F	Invasive carcinoma	T2N0M0	3	IIA	Malignant
E6	48	F	Invasive carcinoma	T2N0M0	3	IIA	Malignant
E7	42	F	Invasive carcinoma	T2N0M0	3	IIA	Malignant
E8	59	F	Invasive carcinoma	T2N0M0	3	IIA	Malignant
E9	46	F	Invasive carcinoma	T2N0M0	3	IIA	Malignant
E10	63	F	Invasive carcinoma	T2N0M0	3	IIA	Malignant
E11	64	F	Invasive carcinoma	T2N1M0	2	IIB	Malignant
F1	43	F	invasive carcinoma	T2N0M0	2	IIA	Malignant
F2	57	F	invasive carcinoma	T3N1M0	3	IIIA	Malignant
F3	62	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
F4	48	F	invasive carcinoma	T2N0M0	2	IIA	Malignant
F5	45	F	invasive carcinoma	T2N0M0	2	IIA	Malignant
F6	47	F	invasive carcinoma	T2N0M0	2	IIA	Malignant
F7	50	F	invasive carcinoma	T2N1M0	2	IIB	Malignant
F8	48	F	invasive carcinoma	T2N0M0	2	IIA	Malignant
F9	42	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
F10	50	F	invasive carcinoma	T3N1M0	3	IIIA	Malignant
F11	32	F	invasive carcinoma	T2N1M0	3	IIB	Malignant
G1	47	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
G2	42	F	invasive carcinoma	T2N2M0	2	IIIA	Malignant
G3	54	F	invasive carcinoma	T2N0M0	2	IIA	Malignant
G4	56	F	invasive carcinoma	T3N1M0	2	IIIA	Malignant
G5	45	F	invasive carcinoma	T2N2M0	2	IIIA	Malignant
G6	48	F	invasive carcinoma	T2N0M0	2	IIA	Malignant
G7	50	F	invasive carcinoma	T1N1M0	3	IIA	Malignant
G8	45	F	invasive carcinoma	T2N3M0	2	IIIC	Malignant
G9	42	F	invasive carcinoma	T3N2M0	3	IIIA	Malignant
G10	36	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
G11	44	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
H1	47	F	invasive carcinoma	T2N1M0	3	IIB	Malignant
H2	50	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
H3	52	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
H4	35	F	invasive carcinoma	T2N0M0	2	IIA	Malignant
H5	30	F	invasive carcinoma	T2N1M0	3	IIB	Malignant
H6	46	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
H7	44	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
H8	43	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
H9	48	F	invasive carcinoma	T4N2M0	3	IIIB	Malignant
H10	42	F	invasive carcinoma	T2N1M0	3	IIB	Malignant
H11	43	F	invasive carcinoma	T1N1M0	3	IIA	Malignant
I1	72	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
I2	68	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
I3	56	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
I4	72	F	invasive carcinoma	T2N1M0	3	IIB	Malignant
I5	45	F	invasive carcinoma	T3N0M0	3	IIB	Malignant
I6	33	F	invasive carcinoma	T3N0M0	3	IIB	Malignant
I7	62	F	invasive carcinoma	T3N1M0	3	IIIA	Malignant
I8	49	F	invasive carcinoma	T4N0M0	3	IIIB	Malignant
I9	44	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
I10	51	F	invasive carcinoma	T3N2M0	3	IIIA	Malignant
I11	45	F	invasive carcinoma	T3M0N0	3	IIB	Malignant
J1	77	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
J2	47	F	carcinoma	T2N0M0		IIA	Malignant
J3	59	F	carcinoma	T2N0M0		IIA	Malignant
J4	50	F	carcinoma	T2N0M0	-	IIA	Malignant
J5	55	F	carcinoma	T2N1M0	-	IIB	Malignant
J6	46	F	carcinoma	T2N0M0	-	IIA	Malignant
J7	46	F	carcinoma	T2N0M0	-	IIA	Malignant
J8	63	F	carcinoma	T2N0M0	-	IIA	Malignant
J9	38	F	carcinoma	T1N0M0	-	IA	Malignant
J10	56	F	carcinoma	T2N0M0	-	IIA	Malignant
J11	42	F	carcinoma	T2N0M0	-	IIA	Malignant
K1	42	F	invasive carcinoma	T2N0M0	2	IIA	Malignant
K2	48	F	invasive carcinoma	T2N0M0	2	IIA	Malignant
K3	50	F	invasive carcinoma	T2N0M0	3	IIA	Malignant
K4	48	F	invasive papillary carcinoma	T2N1M0	-	IIB	Malignant

Figure 131A-131C

PSMGFR-antibody 5C6F3 1 ug/mL

Breast cancer tissue array BR1141a

Fig. 132A

Position: B1
Cell Type: Invasive carcinoma
Tumor Grade: 2
TNM: T2N0M0

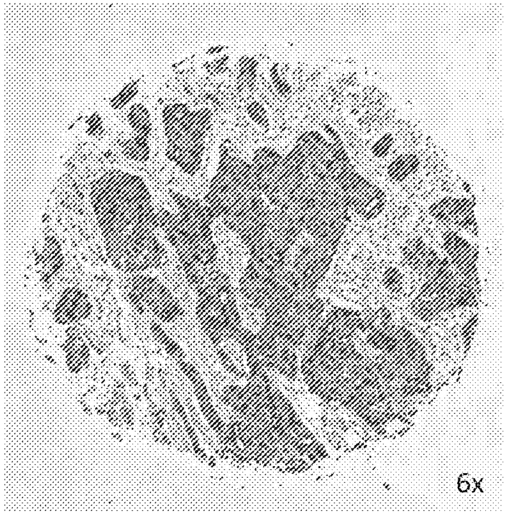


Fig. 132B

Position: B3
Cell Type: Invasive carcinoma
Tumor Grade: 2
TNM: T2N0M0

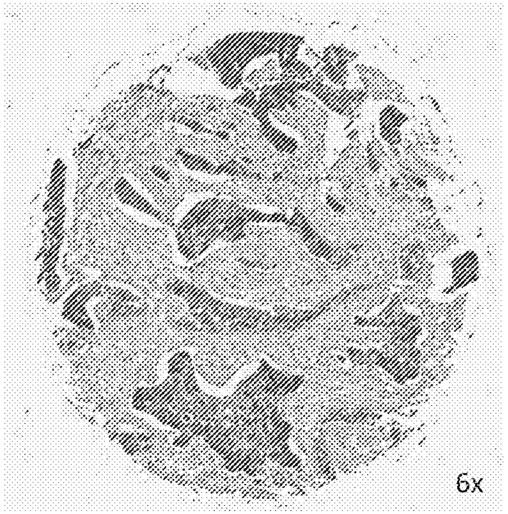


Fig. 132C

Position: B10
Cell Type: Invasive carcinoma
Tumor Grade: 2
TNM: T2N0M0

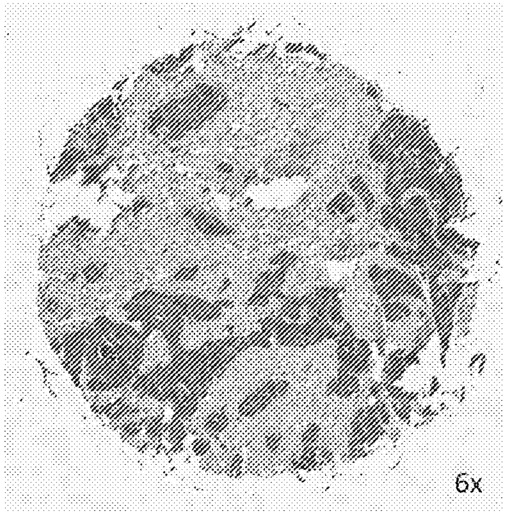


Fig. 132D

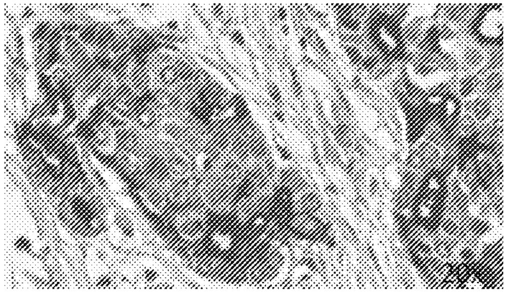


Fig. 132E

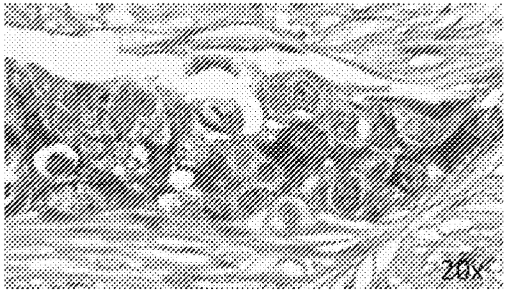


Fig. 132F

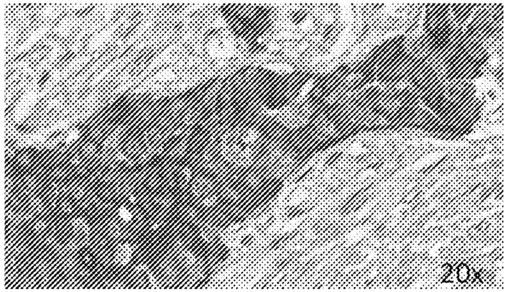


Fig. 132A – 132F

PSMGFR-antibody 18B4 IgG 10 ug/mL

FDA Normal tissue array MNO1021

Fig. 133A

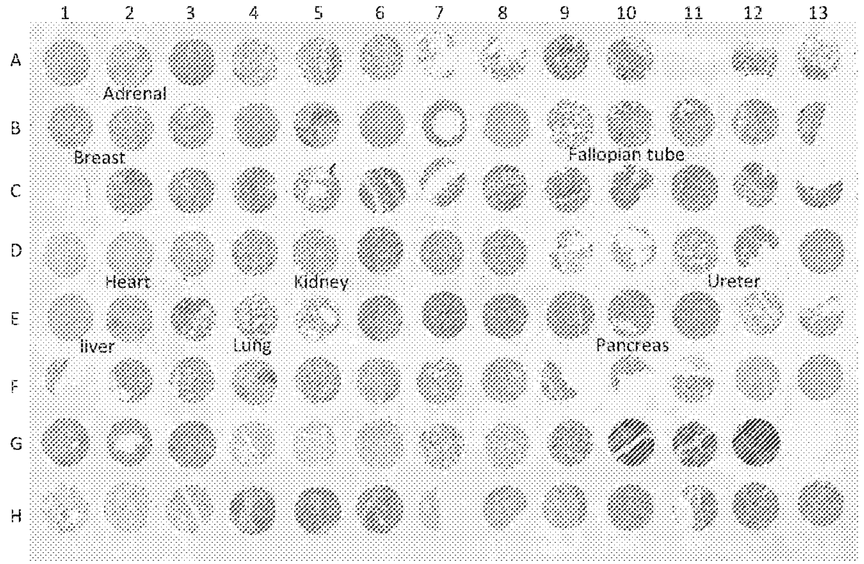


Fig. 133B

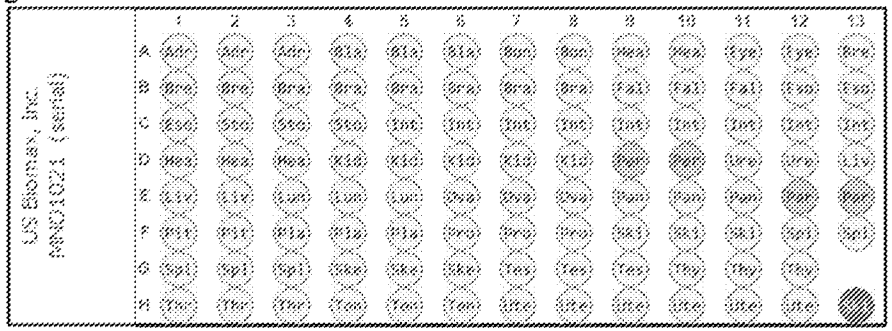


Fig. 133C

Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis	Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis
A1	F	31	Adrenal gland	Normal	E1	M	59	Liver	Normal
A2	M	51	Adrenal gland	Normal	E2	F	27	Liver	Normal
A3	M	53	Adrenal gland	Normal	E3	M	72	Lung	Normal
A4	M	75	Bladder, urinary	Normal	E4	F	55	Lung	Normal
A5	M	72	Bladder, urinary	Normal	E5	M	43	Lung	Normal
A6	M	52	Bladder, urinary	Normal	E6	F	47	Ovary	Normal
A7	M	53	Bone, bone marrow	Normal	E7	F	46	Ovary	Normal
A8	M	43	Bone, bone marrow	Normal	E8	F	40	Ovary	Normal
A9	F	44	Head and neck, salivary gland	Normal	E9	M	42	Pancreas	Normal
A10	M	18	Head and neck, salivary gland	Normal	E10	F	26	Pancreas	Normal
A11	M	55	Eye	Normal	E11	F	59	Pancreas	Normal
A12	M	50	Eye	Normal	E12	M	17	Parathyroid	Adenoma
A13	F	35	Breast	Normal	E13	M	72	Parathyroid	Adenoma
B1	F	38	Breast	Normal	F1	F	3	Pituitary gland	Normal
B2	F	33	Breast	Normal	F2	F		Pituitary gland	Normal
B3	M	58	Brain, cerebellum	Normal	F3	F	32	Placenta	Normal
B4	M	65	Brain, cerebellum	Normal	F4	F	30	Placenta	Normal
B5	F		Brain, cerebellum	Normal	F5	F	27	Placenta	Normal
B6	M	58	Brain, cerebral cortex	Normal	F6	M	64	Prostate	Normal
B7	M	65	Brain, cerebral cortex	Normal	F7	M	65	Prostate	Normal
B8	F		Brain, cerebral cortex	Normal	F8	M	65	Prostate	Normal
B9	F	42	Fallopian tube	Normal	F9	F	32	Skin	Normal
B10	F	32	Fallopian tube	Normal	F10	F	68	Skin	Normal
B11	F	24	Fallopian tube	Normal	F11	M	28	Skin	Normal
B12	M	45	Esophagus	Normal	F12	M	47	Spinal cord	Normal
B13	F	68	Esophagus	Normal	F13	M	56	Spinal cord	Normal
C1	M	54	Esophagus	Normal	G1	M	27	Spleen	Normal
C2	M	45	Stomach	Normal	G2	M	60	Spleen	Normal
C3	M	49	Stomach	Normal	G3	M	31	Spleen	Normal
C4	M	77	Stomach	Normal	G4	F	60	Skeletal muscle	Normal
C5	M	45	Intestine, small intestine	Normal	G5	F	49	Skeletal muscle	Normal
C6	F	75	Intestine, small intestine	Normal	G6	M	70	Skeletal muscle	Normal
C7	F	75	Intestine, small intestine	Normal	G7	M	43	Testis	Normal
C8	M	2	Intestine, colon	Normal	G8	M	30	Testis	Normal
C9	M	46	Intestine, colon	Normal	G9	M	77	Testis	Normal
C10	M	74	Intestine, colon	Normal	G10	M	15	Thymus	Normal
C11	F	47	Intestine, rectum	Normal	G11	M	28	Thymus	Normal
C12	F	75	Intestine, rectum	Normal	G12	F	9	Thymus	Normal
C13	M	66	Intestine, rectum	Normal	G13	-	-	-	-
D1	M	56	Heart	Normal	H1	F	26	Thyroid	Normal
D2	M	46	Heart	Normal	H2	F	37	Thyroid	Normal
D3	F	34	Heart	Normal	H3	F	51	Thyroid	Normal
D4	F	52	Kidney, cortex	Normal	H4	M	46	Tonsil	Normal
D5	M	23	Kidney, cortex	Normal	H5	M	37	Tonsil	Normal
D6	M	63	Kidney, cortex	Normal	H6	M	13	Tonsil	Normal
D7	F	52	Kidney, medulla	Normal	H7	F	38	Uterus, cervix	Normal
D8	M	23	Kidney, medulla	Normal	H8	F	35	Uterus, cervix	Normal
D9	M	59	Peripheral nerve	Schwannoma	H9	F	44	Uterus, cervix	Normal
D10	F	29	Peripheral nerve	Schwannoma	H10	F	38	Uterus, endometrium	Normal
D11	F	44	Ureter	Normal	H11	F	41	Uterus, endometrium	Normal
D12	F	42	Ureter	Normal	H12	F	46	Uterus, endometrium	Normal
D13	F	57	Liver	Normal	H13	M	58	Skin	Malignant melanoma (tissue marker)

Figure 133A-133C

PSMGFR-antibody 18B4 IgG 10 ug/mL

FDA Normal tissue array MNO1021

Fig. 134A
Normal Adrenal Gland

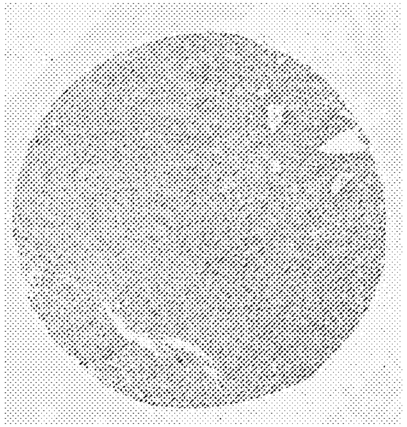


Fig. 134B
Normal Breast

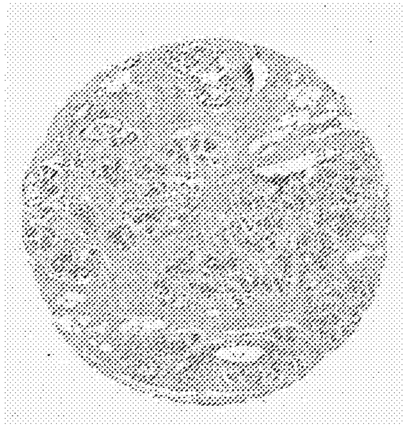


Fig. 134C
Normal Fallopian Tubes

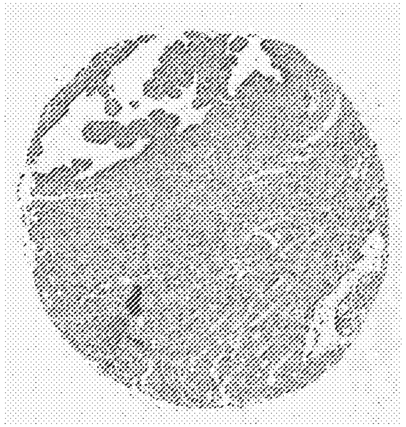


Fig. 134D
Normal Kidney

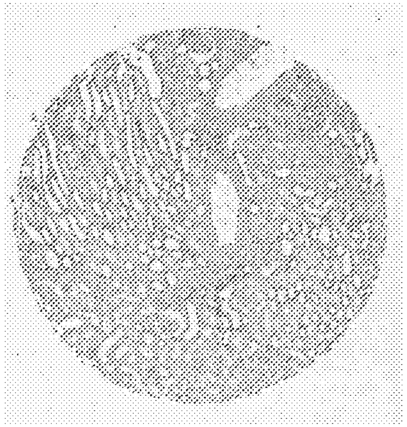


Fig. 134E

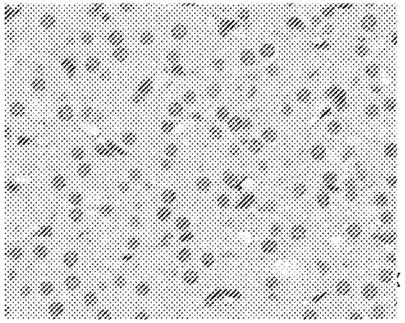


Fig. 134F

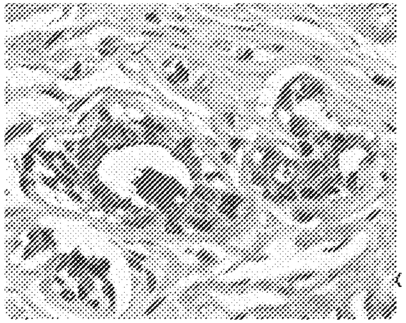


Fig. 134G

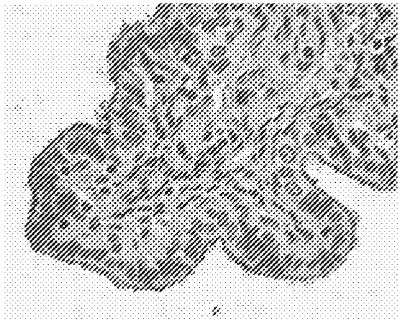


Fig. 134H

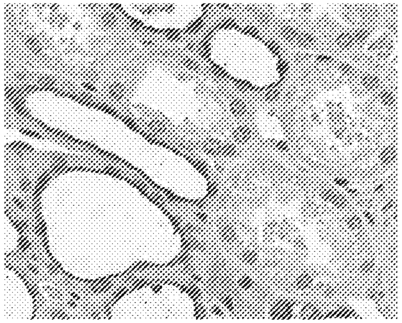


Figure 134A-134H

PSMGFR-antibody 18B4 IgG 10 ug/mL

FDA Normal tissue array MNO1021

Fig. 134I
Normal Heart

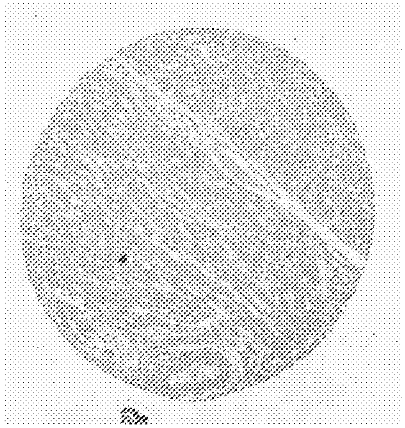


Fig. 134J
Normal Liver

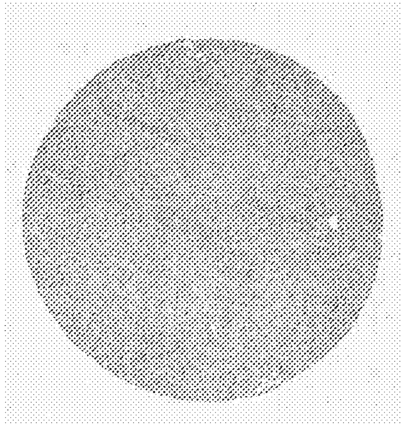


Fig. 134K
Normal Lung

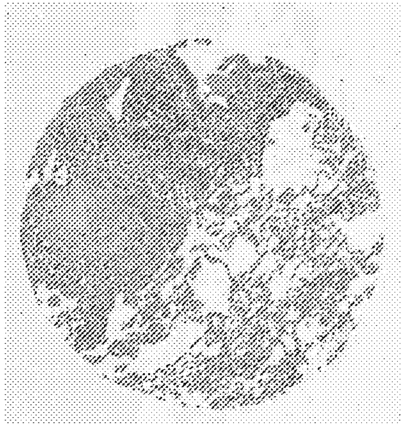


Fig. 134L
Normal Ureter

Fig. 134M

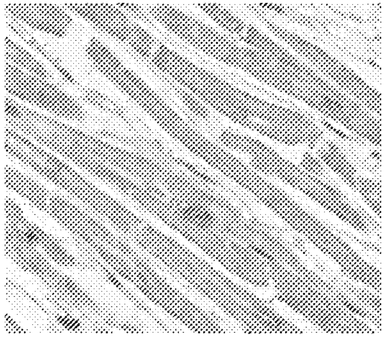


Fig. 134N

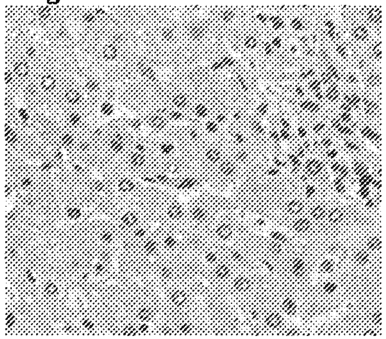


Fig. 134O

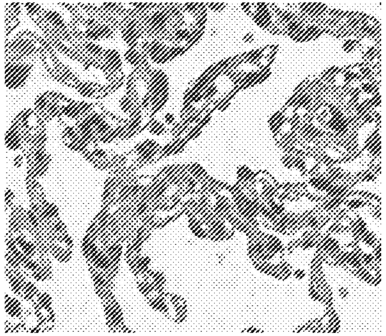


Fig. 134P

Figure 134I-134P

PSMGFR-antibody 18B4 IgG 10 ug/mL
FDA Normal tissue array MNO1021

Fig. 134Q
Normal eye

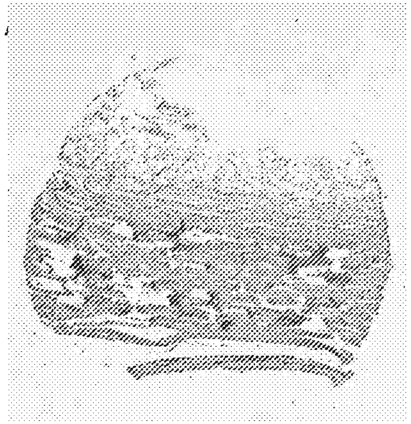


Fig. 134R
Normal Cerebral cortex

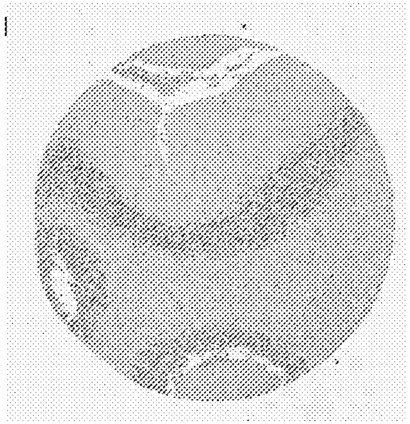


Fig. 134S
Normal Bone marrow

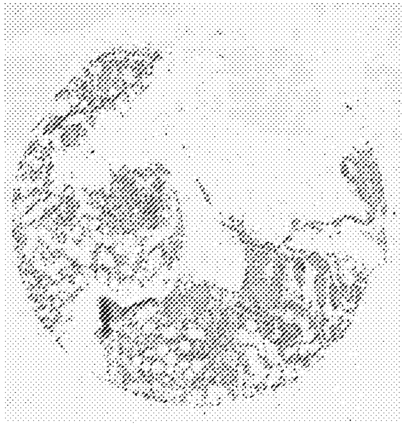


Fig. 134T
Normal Skeletal muscle

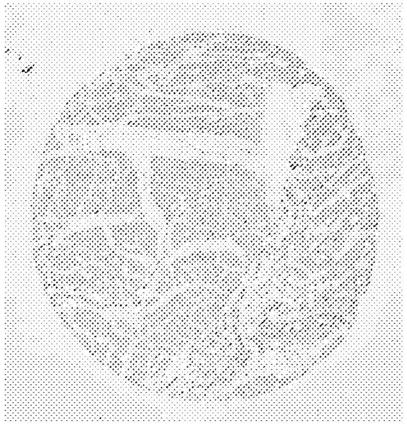


Fig. 134U

Fig. 134V

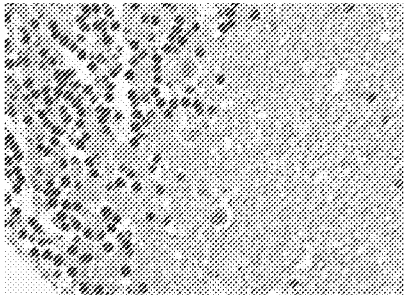


Fig. 134W

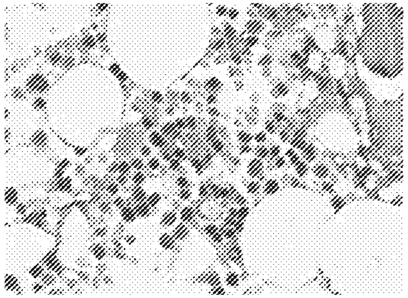


Fig. 134X

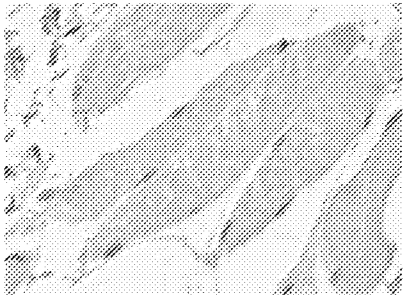


Figure 134Q-134X

PSMGFR-antibody 18B4 10 ug/mL

Breast cancer tissue array BR1141

Fig. 135A

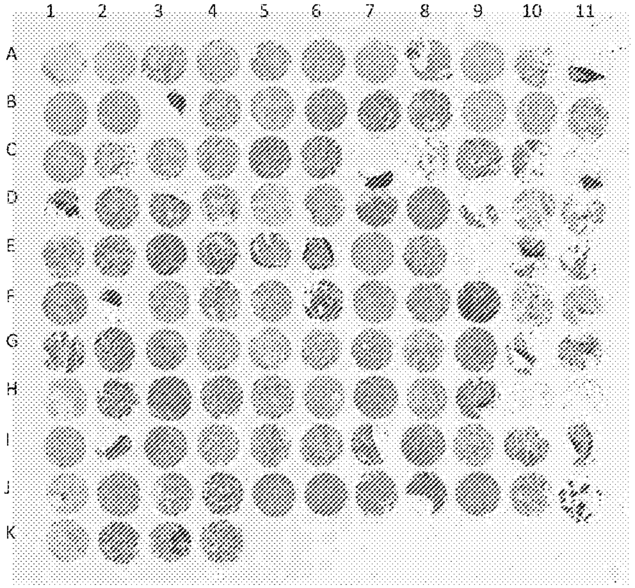
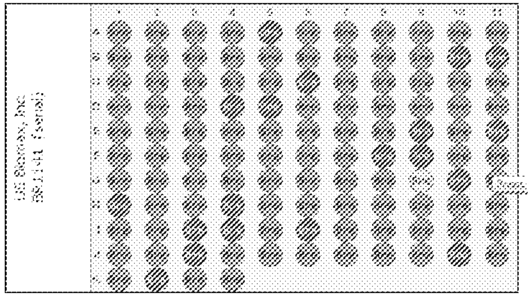
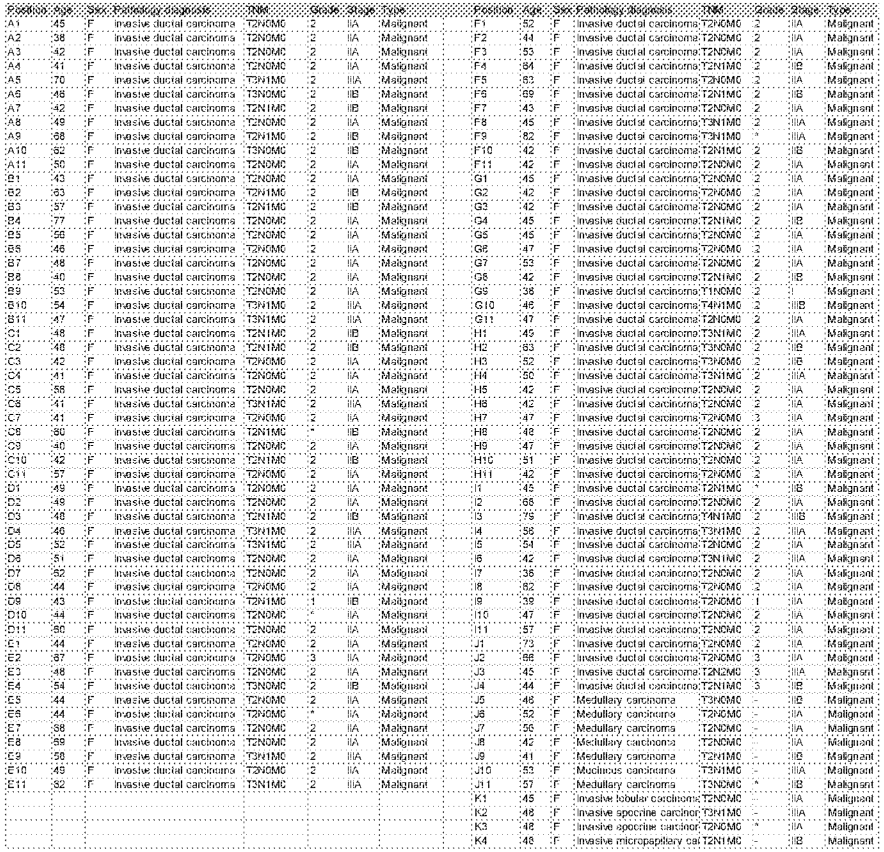


Fig. 135B



Legend: Ore - Breast
- Malignant tumor (stage I), - Malignant tumor (stage IIA), - Malignant tumor (stage IIB), - Malignant tumor (stage IIIA), - Malignant tumor (stage IIIB)

Fig. 135C



Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type
A1	45	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A2	38	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A3	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A4	41	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A5	70	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
A6	46	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
A7	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
A8	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A9	68	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
A10	62	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
A11	50	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B1	43	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B2	63	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
B3	57	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
B4	77	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B5	56	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B6	46	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B7	48	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B8	40	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B9	53	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B10	54	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
B11	47	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
C1	48	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
C2	48	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
C3	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C4	41	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C5	56	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C6	41	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
C7	41	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C8	60	F	Invasive ductal carcinoma	T2N1M0	*	IIB	Malignant
C9	40	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C10	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
C11	57	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D1	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D2	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D3	48	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
D4	46	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
D5	52	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
D6	51	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D7	62	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D8	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D9	43	F	Invasive ductal carcinoma	T2N1M0	1	IIB	Malignant
D10	44	F	Invasive ductal carcinoma	T2N0M0	*	IIA	Malignant
D11	60	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E1	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E2	67	F	Invasive ductal carcinoma	T2N0M0	3	IIA	Malignant
E3	48	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E4	54	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
E5	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E6	44	F	Invasive ductal carcinoma	T2N0M0	*	IIA	Malignant
E7	38	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E8	59	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E9	58	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
E10	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E11	32	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
F1	52	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F2	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F3	53	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F4	64	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
F5	63	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F6	69	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
F7	43	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F8	45	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
F9	82	F	Invasive ductal carcinoma	T3N1M0	*	IIIA	Malignant
F10	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
F11	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G1	45	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G2	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G3	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G4	45	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
G5	45	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G6	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G7	53	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G8	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
G9	38	F	Invasive ductal carcinoma	T1N0M0	2	I	Malignant
G10	46	F	Invasive ductal carcinoma	T4N1M0	2	IIIB	Malignant
G11	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H1	49	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
H2	63	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
H3	52	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
H4	50	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
H5	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H6	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H7	47	F	Invasive ductal carcinoma	T2N0M0	3	IIA	Malignant
H8	48	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H9	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H10	51	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H11	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I1	45	F	Invasive ductal carcinoma	T2N1M0	*	IIB	Malignant
I2	68	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I3	79	F	Invasive ductal carcinoma	T4N1M0	2	IIIB	Malignant
I4	56	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
I5	54	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I6	42	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
I7	38	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I8	62	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I9	39	F	Invasive ductal carcinoma	T2N0M0	1	IIA	Malignant
I10	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I11	57	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
J1	73	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
J2	66	F	Invasive ductal carcinoma	T2N0M0	3	IIA	Malignant
J3	45	F	Invasive ductal carcinoma	T2N2M0	3	IIIA	Malignant
J4	44	F	Invasive ductal carcinoma	T2N1M0	3	IIB	Malignant
J5	46	F	Medullary carcinoma	T3N0M0	-	IIB	Malignant
J6	52	F	Medullary carcinoma	T2N0M0	-	IIA	Malignant
J7	56	F	Medullary carcinoma	T2N0M0	-	IIA	Malignant
J8	42	F	Medullary carcinoma	T2N0M0	-	IIA	Malignant
J9	41	F	Medullary carcinoma	T2N1M0	-	IIB	Malignant
J10	53	F	Mucinous carcinoma	T3N1M0	-	IIIA	Malignant
J11	57	F	Medullary carcinoma	T3N0M0	*	IIB	Malignant
K1	45	F	Invasive lobular carcinoma	T2N0M0	-	IIA	Malignant
K2	48	F	Invasive apocrine carcinor	T3N1M0	-	IIIA	Malignant
K3	48	F	Invasive apocrine carcinor	T2N0M0	*	IIA	Malignant
K4	48	F	Invasive micropapillary cai	T2N1M0	-	IIB	Malignant

Figure 135A-135C

PSMGFR-antibody 18B4 10 ug/mL

Breast cancer tissue array BR1141

Fig. 136A

Position: A4
Cell Type: Invasive Ductal Carcinoma
Tumor Grade: 2
TNM: T2N0M0

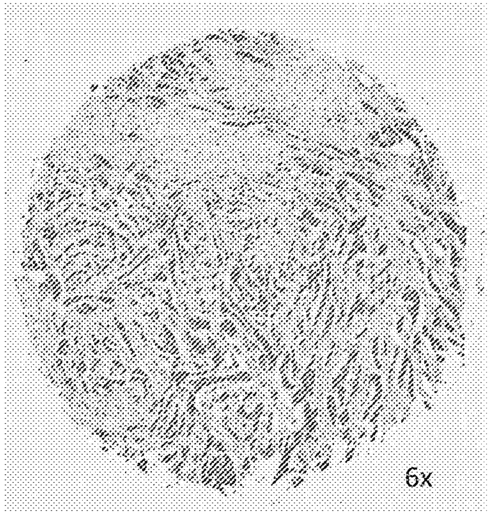


Fig. 136B

Position: G9
Cell Type: Invasive Ductal Carcinoma
Tumor Grade: 2
TNM: T1N0M0

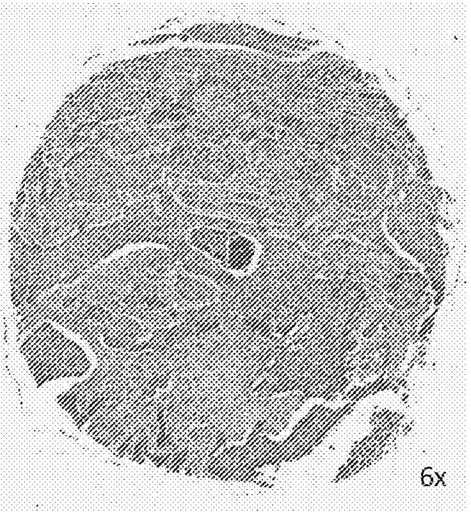


Fig. 136C

Position: G11
Cell Type: Invasive Ductal Carcinoma
Tumor Grade:
TNM: T2N1M0

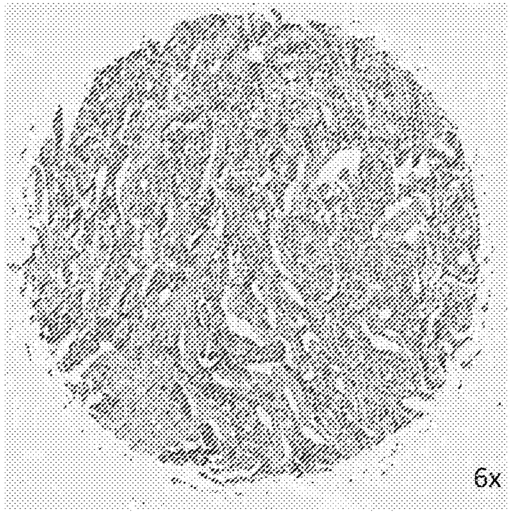


Fig. 136D

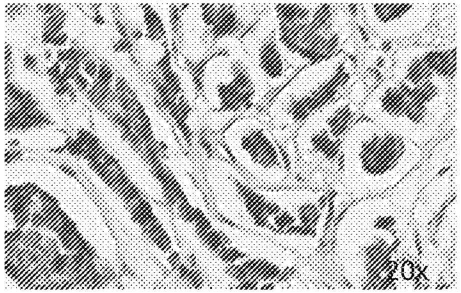


Fig. 136E

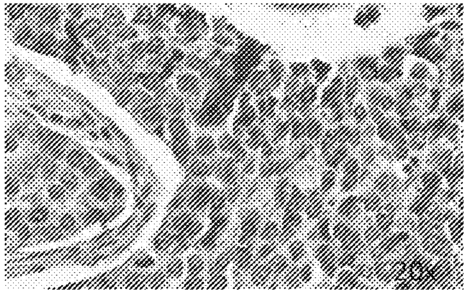


Fig. 136F

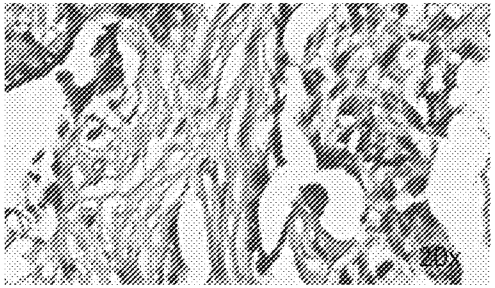


Fig. 136A–136F

PSMGFR antibody 18B4 IgG 10 ug/ml
Esophageal cancer tissue array BC001113

Fig. 137A

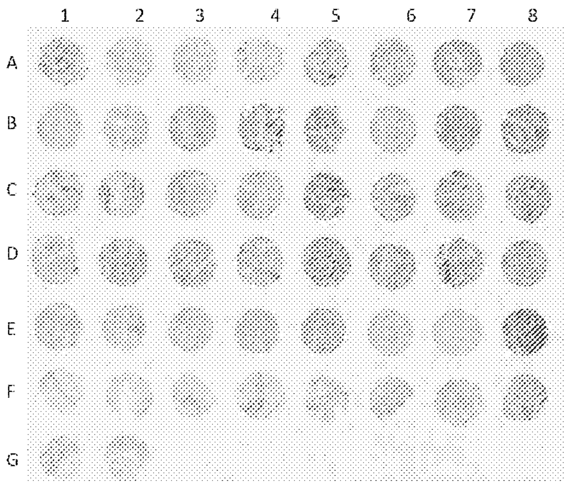


Fig. 137C

Position	Age	Sex	Organ/Anatomic	Pathology diagnosis	Grade	Type	Position	Age	Sex	Organ/Ana	Pathology	Grade	Type
A1	47	F	Esophagus	Adenocarcinoma (smoo	-	malignant	D1	69	M	Cardia	Adenocarc	I	malignant
A2	33	F	Esophagus	Adenocarcinoma	III	malignant	D2	62	M	Cardia	Adenocarc	II	malignant
A3	68	F	Esophagus	Mucinous adenocarcino	I	malignant	D3	65	M	Cardia	Adenocarc	III	malignant
A4	60	M	Esophagus	Adenocarcinoma	III	malignant	D4	72	M	Cardia	Adenocarc	III	malignant
A5	61	M	Esophagus	Adenocarcinoma	II	malignant	D5	74	M	Stomach	Adenocarc	III	malignant
A6	57	M	Esophagus	Adenocarcinoma	III	malignant	D6	51	F	Stomach	Undifferent	IV	malignant
A7	61	M	Esophagus	Undifferentiated adenoc	IV	malignant	D7	51	F	Stomach	Undifferent	IV	malignant
A8	51	F	Esophagus	Adenocarcinoma	III	malignant	D8	53	M	Stomach	Undifferent	IV	malignant
B1	63	M	Esophagus	Undifferentiated adenoc	IV	malignant	E1	64	M	Cardia	Adenocarc	III	malignant
B2	67	F	Esophagus	Adenocarcinoma	III	malignant	E2	70	M	Cardia	Adenocarc	II	malignant
B3	72	M	Cardia	Adenocarcinoma	I	malignant	E3	73	M	Cardia	Undifferent	IV	malignant
B4	36	M	Cardia	Adenocarcinoma	I	malignant	E4	50	M	Cardia	Adenocarc	I	malignant
B5	55	F	Cardia	Adenocarcinoma	II	malignant	E5	64	M	Cardia	Adenocarc	III	malignant
B6	62	M	Cardia	Adenocarcinoma	III	malignant	E6	54	F	Cardia	Cancer adj	-	malignant
B7	64	F	Cardia	Undifferentiated adenoc	IV	malignant	E7	43	M	Cardia	Adenocarc	I	malignant
B8	67	M	Cardia	Adenocarcinoma	I	malignant	E8	59	M	Cardia	Adenocarc	I	malignant
C1	60	F	Cardia	Adenocarcinoma	I	malignant	F1	64	F	Esophagus	Adjacent n	-	normal
C2	66	M	Cardia	Adenocarcinoma	III	malignant	F2	59	M	Esophagus	Adjacent n	-	normal
C3	63	F	Cardia	Adenocarcinoma	II	malignant	F3	67	M	Esophagus	Adjacent n	-	normal
C4	41	M	Cardia	Adenocarcinoma	III	malignant	F4	53	M	Esophagus	Adjacent n	-	normal
C5	70	M	Stomach	Adenocarcinoma	II	malignant	F5	43	M	Esophagus	Adjacent n	-	normal
C6	30	F	Stomach	Adenocarcinoma	II-III	malignant	F6	64	M	Cardia	Adjacent n	-	normal
C7	61	M	Cardia	Adenocarcinoma	II-III	malignant	F7	71	M	Cardia	Adjacent n	-	normal
C8	64	M	Cardia	Adenocarcinoma	III	malignant	F8	66	M	Esophagus	Adjacent n	-	normal
							G1	61	M	Cardia	Adjacent n	-	normal
							G2	56	F	Cardia	Adjacent n	-	normal

Fig. 137B

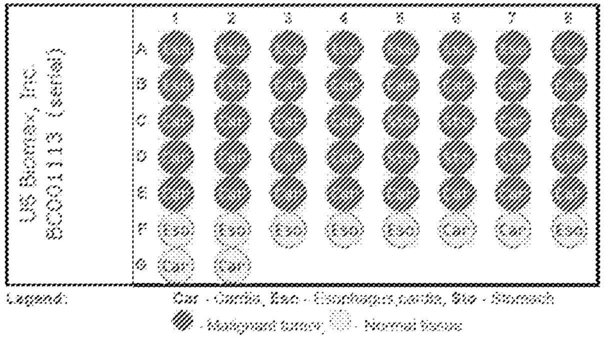


Figure 137A-137C

PSMGFR antibody 18B4 IgG 10 ug/ml

Esophageal cancer tissue array BC001113

Fig. 138A
Esophageal cancer

Fig. 138B
Esophageal cancer

Fig. 138C
Esophageal cancer

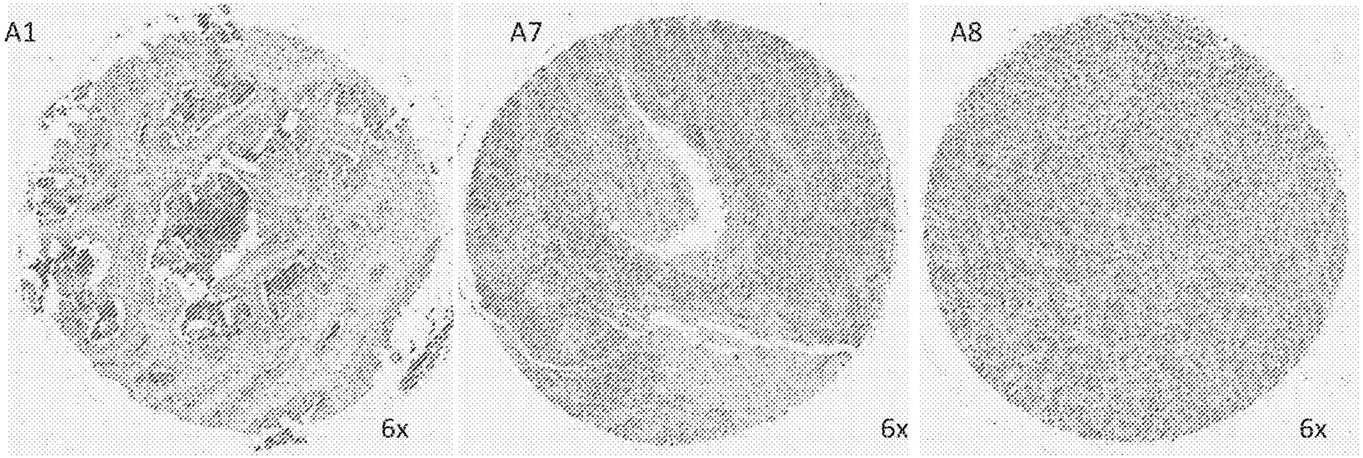


Fig. 138D

Fig. 138E

Fig. 138F

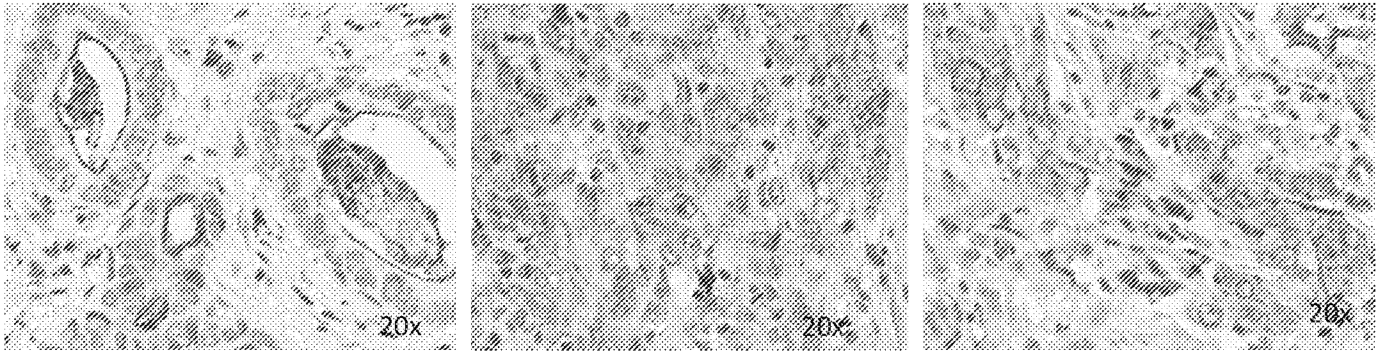


Fig. 138A–138F

PSMGFR-antibody 18G12 IgG 10 ug/mL

FDA Normal tissue array MNO1021

Fig. 139A

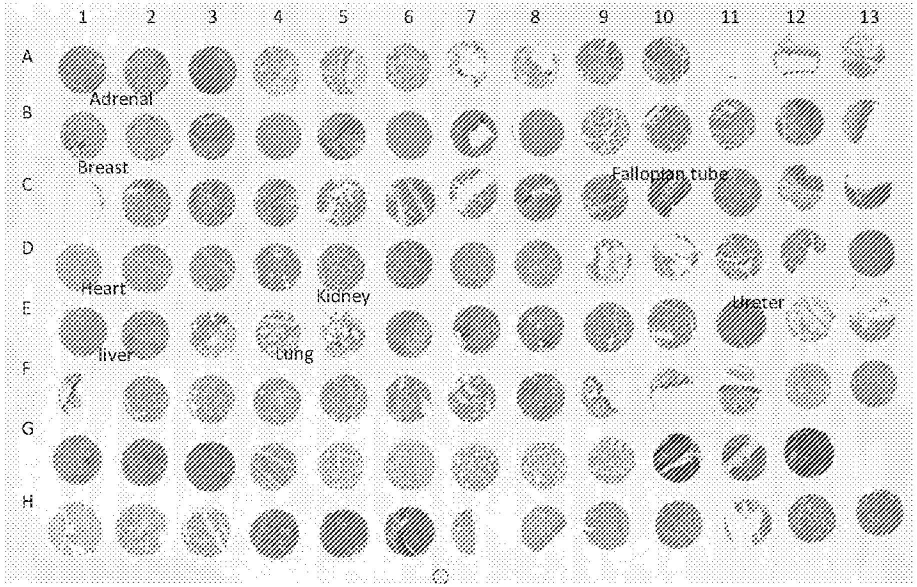


Fig. 139B

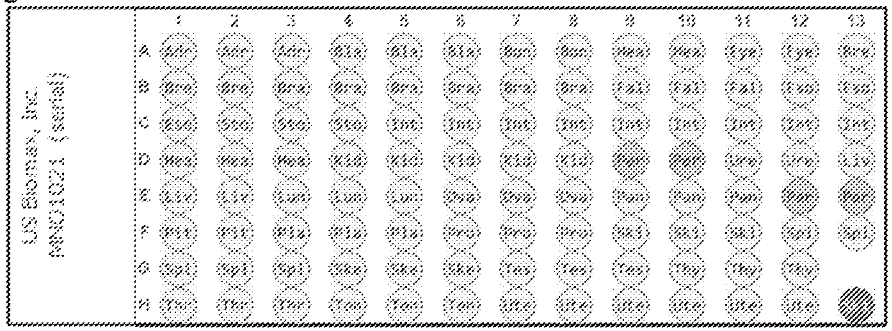


Fig. 139C

Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis	Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis
A1	F	31	Adrenal gland	Normal	E1	M	59	Liver	Normal
A2	M	51	Adrenal gland	Normal	E2	F	27	Liver	Normal
A3	M	53	Adrenal gland	Normal	E3	M	72	Lung	Normal
A4	M	75	Bladder, umary	Normal	E4	F	55	Lung	Normal
A5	M	72	Bladder, umary	Normal	E5	M	43	Lung	Normal
A6	M	52	Bladder, umary	Normal	E6	F	47	Ovary	Normal
A7	M	53	Bone, bone marrow	Normal	E7	F	46	Ovary	Normal
A8	M	43	Bone, bone marrow	Normal	E8	F	40	Ovary	Normal
A9	F	44	Head and neck, salivary gland	Normal	E9	M	42	Pancreas	Normal
A10	M	18	Head and neck, salivary gland	Normal	E10	F	26	Pancreas	Normal
A11	M	55	Eye	Normal	E11	F	59	Pancreas	Normal
A12	M	50	Eye	Normal	E12	M	17	Parathyroid	Adenoma
A13	F	35	Breast	Normal	E13	M	72	Parathyroid	Adenoma
B1	F	38	Breast	Normal	F1	F	3	Pituitary gland	Normal
B2	F	33	Breast	Normal	F2	F		Pituitary gland	Normal
B3	M	58	Brain, cerebellum	Normal	F3	F	32	Placenta	Normal
B4	M	65	Brain, cerebellum	Normal	F4	F	30	Placenta	Normal
B5	F		Brain, cerebellum	Normal	F5	F	27	Placenta	Normal
B6	M	56	Brain, cerebral cortex	Normal	F6	M	64	Prostate	Normal
B7	M	65	Brain, cerebral cortex	Normal	F7	M	65	Prostate	Normal
B8	F		Brain, cerebral cortex	Normal	F8	M	65	Prostate	Normal
B9	F	42	Fallopian tube	Normal	F9	F	32	Skin	Normal
B10	F	32	Fallopian tube	Normal	F10	F	68	Skin	Normal
B11	F	24	Fallopian tube	Normal	F11	M	26	Skin	Normal
B12	M	45	Esophagus	Normal	F12	M	47	Spinal cord	Normal
B13	F	68	Esophagus	Normal	F13	M	58	Spinal cord	Normal
C1	M	54	Esophagus	Normal	G1	M	27	Spleen	Normal
C2	M	45	Stomach	Normal	G2	M	60	Spleen	Normal
C3	M	49	Stomach	Normal	G3	M	31	Spleen	Normal
C4	M	77	Stomach	Normal	G4	F	60	Skeletal muscle	Normal
C5	M	45	Intestine, small intestine	Normal	G5	F	49	Skeletal muscle	Normal
C6	F	75	Intestine, small intestine	Normal	G6	M	70	Skeletal muscle	Normal
C7	F	75	Intestine, small intestine	Normal	G7	M	43	Testis	Normal
C8	M	2	Intestine, colon	Normal	G8	M	30	Testis	Normal
C9	M	46	Intestine, colon	Normal	G9	M	77	Testis	Normal
C10	M	74	Intestine, colon	Normal	G10	M	15	Thymus	Normal
C11	F	47	Intestine, rectum	Normal	G11	M	28	Thymus	Normal
C12	F	75	Intestine, rectum	Normal	G12	F	9	Thymus	Normal
C13	M	66	Intestine, rectum	Normal	G13	-	-	-	-
D1	M	58	Heart	Normal	H1	F	26	Thyroid	Normal
D2	M	46	Heart	Normal	H2	F	37	Thyroid	Normal
D3	F	34	Heart	Normal	H3	F	51	Thyroid	Normal
D4	F	52	Kidney, cortex	Normal	H4	M	46	Tonsil	Normal
D5	M	23	Kidney, cortex	Normal	H5	M	37	Tonsil	Normal
D6	M	63	Kidney, cortex	Normal	H6	M	13	Tonsil	Normal
D7	F	52	Kidney, medulla	Normal	H7	F	38	Uterus, cervix	Normal
D8	M	23	Kidney, medulla	Normal	H8	F	35	Uterus, cervix	Normal
D9	M	59	Peripheral nerve	Schwannoma	H9	F	44	Uterus, cervix	Normal
D10	F	29	Peripheral nerve	Schwannoma	H10	F	38	Uterus, endometrium	Normal
D11	F	44	Ureter	Normal	H11	F	41	Uterus, endometrium	Normal
D12	F	42	Ureter	Normal	H12	F	46	Uterus, endometrium	Normal
D13	F	57	Liver	Normal	H13	M	58	Skin	Malignant melanoma (tissue marker)

Figure 139A-139C

PSMGFR-antibody 18G12 IgG 10 ug/mL

FDA Normal tissue array MNO1021

Fig. 140A
Normal Adrenal Gland

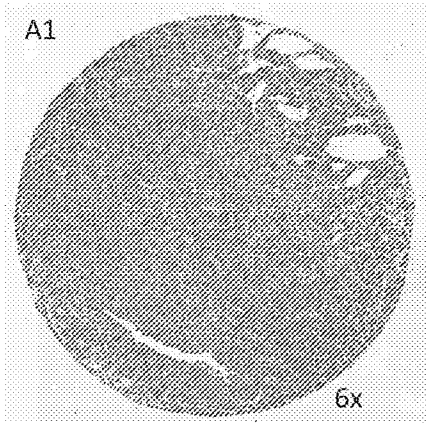


Fig. 140B
Normal Breast

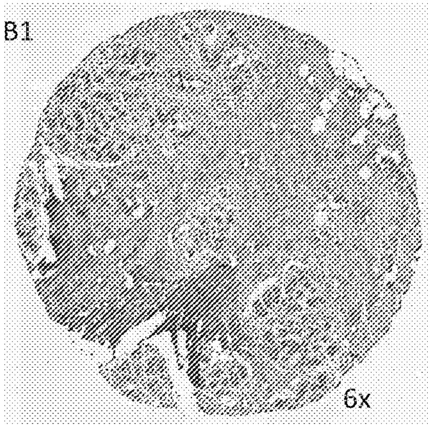


Fig. 140C
Normal Fallopian Tubes

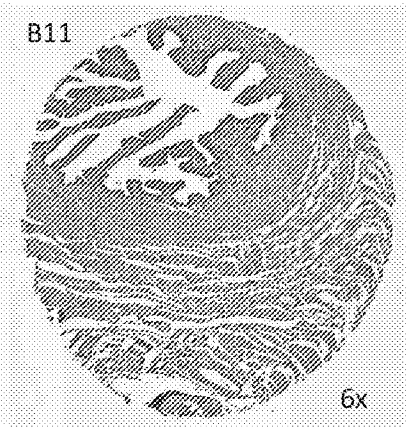


Fig. 140D
Normal Kidney

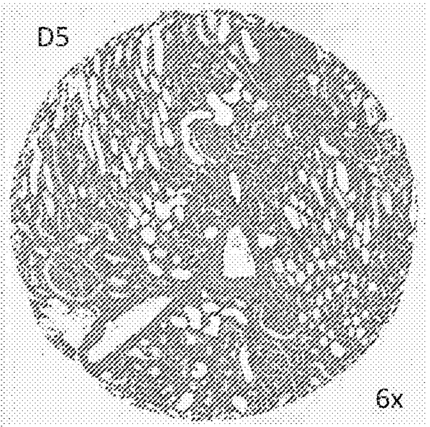


Fig. 140E

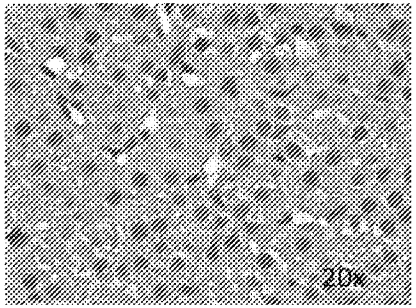


Fig. 140F

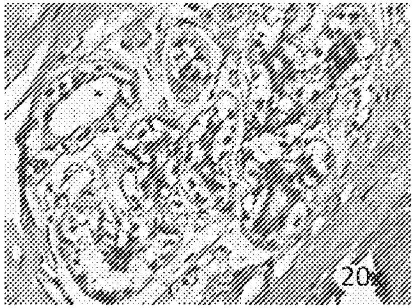


Fig. 140G

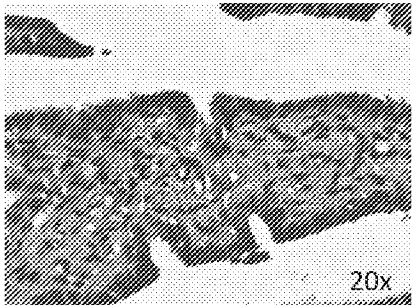


Fig. 140H

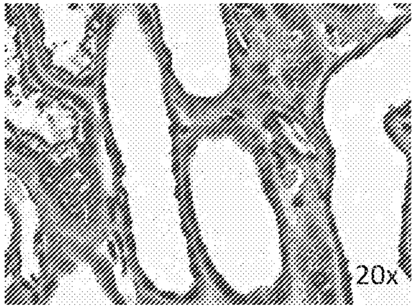


Figure 140A-140H

PSMGFR-antibody 18G12 IgG 10 ug/mL

FDA Normal tissue array MNO1021

Fig. 140I
Normal Heart

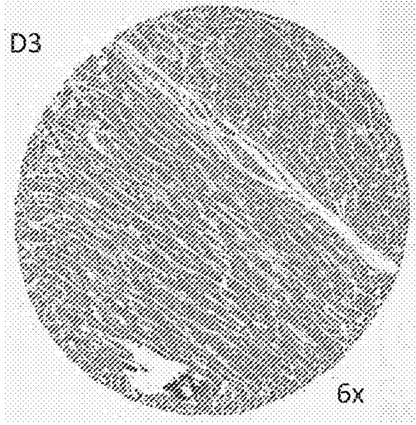


Fig. 140J
Normal Liver

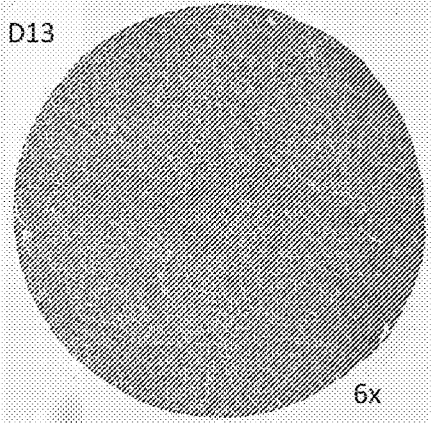


Fig. 140K
Normal Lung

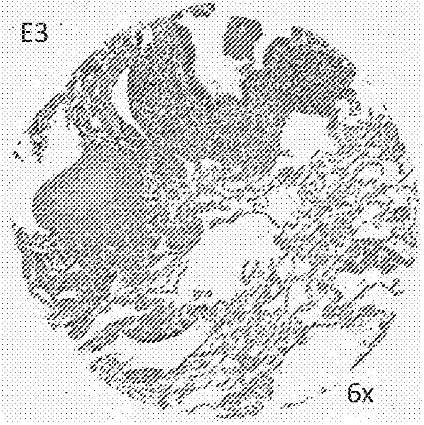


Fig. 140L
Normal Ureter

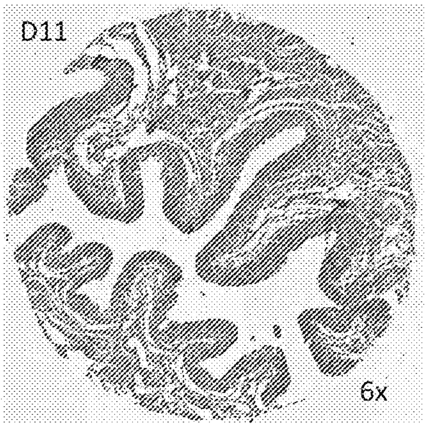


Fig. 140M

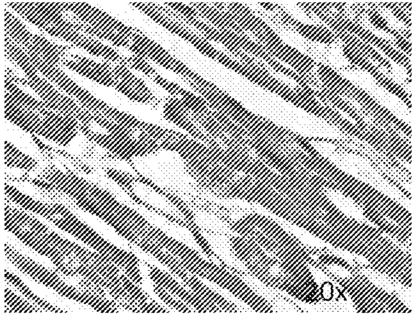


Fig. 140N

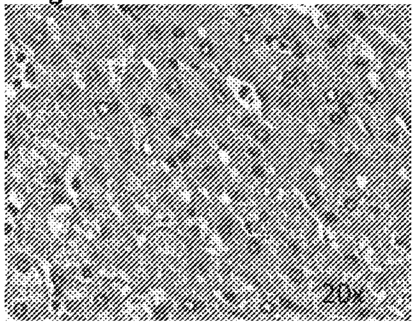


Fig. 140O

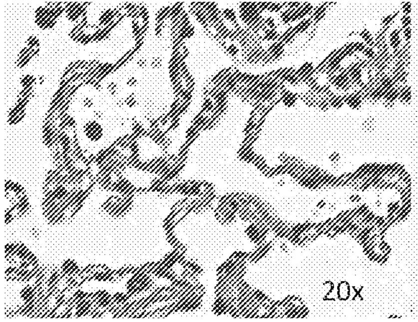


Fig. 140P

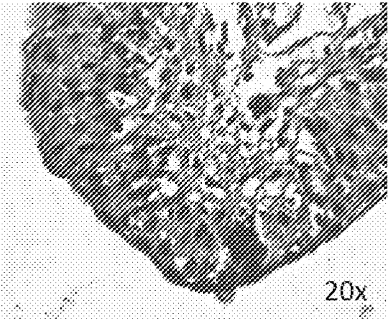


Figure 140I-140P

PSMGFR-antibody 18G12 IgG 10 ug/mL
FDA Normal tissue array MNO1021

Fig. 140Q
Normal eye

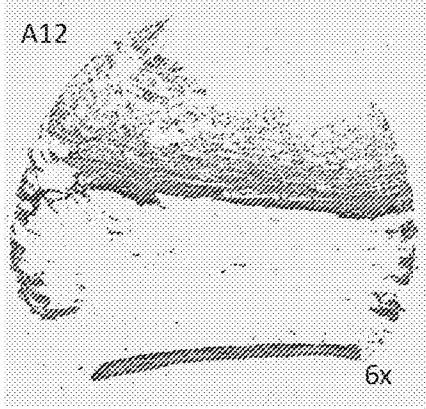


Fig. 140R
Normal Cerebral cortex

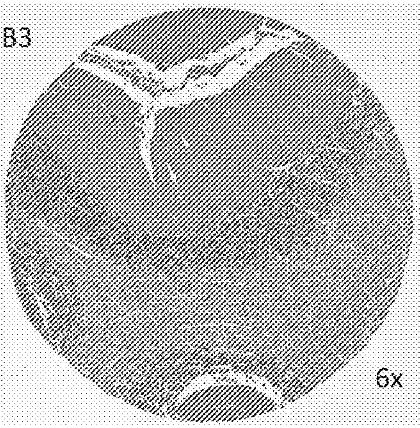


Fig. 140S
Normal Bone marrow

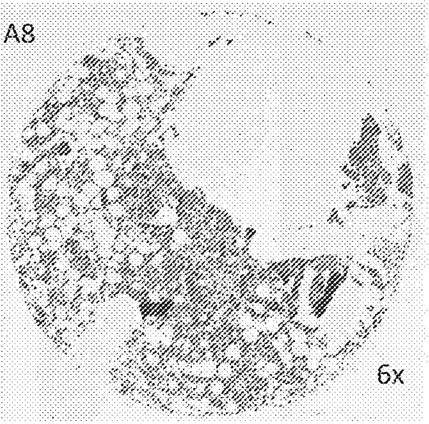


Fig. 140T
Normal Skeletal muscle

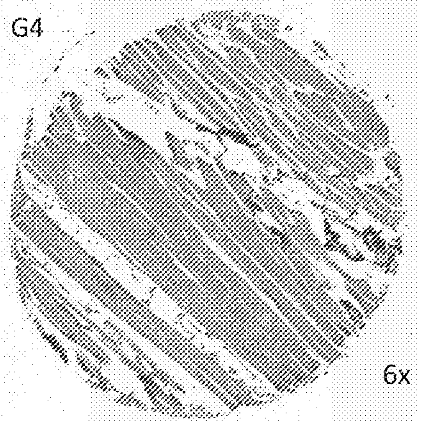


Fig. 140U

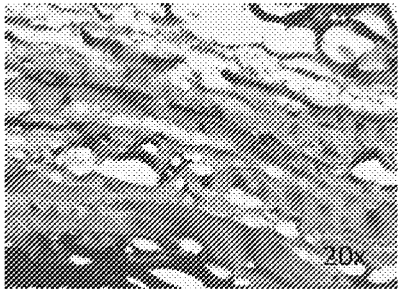


Fig. 140V

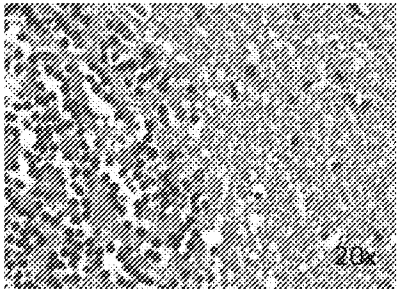


Fig. 140W

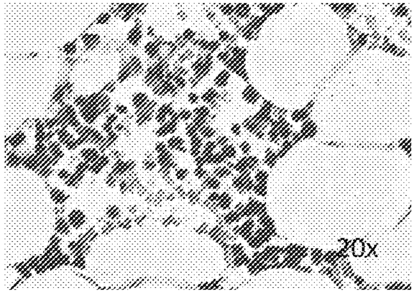


Fig. 140X

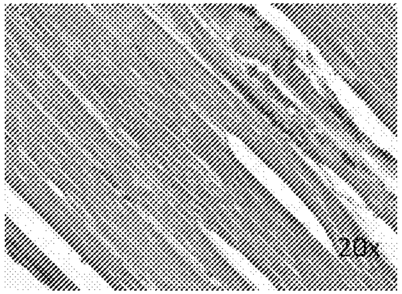


Figure 140Q-140X

PSMGFR-antibody 18G12 15 ug/mL

Breast cancer tissue array BR1141

Fig. 141A

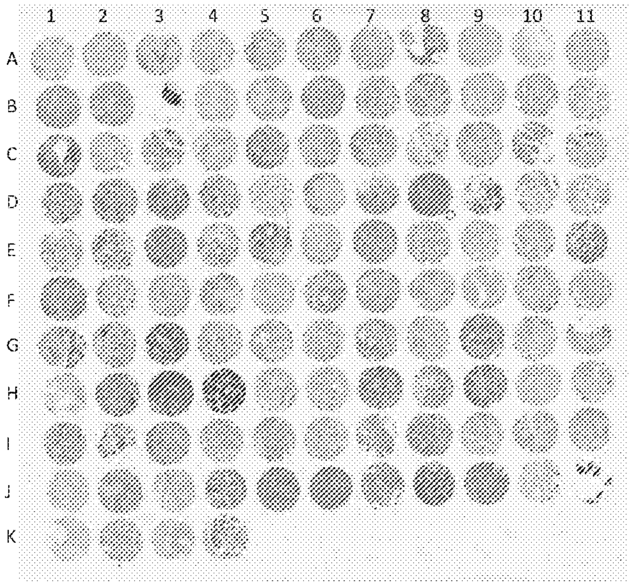


Fig. 141B

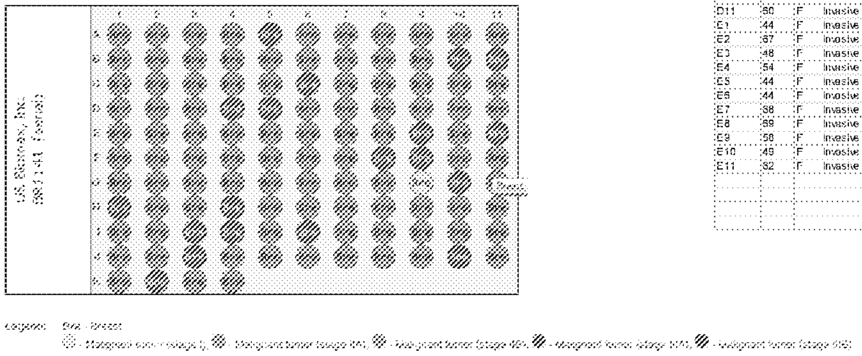
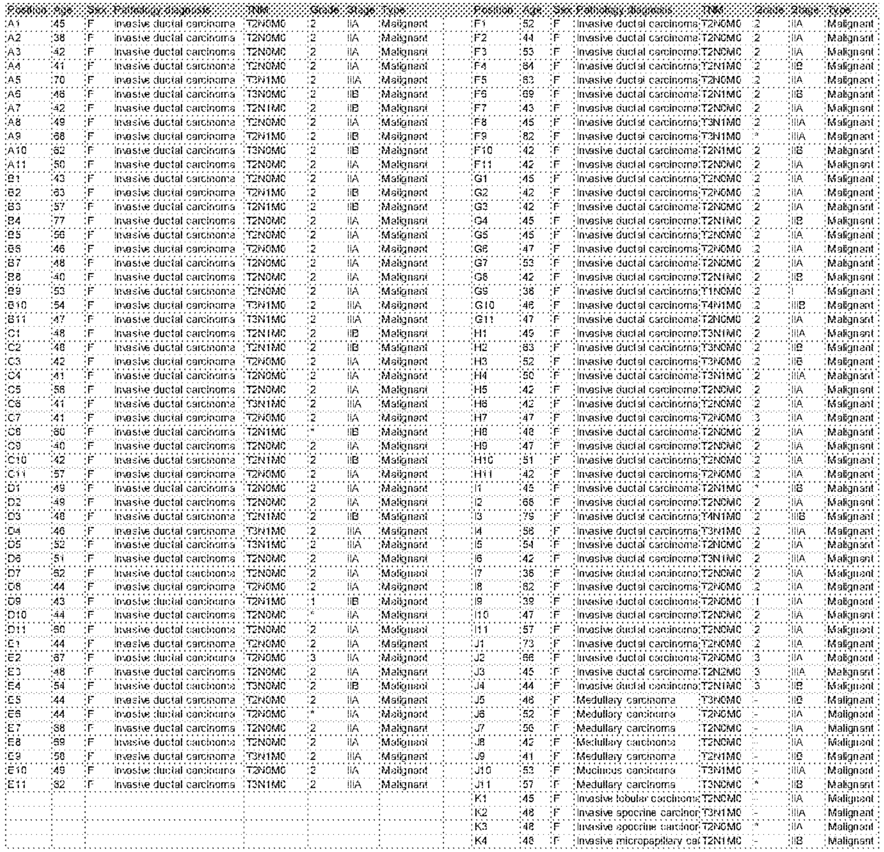


Fig. 141C



Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type	Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type
A1	45	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	F1	52	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A2	38	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	F2	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A3	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	F3	53	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A4	41	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	F4	64	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
A5	70	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant	F5	63	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A6	46	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant	F6	69	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
A7	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant	F7	43	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A8	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	F8	45	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
A9	68	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant	F9	82	F	Invasive ductal carcinoma	T3N1M0	*	IIIA	Malignant
A10	62	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant	F10	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
A11	50	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	F11	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B1	43	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	G1	45	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B2	63	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant	G2	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B3	57	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant	G3	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B4	77	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	G4	45	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
B5	56	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	G5	45	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B6	46	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	G6	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B7	48	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	G7	53	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B8	40	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	G8	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
B9	53	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	G9	38	F	Invasive ductal carcinoma	T1N0M0	2	I	Malignant
B10	54	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant	G10	46	F	Invasive ductal carcinoma	T4N1M0	2	IIIB	Malignant
B11	47	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant	G11	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C1	48	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant	H1	49	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
C2	48	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant	H2	63	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
C3	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	H3	52	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
C4	41	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	H4	50	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
C5	56	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	H5	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C6	41	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant	H6	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C7	41	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	H7	47	F	Invasive ductal carcinoma	T2N0M0	3	IIA	Malignant
C8	60	F	Invasive ductal carcinoma	T2N1M0	*	IIB	Malignant	H8	48	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C9	40	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	H9	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C10	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant	H10	51	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C11	57	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	H11	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D1	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	I1	45	F	Invasive ductal carcinoma	T2N1M0	*	IIB	Malignant
D2	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	I2	68	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D3	48	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant	I3	79	F	Invasive ductal carcinoma	T4N1M0	2	IIIB	Malignant
D4	46	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant	I4	56	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
D5	52	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant	I5	54	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D6	51	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	I6	42	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
D7	62	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	I7	38	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D8	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	I8	62	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D9	43	F	Invasive ductal carcinoma	T2N1M0	1	IIB	Malignant	I9	39	F	Invasive ductal carcinoma	T2N0M0	1	IIA	Malignant
D10	44	F	Invasive ductal carcinoma	T2N0M0	*	IIA	Malignant	I10	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D11	60	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	I11	57	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E1	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	J1	73	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E2	67	F	Invasive ductal carcinoma	T2N0M0	3	IIA	Malignant	J2	66	F	Invasive ductal carcinoma	T2N0M0	3	IIA	Malignant
E3	48	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	J3	45	F	Invasive ductal carcinoma	T2N2M0	3	IIIA	Malignant
E4	54	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant	J4	44	F	Invasive ductal carcinoma	T2N1M0	3	IIB	Malignant
E5	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	J5	46	F	Medullary carcinoma	T3N0M0	-	IIB	Malignant
E6	44	F	Invasive ductal carcinoma	T2N0M0	*	IIA	Malignant	J6	52	F	Medullary carcinoma	T2N0M0	-	IIA	Malignant
E7	38	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	J7	56	F	Medullary carcinoma	T2N0M0	-	IIA	Malignant
E8	59	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	J8	42	F	Medullary carcinoma	T2N0M0	-	IIA	Malignant
E9	58	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant	J9	41	F	Medullary carcinoma	T2N1M0	-	IIB	Malignant
E10	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	J10	53	F	Mucinous carcinoma	T3N1M0	-	IIIA	Malignant
E11	32	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant	J11	57	F	Medullary carcinoma	T3N0M0	*	IIB	Malignant
								K1	45	F	Invasive lobular carcinoma	T2N0M0	-	IIA	Malignant
								K2	48	F	Invasive apocrine carcinor	T3N1M0	-	IIIA	Malignant
								K3	48	F	Invasive apocrine carcinor	T2N0M0	*	IIA	Malignant
								K4	48	F	Invasive micropapillary cal	T2N1M0	-	IIB	Malignant

Figure 141A-141C

PSMGFR-antibody 18G12 15 ug/mL

Breast cancer tissue array BR1141

Fig. 142A

Position: C5
Cell Type: Invasive Ductal Carcinoma
Tumor Grade: 2
TNM: T2N0M0

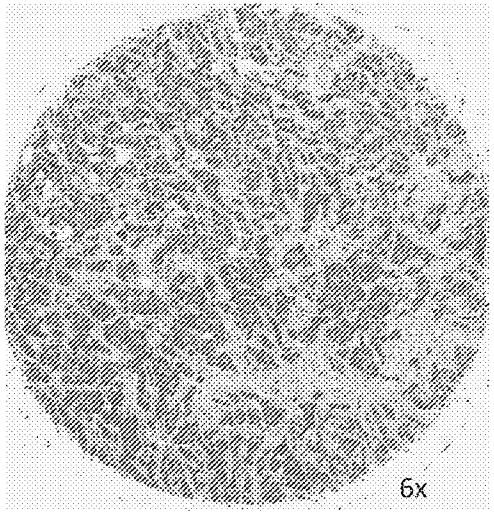


Fig. 142B

Position: G9
Cell Type: Invasive Ductal Carcinoma
Tumor Grade: 2
TNM: T1N0M0

Fig. 142C

Position: I1
Cell Type: Invasive Ductal Carcinoma
Tumor Grade:
TNM: T2N1M0

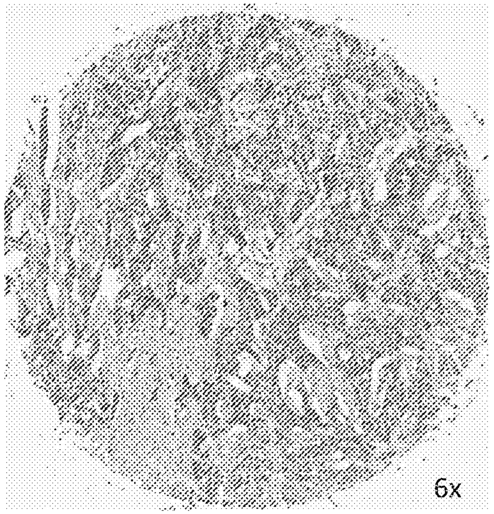


Fig. 142D

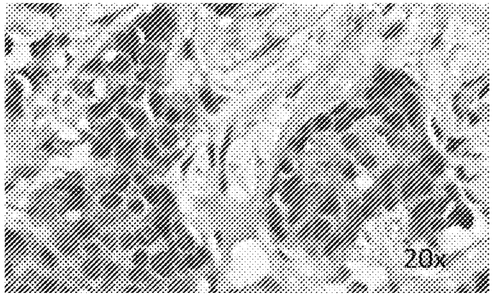


Fig. 142E

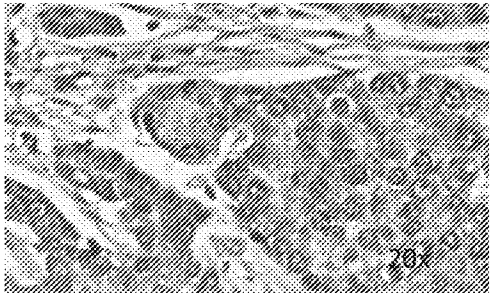


Fig. 142F

Fig. 142A–142F

PSMGFR-antibody 18G12 1.0 – 15 ug/mL

Pancreatic cancer tissue array PA1003

Fig. 143A

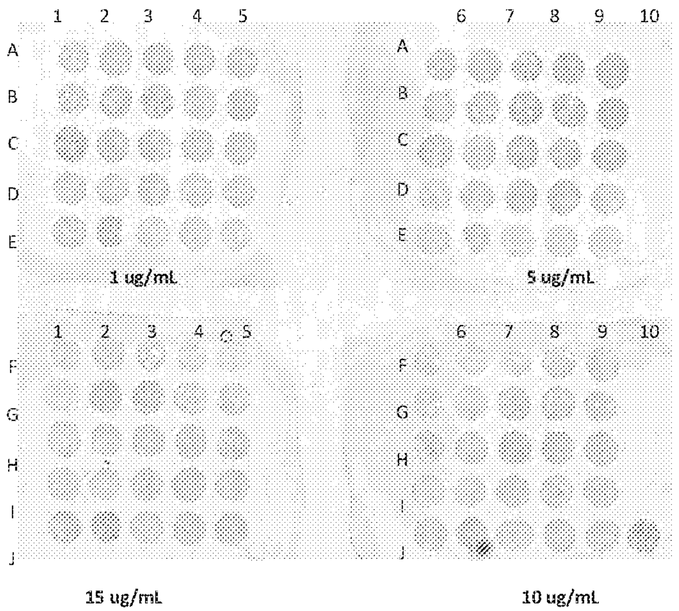


Fig. 143B

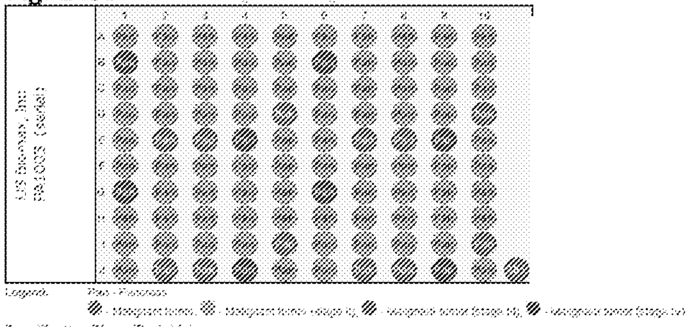


Fig. 143A – 143C

Fig. 143C

Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type	Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type
A1	39	F	Adenocarcinoma	T3N0M0	2	II	malignant	F1	39	F	Adenocarcinoma	T3N0M0	2	II	malignant
A2	44	M	Adenocarcinoma	T3N0M0	2	II	malignant	F2	44	M	Adenocarcinoma	T3N0M0	2	II	malignant
A3	59	M	Adenocarcinoma	T3N0M0	2	II	malignant	F3	59	M	Adenocarcinoma	T3N0M0	2	II	malignant
A4	65	M	Adenocarcinoma	T3N0M0	2	II	malignant	F4	65	M	Adenocarcinoma	T3N0M0	2	II	malignant
A5	53	M	Adenocarcinoma	T3N0M0	2	II	malignant	F5	53	M	Adenocarcinoma	T3N0M0	2	II	malignant
A6	39	F	Adenocarcinoma	T3N0M0	2	II	malignant	F6	39	F	Adenocarcinoma	T3N0M0	2	II	malignant
A7	44	M	Adenocarcinoma	T3N0M0	2	II	malignant	F7	44	M	Adenocarcinoma	T3N0M0	2	II	malignant
A8	59	M	Adenocarcinoma	T3N0M0	2	II	malignant	F8	59	M	Adenocarcinoma	T3N0M0	2	II	malignant
A9	65	M	Adenocarcinoma	T3N0M0	2	II	malignant	F9	65	M	Adenocarcinoma	T3N0M0	-	II	malignant
A10	53	M	Adenocarcinoma	T3N0M0	2	II	malignant	F10	53	M	Adenocarcinoma	T3N0M0	2	II	malignant
B1	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant	G1	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant
B2	52	M	Adenocarcinoma	T3N0M0	1	II	malignant	G2	52	M	Adenocarcinoma	T3N0M0	1	II	malignant
B3	57	M	Adenocarcinoma	T3N0M0	2	II	malignant	G3	57	M	Adenocarcinoma	T3N0M0	2	II	malignant
B4	34	M	Adenocarcinoma	T3N0M0	2	II	malignant	G4	34	M	Adenocarcinoma	T3N0M0	2	II	malignant
B5	72	F	Adenocarcinoma	T3N0M0	2	II	malignant	G5	72	F	Adenocarcinoma	T3N0M0	1	II	malignant
B6	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant	G6	42	M	Adenocarcinoma	T2N0M1	-	IV	malignant
B7	52	M	Adenocarcinoma	T3N0M0	2	II	malignant	G7	52	M	Adenocarcinoma	T3N0M0	2	II	malignant
B8	57	M	Adenocarcinoma	T3N0M0	2	II	malignant	G8	57	M	Adenocarcinoma	T3N0M0	2	II	malignant
B9	34	M	Adenocarcinoma	T3N0M0	1	II	malignant	G9	34	M	Adenocarcinoma	T3N0M0	2	II	malignant
B10	72	F	Adenocarcinoma	T3N0M0	2	II	malignant	G10	72	F	Adenocarcinoma	T3N0M0	2	II	malignant
C1	47	M	Adenocarcinoma	T3N0M0	1	II	malignant	H1	47	M	Adenocarcinoma	T3N0M0	1	II	malignant
C2	64	F	Adenocarcinoma	T3N0M0	1	II	malignant	H2	64	F	Adenocarcinoma	T3N0M0	-	II	malignant
C3	51	M	Adenocarcinoma	T3N0M0	2	II	malignant	H3	51	M	Adenocarcinoma	T3N0M0	2	II	malignant
C4	68	F	Adenocarcinoma	T3N0M0	2	II	malignant	H4	68	F	Adenocarcinoma	T3N0M0	3	II	malignant
C5	41	M	Adenocarcinoma	T3N0M0		II	malignant	H5	41	M	Adenocarcinoma	T3N0M0	2	II	malignant
C6	47	M	Adenocarcinoma	T3N0M0	1	II	malignant	H6	47	M	Adenocarcinoma	T3N0M0	1	II	malignant
C7	64	F	Adenocarcinoma	T3N0M0	2	II	malignant	H7	64	F	Adenocarcinoma	T3N0M0	2	II	malignant
C8	51	M	Adenocarcinoma	T3N0M0	2	II	malignant	H8	51	M	Adenocarcinoma	T3N0M0	-	II	malignant
C9	68	F	Adenocarcinoma	T3N0M0	2	II	malignant	H9	68	F	Adenocarcinoma	T3N0M0	2	II	malignant
C10	41	M	Adenocarcinoma	T3N0M0	2	II	malignant	H10	41	M	Adenocarcinoma	T3N0M0	2	II	malignant
D1	58	F	Adenocarcinoma	T3N0M0	2	II	malignant	I1	58	F	Adenocarcinoma	T3N0M0	2	II	malignant
D2	41	F	Adenocarcinoma	T3N0M0	3	II	malignant	I2	41	F	Adenocarcinoma	T3N0M0	3	II	malignant
D3	72	F	Adenocarcinoma	T3N0M0	3	II	malignant	I3	72	F	Adenocarcinoma	T3N0M0	3	II	malignant
D4	59	M	Adenocarcinoma	T3N0M0	3	II	malignant	I4	59	M	Adenocarcinoma	T3N0M0	3	II	malignant
D5	50	M	Adenocarcinoma	T3N1M0	3	III	malignant	I5	50	M	Adenocarcinoma	T3N1M0	3	III	malignant
D6	58	F	Adenocarcinoma	T3N0M0	2	II	malignant	I6	58	F	Adenocarcinoma	T3N0M0	2	II	malignant
D7	41	F	Adenocarcinoma	T3N0M0	3	II	malignant	I7	41	F	Adenocarcinoma	T3N0M0	2	II	malignant
D8	72	F	Adenocarcinoma	T3N0M0	3	II	malignant	I8	72	F	Adenocarcinoma	T3N0M0	3	II	malignant
D9	59	M	Adenocarcinoma	T3N0M0	3	II	malignant	I9	59	M	Adenocarcinoma	T3N0M0	3	II	malignant
D10	50	M	Adenocarcinoma	T3N1M0	3	III	malignant	I10	50	M	Adenocarcinoma	T3N1M0	3	III	malignant
E1	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant	J1	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant
E2	60	M	Adenocarcinoma	T3N1M0	2--3	III	malignant	J2	60	M	Adenocarcinoma	T3N1M0	2--3	III	malignant
E3	56	M	Adenocarcinoma	T2N1M0	3	III	malignant	J3	56	M	Adenocarcinoma	T2N1M0	3	III	malignant
E4	60	F	Adenocarcinoma	T2N1M1	3	IV	malignant	J4	60	F	Adenocarcinoma	T2N1M1	2	IV	malignant
E5	66	F	Adenocarcinoma	T3N0M0	-	II	malignant	J5	66	F	Adenocarcinoma	T3N0M0	3	II	malignant
E6	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant	J6	53	F	Adenocarcinoma	T3N0M0	3	II	malignant
E7	60	M	Adenocarcinoma	T3N1M0	2	III	malignant	J7	60	M	Adenocarcinoma	T3N1M0	3	III	malignant
E8	56	M	Adenocarcinoma	T2N1M0	3	III	malignant	J8	56	M	Adenocarcinoma	T2N1M0	3	III	malignant
E9	60	F	Adenocarcinoma	T2N1M1	3	IV	malignant	J9	60	F	Adenocarcinoma	T2N1M1	-	IV	malignant
E10	66	F	Adenocarcinoma	T3N0M0	3	II	malignant	J10	66	F	Adenocarcinoma	T3N0M0	3	II	malignant

PSMGFR-antibody 18G12 15 ug/mL

Pancreatic cancer tissue array PA1003

Fig. 144A

Position: A2
Cell Type: Adenocarcinoma
Tumor Grade: 2
TNM: T3N0M0

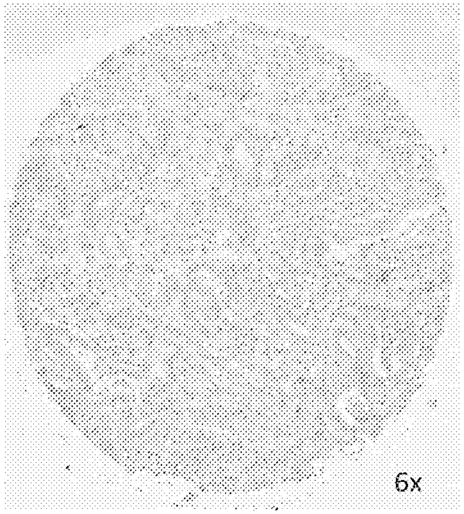


Fig. 144B

Position: B2
Cell Type: Adenocarcinoma
Tumor Grade: 1
TNM: T3N0M0

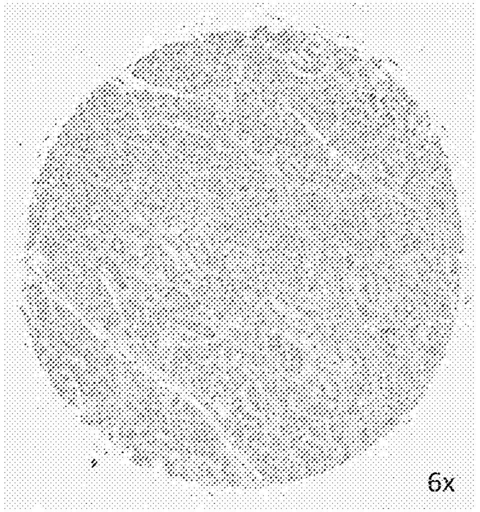


Fig. 144C

Position: C2
Cell Type: Adenocarcinoma
Tumor Grade: 1
TNM: T3N0M0

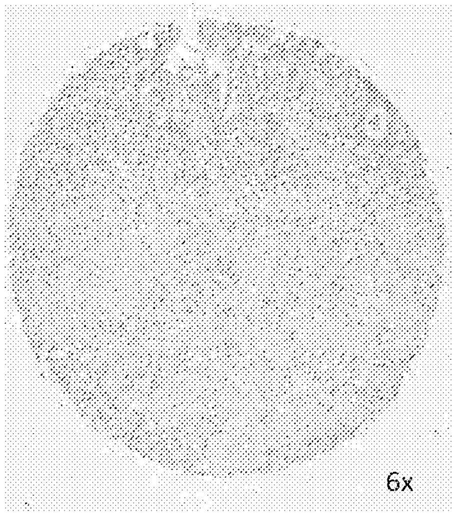


Fig. 144D

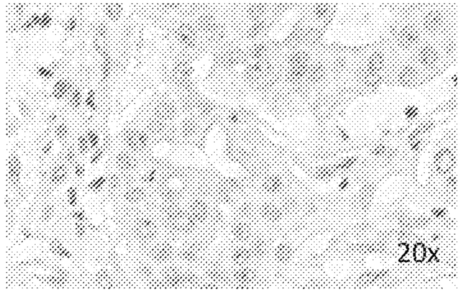


Fig. 144E

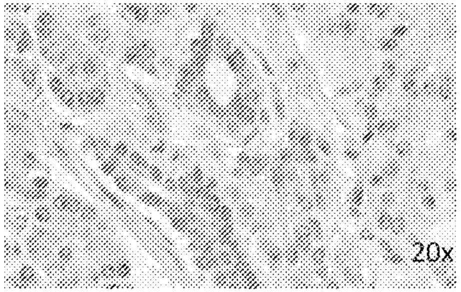


Fig. 144F

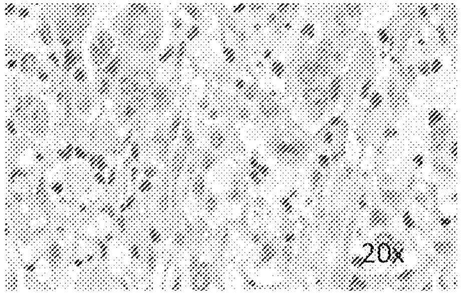


Fig. 144A–144F

PSMGFR antibody 18G12 IgG 30 ug/ml

Esophageal cancer tissue array BC001113

Fig. 145A

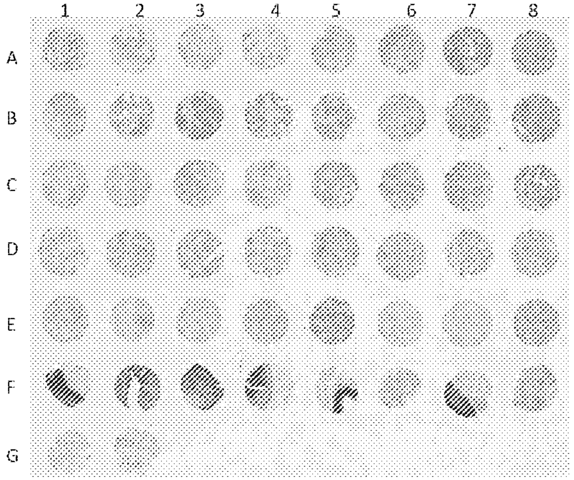


Fig. 145C

Position	Age	Sex	Organ/Anatomic	Pathology diagnosis	Grade	Type	Position	Age	Sex	Organ/Ana	Pathology	Grade	Type
A1	47	F	Esophagus	Adenocarcinoma (smoo	-	malignant	D1	69	M	Cardia	Adenocarc	I	malignant
A2	33	F	Esophagus	Adenocarcinoma	III	malignant	D2	62	M	Cardia	Adenocarc	II	malignant
A3	68	F	Esophagus	Mucinous adenocarcino	I	malignant	D3	65	M	Cardia	Adenocarc	III	malignant
A4	60	M	Esophagus	Adenocarcinoma	III	malignant	D4	72	M	Cardia	Adenocarc	III	malignant
A5	61	M	Esophagus	Adenocarcinoma	II	malignant	D5	74	M	Stomach	Adenocarc	III	malignant
A6	57	M	Esophagus	Adenocarcinoma	III	malignant	D6	51	F	Stomach	Undifferent	IV	malignant
A7	61	M	Esophagus	Undifferentiated adenoc	IV	malignant	D7	51	F	Stomach	Undifferent	IV	malignant
A8	51	F	Esophagus	Adenocarcinoma	III	malignant	D8	53	M	Stomach	Undifferent	IV	malignant
B1	63	M	Esophagus	Undifferentiated adenoc	IV	malignant	E1	64	M	Cardia	Adenocarc	III	malignant
B2	67	F	Esophagus	Adenocarcinoma	III	malignant	E2	70	M	Cardia	Adenocarc	II	malignant
B3	72	M	Cardia	Adenocarcinoma	I	malignant	E3	73	M	Cardia	Undifferent	IV	malignant
B4	36	M	Cardia	Adenocarcinoma	I	malignant	E4	50	M	Cardia	Adenocarc	I	malignant
B5	55	F	Cardia	Adenocarcinoma	II	malignant	E5	64	M	Cardia	Adenocarc	III	malignant
B6	62	M	Cardia	Adenocarcinoma	III	malignant	E6	54	F	Cardia	Cancer adj	-	malignant
B7	64	F	Cardia	Undifferentiated adenoc	IV	malignant	E7	43	M	Cardia	Adenocarc	I	malignant
B8	67	M	Cardia	Adenocarcinoma	I	malignant	E8	59	M	Cardia	Adenocarc	I	malignant
C1	60	F	Cardia	Adenocarcinoma	I	malignant	F1	64	F	Esophagus	Adjacent n	-	normal
C2	66	M	Cardia	Adenocarcinoma	III	malignant	F2	59	M	Esophagus	Adjacent n	-	normal
C3	63	F	Cardia	Adenocarcinoma	II	malignant	F3	67	M	Esophagus	Adjacent n	-	normal
C4	41	M	Cardia	Adenocarcinoma	III	malignant	F4	53	M	Esophagus	Adjacent n	-	normal
C5	70	M	Stomach	Adenocarcinoma	II	malignant	F5	43	M	Esophagus	Adjacent n	-	normal
C6	30	F	Stomach	Adenocarcinoma	II-III	malignant	F6	64	M	Cardia	Adjacent n	-	normal
C7	61	M	Cardia	Adenocarcinoma	II-III	malignant	F7	71	M	Cardia	Adjacent n	-	normal
C8	64	M	Cardia	Adenocarcinoma	III	malignant	F8	66	M	Esophagus	Adjacent n	-	normal
							G1	61	M	Cardia	Adjacent n	-	normal
							G2	56	F	Cardia	Adjacent n	-	normal

Fig. 145B

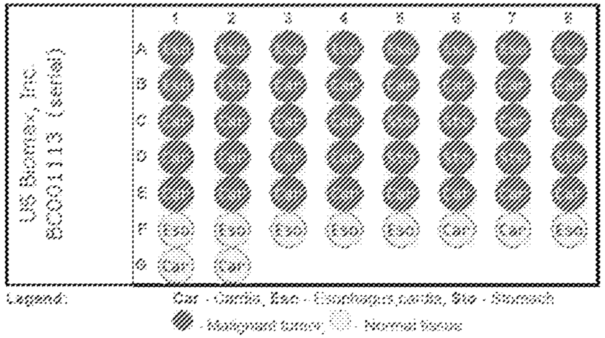


Figure 145A-145C

PSMGFR antibody 18G12 IgG 30 ug/ml

Esophageal cancer tissue array BC001113

Fig. 146A
Esophageal cancer

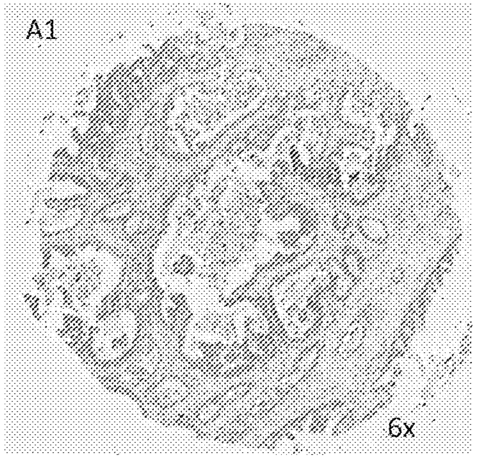


Fig. 146B
Esophageal cancer

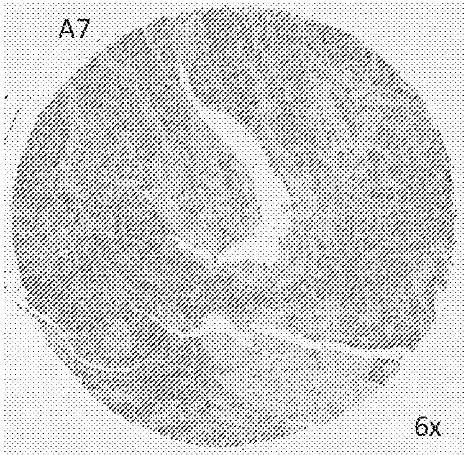


Fig. 146C
Esophageal cancer

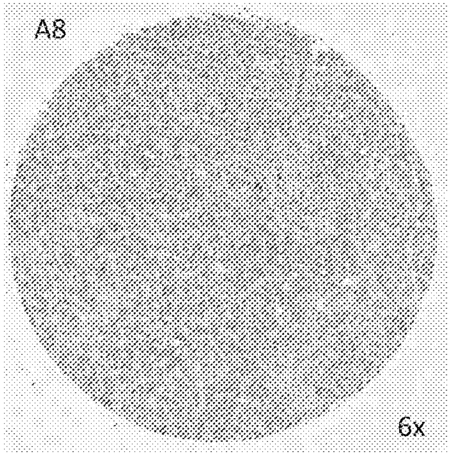


Fig. 146D

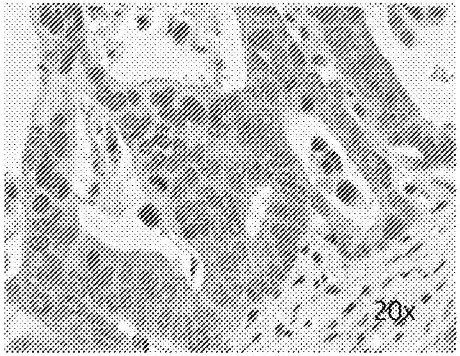


Fig. 146E

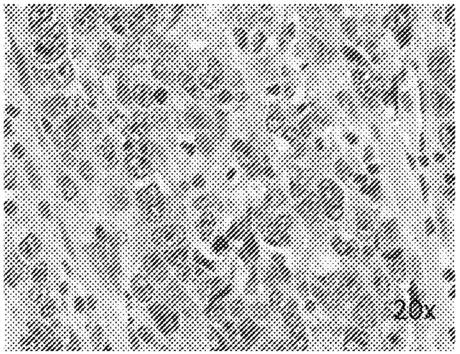


Fig. 146F

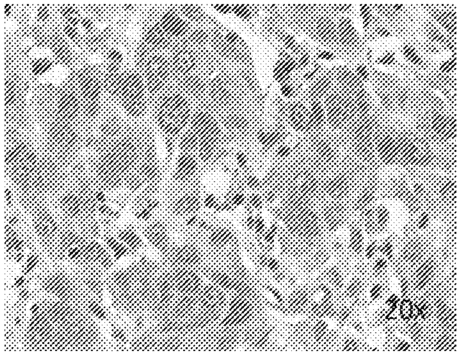


Fig. 146A–146F

PSMGFR-antibody 25E6 IgG 5.0 ug/mL

FDA Normal tissue array MNO1021

Fig. 147A

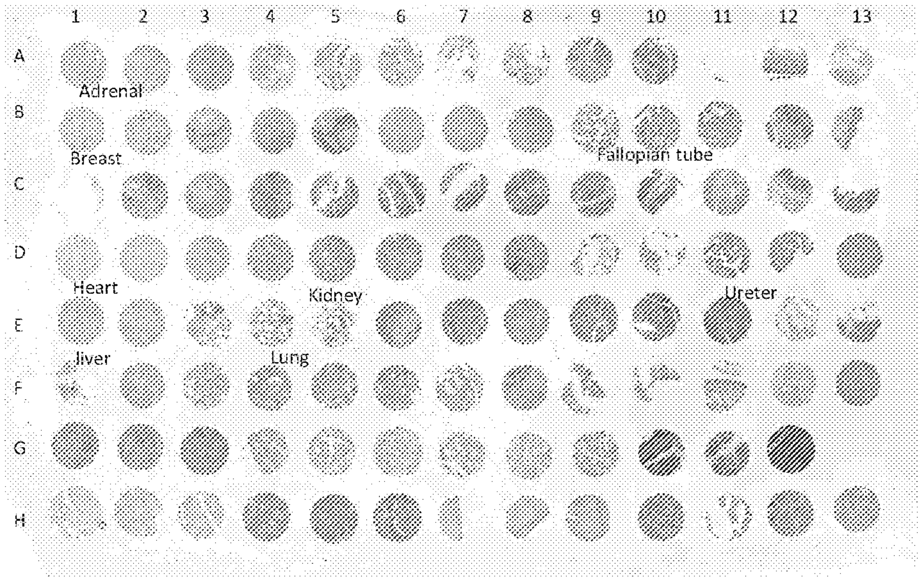


Fig. 147B

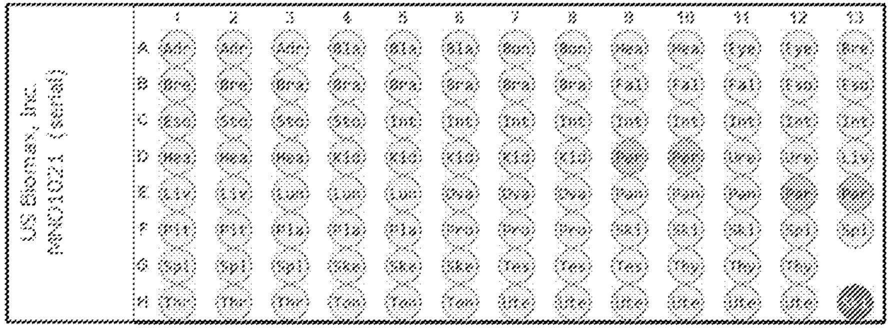


Fig. 147C

Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis	Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis
A1	F	31	Adrenal gland	Normal	E1	M	59	Liver	Normal
A2	M	51	Adrenal gland	Normal	E2	F	27	Liver	Normal
A3	M	53	Adrenal gland	Normal	E3	M	72	Lung	Normal
A4	M	75	Bladder, urinary	Normal	E4	F	55	Lung	Normal
A5	M	72	Bladder, urinary	Normal	E5	M	43	Lung	Normal
A6	M	52	Bladder, urinary	Normal	E6	F	47	Ovary	Normal
A7	M	53	Bone, bone marrow	Normal	E7	F	46	Ovary	Normal
A8	M	43	Bone, bone marrow	Normal	E8	F	40	Ovary	Normal
A9	F	44	Head and neck, salivary gland	Normal	E9	M	42	Pancreas	Normal
A10	M	18	Head and neck, salivary gland	Normal	E10	F	26	Pancreas	Normal
A11	M	55	Eye	Normal	E11	F	59	Pancreas	Normal
A12	M	50	Eye	Normal	E12	M	17	Parathyroid	Adenoma
A13	F	35	Breast	Normal	E13	M	72	Parathyroid	Adenoma
B1	F	38	Breast	Normal	F1	F	3	Pituitary gland	Normal
B2	F	33	Breast	Normal	F2	F		Pituitary gland	Normal
B3	M	58	Brain, cerebellum	Normal	F3	F	32	Placenta	Normal
B4	M	65	Brain, cerebellum	Normal	F4	F	30	Placenta	Normal
B5	F		Brain, cerebellum	Normal	F5	F	27	Placenta	Normal
B6	M	58	Brain, cerebral cortex	Normal	F6	M	64	Prostate	Normal
B7	M	65	Brain, cerebral cortex	Normal	F7	M	65	Prostate	Normal
B8	F		Brain, cerebral cortex	Normal	F8	M	65	Prostate	Normal
B9	F	42	Fallopian tube	Normal	F9	F	32	Skin	Normal
B10	F	32	Fallopian tube	Normal	F10	F	68	Skin	Normal
B11	F	24	Fallopian tube	Normal	F11	M	28	Skin	Normal
B12	M	45	Esophagus	Normal	F12	M	47	Spinal cord	Normal
B13	F	68	Esophagus	Normal	F13	M	58	Spinal cord	Normal
C1	M	54	Esophagus	Normal	G1	M	27	Spleen	Normal
C2	M	45	Stomach	Normal	G2	M	60	Spleen	Normal
C3	M	49	Stomach	Normal	G3	M	31	Spleen	Normal
C4	M	77	Stomach	Normal	G4	F	60	Skeletal muscle	Normal
C5	M	45	Intestine, small intestine	Normal	G5	F	49	Skeletal muscle	Normal
C6	F	75	Intestine, small intestine	Normal	G6	M	70	Skeletal muscle	Normal
C7	F	75	Intestine, small intestine	Normal	G7	M	43	Testis	Normal
C8	M	2	Intestine, colon	Normal	G8	M	30	Testis	Normal
C9	M	46	Intestine, colon	Normal	G9	M	77	Testis	Normal
C10	M	74	Intestine, colon	Normal	G10	M	15	Thymus	Normal
C11	F	47	Intestine, rectum	Normal	G11	M	26	Thymus	Normal
C12	F	75	Intestine, rectum	Normal	G12	F	9	Thymus	Normal
C13	M	66	Intestine, rectum	Normal	G13	-	-	-	-
D1	M	58	Heart	Normal	H1	F	26	Thyroid	Normal
D2	M	46	Heart	Normal	H2	F	37	Thyroid	Normal
D3	F	34	Heart	Normal	H3	F	51	Thyroid	Normal
D4	F	52	Kidney, cortex	Normal	H4	M	46	Tonsil	Normal
D5	M	23	Kidney, cortex	Normal	H5	M	37	Tonsil	Normal
D6	M	63	Kidney, cortex	Normal	H6	M	13	Tonsil	Normal
D7	F	52	Kidney, medulla	Normal	H7	F	36	Uterus, cervix	Normal
D8	M	23	Kidney, medulla	Normal	H8	F	35	Uterus, cervix	Normal
D9	M	59	Peripheral nerve	Schwannoma	H9	F	44	Uterus, cervix	Normal
D10	F	29	Peripheral nerve	Schwannoma	H10	F	38	Uterus, endometrium	Normal
D11	F	44	Ureter	Normal	H11	F	41	Uterus, endometrium	Normal
D12	F	42	Ureter	Normal	H12	F	46	Uterus, endometrium	Normal
D13	F	57	Liver	Normal	H13	M	58	Skin	Malignant melanoma (tissue marker)

Figure 147A-147C

PSMGFR-antibody 25E6 IgG 5.0 ug/mL

FDA Normal tissue array MNO1021

Fig. 148A
Normal Adrenal Gland

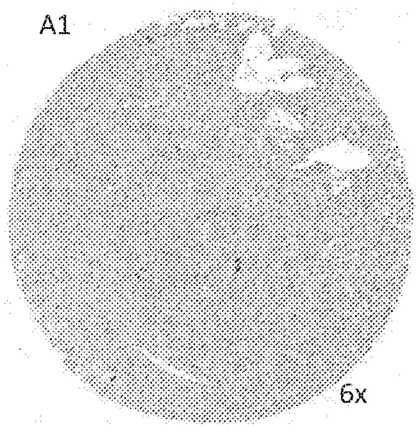


Fig. 148B
Normal Breast

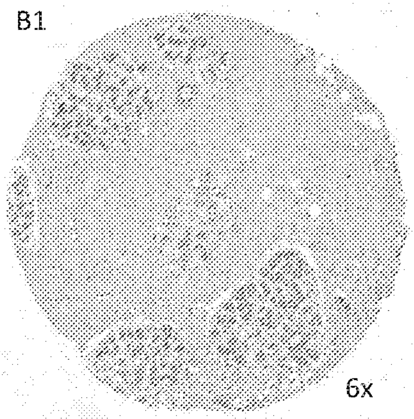


Fig. 148C
Normal Fallopian Tubes

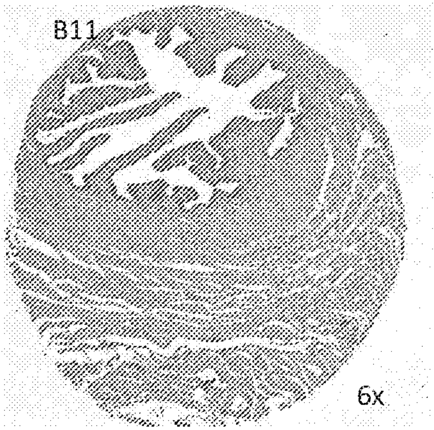


Fig. 148D
Normal Kidney

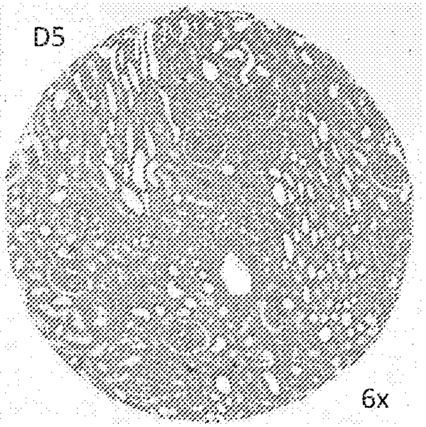


Fig. 148E

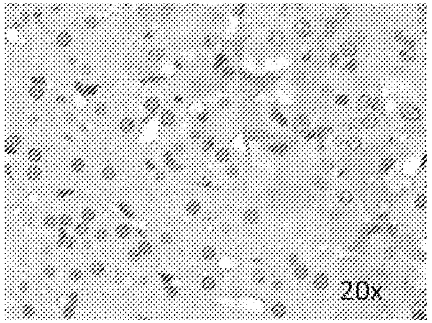


Fig. 148F

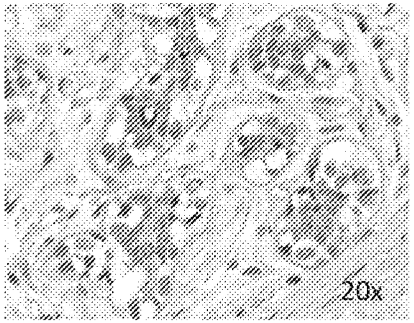


Fig. 148G

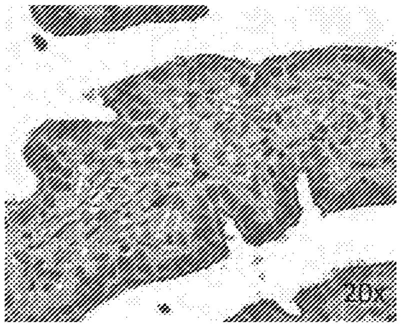


Fig. 148H

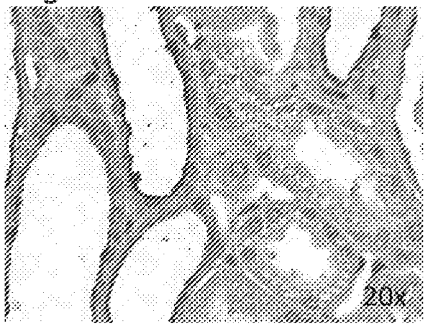


Figure 148A-148H

PSMGFR-antibody 25E6 IgG 5.0 ug/mL

FDA Normal tissue array MNO1021

Fig. 148I
Normal Heart

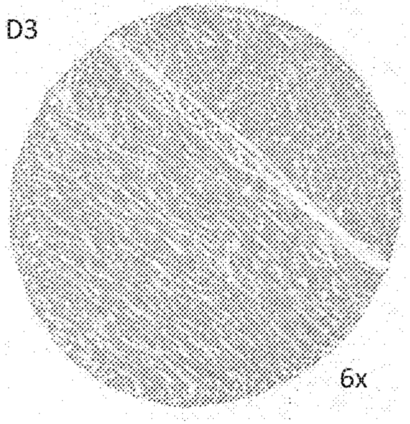


Fig. 148J
Normal Liver

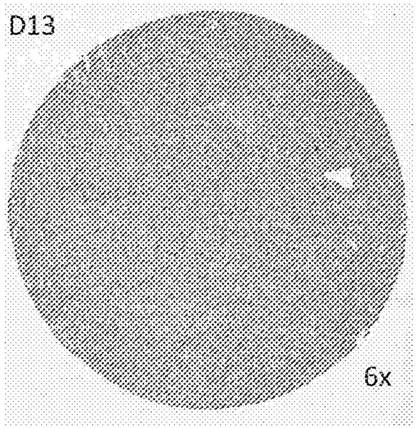


Fig. 148K
Normal Lung

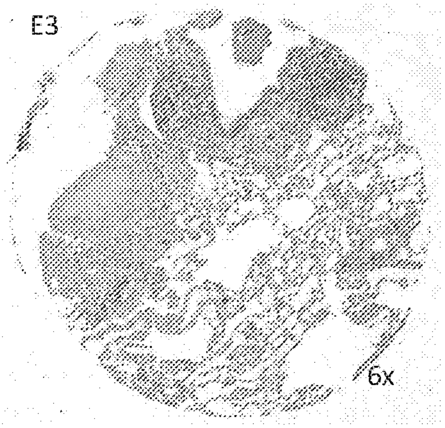


Fig. 148L
Normal Ureter

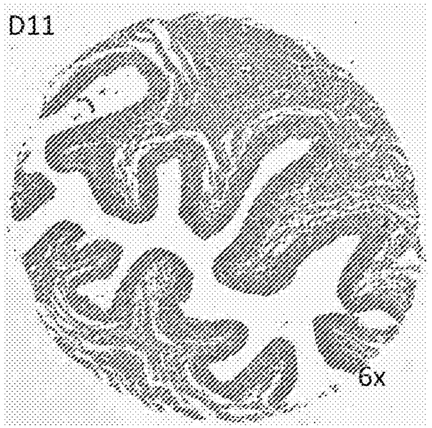


Fig. 148M

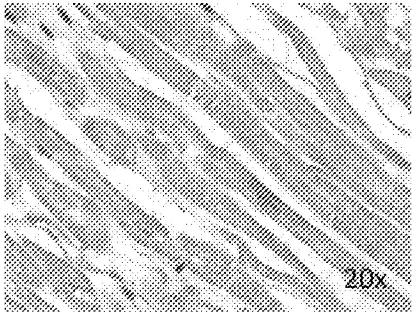


Fig. 148N

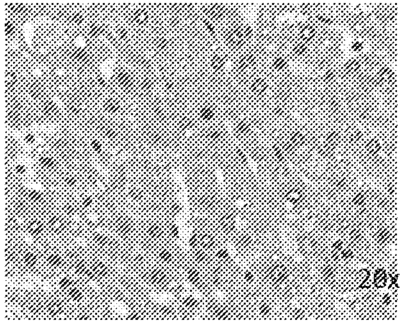


Fig. 148O

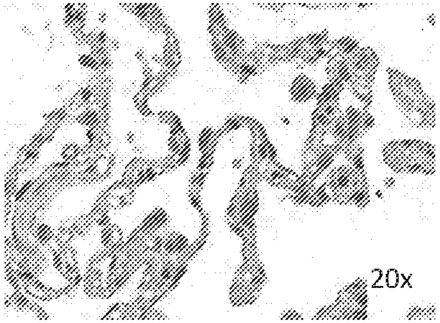


Fig. 148P

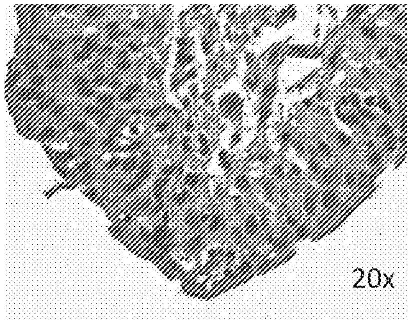


Figure 148I-148P

PSMGFR-antibody 25E6 IgG 5.0 ug/mL

FDA Normal tissue array MNO1021

Fig. 148Q
Normal eye

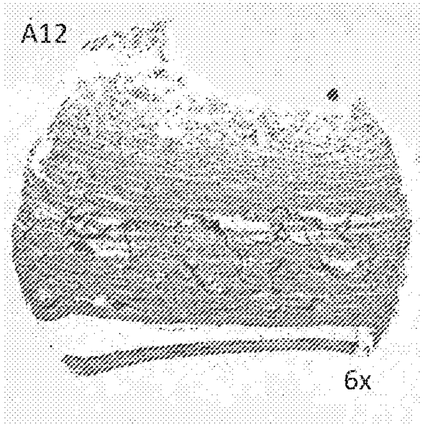


Fig. 148R
Normal Cerebral cortex

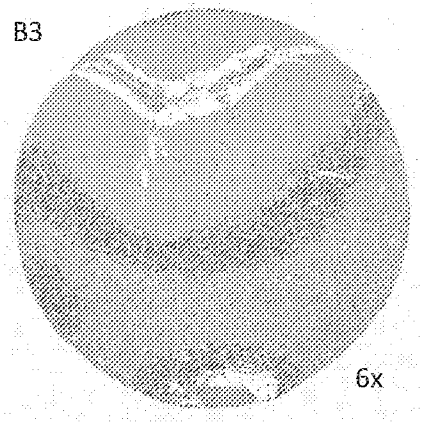


Fig. 148S
Normal Bone marrow

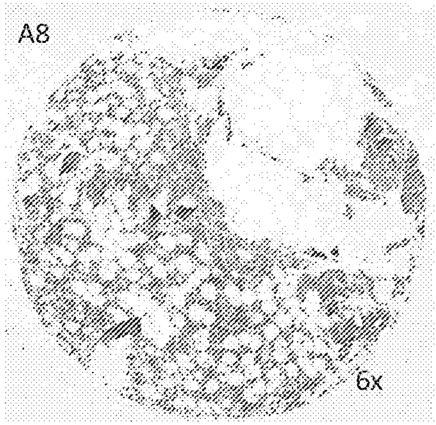


Fig. 148T
Normal Skeletal muscle

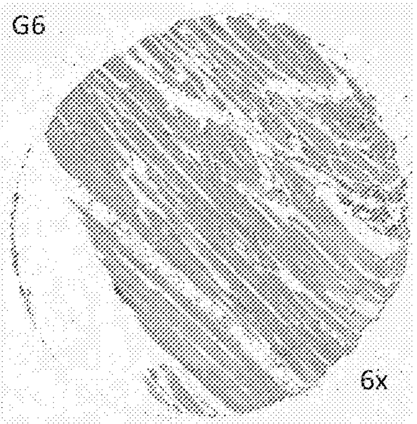


Fig. 148U

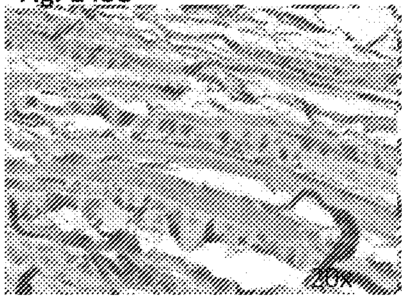


Fig. 148V

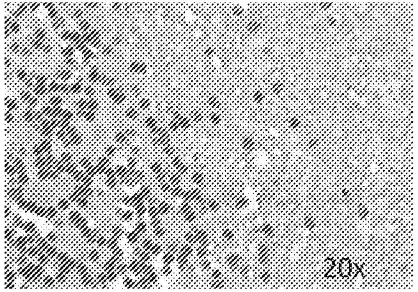


Fig. 148W

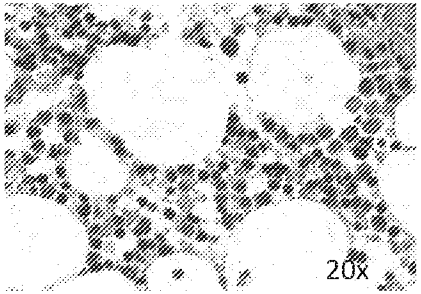


Fig. 148X

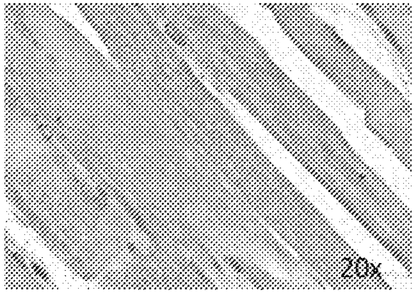


Figure 148Q-148X

PSMGFR-antibody 25E6 5 ug/mL

Breast cancer tissue array BR1141

Fig. 149A

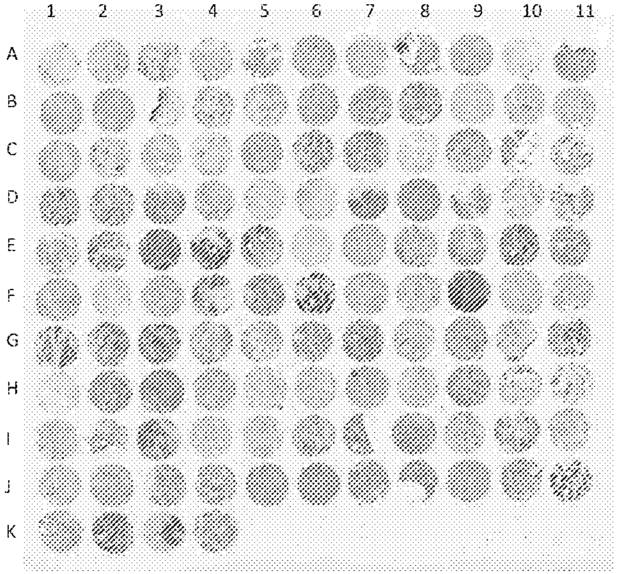


Fig. 149B

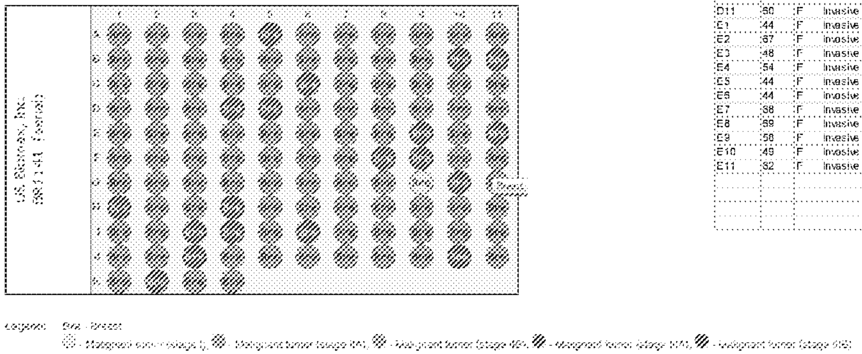


Fig. 149C

Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type	Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type
A1	45	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	F1	52	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A2	38	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	F2	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A3	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	F3	53	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A4	41	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	F4	64	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
A5	70	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant	F5	63	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A6	46	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant	F6	69	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
A7	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant	F7	43	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A8	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	F8	45	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
A9	68	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant	F9	82	F	Invasive ductal carcinoma	T3N1M0	*	IIIA	Malignant
A10	62	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant	F10	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
A11	50	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	F11	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B1	43	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	G1	45	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B2	63	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant	G2	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B3	57	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant	G3	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B4	77	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	G4	45	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
B5	56	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	G5	45	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B6	46	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	G6	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B7	48	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	G7	53	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B8	40	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	G8	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
B9	53	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	G9	38	F	Invasive ductal carcinoma	T1N0M0	2	I	Malignant
B10	54	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant	G10	46	F	Invasive ductal carcinoma	T4N1M0	2	IIIB	Malignant
B11	47	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant	G11	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C1	48	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant	H1	49	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
C2	48	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant	H2	63	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
C3	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	H3	52	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
C4	41	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	H4	50	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
C5	56	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	H5	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C6	41	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant	H6	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C7	41	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	H7	47	F	Invasive ductal carcinoma	T2N0M0	3	IIA	Malignant
C8	60	F	Invasive ductal carcinoma	T2N1M0	*	IIB	Malignant	H8	48	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C9	40	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	H9	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C10	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant	H10	51	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C11	57	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	H11	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D1	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	I1	45	F	Invasive ductal carcinoma	T2N1M0	*	IIB	Malignant
D2	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	I2	68	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D3	48	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant	I3	79	F	Invasive ductal carcinoma	T4N1M0	2	IIIB	Malignant
D4	46	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant	I4	56	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
D5	52	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant	I5	54	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D6	51	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	I6	42	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
D7	62	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	I7	38	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D8	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	I8	62	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D9	43	F	Invasive ductal carcinoma	T2N1M0	1	IIB	Malignant	I9	39	F	Invasive ductal carcinoma	T2N0M0	1	IIA	Malignant
D10	44	F	Invasive ductal carcinoma	T2N0M0	*	IIA	Malignant	I10	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D11	60	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	I11	57	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E1	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	J1	73	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E2	67	F	Invasive ductal carcinoma	T2N0M0	3	IIA	Malignant	J2	66	F	Invasive ductal carcinoma	T2N0M0	3	IIA	Malignant
E3	48	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	J3	45	F	Invasive ductal carcinoma	T2N2M0	3	IIIA	Malignant
E4	54	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant	J4	44	F	Invasive ductal carcinoma	T2N1M0	3	IIB	Malignant
E5	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	J5	46	F	Medullary carcinoma	T3N0M0	-	IIB	Malignant
E6	44	F	Invasive ductal carcinoma	T2N0M0	*	IIA	Malignant	J6	52	F	Medullary carcinoma	T2N0M0	-	IIA	Malignant
E7	38	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	J7	56	F	Medullary carcinoma	T2N0M0	-	IIA	Malignant
E8	69	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	J8	42	F	Medullary carcinoma	T2N0M0	-	IIA	Malignant
E9	58	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant	J9	41	F	Medullary carcinoma	T2N1M0	-	IIB	Malignant
E10	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant	J10	53	F	Mucinous carcinoma	T3N1M0	-	IIIA	Malignant
E11	32	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant	J11	57	F	Medullary carcinoma	T3N0M0	*	IIB	Malignant
								K1	45	F	Invasive lobular carcinoma	T2N0M0	-	IIA	Malignant
								K2	48	F	Invasive apocrine carcinor	T3N1M0	-	IIIA	Malignant
								K3	48	F	Invasive apocrine carcinor	T2N0M0	*	IIA	Malignant
								K4	48	F	Invasive micropapillary cal	T2N1M0	-	IIB	Malignant

Figure 149A-149C

PSMGFR-antibody 25E6 5 ug/mL

Breast cancer tissue array BR1141

Fig. 150A

Position: C5
Cell Type: Invasive Ductal Carcinoma
Tumor Grade: 2
TNM: T2N0M0

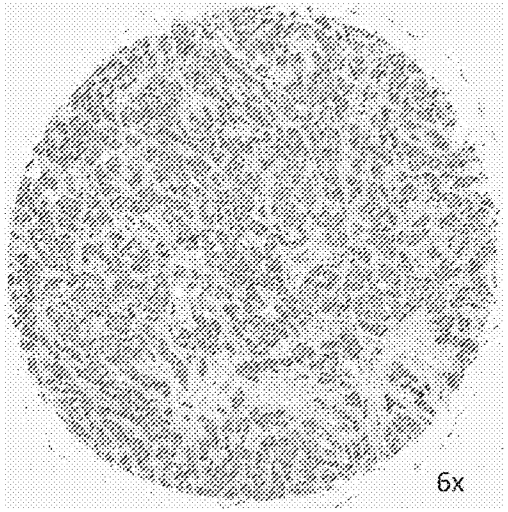


Fig. 150B

Position: G9
Cell Type: Invasive Ductal Carcinoma
Tumor Grade: 2
TNM: T1N0M0

Fig. 150C

Position: I1
Cell Type: Invasive Ductal Carcinoma
Tumor Grade:
TNM: T2N1M0

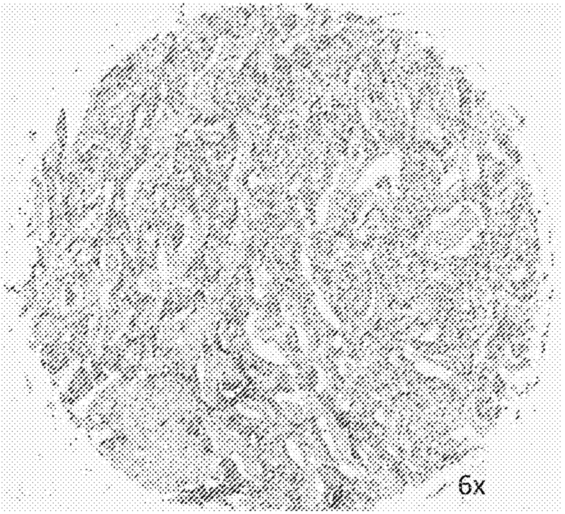


Fig. 150D

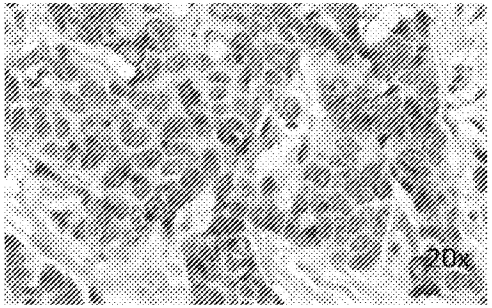


Fig. 150E

Fig. 150F

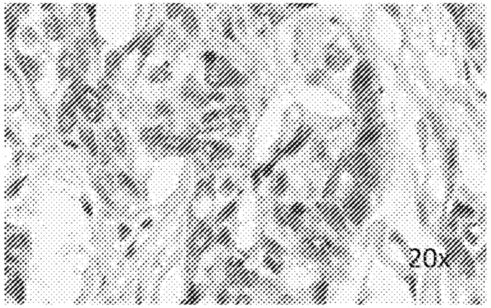


Fig. 150A–150F

PSMGFR-antibody 25E6 0.1-5 ug/mL
Pancreatic cancer tissue array PA1003

Fig. 151A

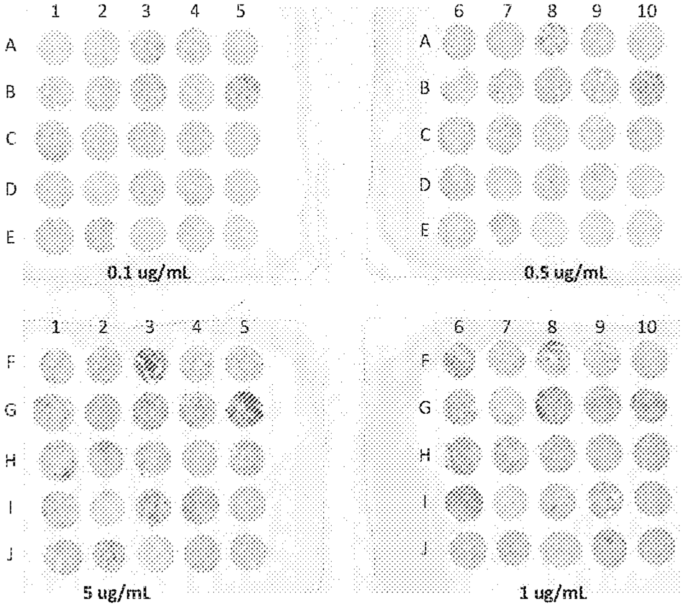


Fig. 151B

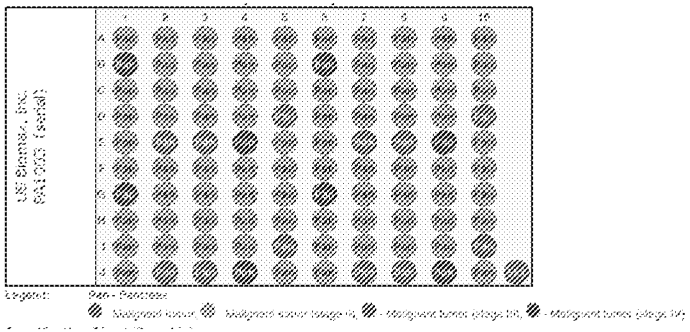
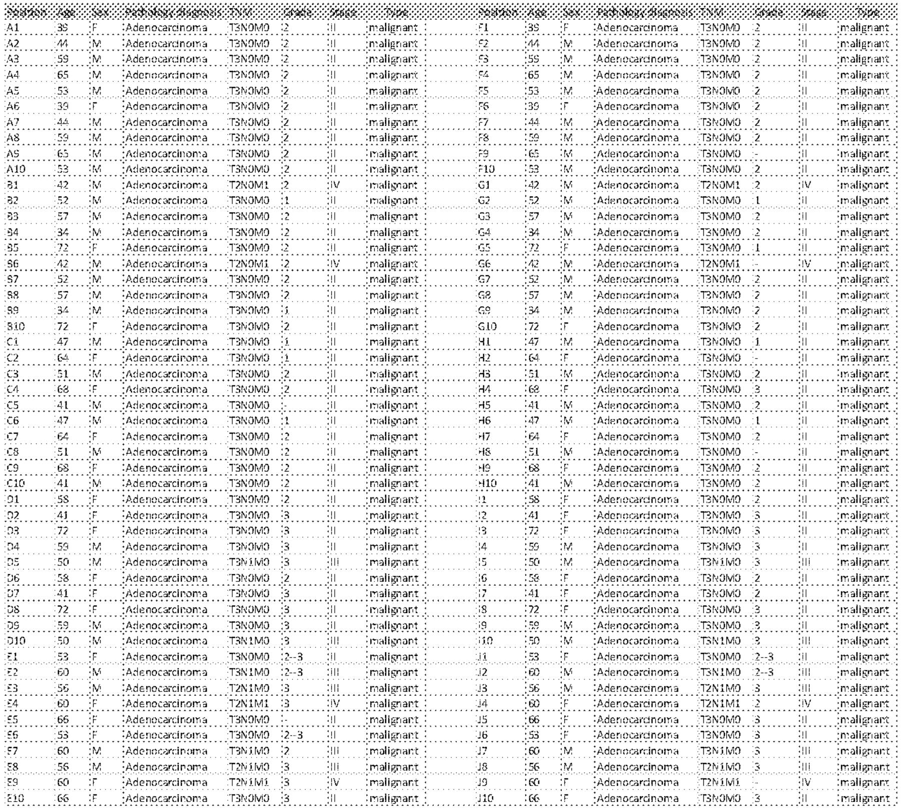


Fig. 151C



Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type	Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type
A1	39	F	Adenocarcinoma	T3N0M0	2	II	malignant	F1	39	F	Adenocarcinoma	T3N0M0	2	II	malignant
A2	44	M	Adenocarcinoma	T3N0M0	2	II	malignant	F2	44	M	Adenocarcinoma	T3N0M0	2	II	malignant
A3	59	M	Adenocarcinoma	T3N0M0	2	II	malignant	F3	59	M	Adenocarcinoma	T3N0M0	2	II	malignant
A4	65	M	Adenocarcinoma	T3N0M0	2	II	malignant	F4	65	M	Adenocarcinoma	T3N0M0	2	II	malignant
A5	53	M	Adenocarcinoma	T3N0M0	2	II	malignant	F5	53	M	Adenocarcinoma	T3N0M0	2	II	malignant
A6	39	F	Adenocarcinoma	T3N0M0	2	II	malignant	F6	39	F	Adenocarcinoma	T3N0M0	2	II	malignant
A7	44	M	Adenocarcinoma	T3N0M0	2	II	malignant	F7	44	M	Adenocarcinoma	T3N0M0	2	II	malignant
A8	59	M	Adenocarcinoma	T3N0M0	2	II	malignant	F8	59	M	Adenocarcinoma	T3N0M0	2	II	malignant
A9	65	M	Adenocarcinoma	T3N0M0	2	II	malignant	F9	65	M	Adenocarcinoma	T3N0M0	-	II	malignant
A10	53	M	Adenocarcinoma	T3N0M0	2	II	malignant	F10	53	M	Adenocarcinoma	T3N0M0	2	II	malignant
B1	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant	G1	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant
B2	52	M	Adenocarcinoma	T3N0M0	1	II	malignant	G2	52	M	Adenocarcinoma	T3N0M0	1	II	malignant
B3	57	M	Adenocarcinoma	T3N0M0	2	II	malignant	G3	57	M	Adenocarcinoma	T3N0M0	2	II	malignant
B4	34	M	Adenocarcinoma	T3N0M0	2	II	malignant	G4	34	M	Adenocarcinoma	T3N0M0	2	II	malignant
B5	72	F	Adenocarcinoma	T3N0M0	2	II	malignant	G5	72	F	Adenocarcinoma	T3N0M0	1	II	malignant
B6	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant	G6	42	M	Adenocarcinoma	T2N0M1	-	IV	malignant
B7	52	M	Adenocarcinoma	T3N0M0	2	II	malignant	G7	52	M	Adenocarcinoma	T3N0M0	2	II	malignant
B8	57	M	Adenocarcinoma	T3N0M0	2	II	malignant	G8	57	M	Adenocarcinoma	T3N0M0	2	II	malignant
B9	34	M	Adenocarcinoma	T3N0M0	1	II	malignant	G9	34	M	Adenocarcinoma	T3N0M0	2	II	malignant
B10	72	F	Adenocarcinoma	T3N0M0	2	II	malignant	G10	72	F	Adenocarcinoma	T3N0M0	2	II	malignant
C1	47	M	Adenocarcinoma	T3N0M0	1	II	malignant	H1	47	M	Adenocarcinoma	T3N0M0	1	II	malignant
C2	64	F	Adenocarcinoma	T3N0M0	1	II	malignant	H2	64	F	Adenocarcinoma	T3N0M0	-	II	malignant
C3	51	M	Adenocarcinoma	T3N0M0	2	II	malignant	H3	51	M	Adenocarcinoma	T3N0M0	2	II	malignant
C4	68	F	Adenocarcinoma	T3N0M0	2	II	malignant	H4	68	F	Adenocarcinoma	T3N0M0	3	II	malignant
C5	41	M	Adenocarcinoma	T3N0M0	-	II	malignant	H5	41	M	Adenocarcinoma	T3N0M0	2	II	malignant
C6	47	M	Adenocarcinoma	T3N0M0	1	II	malignant	H6	47	M	Adenocarcinoma	T3N0M0	1	II	malignant
C7	64	F	Adenocarcinoma	T3N0M0	2	II	malignant	H7	64	F	Adenocarcinoma	T3N0M0	2	II	malignant
C8	51	M	Adenocarcinoma	T3N0M0	2	II	malignant	H8	51	M	Adenocarcinoma	T3N0M0	-	II	malignant
C9	68	F	Adenocarcinoma	T3N0M0	2	II	malignant	H9	68	F	Adenocarcinoma	T3N0M0	2	II	malignant
C10	41	M	Adenocarcinoma	T3N0M0	2	II	malignant	H10	41	M	Adenocarcinoma	T3N0M0	2	II	malignant
D1	58	F	Adenocarcinoma	T3N0M0	2	II	malignant	I1	58	F	Adenocarcinoma	T3N0M0	2	II	malignant
D2	41	F	Adenocarcinoma	T3N0M0	3	II	malignant	I2	41	F	Adenocarcinoma	T3N0M0	3	II	malignant
D3	72	F	Adenocarcinoma	T3N0M0	3	II	malignant	I3	72	F	Adenocarcinoma	T3N0M0	3	II	malignant
D4	59	M	Adenocarcinoma	T3N0M0	3	II	malignant	I4	59	M	Adenocarcinoma	T3N0M0	3	II	malignant
D5	50	M	Adenocarcinoma	T3N1M0	3	III	malignant	I5	50	M	Adenocarcinoma	T3N1M0	3	III	malignant
D6	58	F	Adenocarcinoma	T3N0M0	2	II	malignant	I6	58	F	Adenocarcinoma	T3N0M0	2	II	malignant
D7	41	F	Adenocarcinoma	T3N0M0	3	II	malignant	I7	41	F	Adenocarcinoma	T3N0M0	2	II	malignant
D8	72	F	Adenocarcinoma	T3N0M0	3	II	malignant	I8	72	F	Adenocarcinoma	T3N0M0	3	II	malignant
D9	59	M	Adenocarcinoma	T3N0M0	3	II	malignant	I9	59	M	Adenocarcinoma	T3N0M0	3	II	malignant
D10	50	M	Adenocarcinoma	T3N1M0	3	III	malignant	I10	50	M	Adenocarcinoma	T3N1M0	3	III	malignant
E1	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant	J1	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant
E2	60	M	Adenocarcinoma	T3N1M0	2--3	III	malignant	J2	60	M	Adenocarcinoma	T3N1M0	2--3	III	malignant
E3	56	M	Adenocarcinoma	T2N1M0	3	III	malignant	J3	56	M	Adenocarcinoma	T2N1M0	3	III	malignant
E4	60	F	Adenocarcinoma	T2N1M1	3	IV	malignant	J4	60	F	Adenocarcinoma	T2N1M1	2	IV	malignant
E5	66	F	Adenocarcinoma	T3N0M0	-	II	malignant	J5	66	F	Adenocarcinoma	T3N0M0	3	II	malignant
E6	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant	J6	53	F	Adenocarcinoma	T3N0M0	3	II	malignant
E7	60	M	Adenocarcinoma	T3N1M0	2	III	malignant	J7	60	M	Adenocarcinoma	T3N1M0	3	III	malignant
E8	56	M	Adenocarcinoma	T2N1M0	3	III	malignant	J8	56	M	Adenocarcinoma	T2N1M0	3	III	malignant
E9	60	F	Adenocarcinoma	T2N1M1	3	IV	malignant	J9	60	F	Adenocarcinoma	T2N1M1	-	IV	malignant
E10	66	F	Adenocarcinoma	T3N0M0	3	II	malignant	J10	66	F	Adenocarcinoma	T3N0M0	3	II	malignant

Fig. 151A–151C

PSMGFR-antibody 25E6 0.1 ug/mL

Pancreatic cancer tissue array PA1003

Fig. 152A

Position: A2
Cell Type: Adenocarcinoma
Tumor Grade: 2
TNM: T3N0M0

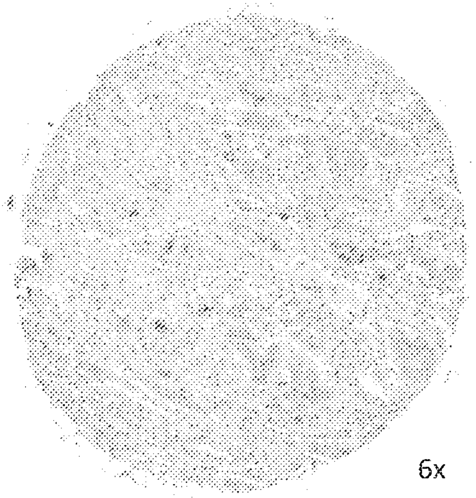


Fig. 152B

Position: B2
Cell Type: Adenocarcinoma
Tumor Grade: 1
TNM: T3N0M0

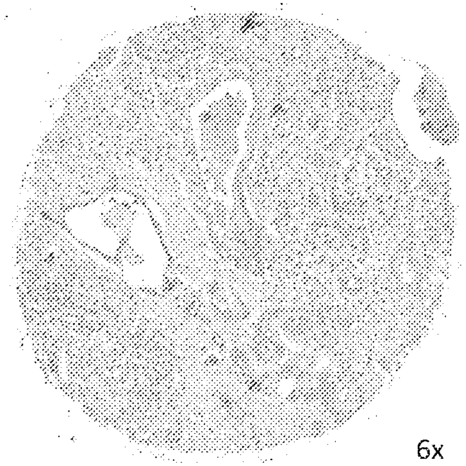


Fig. 152C

Position: C2
Cell Type: Adenocarcinoma
Tumor Grade: 1
TNM: T3N0M0

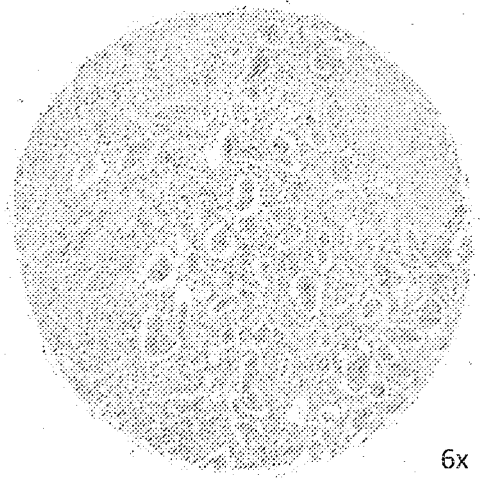


Fig. 152D

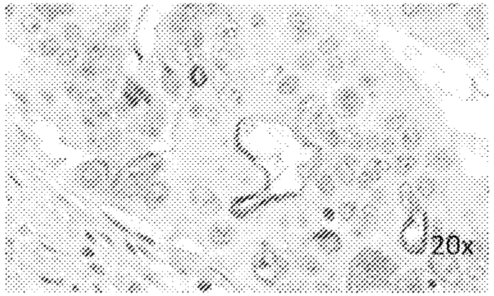


Fig. 152E

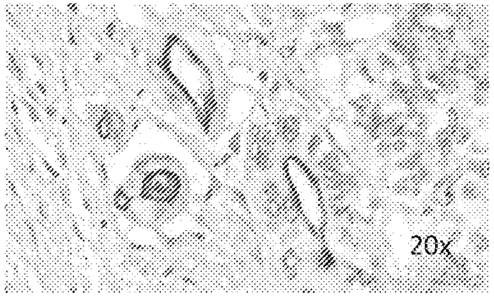


Fig. 152F

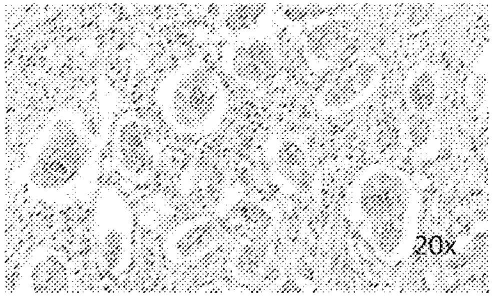


Fig. 152A–152F

PSMGFR-antibody 28F9 IgG 15 ug/mL

FDA Normal tissue array MNO1021

Fig. 153A

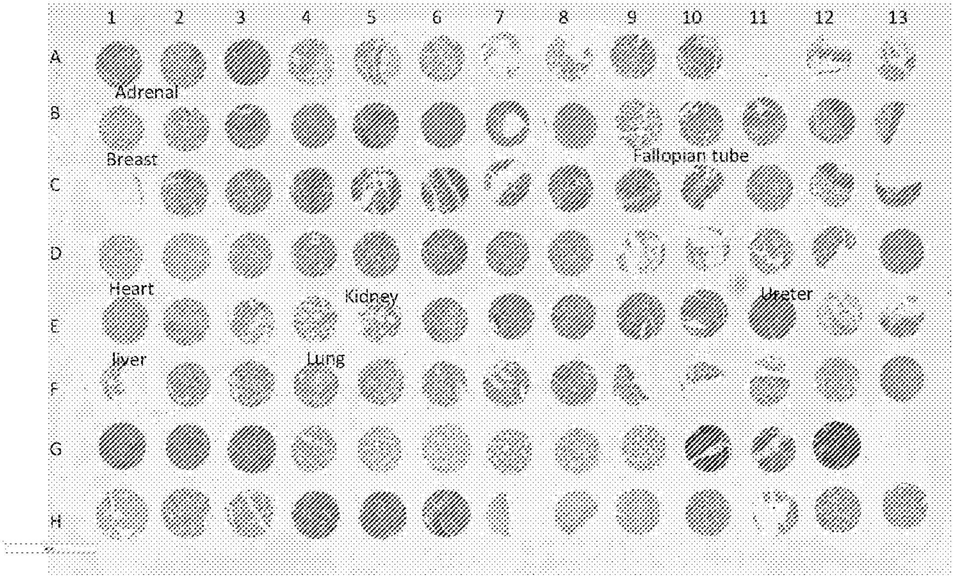


Fig. 153B

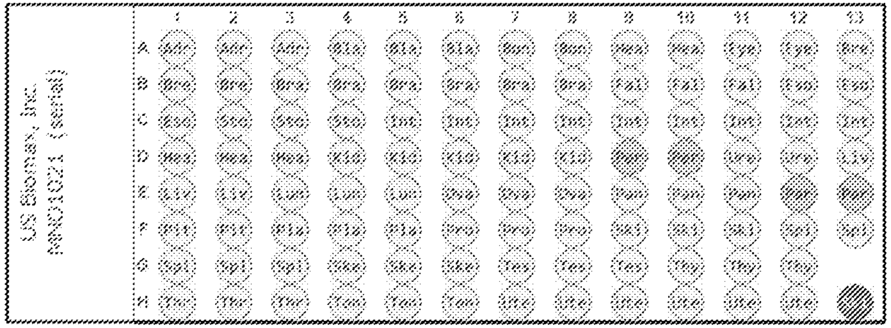


Figure 153A-153C

Fig. 153C

Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis	Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis
A1	F	31	Adrenal gland	Normal	E1	M	59	Liver	Normal
A2	M	51	Adrenal gland	Normal	E2	F	27	Liver	Normal
A3	M	53	Adrenal gland	Normal	E3	M	72	Lung	Normal
A4	M	75	Bladder, urinary	Normal	E4	F	55	Lung	Normal
A5	M	72	Bladder, urinary	Normal	E5	M	43	Lung	Normal
A6	M	52	Bladder, urinary	Normal	E6	F	47	Ovary	Normal
A7	M	53	Bone, bone marrow	Normal	E7	F	46	Ovary	Normal
A8	M	43	Bone, bone marrow	Normal	E8	F	40	Ovary	Normal
A9	F	44	Head and neck, salivary gland	Normal	E9	M	42	Pancreas	Normal
A10	M	18	Head and neck, salivary gland	Normal	E10	F	26	Pancreas	Normal
A11	M	55	Eye	Normal	E11	F	59	Pancreas	Normal
A12	M	50	Eye	Normal	E12	M	17	Parathyroid	Adenoma
A13	F	35	Breast	Normal	E13	M	72	Parathyroid	Adenoma
B1	F	38	Breast	Normal	F1	F	3	Pituitary gland	Normal
B2	F	33	Breast	Normal	F2	F		Pituitary gland	Normal
B3	M	58	Brain, cerebellum	Normal	F3	F	32	Placenta	Normal
B4	M	65	Brain, cerebellum	Normal	F4	F	30	Placenta	Normal
B5	F		Brain, cerebellum	Normal	F5	F	27	Placenta	Normal
B6	M	58	Brain, cerebral cortex	Normal	F6	M	64	Prostate	Normal
B7	M	65	Brain, cerebral cortex	Normal	F7	M	65	Prostate	Normal
B8	F		Brain, cerebral cortex	Normal	F8	M	65	Prostate	Normal
B9	F	42	Fallopian tube	Normal	F9	F	32	Skin	Normal
B10	F	32	Fallopian tube	Normal	F10	F	68	Skin	Normal
B11	F	24	Fallopian tube	Normal	F11	M	28	Skin	Normal
B12	M	45	Esophagus	Normal	F12	M	47	Spinal cord	Normal
B13	F	68	Esophagus	Normal	F13	M	58	Spinal cord	Normal
C1	M	54	Esophagus	Normal	G1	M	27	Spleen	Normal
C2	M	45	Stomach	Normal	G2	M	60	Spleen	Normal
C3	M	49	Stomach	Normal	G3	M	31	Spleen	Normal
C4	M	77	Stomach	Normal	G4	F	60	Skeletal muscle	Normal
C5	M	45	Intestine, small intestine	Normal	G5	F	49	Skeletal muscle	Normal
C6	F	75	Intestine, small intestine	Normal	G6	M	70	Skeletal muscle	Normal
C7	F	75	Intestine, small intestine	Normal	G7	M	43	Testis	Normal
C8	M	2	Intestine, colon	Normal	G8	M	30	Testis	Normal
C9	M	46	Intestine, colon	Normal	G9	M	77	Testis	Normal
C10	M	74	Intestine, colon	Normal	G10	M	15	Thymus	Normal
C11	F	47	Intestine, rectum	Normal	G11	M	26	Thymus	Normal
C12	F	75	Intestine, rectum	Normal	G12	F	9	Thymus	Normal
C13	M	66	Intestine, rectum	Normal	G13	-	-	-	-
D1	M	58	Heart	Normal	H1	F	26	Thyroid	Normal
D2	M	46	Heart	Normal	H2	F	37	Thyroid	Normal
D3	F	34	Heart	Normal	H3	F	51	Thyroid	Normal
D4	F	52	Kidney, cortex	Normal	H4	M	46	Tonsil	Normal
D5	M	23	Kidney, cortex	Normal	H5	M	37	Tonsil	Normal
D6	M	63	Kidney, cortex	Normal	H6	M	13	Tonsil	Normal
D7	F	52	Kidney, medulla	Normal	H7	F	38	Uterus, cervix	Normal
D8	M	23	Kidney, medulla	Normal	H8	F	35	Uterus, cervix	Normal
D9	M	59	Peripheral nerve	Schwannoma	H9	F	44	Uterus, cervix	Normal
D10	F	29	Peripheral nerve	Schwannoma	H10	F	38	Uterus, endometrium	Normal
D11	F	44	Ureter	Normal	H11	F	41	Uterus, endometrium	Normal
D12	F	42	Ureter	Normal	H12	F	46	Uterus, endometrium	Normal
D13	F	57	Liver	Normal	H13	M	58	Skin	Malignant melanoma (tissue marker)

PSMGFR-antibody 28F9 IgG 15 ug/mL

FDA Normal tissue array MNO1021

Fig. 154A
Normal Adrenal Gland

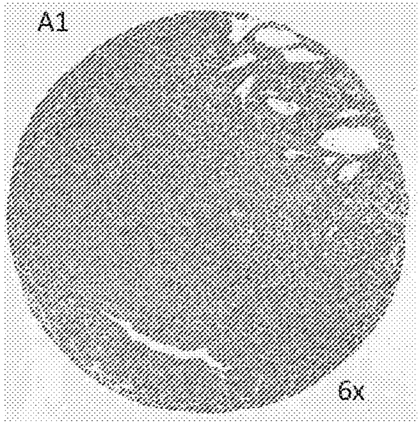


Fig. 154B
Normal Breast

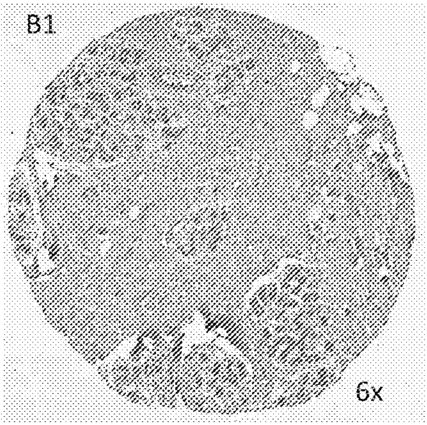


Fig. 154C
Normal Fallopian Tubes

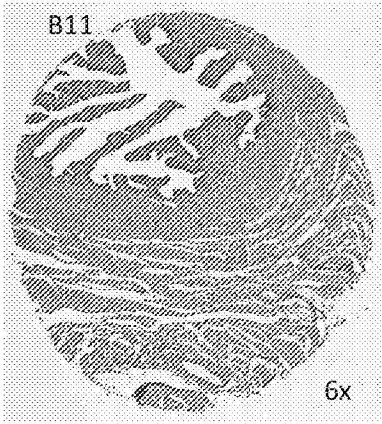


Fig. 154D
Normal Kidney

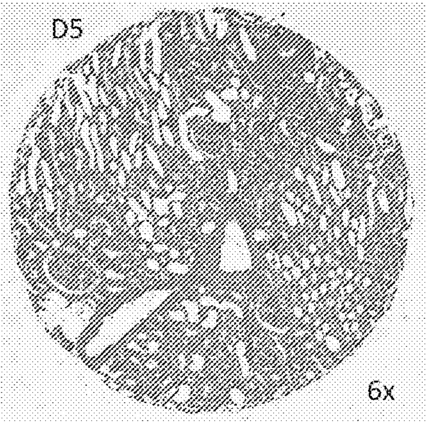


Fig. 154E

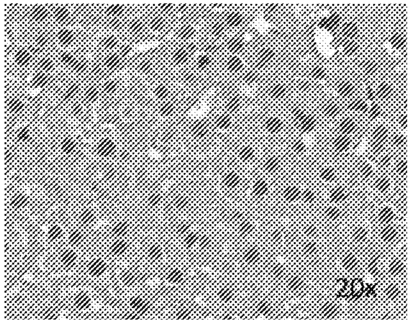


Fig. 154F

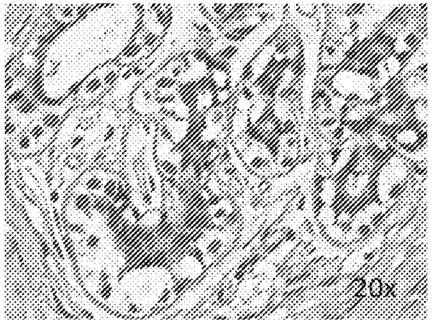


Fig. 154G

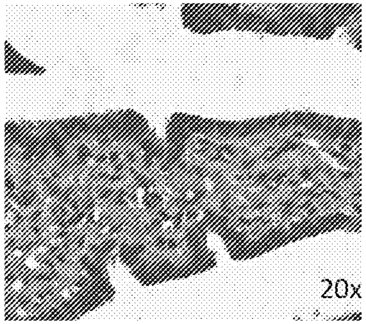


Fig. 154H

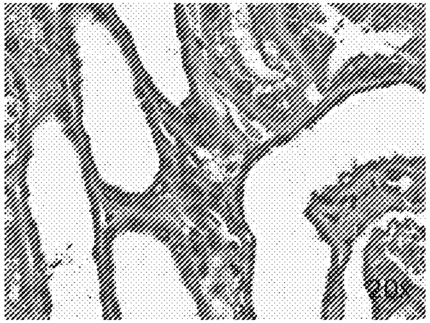


Figure 154A-154H

PSMGFR-antibody 28F9 IgG 15 ug/mL

FDA Normal tissue array MNO1021

Fig. 154I
Normal Heart

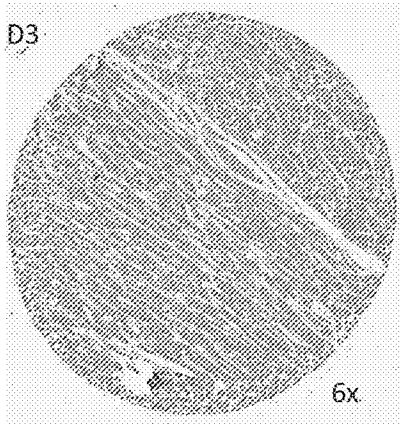


Fig. 154J
Normal Liver

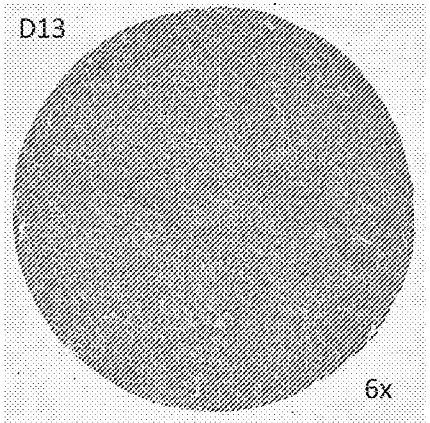


Fig. 154K
Normal Lung

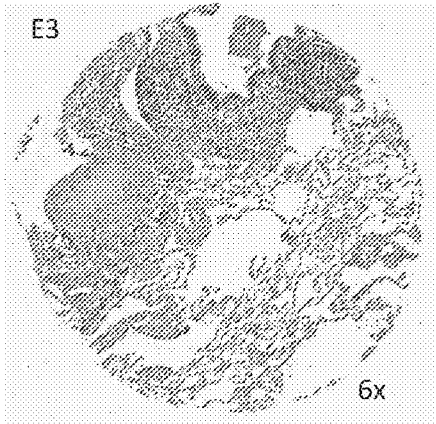


Fig. 154L
Normal Ureter

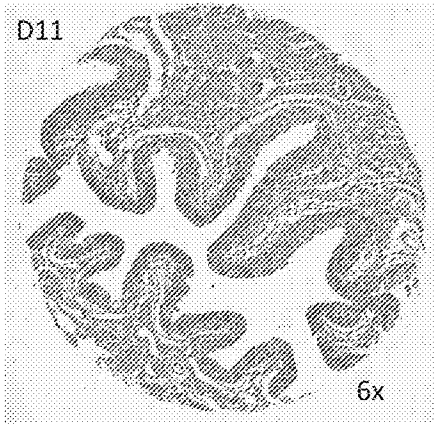


Fig. 154M

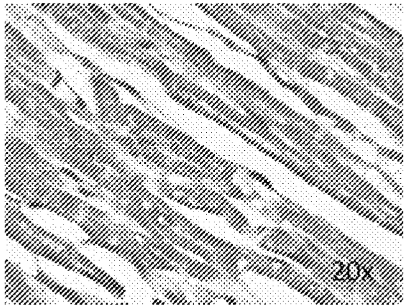


Fig. 154N

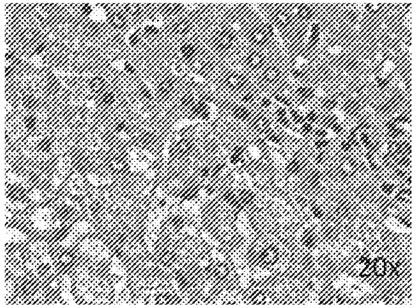


Fig. 154O

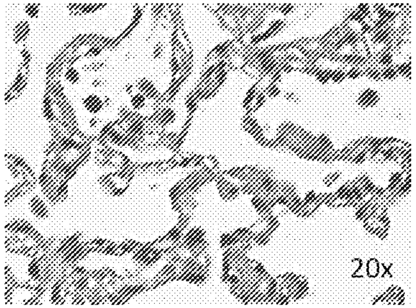


Fig. 154P

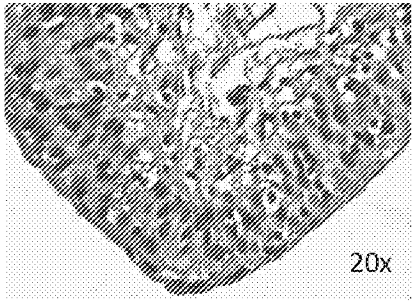


Figure 154I-154P

PSMGFR-antibody 28F9 IgG 15 ug/mL

FDA Normal tissue array MNO1021

Fig. 154Q
Normal eye

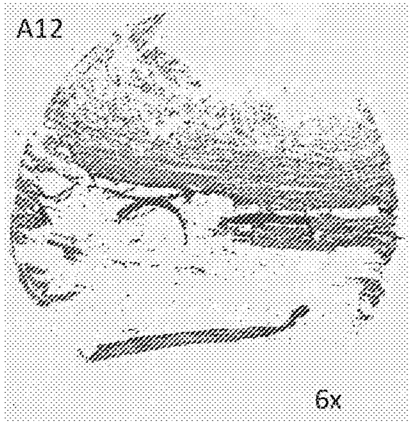


Fig. 154R
Normal Cerebral cortex

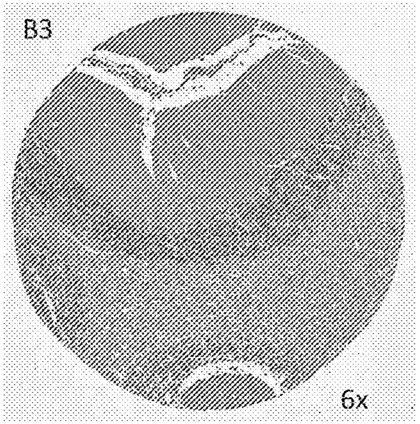


Fig. 154S
Normal Bone marrow

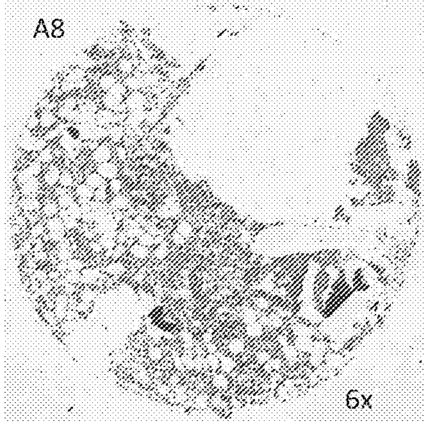


Fig. 154T
Normal Skeletal muscle

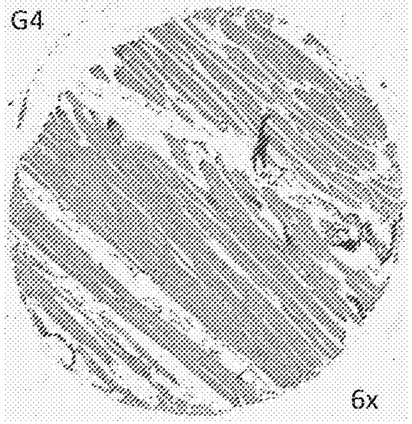


Fig. 154U

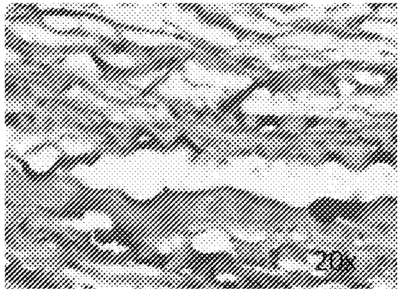


Fig. 154V

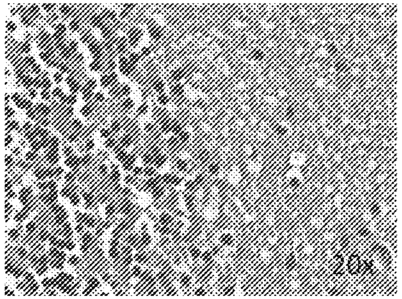


Fig. 154W

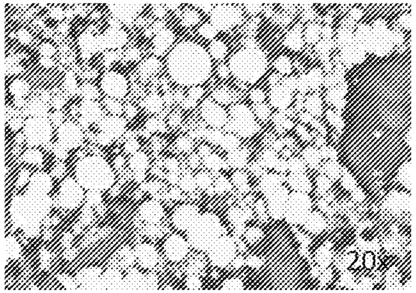


Fig. 154X

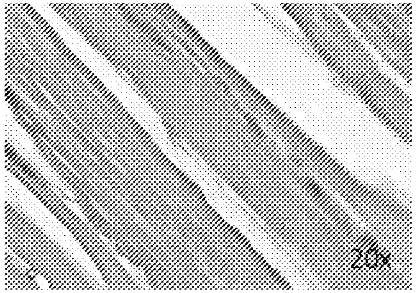


Figure 154Q-154X

PSMGFR-antibody 28F9 15ug/mL

Breast cancer tissue array BR1141

Fig. 155A

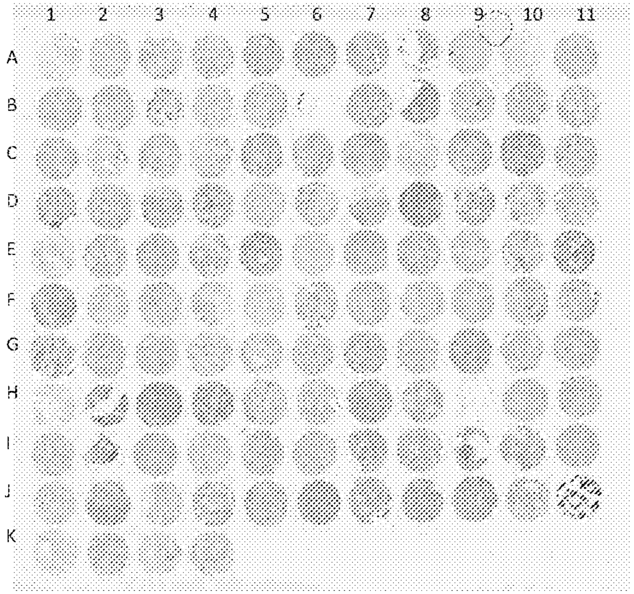


Fig. 155B

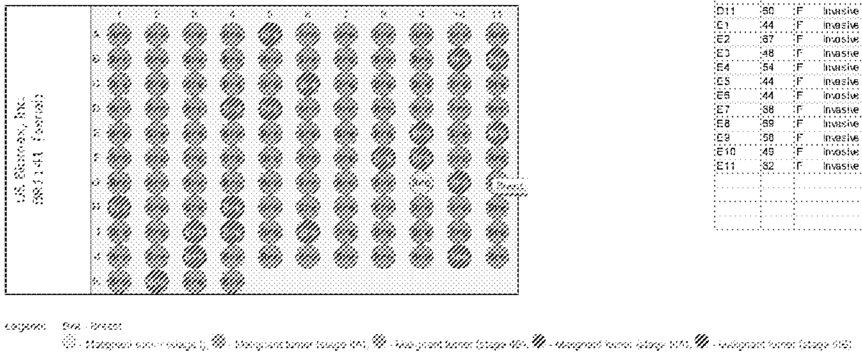
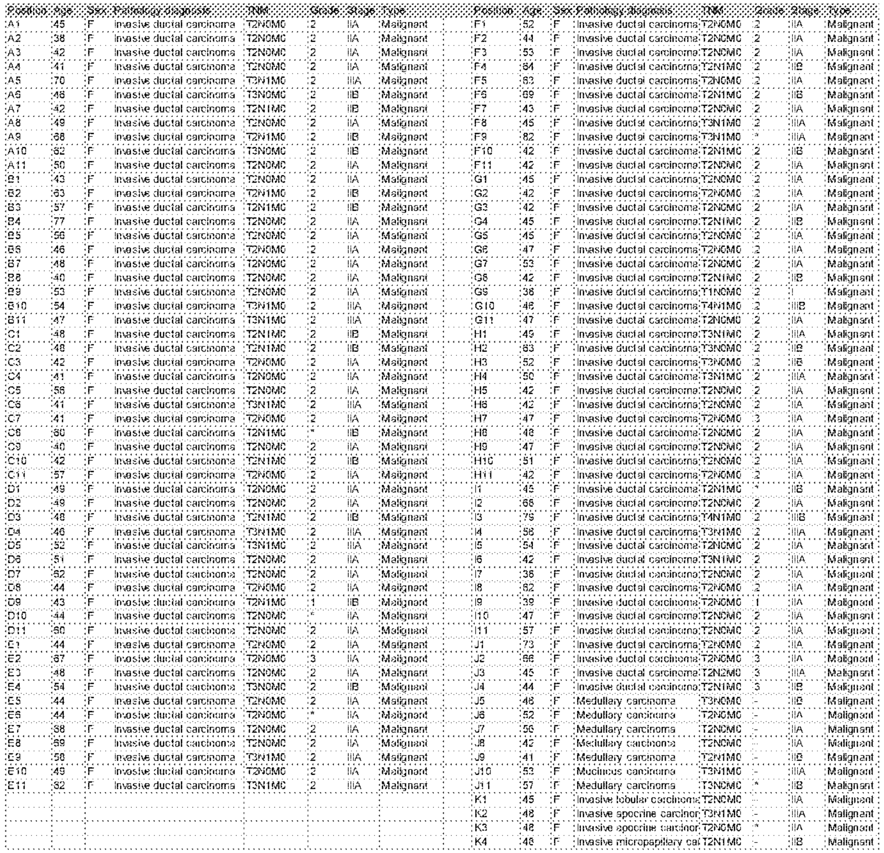


Fig. 155C



Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type
A1	45	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A2	38	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A3	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A4	41	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A5	70	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
A6	46	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
A7	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
A8	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A9	68	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
A10	62	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
A11	50	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B1	43	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B2	63	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
B3	57	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
B4	77	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B5	56	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B6	46	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B7	48	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B8	40	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B9	53	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B10	54	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
B11	47	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
C1	48	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
C2	48	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
C3	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C4	41	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C5	56	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C6	41	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
C7	41	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C8	60	F	Invasive ductal carcinoma	T2N1M0	*	IIB	Malignant
C9	40	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C10	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
C11	57	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D1	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D2	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D3	48	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
D4	46	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
D5	52	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
D6	51	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D7	62	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D8	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D9	43	F	Invasive ductal carcinoma	T2N1M0	1	IIB	Malignant
D10	44	F	Invasive ductal carcinoma	T2N0M0	*	IIA	Malignant
D11	60	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E1	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E2	67	F	Invasive ductal carcinoma	T2N0M0	3	IIA	Malignant
E3	48	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E4	54	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
E5	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E6	44	F	Invasive ductal carcinoma	T2N0M0	*	IIA	Malignant
E7	38	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E8	69	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E9	58	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
E10	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E11	32	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
F1	52	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F2	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F3	53	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F4	64	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
F5	63	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F6	69	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
F7	43	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F8	45	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
F9	82	F	Invasive ductal carcinoma	T3N1M0	*	IIIA	Malignant
F10	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
F11	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G1	45	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G2	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G3	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G4	45	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
G5	45	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G6	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G7	53	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G8	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
G9	38	F	Invasive ductal carcinoma	T1N0M0	2	I	Malignant
G10	46	F	Invasive ductal carcinoma	T4N1M0	2	IIIB	Malignant
G11	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H1	49	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
H2	63	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
H3	52	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
H4	50	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
H5	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H6	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H7	47	F	Invasive ductal carcinoma	T2N0M0	3	IIA	Malignant
H8	48	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H9	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H10	51	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H11	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I1	45	F	Invasive ductal carcinoma	T2N1M0	*	IIB	Malignant
I2	68	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I3	79	F	Invasive ductal carcinoma	T4N1M0	2	IIIB	Malignant
I4	56	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
I5	54	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I6	42	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
I7	38	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I8	62	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I9	39	F	Invasive ductal carcinoma	T2N0M0	1	IIA	Malignant
I10	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I11	57	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
J1	73	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
J2	66	F	Invasive ductal carcinoma	T2N0M0	3	IIA	Malignant
J3	45	F	Invasive ductal carcinoma	T2N2M0	3	IIIA	Malignant
J4	44	F	Invasive ductal carcinoma	T2N1M0	3	IIB	Malignant
J5	46	F	Medullary carcinoma	T3N0M0	-	IIB	Malignant
J6	52	F	Medullary carcinoma	T2N0M0	-	IIA	Malignant
J7	56	F	Medullary carcinoma	T2N0M0	-	IIA	Malignant
J8	42	F	Medullary carcinoma	T2N0M0	-	IIA	Malignant
J9	41	F	Medullary carcinoma	T2N1M0	-	IIB	Malignant
J10	53	F	Mucinous carcinoma	T3N1M0	-	IIIA	Malignant
J11	57	F	Medullary carcinoma	T3N0M0	*	IIB	Malignant
K1	45	F	Invasive lobular carcinoma	T2N0M0	-	IIA	Malignant
K2	48	F	Invasive apocrine carcinor	T3N1M0	-	IIIA	Malignant
K3	48	F	Invasive apocrine carcinor	T2N0M0	*	IIA	Malignant
K4	48	F	Invasive micropapillary ca	T2N1M0	-	IIB	Malignant

Figure 155A-155C

PSMGFR-antibody 28F9 15ug/mL

Breast cancer tissue array BR1141

Fig. 156A

Position: C5

Cell Type: Invasive Ductal Carcinoma

Tumor Grade: 2

TNM: T2N0M0

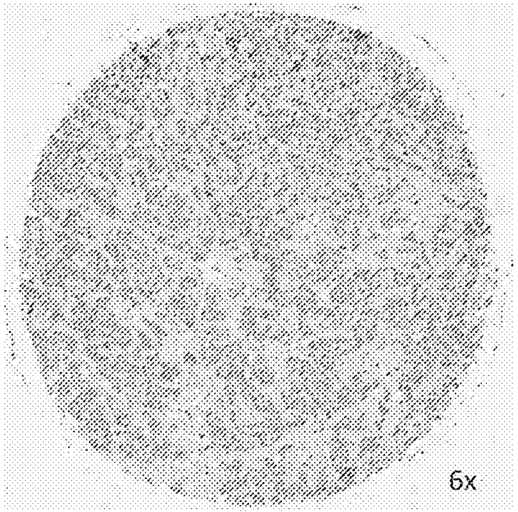


Fig. 156B

Position: G9

Cell Type: Invasive Ductal Carcinoma

Tumor Grade: 2

TNM: T1N0M0

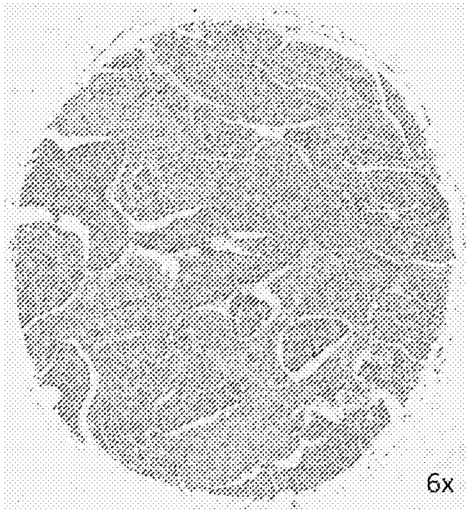


Fig. 156C

Position: I1

Cell Type: Invasive Ductal Carcinoma

Tumor Grade:

TNM: T2N1M0

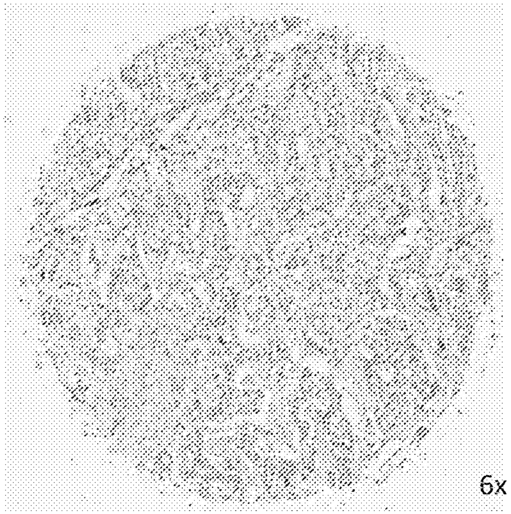


Fig. 156D

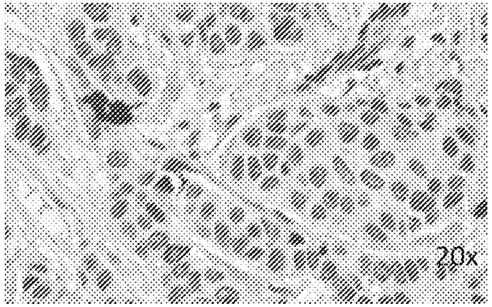


Fig. 156E

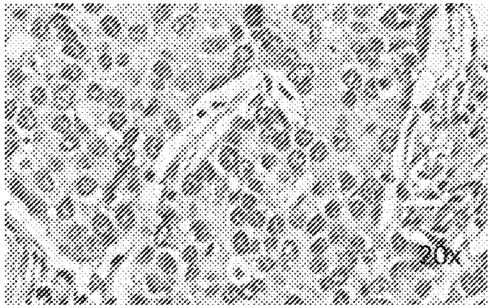


Fig. 156F

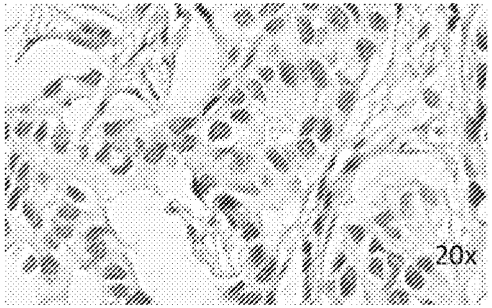


Fig. 156A–156F

N+20/C-27 antibody 1E4 IgG 7.5 ug/mL

FDA Normal tissue array MNO1021

Fig. 157A

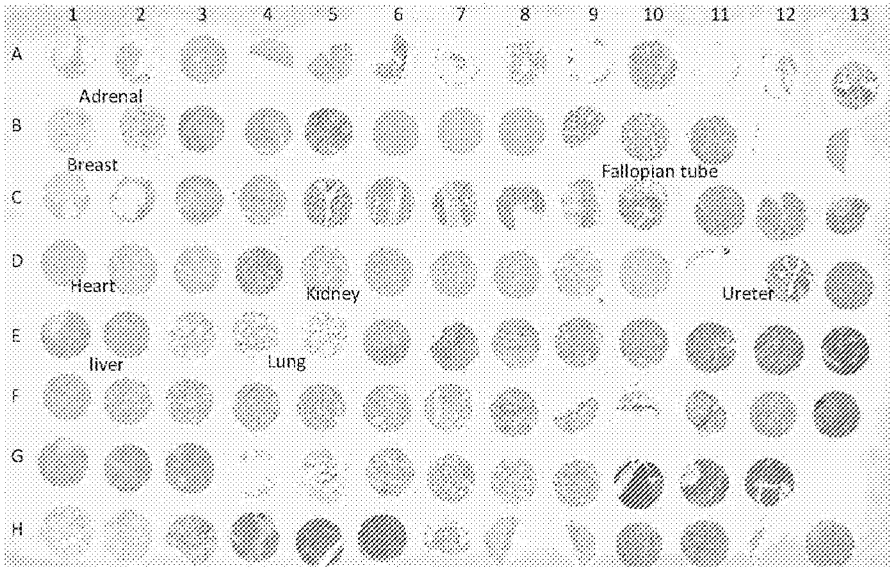


Fig. 157B

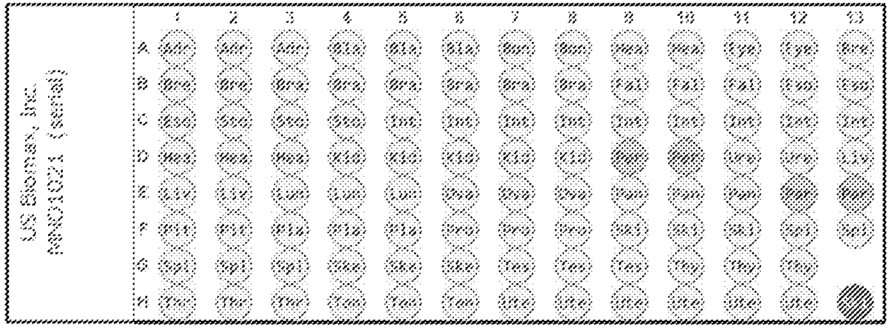


Figure 157A-157C

Fig. 157C

Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis	Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis
A1	F	31	Adrenal gland	Normal	E1	M	59	Liver	Normal
A2	M	51	Adrenal gland	Normal	E2	F	27	Liver	Normal
A3	M	53	Adrenal gland	Normal	E3	M	72	Lung	Normal
A4	M	75	Bladder, umary	Normal	E4	F	55	Lung	Normal
A5	M	72	Bladder, umary	Normal	E5	M	43	Lung	Normal
A6	M	52	Bladder, umary	Normal	E6	F	47	Ovary	Normal
A7	M	53	Bone, bone marrow	Normal	E7	F	46	Ovary	Normal
A8	M	43	Bone, bone marrow	Normal	E8	F	40	Ovary	Normal
A9	F	44	Head and neck, salivary gland	Normal	E9	M	42	Pancreas	Normal
A10	M	18	Head and neck, salivary gland	Normal	E10	F	26	Pancreas	Normal
A11	M	55	Eye	Normal	E11	F	59	Pancreas	Normal
A12	M	50	Eye	Normal	E12	M	17	Parathyroid	Adenoma
A13	F	35	Breast	Normal	E13	M	72	Parathyroid	Adenoma
B1	F	38	Breast	Normal	F1	F	3	Pituitary gland	Normal
B2	F	33	Breast	Normal	F2	F		Pituitary gland	Normal
B3	M	58	Brain, cerebellum	Normal	F3	F	32	Placenta	Normal
B4	M	65	Brain, cerebellum	Normal	F4	F	30	Placenta	Normal
B5	F		Brain, cerebellum	Normal	F5	F	27	Placenta	Normal
B6	M	56	Brain, cerebral cortex	Normal	F6	M	64	Prostate	Normal
B7	M	65	Brain, cerebral cortex	Normal	F7	M	65	Prostate	Normal
B8	F		Brain, cerebral cortex	Normal	F8	M	65	Prostate	Normal
B9	F	42	Fallopian tube	Normal	F9	F	32	Skin	Normal
B10	F	32	Fallopian tube	Normal	F10	F	68	Skin	Normal
B11	F	24	Fallopian tube	Normal	F11	M	26	Skin	Normal
B12	M	45	Esophagus	Normal	F12	M	47	Spinal cord	Normal
B13	F	68	Esophagus	Normal	F13	M	58	Spinal cord	Normal
C1	M	54	Esophagus	Normal	G1	M	27	Spleen	Normal
C2	M	45	Stomach	Normal	G2	M	60	Spleen	Normal
C3	M	49	Stomach	Normal	G3	M	31	Spleen	Normal
C4	M	77	Stomach	Normal	G4	F	60	Skeletal muscle	Normal
C5	M	45	Intestine, small intestine	Normal	G5	F	49	Skeletal muscle	Normal
C6	F	75	Intestine, small intestine	Normal	G6	M	70	Skeletal muscle	Normal
C7	F	75	Intestine, small intestine	Normal	G7	M	43	Testis	Normal
C8	M	2	Intestine, colon	Normal	G8	M	30	Testis	Normal
C9	M	46	Intestine, colon	Normal	G9	M	77	Testis	Normal
C10	M	74	Intestine, colon	Normal	G10	M	15	Thymus	Normal
C11	F	47	Intestine, rectum	Normal	G11	M	28	Thymus	Normal
C12	F	75	Intestine, rectum	Normal	G12	F	9	Thymus	Normal
C13	M	66	Intestine, rectum	Normal	G13	-	-	-	-
D1	M	58	Heart	Normal	H1	F	26	Thyroid	Normal
D2	M	46	Heart	Normal	H2	F	37	Thyroid	Normal
D3	F	34	Heart	Normal	H3	F	51	Thyroid	Normal
D4	F	52	Kidney, cortex	Normal	H4	M	46	Tonsil	Normal
D5	M	23	Kidney, cortex	Normal	H5	M	37	Tonsil	Normal
D6	M	63	Kidney, cortex	Normal	H6	M	13	Tonsil	Normal
D7	F	52	Kidney, medulla	Normal	H7	F	38	Uterus, cervix	Normal
D8	M	23	Kidney, medulla	Normal	H8	F	35	Uterus, cervix	Normal
D9	M	59	Peripheral nerve	Schwannoma	H9	F	44	Uterus, cervix	Normal
D10	F	29	Peripheral nerve	Schwannoma	H10	F	38	Uterus, endometrium	Normal
D11	F	44	Ureter	Normal	H11	F	41	Uterus, endometrium	Normal
D12	F	42	Ureter	Normal	H12	F	46	Uterus, endometrium	Normal
D13	F	57	Liver	Normal	H13	M	58	Skin	Malignant melanoma (tissue marker)

N+20/C-27 antibody 1E4 IgG 7.5 ug/mL

FDA Normal tissue array MNO1021

Fig. 158A
Normal Adrenal Gland

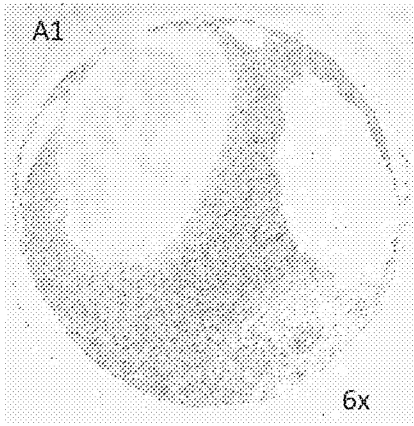


Fig. 158B
Normal Breast

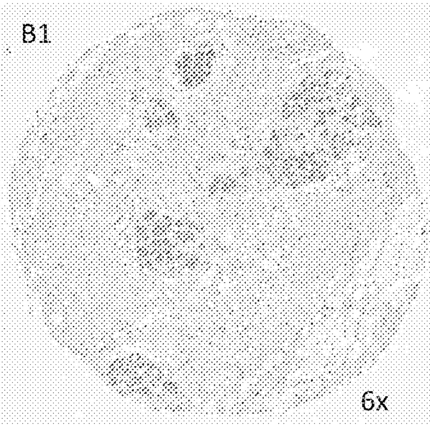


Fig. 158C
Normal Fallopian Tubes

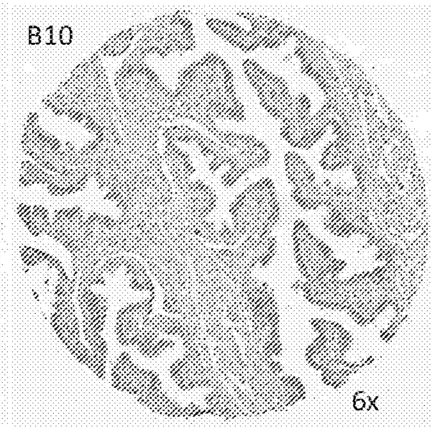


Fig. 158D
Normal Kidney

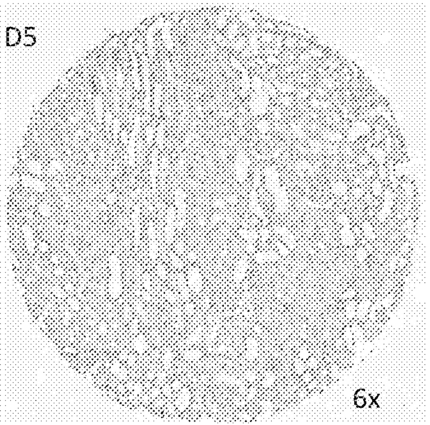


Fig. 158E

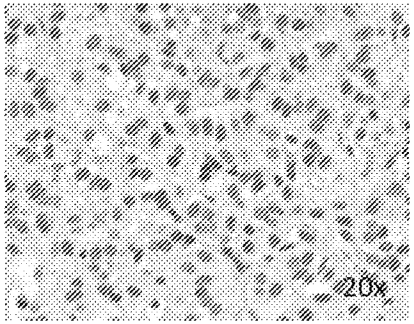


Fig. 158F

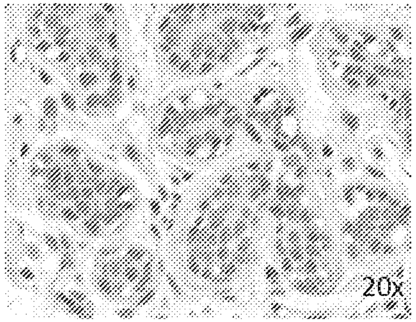


Fig. 158G

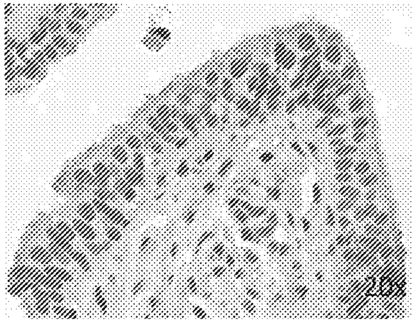


Fig. 158H

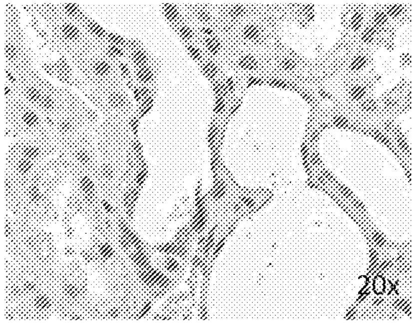


Figure 158A-158H

N+20/C-27 antibody 1E4 IgG 7.5 ug/mL

FDA Normal tissue array MNO1021

Fig. 158I
Normal Heart

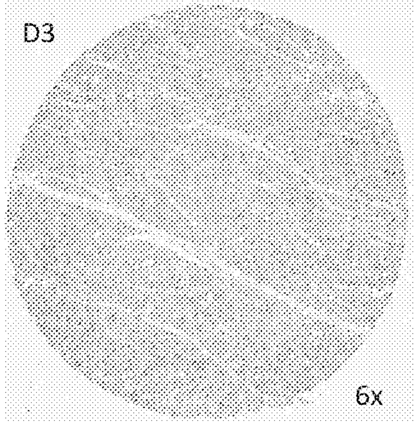


Fig. 158J
Normal Liver

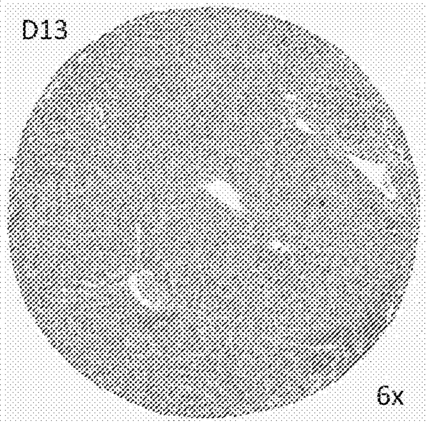


Fig. 158K
Normal Lung

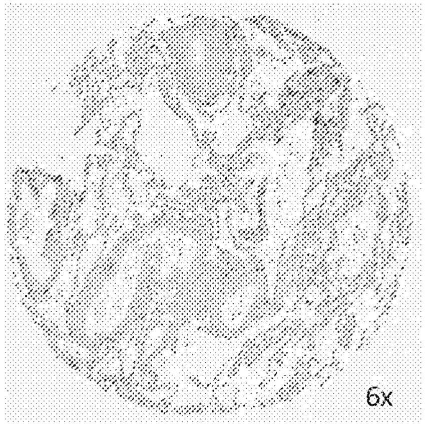


Fig. 158L
Normal Ureter

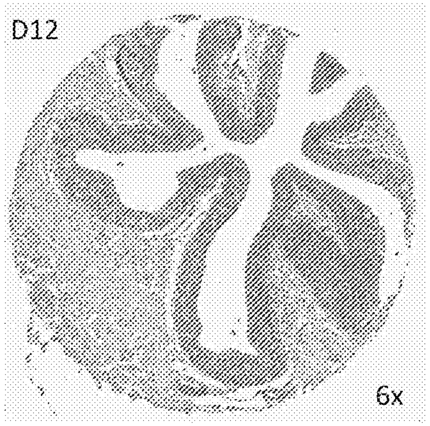


Fig. 158M

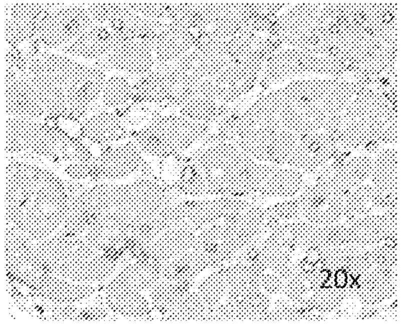


Fig. 158N

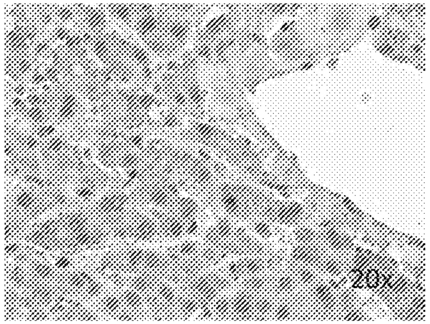


Fig. 158O

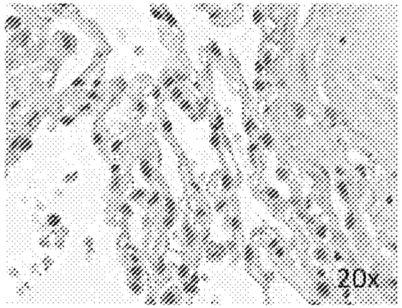


Fig. 158P

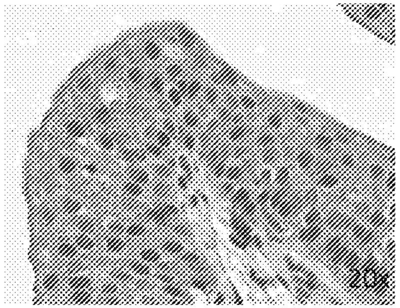


Figure 158I-158P

N+20/C-27 antibody 1E4 IgG 7.5 ug/mL

FDA Normal tissue array MNO1021

Fig. 158Q
Normal eye

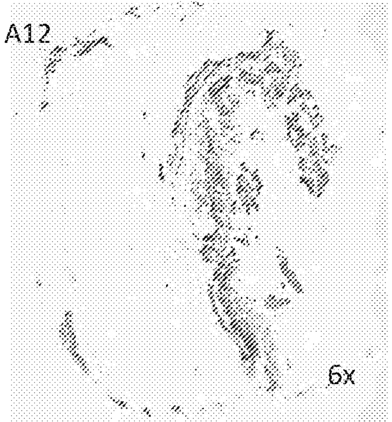


Fig. 158R
Normal Cerebral cortex

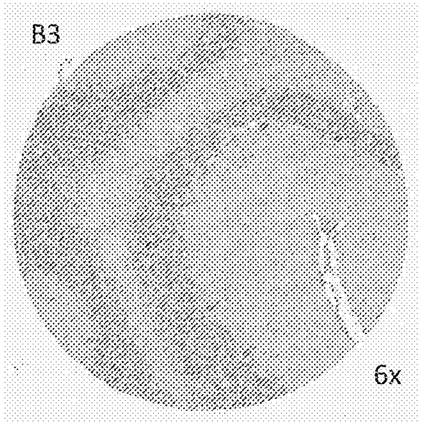


Fig. 158S
Normal Bone marrow

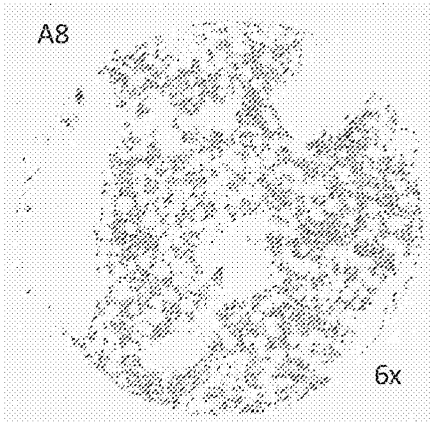


Fig. 158T
Normal Skeletal muscle

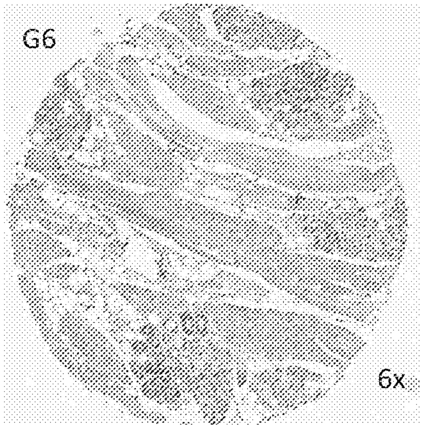


Fig. 158U

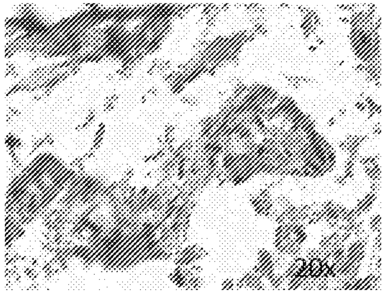


Fig. 158V

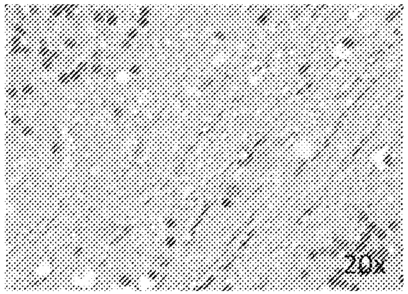


Fig. 158W

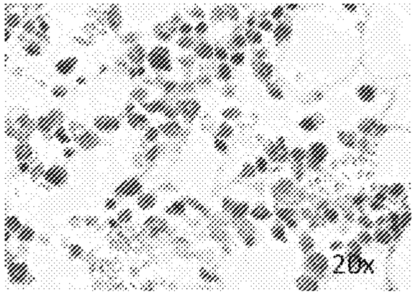


Fig. 158X

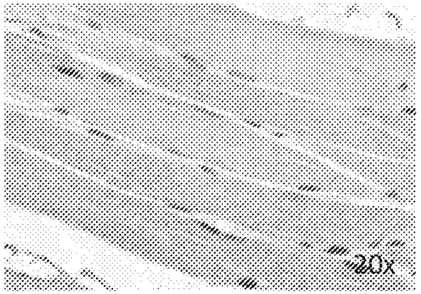


Figure 158Q-158X

N+20/C-27 antibody 1E4 IgG 10 ug/mL

Breast cancer tissue array BR1007

Fig. 159A

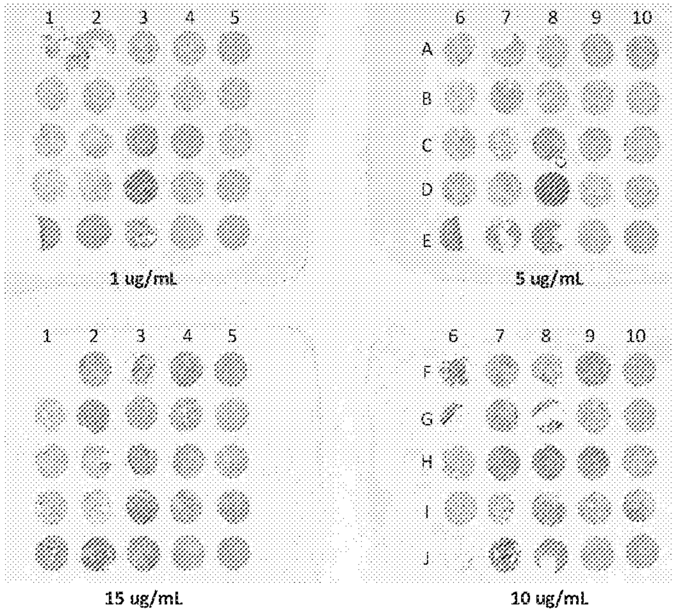


Fig. 159B

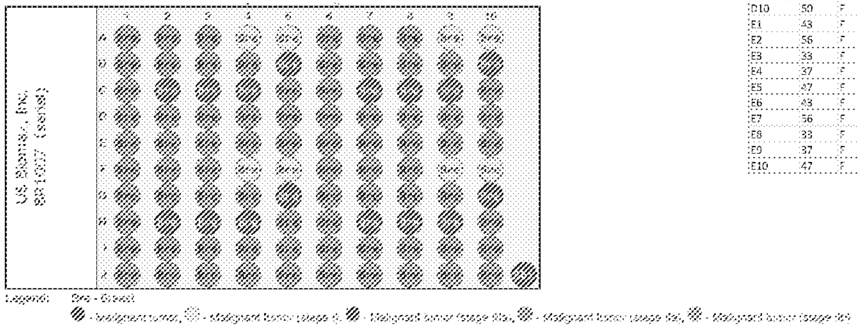


Fig. 159C

Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type
A1	63	F	Invasive ductal carcinoma	T3N1M0	2	IIb	malignant
A2	43	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
A3	52	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
A4	52	F	Invasive ductal carcinoma	T1N0M0	2	I	malignant
A5	34	F	Invasive ductal carcinoma	T1N0M0	2	I	malignant
A6	63	F	Invasive ductal carcinoma	T3N1M0	2	IIb	malignant
A7	43	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
A8	52	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
A9	52	F	Invasive ductal carcinoma	T1N0M0	2	I	malignant
A10	34	F	Invasive ductal carcinoma	T1N0M0	2	I	malignant
B1	47	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
B2	45	F	Invasive ductal carcinoma	T2N0M0	2	IIa	malignant
B3	55	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
B4	64	F	Invasive ductal carcinoma	T1N1M0	2	IIa	malignant
B5	39	F	Invasive ductal carcinoma	T2N2M0	2	IIIa	malignant
B6	47	F	Invasive ductal carcinoma	T2N1M0	-	IIb	malignant
B7	45	F	Invasive ductal carcinoma	T2N0M0	2	IIa	malignant
B8	55	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
B9	64	F	Invasive ductal carcinoma	T1N1M0	2	IIa	malignant
B10	39	F	Invasive ductal carcinoma	T2N2M0	2	IIIa	malignant
C1	49	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
C2	61	F	Invasive ductal carcinoma	T2N2M0	2	IIIa	malignant
C3	52	F	Invasive ductal carcinoma	T2N2M0	2	IIIa	malignant
C4	48	F	Invasive ductal carcinoma	T4N0M0	2	IIIa	malignant
C5	57	F	Invasive ductal carcinoma	T2N0M0	2	IIa	malignant
C6	49	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
C7	61	F	Invasive ductal carcinoma	T2N2M0	-	IIIa	malignant
C8	52	F	Invasive ductal carcinoma	T2N2M0	2	IIIa	malignant
C9	48	F	Invasive ductal carcinoma	T4N0M0	2	IIIa	malignant
C10	57	F	Invasive ductal carcinoma	T2N0M0	2	IIa	malignant
D1	50	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
D2	33	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
D3	54	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
D4	46	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
D5	50	F	Invasive ductal carcinoma	T2N0M0	2	IIa	malignant
D6	50	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
D7	33	F	Invasive ductal carcinoma	T2N1M0	-	IIb	malignant
D8	54	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
D9	46	F	Invasive ductal carcinoma	T2N1M0	3	IIb	malignant
D10	50	F	Invasive ductal carcinoma	T2N0M0	2	IIa	malignant
E1	43	F	Invasive ductal carcinoma	T2N1M0	3	IIb	malignant
E2	56	F	Invasive ductal carcinoma	T2N0M0	3	IIa	malignant
E3	33	F	Invasive ductal carcinoma	T2N0M0	3	IIa	malignant
E4	37	F	Invasive ductal carcinoma	T2N1M0	3	IIb	malignant
E5	47	F	Invasive ductal carcinoma	T3N1M0	3	IIb	malignant
E6	43	F	Invasive ductal carcinoma	T2N1M0	3	IIb	malignant
E7	56	F	Invasive ductal carcinoma	T2N0M0	3	IIa	malignant
E8	33	F	Invasive ductal carcinoma	T2N0M0	3	IIa	malignant
E9	37	F	Invasive ductal carcinoma	T2N1M0	3	IIb	malignant
E10	47	F	Invasive ductal carcinoma	T3N1M0	3	IIb	malignant
F1	63	F	Invasive ductal carcinoma	T3N1M0	2	IIb	malignant
F2	43	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
F3	52	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
F4	52	F	Invasive ductal carcinoma	T1N0M0	2	I	malignant
F5	34	F	Invasive ductal carcinoma	T1N0M0	2	I	malignant
F6	63	F	Invasive ductal carcinoma	T3N1M0	2	IIb	malignant
F7	43	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
F8	52	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
F9	52	F	Invasive ductal carcinoma	T1N0M0	2	I	malignant
F10	34	F	Invasive ductal carcinoma	T1N0M0	2	I	malignant
G1	47	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
G2	45	F	Invasive ductal carcinoma	T2N0M0	2	IIa	malignant
G3	55	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
G4	64	F	Invasive ductal carcinoma	T1N1M0	2	IIa	malignant
G5	39	F	Invasive ductal carcinoma	T2N2M0	2	IIIa	malignant
G6	47	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
G7	45	F	Invasive ductal carcinoma	T2N0M0	2	IIa	malignant
G8	55	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
G9	64	F	Invasive ductal carcinoma	T1N1M0	2	IIa	malignant
G10	39	F	Invasive ductal carcinoma	T2N2M0	2	IIIa	malignant
H1	49	F	Invasive ductal carcinoma	T2N1M0	-	IIb	malignant
H2	61	F	Invasive ductal carcinoma	T2N2M0	2	IIIa	malignant
H3	52	F	Invasive ductal carcinoma	T2N2M0	2	IIIa	malignant
H4	48	F	Invasive ductal carcinoma	T4N0M0	2	IIIa	malignant
H5	57	F	Invasive ductal carcinoma	T2N0M0	2	IIa	malignant
H6	49	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
H7	61	F	Invasive ductal carcinoma	T2N2M0	2	IIIa	malignant
H8	52	F	Invasive ductal carcinoma	T2N2M0	2	IIIa	malignant
H9	48	F	Invasive ductal carcinoma	T4N0M0	2	IIIa	malignant
H10	57	F	Invasive ductal carcinoma	T2N0M0	2	IIa	malignant
I1	50	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
I2	33	F	Invasive ductal carcinoma	T2N1M0	-	IIb	malignant
I3	54	F	Invasive ductal carcinoma	T2N1M0	3	IIb	malignant
I4	46	F	Invasive ductal carcinoma	T2N1M0	3	IIb	malignant
I5	50	F	Invasive ductal carcinoma	T2N0M0	2	IIa	malignant
I6	50	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
I7	33	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
I8	54	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
I9	46	F	Invasive ductal carcinoma	T2N1M0	3	IIb	malignant
I10	50	F	Invasive ductal carcinoma	T2N0M0	2	IIa	malignant
J1	43	F	Invasive ductal carcinoma	T2N1M0	3	IIb	malignant
J2	56	F	Invasive ductal carcinoma	T2N0M0	3	IIa	malignant
J3	33	F	Invasive ductal carcinoma	T2N0M0	3	IIa	malignant
J4	37	F	Invasive ductal carcinoma	T2N1M0	3	IIb	malignant
J5	47	F	Invasive ductal carcinoma	T3N1M0	3	IIb	malignant
J6	43	F	Invasive ductal carcinoma	T2N1M0	3	IIb	malignant
J7	56	F	Invasive ductal carcinoma	T2N0M0	3	IIa	malignant
J8	33	F	Invasive ductal carcinoma	T2N0M0	3	IIa	malignant
J9	37	F	Invasive ductal carcinoma	T2N1M0	3	IIb	malignant
J10	47	F	Invasive ductal carcinoma	T3N1M0	3	IIb	malignant

Figure 159A-159C

N+20/C-27 antibody 1E4 IgG 10 ug/mL

Breast cancer tissue array BR1007

Fig. 160A

Position: B4

Cell Type: Invasive Ductal Carcinoma
Tumor Grade: 2
TNM: T1N1M0

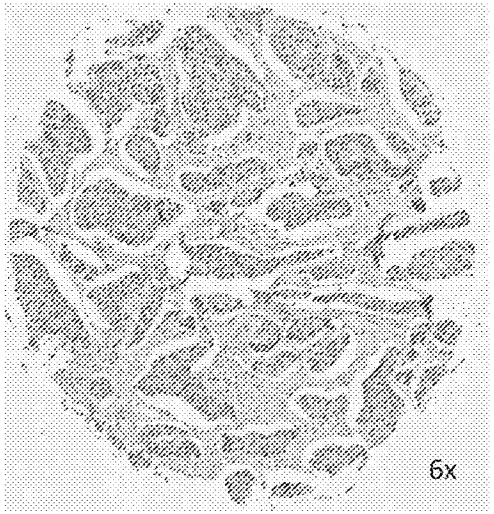


Fig. 160B

Position: C4

Cell Type: Invasive Ductal Carcinoma
Tumor Grade: 2
TNM: T4N0M0

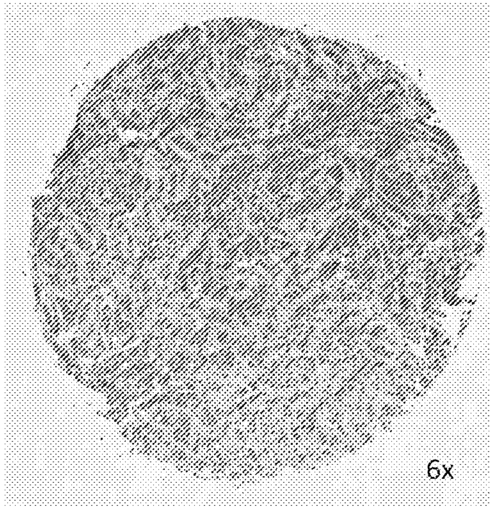


Fig. 160C

Position: D5

Cell Type: Invasive Ductal Carcinoma
Tumor Grade: 2
TNM: T2N0M0

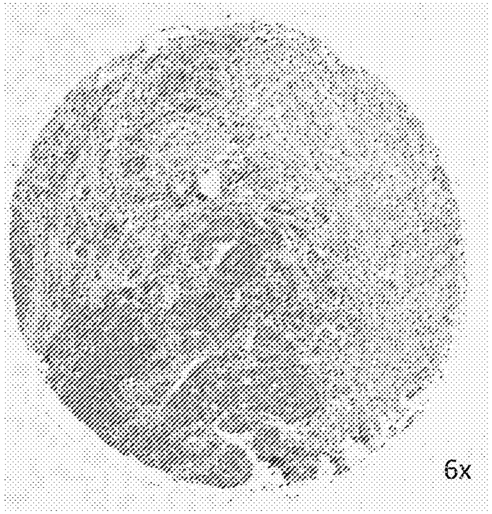


Fig. 160D

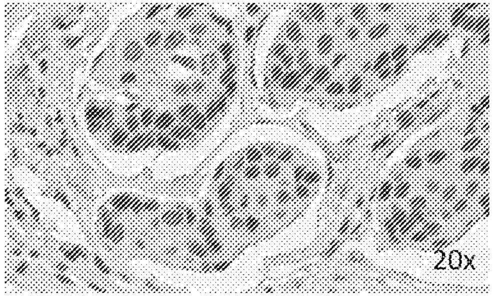


Fig. 160E

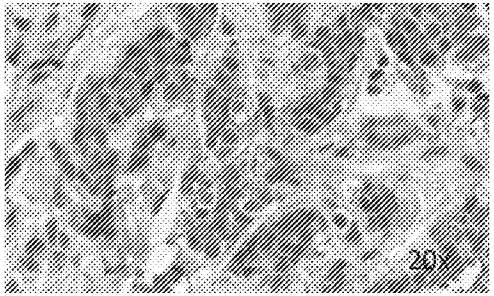


Fig. 160F

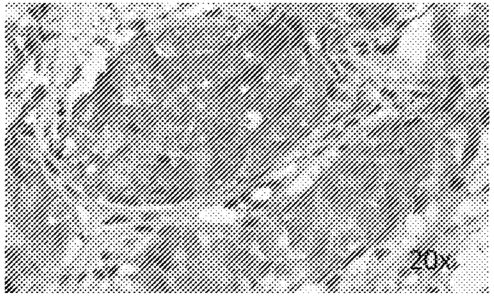


Fig. 160A– 160F

N+20/C-27 antibody 29H1 IgG 0.5 ug/mL

FDA Normal tissue array MNO1021

Fig. 161A

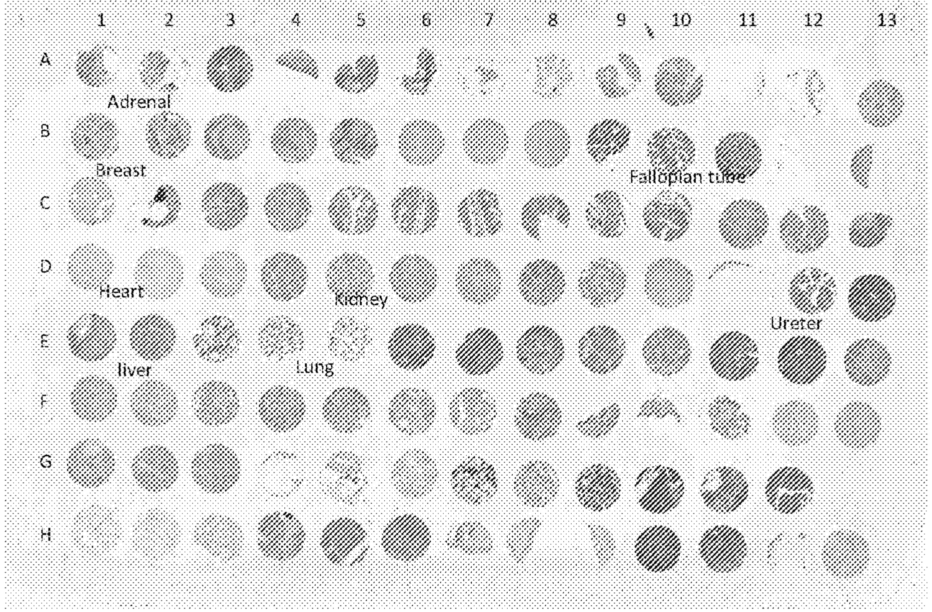


Fig. 161B

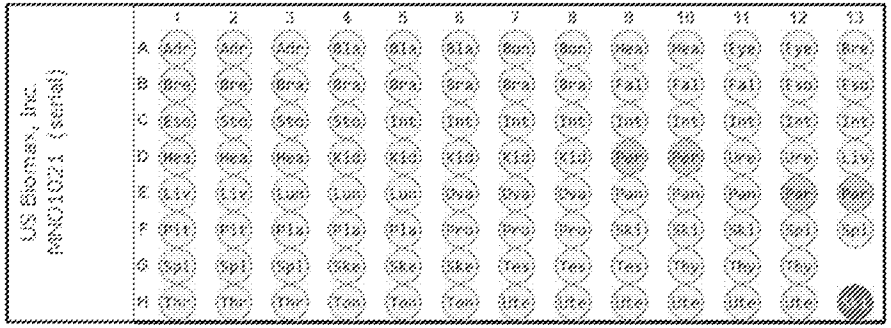


Figure 161A-161C

Fig. 161C

Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis	Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis
A1	F	31	Adrenal gland	Normal	E1	M	59	Liver	Normal
A2	M	51	Adrenal gland	Normal	E2	F	27	Liver	Normal
A3	M	53	Adrenal gland	Normal	E3	M	72	Lung	Normal
A4	M	75	Bladder, urnary	Normal	E4	F	55	Lung	Normal
A5	M	72	Bladder, urnary	Normal	E5	M	43	Lung	Normal
A6	M	52	Bladder, urnary	Normal	E6	F	47	Ovary	Normal
A7	M	53	Bone, bone marrow	Normal	E7	F	46	Ovary	Normal
A8	M	43	Bone, bone marrow	Normal	E8	F	40	Ovary	Normal
A9	F	44	Head and neck, salivary gland	Normal	E9	M	42	Pancreas	Normal
A10	M	18	Head and neck, salivary gland	Normal	E10	F	26	Pancreas	Normal
A11	M	55	Eye	Normal	E11	F	59	Pancreas	Normal
A12	M	50	Eye	Normal	E12	M	17	Parathyroid	Adenoma
A13	F	35	Breast	Normal	E13	M	72	Parathyroid	Adenoma
B1	F	38	Breast	Normal	F1	F	3	Pituitary gland	Normal
B2	F	33	Breast	Normal	F2	F		Pituitary gland	Normal
B3	M	58	Brain, cerebellum	Normal	F3	F	32	Placenta	Normal
B4	M	65	Brain, cerebellum	Normal	F4	F	30	Placenta	Normal
B5	F		Brain, cerebellum	Normal	F5	F	27	Placenta	Normal
B6	M	56	Brain, cerebral cortex	Normal	F6	M	64	Prostate	Normal
B7	M	65	Brain, cerebral cortex	Normal	F7	M	65	Prostate	Normal
B8	F		Brain, cerebral cortex	Normal	F8	M	65	Prostate	Normal
B9	F	42	Fallopian tube	Normal	F9	F	32	Skin	Normal
B10	F	32	Fallopian tube	Normal	F10	F	68	Skin	Normal
B11	F	24	Fallopian tube	Normal	F11	M	26	Skin	Normal
B12	M	45	Esophagus	Normal	F12	M	47	Spinal cord	Normal
B13	F	68	Esophagus	Normal	F13	M	58	Spinal cord	Normal
C1	M	54	Esophagus	Normal	G1	M	27	Spleen	Normal
C2	M	45	Stomach	Normal	G2	M	60	Spleen	Normal
C3	M	49	Stomach	Normal	G3	M	31	Spleen	Normal
C4	M	77	Stomach	Normal	G4	F	60	Skeletal muscle	Normal
C5	M	45	Intestine, small intestine	Normal	G5	F	49	Skeletal muscle	Normal
C6	F	75	Intestine, small intestine	Normal	G6	M	70	Skeletal muscle	Normal
C7	F	75	Intestine, small intestine	Normal	G7	M	43	Testis	Normal
C8	M	2	Intestine, colon	Normal	G8	M	30	Testis	Normal
C9	M	46	Intestine, colon	Normal	G9	M	77	Testis	Normal
C10	M	74	Intestine, colon	Normal	G10	M	15	Thymus	Normal
C11	F	47	Intestine, rectum	Normal	G11	M	28	Thymus	Normal
C12	F	75	Intestine, rectum	Normal	G12	F	9	Thymus	Normal
C13	M	66	Intestine, rectum	Normal	G13	-	-	-	-
D1	M	58	Heart	Normal	H1	F	26	Thyroid	Normal
D2	M	46	Heart	Normal	H2	F	37	Thyroid	Normal
D3	F	34	Heart	Normal	H3	F	51	Thyroid	Normal
D4	F	52	Kidney, cortex	Normal	H4	M	46	Tonsil	Normal
D5	M	23	Kidney, cortex	Normal	H5	M	37	Tonsil	Normal
D6	M	63	Kidney, cortex	Normal	H6	M	13	Tonsil	Normal
D7	F	52	Kidney, medulla	Normal	H7	F	38	Uterus, cervix	Normal
D8	M	23	Kidney, medulla	Normal	H8	F	35	Uterus, cervix	Normal
D9	M	59	Peripheral nerve	Schwannoma	H9	F	44	Uterus, cervix	Normal
D10	F	29	Peripheral nerve	Schwannoma	H10	F	38	Uterus, endometrium	Normal
D11	F	44	Ureter	Normal	H11	F	41	Uterus, endometrium	Normal
D12	F	42	Ureter	Normal	H12	F	46	Uterus, endometrium	Normal
D13	F	57	Liver	Normal	H13	M	58	Skin	Malignant melanoma (tissue marker)

N+20/C-27 antibody 29H1 IgG 0.5 ug/mL

FDA Normal tissue array MNO1021

Fig. 162A
Normal Adrenal Gland

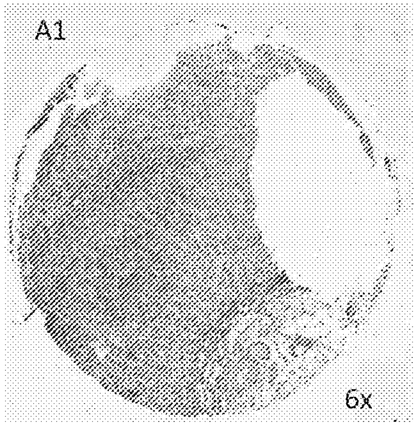


Fig. 162B
Normal Breast

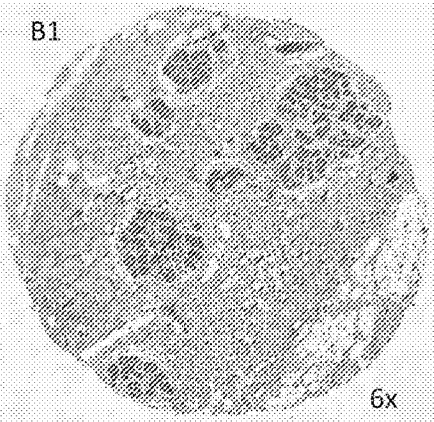


Fig. 162C
Normal Fallopian Tubes

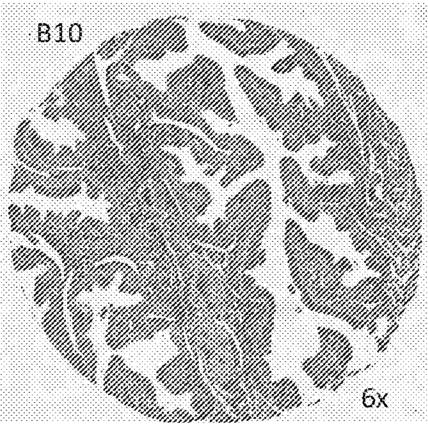


Fig. 162D
Normal Kidney

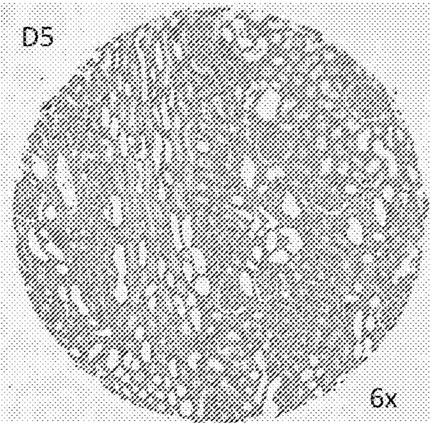


Fig. 162E

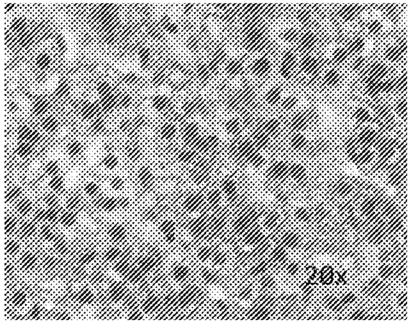


Fig. 162F

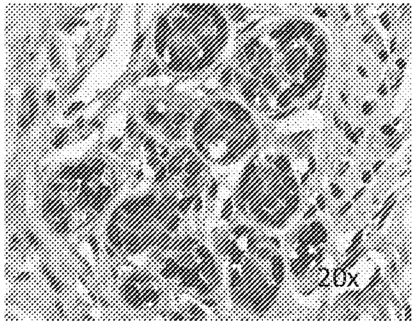


Fig. 162G

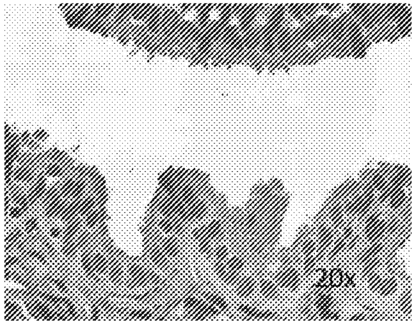


Fig. 162H

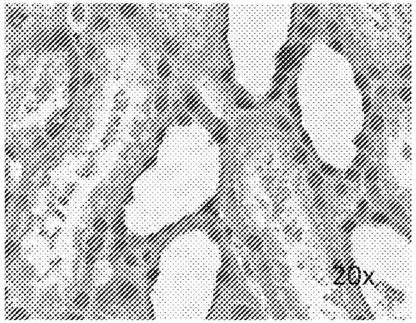


Figure 162A-162H

N+20/C-27 antibody 29H1 IgG 0.5 ug/mL
FDA Normal tissue array MNO1021

Fig. 162I
Normal Heart

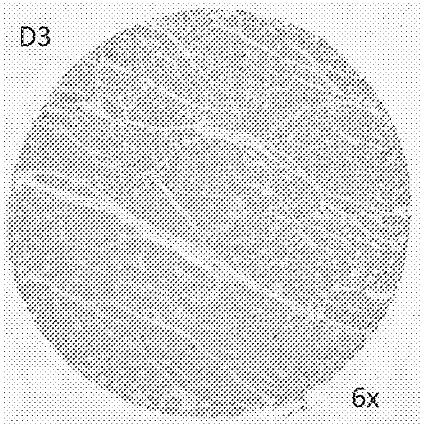


Fig. 162J
Normal Liver

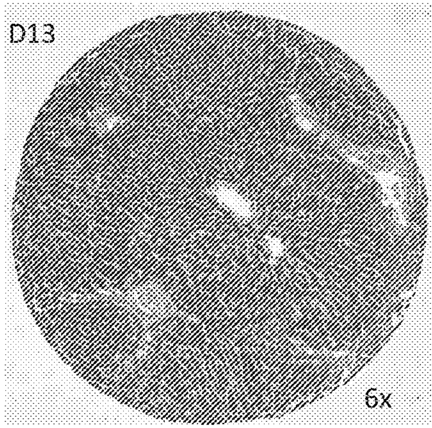


Fig. 162K
Normal Lung

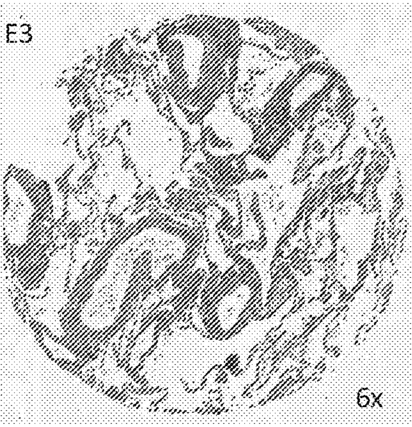


Fig. 162L
Normal Ureter

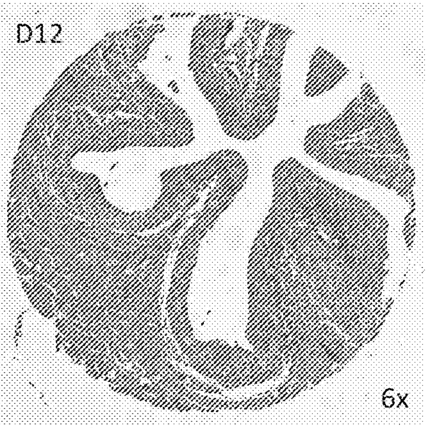


Fig. 162M

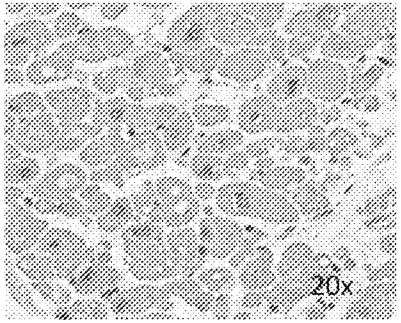


Fig. 162N

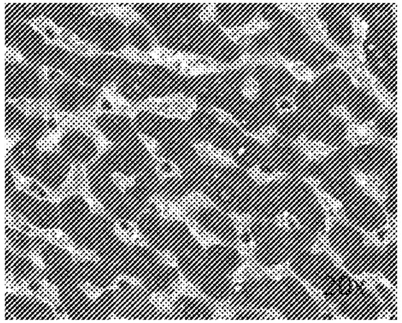


Fig. 162O

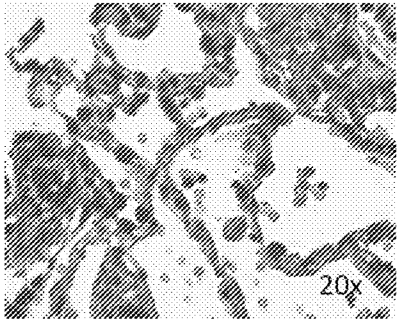


Fig. 162P

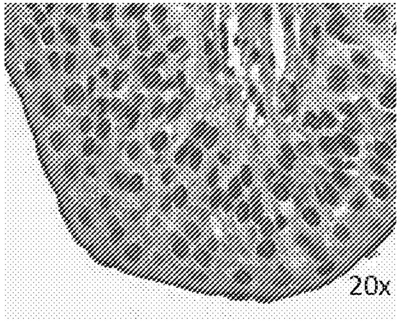


Figure 162I-162P

N+20/C-27 antibody 29H1 IgG 0.5 ug/mL

FDA Normal tissue array MNO1021

Fig. 162Q
Normal eye

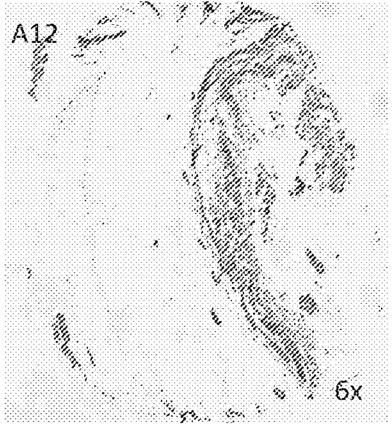


Fig. 162R
Normal Cerebral cortex

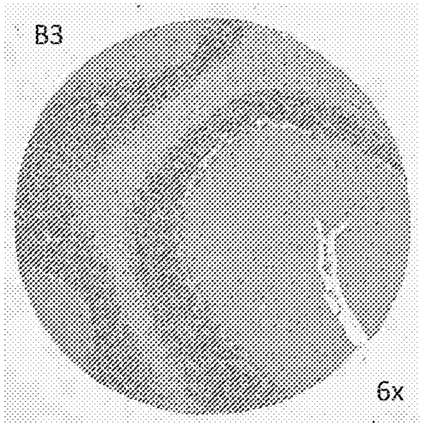


Fig. 162S
Normal Bone marrow

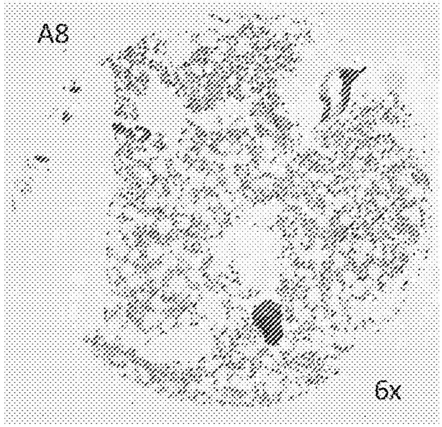


Fig. 162T
Normal Skeletal muscle

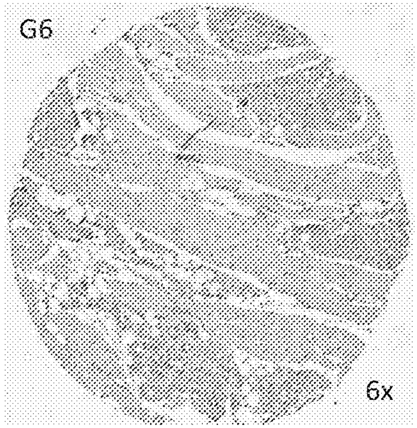


Fig. 162U

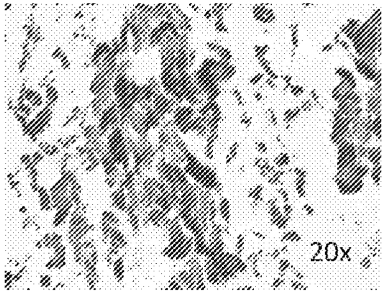


Fig. 162V

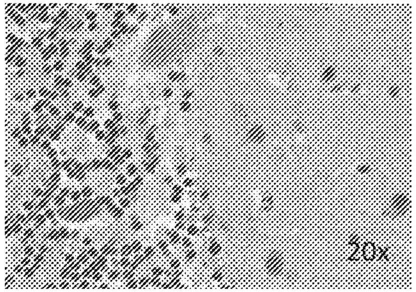


Fig. 162W

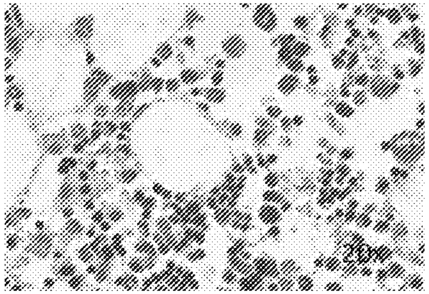


Fig. 162X

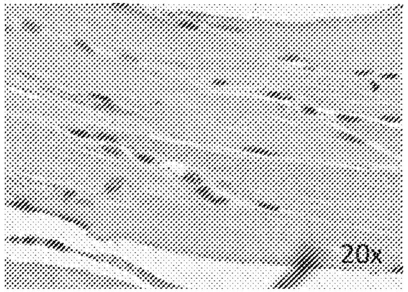


Figure 162Q-162X

N+20/C-27 antibody 29H1 IgG 0.5 ug/mL

Breast cancer tissue array Br1141

Fig. 163A

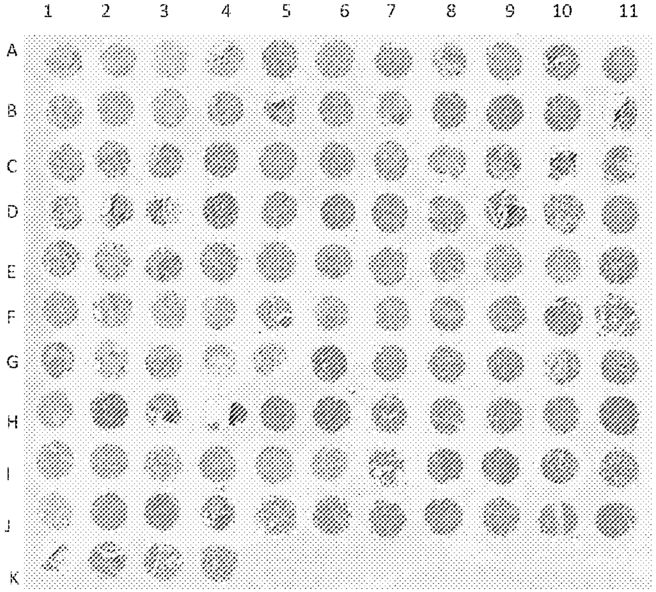


Fig. 163B

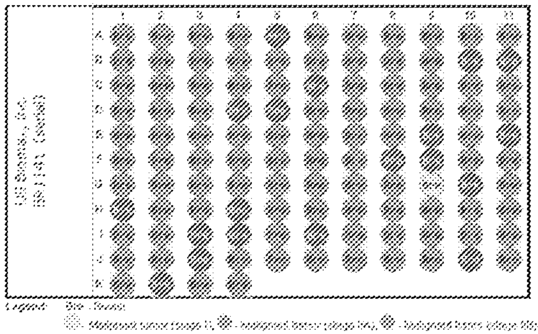
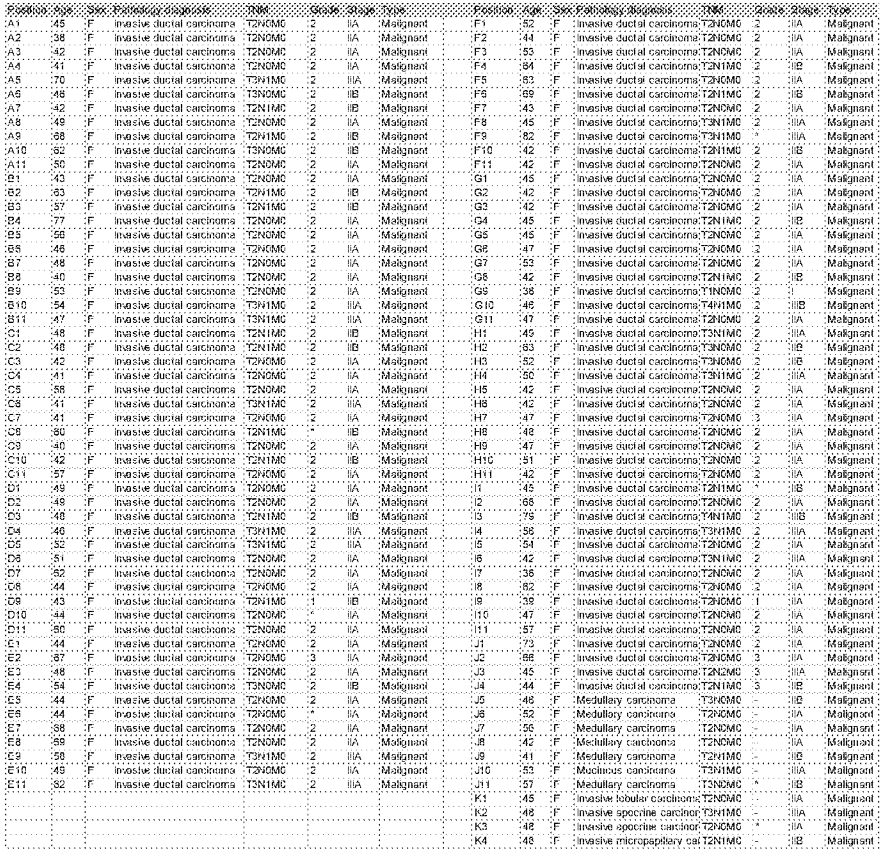


Figure 163A-163C

Fig. 163C



Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type
A1	45	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A2	38	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A3	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A4	41	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A5	70	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
A6	46	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
A7	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
A8	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A9	68	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
A10	62	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
A11	50	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B1	43	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B2	63	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
B3	57	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
B4	77	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B5	56	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B6	46	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B7	48	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B8	40	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B9	53	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B10	54	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
B11	47	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
C1	48	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
C2	48	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
C3	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C4	41	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C5	56	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C6	41	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
C7	41	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C8	60	F	Invasive ductal carcinoma	T2N1M0	*	IIB	Malignant
C9	40	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C10	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
C11	57	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D1	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D2	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D3	48	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
D4	46	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
D5	52	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
D6	51	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D7	62	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D8	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D9	43	F	Invasive ductal carcinoma	T2N1M0	1	IIB	Malignant
D10	44	F	Invasive ductal carcinoma	T2N0M0	*	IIA	Malignant
D11	60	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E1	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E2	67	F	Invasive ductal carcinoma	T2N0M0	3	IIA	Malignant
E3	48	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E4	54	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
E5	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E6	44	F	Invasive ductal carcinoma	T2N0M0	*	IIA	Malignant
E7	38	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E8	59	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E9	58	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
E10	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E11	32	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
F1	52	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F2	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F3	53	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F4	64	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
F5	63	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F6	69	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
F7	43	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F8	45	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
F9	82	F	Invasive ductal carcinoma	T3N1M0	*	IIIA	Malignant
F10	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
F11	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G1	45	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G2	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G3	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G4	45	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
G5	45	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G6	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G7	53	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G8	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
G9	38	F	Invasive ductal carcinoma	T1N0M0	2	I	Malignant
G10	46	F	Invasive ductal carcinoma	T4N1M0	2	IIIB	Malignant
G11	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H1	49	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
H2	63	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
H3	52	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
H4	50	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
H5	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H6	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H7	47	F	Invasive ductal carcinoma	T2N0M0	3	IIA	Malignant
H8	48	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H9	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H10	51	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H11	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I1	45	F	Invasive ductal carcinoma	T2N1M0	*	IIB	Malignant
I2	68	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I3	79	F	Invasive ductal carcinoma	T4N1M0	2	IIIB	Malignant
I4	56	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
I5	54	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I6	42	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
I7	38	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I8	62	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I9	39	F	Invasive ductal carcinoma	T2N0M0	1	IIA	Malignant
I10	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I11	57	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
J1	73	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
J2	66	F	Invasive ductal carcinoma	T2N0M0	3	IIA	Malignant
J3	45	F	Invasive ductal carcinoma	T2N2M0	3	IIIA	Malignant
J4	44	F	Invasive ductal carcinoma	T2N1M0	3	IIB	Malignant
J5	46	F	Medullary carcinoma	T3N0M0	-	IIB	Malignant
J6	52	F	Medullary carcinoma	T2N0M0	-	IIA	Malignant
J7	56	F	Medullary carcinoma	T2N0M0	-	IIA	Malignant
J8	42	F	Medullary carcinoma	T2N0M0	-	IIA	Malignant
J9	41	F	Medullary carcinoma	T2N1M0	-	IIB	Malignant
J10	53	F	Mucinous carcinoma	T3N1M0	-	IIIA	Malignant
J11	57	F	Medullary carcinoma	T3N0M0	*	IIB	Malignant
K1	45	F	Invasive lobular carcinoma	T2N0M0	-	IIA	Malignant
K2	48	F	Invasive apocrine carcinor	T3N1M0	-	IIIA	Malignant
K3	48	F	Invasive apocrine carcinor	T2N0M0	*	IIA	Malignant
K4	48	F	Invasive micropapillary cai	T2N1M0	-	IIB	Malignant

N+20/C-27 antibody 29H1 IgG 0.5ug/mL

Breast cancer tissue array Br1141

Fig. 164A

Position: A4
Cell Type: Invasive Ductal Carcinoma
Tumor Grade: 2
TNM: T2N0M0

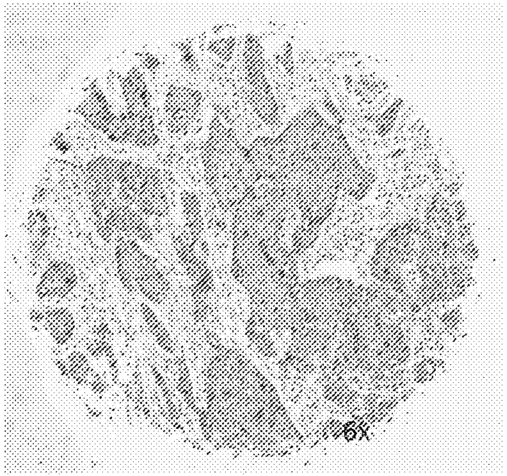


Fig. 164B

Position: A11
Cell Type: Invasive Ductal Carcinoma
Tumor Grade: 2
TNM: T2N0M0

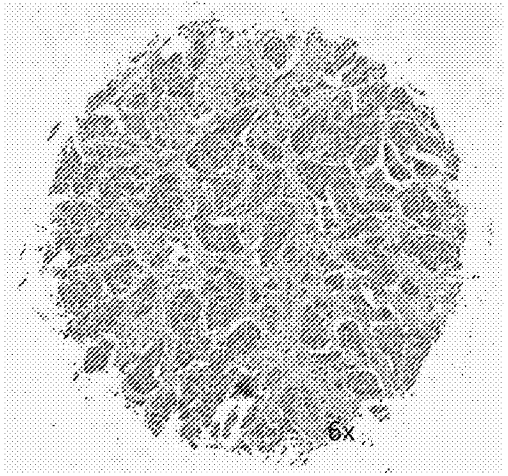


Fig. 164C

Position: G11
Cell Type: Invasive Ductal Carcinoma
Tumor Grade: 2
TNM: T2N0M0

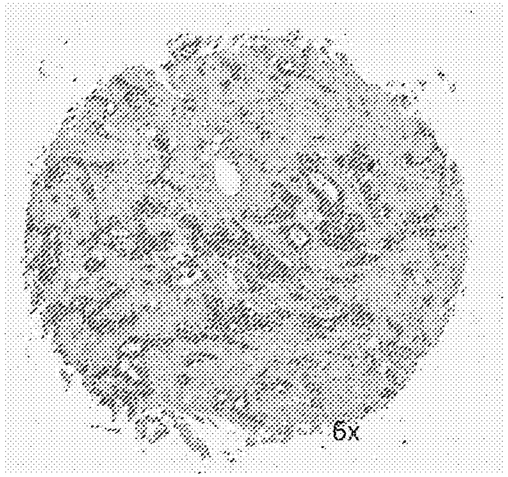


Fig. 164D

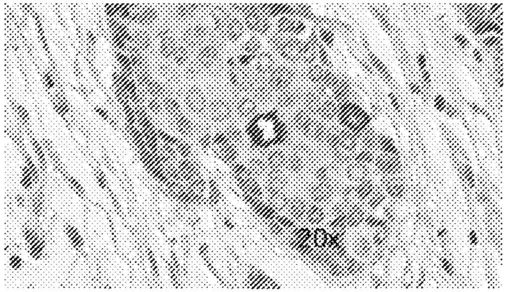


Fig. 164E

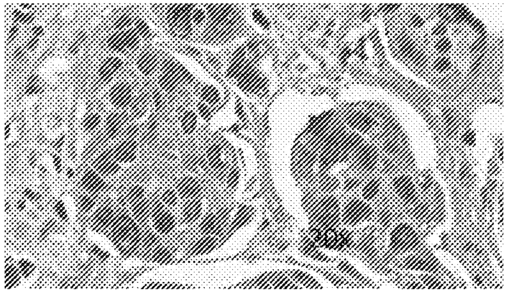


Fig. 164F

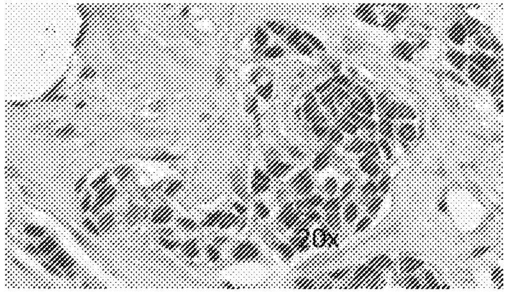


Fig. 164A–164F

N+20/C-27-antibody 29H1 0.1 - 4 ug/mL

Pancreatic cancer tissue array PA1003

Fig. 165A

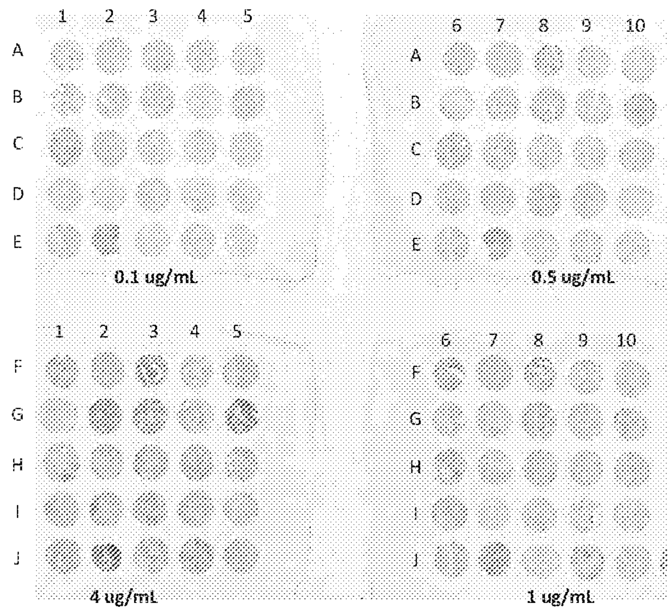


Fig. 165B

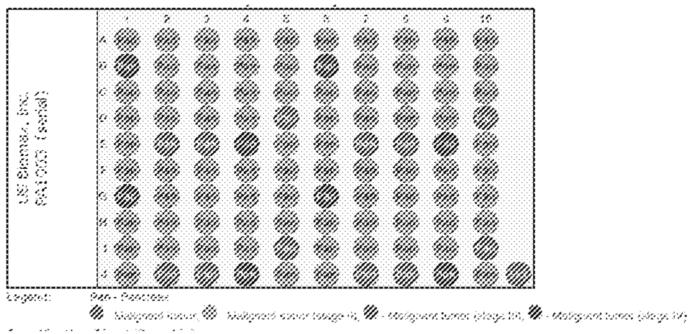


Fig. 165C

Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type	Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type
A1	39	F	Adenocarcinoma	T3N0M0	2	II	malignant	F1	39	F	Adenocarcinoma	T3N0M0	2	II	malignant
A2	44	M	Adenocarcinoma	T3N0M0	2	II	malignant	F2	44	M	Adenocarcinoma	T3N0M0	2	II	malignant
A3	59	M	Adenocarcinoma	T3N0M0	2	II	malignant	F3	59	M	Adenocarcinoma	T3N0M0	2	II	malignant
A4	65	M	Adenocarcinoma	T3N0M0	2	II	malignant	F4	65	M	Adenocarcinoma	T3N0M0	2	II	malignant
A5	53	M	Adenocarcinoma	T3N0M0	2	II	malignant	F5	53	M	Adenocarcinoma	T3N0M0	2	II	malignant
A6	39	F	Adenocarcinoma	T3N0M0	2	II	malignant	F6	39	F	Adenocarcinoma	T3N0M0	2	II	malignant
A7	44	M	Adenocarcinoma	T3N0M0	2	II	malignant	F7	44	M	Adenocarcinoma	T3N0M0	2	II	malignant
A8	59	M	Adenocarcinoma	T3N0M0	2	II	malignant	F8	59	M	Adenocarcinoma	T3N0M0	2	II	malignant
A9	65	M	Adenocarcinoma	T3N0M0	2	II	malignant	F9	65	M	Adenocarcinoma	T3N0M0	-	II	malignant
A10	53	M	Adenocarcinoma	T3N0M0	2	II	malignant	F10	53	M	Adenocarcinoma	T3N0M0	2	II	malignant
B1	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant	G1	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant
B2	52	M	Adenocarcinoma	T3N0M0	1	II	malignant	G2	52	M	Adenocarcinoma	T3N0M0	1	II	malignant
B3	57	M	Adenocarcinoma	T3N0M0	2	II	malignant	G3	57	M	Adenocarcinoma	T3N0M0	2	II	malignant
B4	34	M	Adenocarcinoma	T3N0M0	2	II	malignant	G4	34	M	Adenocarcinoma	T3N0M0	2	II	malignant
B5	72	F	Adenocarcinoma	T3N0M0	2	II	malignant	G5	72	F	Adenocarcinoma	T3N0M0	1	II	malignant
B6	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant	G6	42	M	Adenocarcinoma	T2N0M1	-	IV	malignant
B7	52	M	Adenocarcinoma	T3N0M0	2	II	malignant	G7	52	M	Adenocarcinoma	T3N0M0	2	II	malignant
B8	57	M	Adenocarcinoma	T3N0M0	2	II	malignant	G8	57	M	Adenocarcinoma	T3N0M0	2	II	malignant
B9	34	M	Adenocarcinoma	T3N0M0	1	II	malignant	G9	34	M	Adenocarcinoma	T3N0M0	2	II	malignant
B10	72	F	Adenocarcinoma	T3N0M0	2	II	malignant	G10	72	F	Adenocarcinoma	T3N0M0	2	II	malignant
C1	47	M	Adenocarcinoma	T3N0M0	1	II	malignant	H1	47	M	Adenocarcinoma	T3N0M0	1	II	malignant
C2	64	F	Adenocarcinoma	T3N0M0	1	II	malignant	H2	64	F	Adenocarcinoma	T3N0M0	-	II	malignant
C3	51	M	Adenocarcinoma	T3N0M0	2	II	malignant	H3	51	M	Adenocarcinoma	T3N0M0	2	II	malignant
C4	68	F	Adenocarcinoma	T3N0M0	2	II	malignant	H4	68	F	Adenocarcinoma	T3N0M0	3	II	malignant
C5	41	M	Adenocarcinoma	T3N0M0	-	II	malignant	H5	41	M	Adenocarcinoma	T3N0M0	2	II	malignant
C6	47	M	Adenocarcinoma	T3N0M0	1	II	malignant	H6	47	M	Adenocarcinoma	T3N0M0	1	II	malignant
C7	64	F	Adenocarcinoma	T3N0M0	2	II	malignant	H7	64	F	Adenocarcinoma	T3N0M0	2	II	malignant
C8	51	M	Adenocarcinoma	T3N0M0	2	II	malignant	H8	51	M	Adenocarcinoma	T3N0M0	-	II	malignant
C9	68	F	Adenocarcinoma	T3N0M0	2	II	malignant	H9	68	F	Adenocarcinoma	T3N0M0	2	II	malignant
C10	41	M	Adenocarcinoma	T3N0M0	2	II	malignant	H10	41	M	Adenocarcinoma	T3N0M0	2	II	malignant
D1	58	F	Adenocarcinoma	T3N0M0	2	II	malignant	I1	58	F	Adenocarcinoma	T3N0M0	2	II	malignant
D2	41	F	Adenocarcinoma	T3N0M0	3	II	malignant	I2	41	F	Adenocarcinoma	T3N0M0	3	II	malignant
D3	72	F	Adenocarcinoma	T3N0M0	3	II	malignant	I3	72	F	Adenocarcinoma	T3N0M0	3	II	malignant
D4	59	M	Adenocarcinoma	T3N0M0	3	II	malignant	I4	59	M	Adenocarcinoma	T3N0M0	3	II	malignant
D5	50	M	Adenocarcinoma	T3N1M0	3	III	malignant	I5	50	M	Adenocarcinoma	T3N1M0	3	III	malignant
D6	58	F	Adenocarcinoma	T3N0M0	2	II	malignant	I6	58	F	Adenocarcinoma	T3N0M0	2	II	malignant
D7	41	F	Adenocarcinoma	T3N0M0	3	II	malignant	I7	41	F	Adenocarcinoma	T3N0M0	2	II	malignant
D8	72	F	Adenocarcinoma	T3N0M0	3	II	malignant	I8	72	F	Adenocarcinoma	T3N0M0	3	II	malignant
D9	59	M	Adenocarcinoma	T3N0M0	3	II	malignant	I9	59	M	Adenocarcinoma	T3N0M0	3	II	malignant
D10	50	M	Adenocarcinoma	T3N1M0	3	III	malignant	I10	50	M	Adenocarcinoma	T3N1M0	3	III	malignant
E1	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant	J1	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant
E2	60	M	Adenocarcinoma	T3N1M0	2--3	III	malignant	J2	60	M	Adenocarcinoma	T3N1M0	2--3	III	malignant
E3	56	M	Adenocarcinoma	T2N1M0	3	III	malignant	J3	56	M	Adenocarcinoma	T2N1M0	3	III	malignant
E4	60	F	Adenocarcinoma	T2N1M1	3	IV	malignant	J4	60	F	Adenocarcinoma	T2N1M1	2	IV	malignant
E5	66	F	Adenocarcinoma	T3N0M0	-	II	malignant	J5	66	F	Adenocarcinoma	T3N0M0	3	II	malignant
E6	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant	J6	53	F	Adenocarcinoma	T3N0M0	3	II	malignant
E7	60	M	Adenocarcinoma	T3N1M0	2	III	malignant	J7	60	M	Adenocarcinoma	T3N1M0	3	III	malignant
E8	56	M	Adenocarcinoma	T2N1M0	3	III	malignant	J8	56	M	Adenocarcinoma	T2N1M0	3	III	malignant
E9	60	F	Adenocarcinoma	T2N1M1	3	IV	malignant	J9	60	F	Adenocarcinoma	T2N1M1	-	IV	malignant
E10	66	F	Adenocarcinoma	T3N0M0	3	II	malignant	J10	66	F	Adenocarcinoma	T3N0M0	3	II	malignant

Fig. 165A–165C

N+20 antibody 29H1 0.5 ug/mL

Pancreatic cancer tissue array PA1003

Fig. 166A

Position: A8
Cell Type: Adenocarcinoma
Tumor Grade: 2
TNM: T3N0M0

Fig. 166B

Position: B10
Cell Type: Adenocarcinoma
Tumor Grade: 2
TNM: T3N0M0

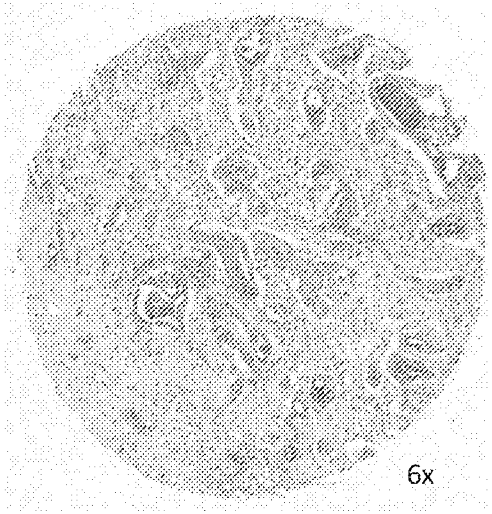


Fig. 166C

Position: D8
Cell Type: Adenocarcinoma
Tumor Grade: 3
TNM: T3N0M0

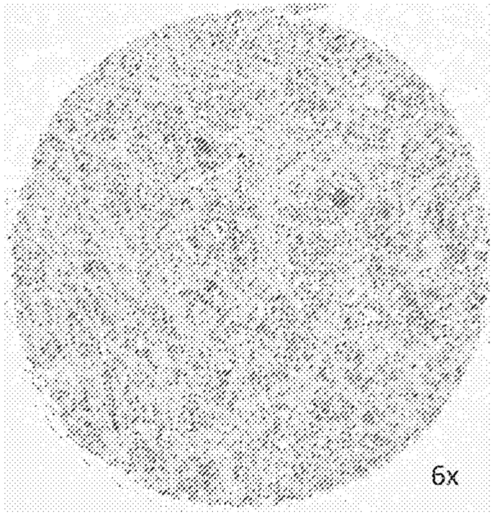


Fig. 166D

Fig. 166E

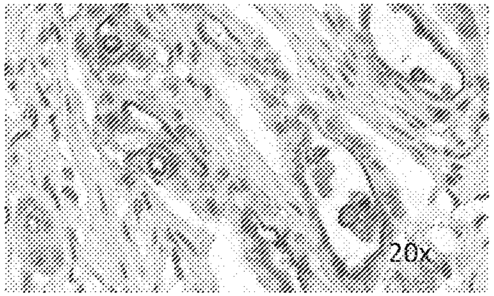


Fig. 166F

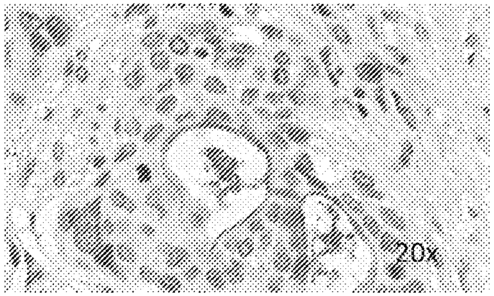


Fig. 166A–166F

N+20/C-27 antibody 31A1 IgG 0.5 ug/mL

FDA Normal tissue array MNO1021

Fig. 167A

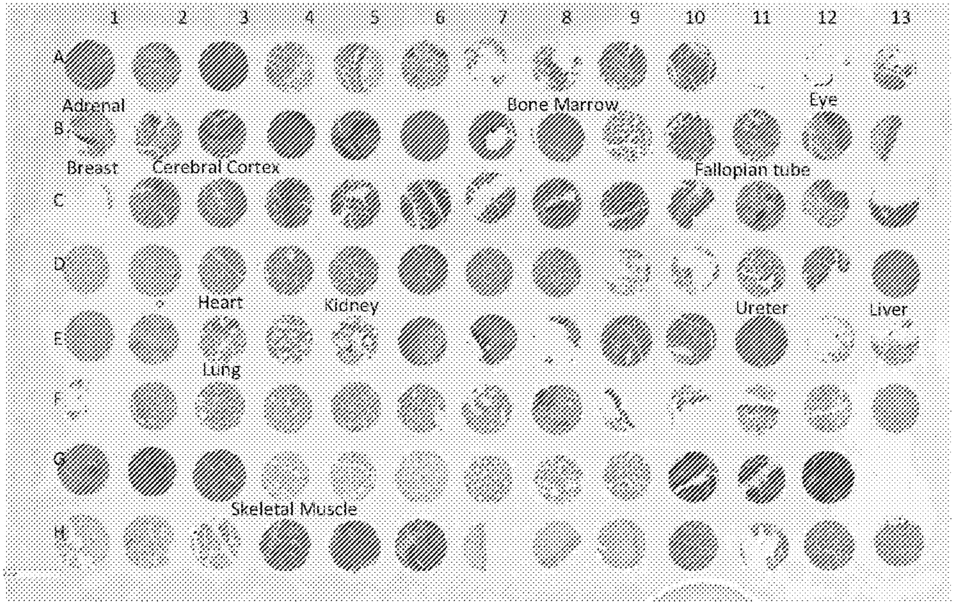


Fig. 167B

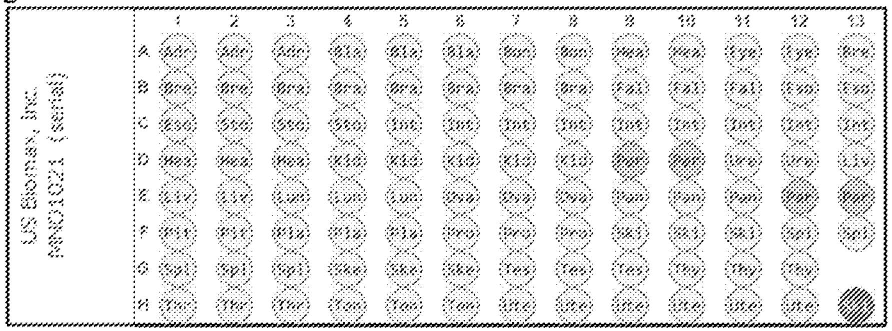


Figure 167A-167C

Fig. 167C

Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis	Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis
A1	F	31	Adrenal gland	Normal	E1	M	59	Liver	Normal
A2	M	51	Adrenal gland	Normal	E2	F	27	Liver	Normal
A3	M	53	Adrenal gland	Normal	E3	M	72	Lung	Normal
A4	M	75	Bladder, umary	Normal	E4	F	55	Lung	Normal
A5	M	72	Bladder, umary	Normal	E5	M	43	Lung	Normal
A6	M	52	Bladder, umary	Normal	E6	F	47	Ovary	Normal
A7	M	53	Bone, bone marrow	Normal	E7	F	46	Ovary	Normal
A8	M	43	Bone, bone marrow	Normal	E8	F	40	Ovary	Normal
A9	F	44	Head and neck, salivary gland	Normal	E9	M	42	Pancreas	Normal
A10	M	18	Head and neck, salivary gland	Normal	E10	F	26	Pancreas	Normal
A11	M	55	Eye	Normal	E11	F	59	Pancreas	Normal
A12	M	50	Eye	Normal	E12	M	17	Parathyroid	Adenoma
A13	F	35	Breast	Normal	E13	M	72	Parathyroid	Adenoma
B1	F	38	Breast	Normal	F1	F	3	Pituitary gland	Normal
B2	F	33	Breast	Normal	F2	F		Pituitary gland	Normal
B3	M	58	Brain, cerebellum	Normal	F3	F	32	Placenta	Normal
B4	M	65	Brain, cerebellum	Normal	F4	F	30	Placenta	Normal
B5	F		Brain, cerebellum	Normal	F5	F	27	Placenta	Normal
B6	M	56	Brain, cerebral cortex	Normal	F6	M	64	Prostate	Normal
B7	M	65	Brain, cerebral cortex	Normal	F7	M	65	Prostate	Normal
B8	F		Brain, cerebral cortex	Normal	F8	M	65	Prostate	Normal
B9	F	42	Fallopian tube	Normal	F9	F	32	Skin	Normal
B10	F	32	Fallopian tube	Normal	F10	F	68	Skin	Normal
B11	F	24	Fallopian tube	Normal	F11	M	26	Skin	Normal
B12	M	45	Esophagus	Normal	F12	M	47	Spinal cord	Normal
B13	F	68	Esophagus	Normal	F13	M	58	Spinal cord	Normal
C1	M	54	Esophagus	Normal	G1	M	27	Spleen	Normal
C2	M	45	Stomach	Normal	G2	M	60	Spleen	Normal
C3	M	49	Stomach	Normal	G3	M	31	Spleen	Normal
C4	M	77	Stomach	Normal	G4	F	60	Skeletal muscle	Normal
C5	M	45	Intestine, small intestine	Normal	G5	F	49	Skeletal muscle	Normal
C6	F	75	Intestine, small intestine	Normal	G6	M	70	Skeletal muscle	Normal
C7	F	75	Intestine, small intestine	Normal	G7	M	43	Testis	Normal
C8	M	2	Intestine, colon	Normal	G8	M	30	Testis	Normal
C9	M	46	Intestine, colon	Normal	G9	M	77	Testis	Normal
C10	M	74	Intestine, colon	Normal	G10	M	15	Thymus	Normal
C11	F	47	Intestine, rectum	Normal	G11	M	28	Thymus	Normal
C12	F	75	Intestine, rectum	Normal	G12	F	9	Thymus	Normal
C13	M	66	Intestine, rectum	Normal	G13	-	-	-	-
D1	M	58	Heart	Normal	H1	F	26	Thyroid	Normal
D2	M	46	Heart	Normal	H2	F	37	Thyroid	Normal
D3	F	34	Heart	Normal	H3	F	51	Thyroid	Normal
D4	F	52	Kidney, cortex	Normal	H4	M	46	Tonsil	Normal
D5	M	23	Kidney, cortex	Normal	H5	M	37	Tonsil	Normal
D6	M	63	Kidney, cortex	Normal	H6	M	13	Tonsil	Normal
D7	F	52	Kidney, medulla	Normal	H7	F	38	Uterus, cervix	Normal
D8	M	23	Kidney, medulla	Normal	H8	F	35	Uterus, cervix	Normal
D9	M	59	Peripheral nerve	Schwannoma	H9	F	44	Uterus, cervix	Normal
D10	F	29	Peripheral nerve	Schwannoma	H10	F	38	Uterus, endometrium	Normal
D11	F	44	Ureter	Normal	H11	F	41	Uterus, endometrium	Normal
D12	F	42	Ureter	Normal	H12	F	46	Uterus, endometrium	Normal
D13	F	57	Liver	Normal	H13	M	58	Skin	Malignant melanoma (tissue marker)

N+20/C-27 antibody 31A1 IgG 0.5 ug/mL

FDA Normal tissue array MNO1021

Fig. 168A
Normal Adrenal Gland

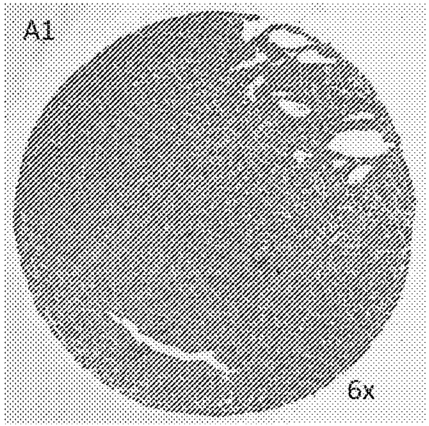


Fig. 168B
Normal Breast

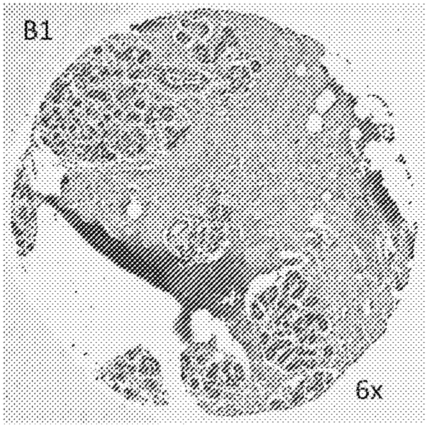


Fig. 168C
Normal Fallopian Tubes

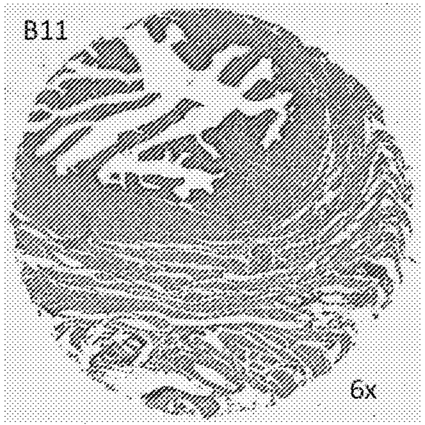


Fig. 168D
Normal Kidney

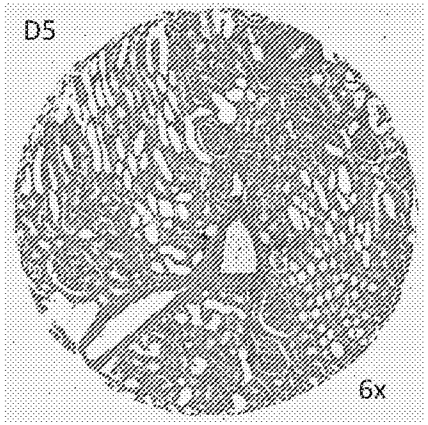


Fig. 168E

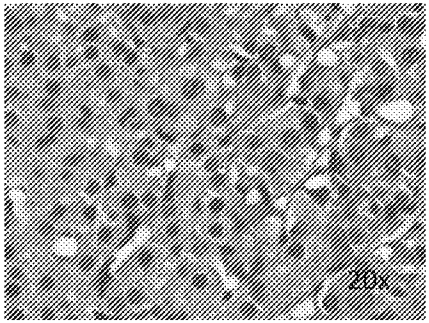


Fig. 168F

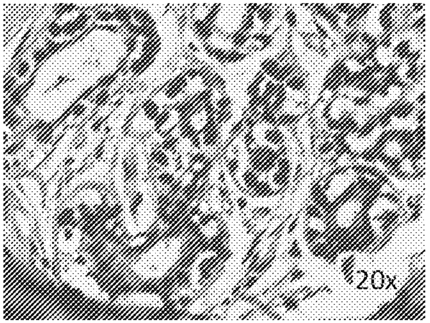


Fig. 168G

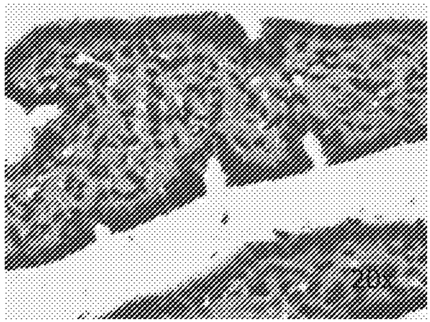


Fig. 168H

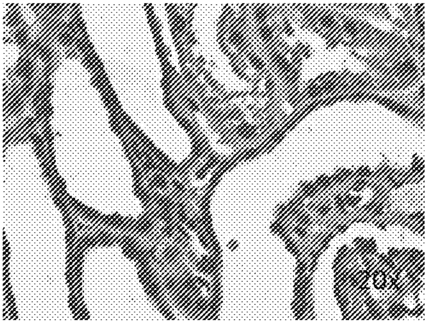


Figure 168A-168H

N+20/C-27 antibody 31A1 IgG 0.5 ug/mL

FDA Normal tissue array MNO1021

Fig. 168I
Normal Heart

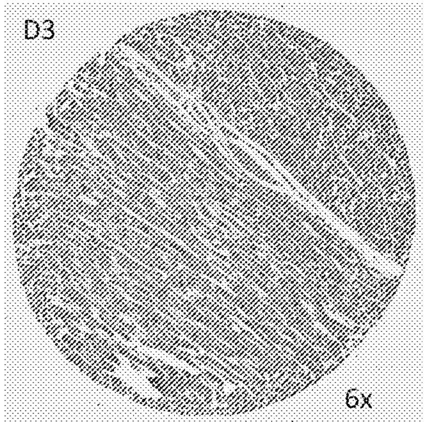


Fig. 168J
Normal Liver

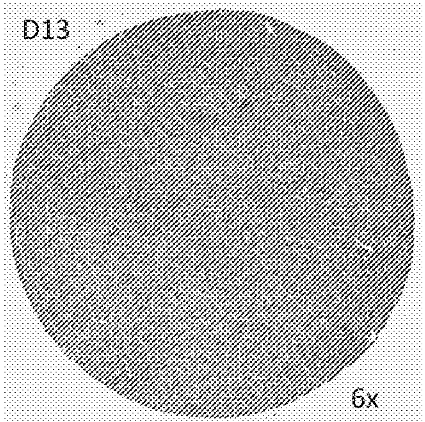


Fig. 168K
Normal Lung

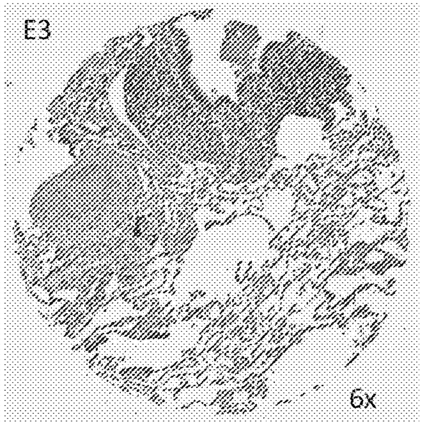


Fig. 168L
Normal Ureter

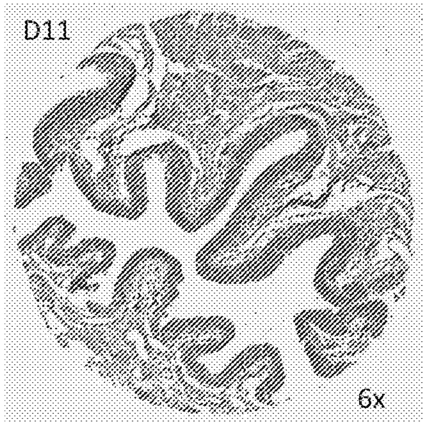


Fig. 168M

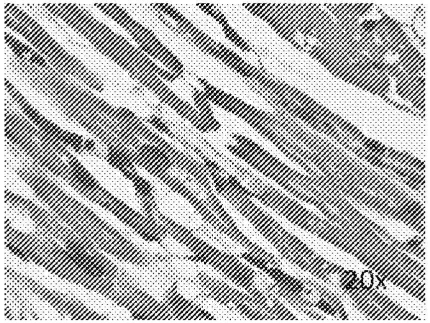


Fig. 168N

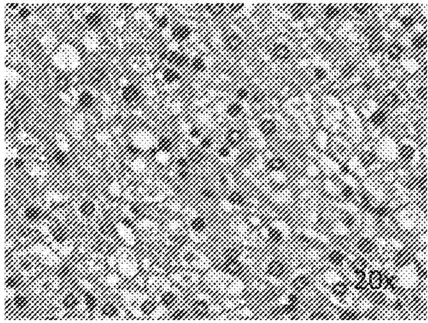


Fig. 168O

Fig. 168P

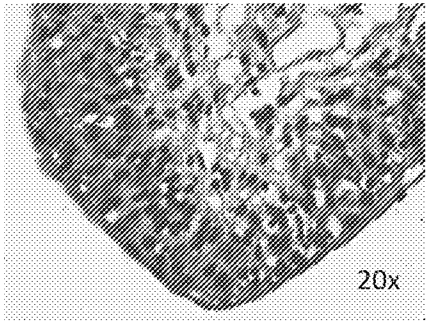


Figure 168I-168P

N+20/C-27 antibody 31A1 IgG 0.5 ug/mL

FDA Normal tissue array MNO1021

Fig. 168Q
Normal Eye

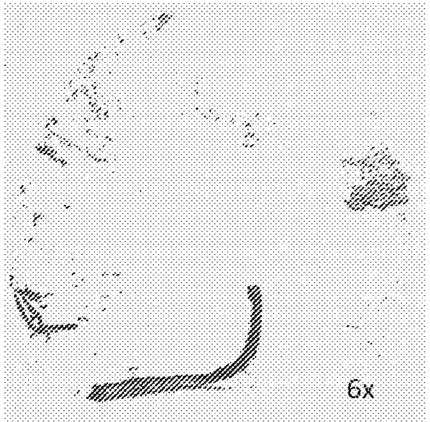


Fig. 168R
Normal Cerebral Cortex

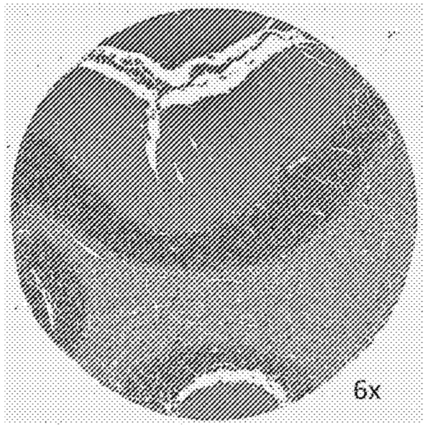


Fig. 168S
Normal Bone Marrow

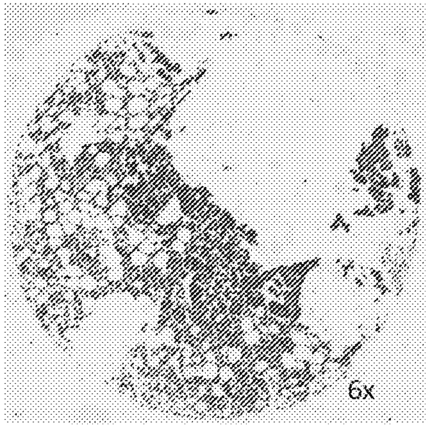


Fig. 168T
Normal Skeletal Muscle

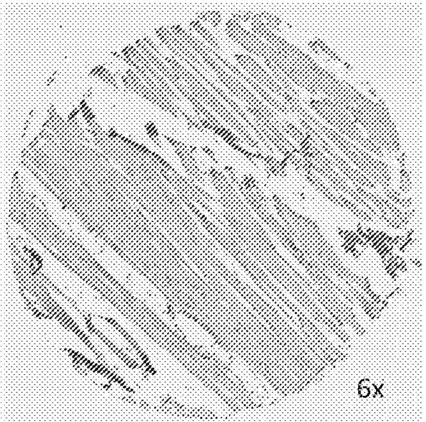


Fig. 168U

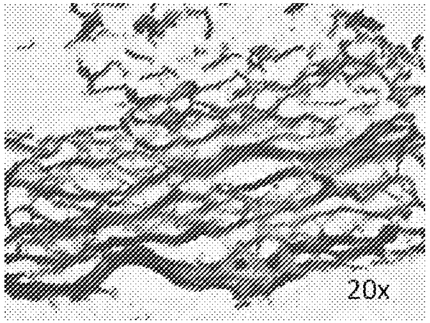


Fig. 168V

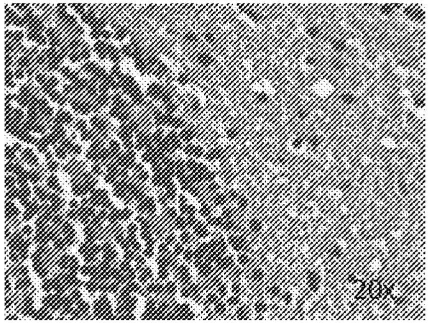


Fig. 168W

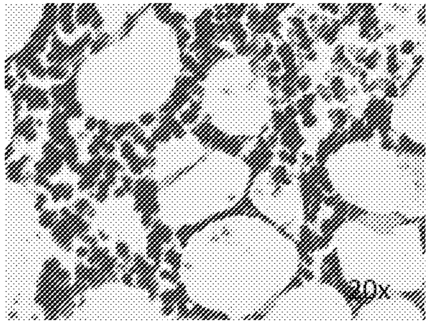


Fig. 168X

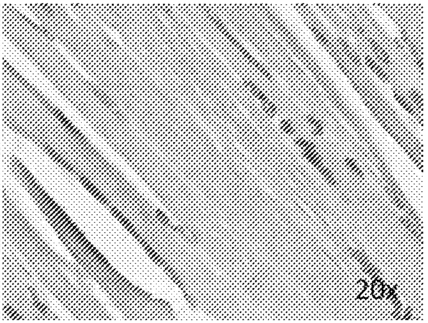


Figure 168Q-168X

N+20/C-27 antibody 31A1 IgG 0.5 ug/mL

Breast cancer tissue array Br1141

Fig. 169A

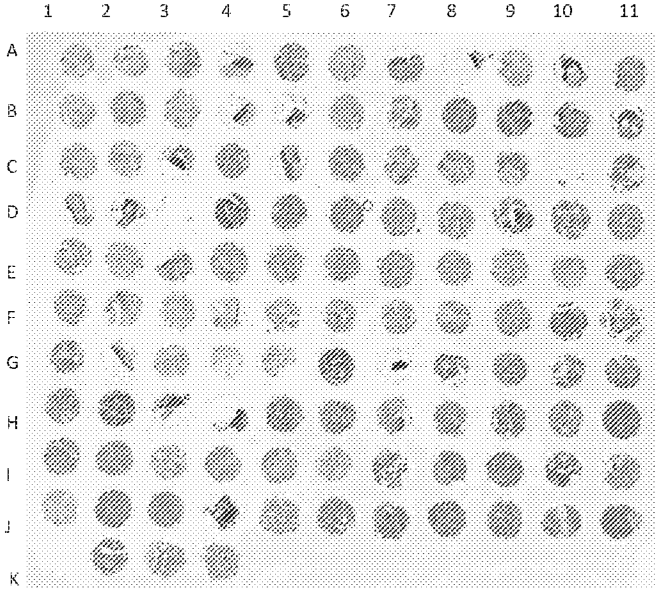


Fig. 169B

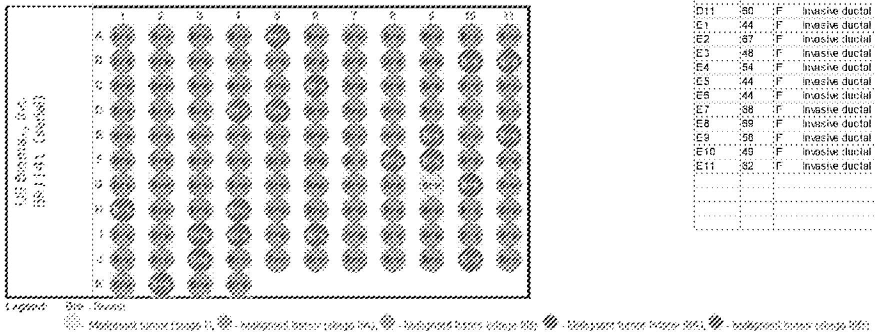


Fig. 169C

Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type
A1	45	F	invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A2	38	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A3	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A4	41	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A5	70	F	invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
A6	46	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
A7	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
A8	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A9	68	F	invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
A10	62	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
A11	50	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B1	43	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B2	63	F	invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
B3	57	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
B4	77	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B5	56	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B6	46	F	invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B7	48	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B8	40	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B9	53	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B10	54	F	invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
B11	47	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
C1	48	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
C2	48	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
C3	42	F	invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C4	41	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C5	56	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C6	41	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
C7	41	F	invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C8	60	F	Invasive ductal carcinoma	T2N1M0	*	IIB	Malignant
C9	40	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C10	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
C11	57	F	invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D1	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D2	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D3	48	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
D4	46	F	invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
D5	52	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
D6	51	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D7	62	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D8	44	F	invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D9	43	F	invasive ductal carcinoma	T2N1M0	1	IIB	Malignant
D10	44	F	Invasive ductal carcinoma	T2N0M0	*	IIA	Malignant
D11	60	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E1	44	F	invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E2	67	F	invasive ductal carcinoma	T2N0M0	3	IIA	Malignant
E3	48	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E4	54	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
E5	44	F	invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E6	44	F	invasive ductal carcinoma	T2N0M0	*	IIA	Malignant
E7	38	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E8	69	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E9	58	F	invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
E10	49	F	invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E11	32	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
F1	52	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F2	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F3	53	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F4	64	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
F5	63	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F6	69	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
F7	43	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F8	45	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
F9	82	F	Invasive ductal carcinoma	T3N1M0	*	IIIA	Malignant
F10	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
F11	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G1	45	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G2	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G3	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G4	45	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
G5	45	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G6	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G7	53	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G8	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
G9	38	F	Invasive ductal carcinoma	T1N0M0	2	I	Malignant
G10	46	F	Invasive ductal carcinoma	T4N1M0	2	IIIB	Malignant
G11	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H1	49	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
H2	63	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
H3	52	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
H4	50	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
H5	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H6	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H7	47	F	Invasive ductal carcinoma	T2N0M0	3	IIA	Malignant
H8	48	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H9	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H10	51	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H11	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I1	45	F	Invasive ductal carcinoma	T2N1M0	*	IIB	Malignant
I2	68	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I3	79	F	Invasive ductal carcinoma	T4N1M0	2	IIIB	Malignant
I4	56	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
I5	54	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I6	42	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
I7	38	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I8	62	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I9	39	F	Invasive ductal carcinoma	T2N0M0	1	IIA	Malignant
I10	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I11	57	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
J1	73	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
J2	66	F	Invasive ductal carcinoma	T2N0M0	3	IIA	Malignant
J3	45	F	Invasive ductal carcinoma	T2N2M0	3	IIIA	Malignant
J4	44	F	Invasive ductal carcinoma	T2N1M0	3	IIB	Malignant
J5	46	F	Medullary carcinoma	T3N0M0	-	IIB	Malignant
J6	52	F	Medullary carcinoma	T2N0M0	-	IIA	Malignant
J7	56	F	Medullary carcinoma	T2N0M0	-	IIA	Malignant
J8	42	F	Medullary carcinoma	T2N0M0	-	IIA	Malignant
J9	41	F	Medullary carcinoma	T2N1M0	-	IIB	Malignant
J10	53	F	Mucinous carcinoma	T3N1M0	-	IIIA	Malignant
J11	57	F	Medullary carcinoma	T3N0M0	*	IIB	Malignant
K1	45	F	Invasive lobular carcinoma	T2N0M0	-	IIA	Malignant
K2	48	F	Invasive apocrine carcinor	T3N1M0	-	IIIA	Malignant
K3	48	F	Invasive apocrine carcinor	T2N0M0	*	IIA	Malignant
K4	48	F	Invasive micropapillary cal	T2N1M0	-	IIB	Malignant

Figure 169A-169C

N+20/C-27 antibody 31A1 IgG 15 ug/mL

Breast cancer tissue array Br1141

Fig. 170A

Position: A4
Cell Type: Invasive Ductal Carcinoma
Tumor Grade: 2
TNM: T2N0M0

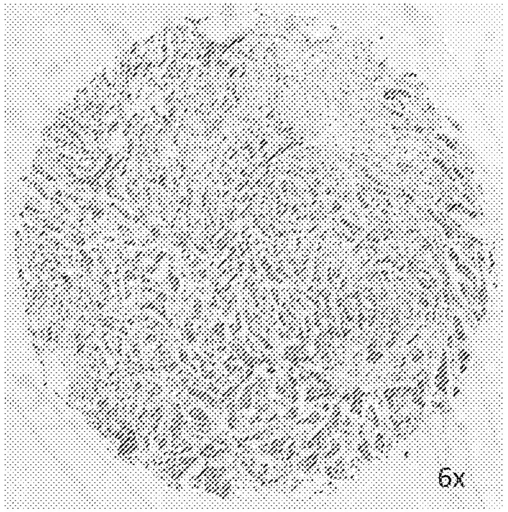


Fig. 170B

Position: A11
Cell Type: Invasive Ductal Carcinoma
Tumor Grade: 2
TNM: T2N0M0

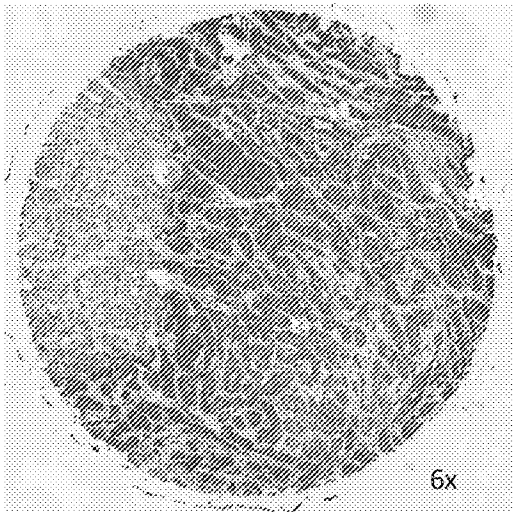


Fig. 170C

Position: G11
Cell Type: Invasive Ductal Carcinoma
Tumor Grade: 2
TNM: T2N0M0

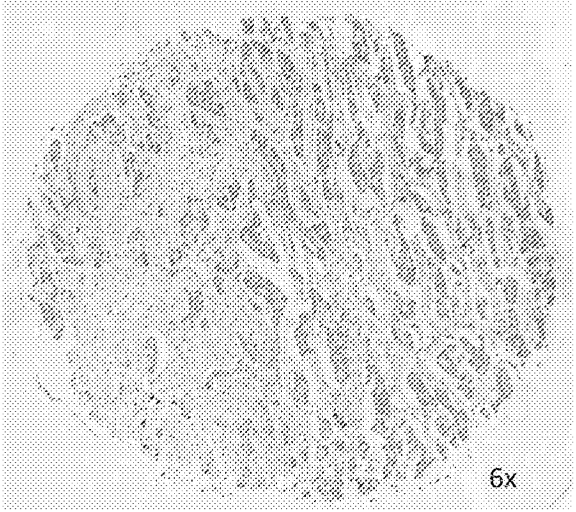


Fig. 170D

Fig. 170E

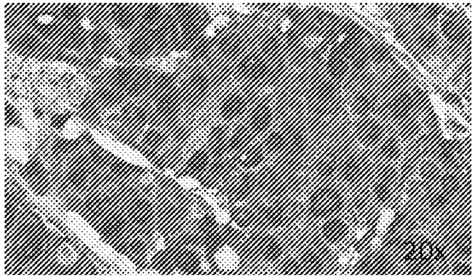


Fig. 170F

Fig. 170A–170F

N+20 antibody 31A1 0.1 - 10 ug/mL

Pancreatic cancer tissue array PA1003

Fig. 171A

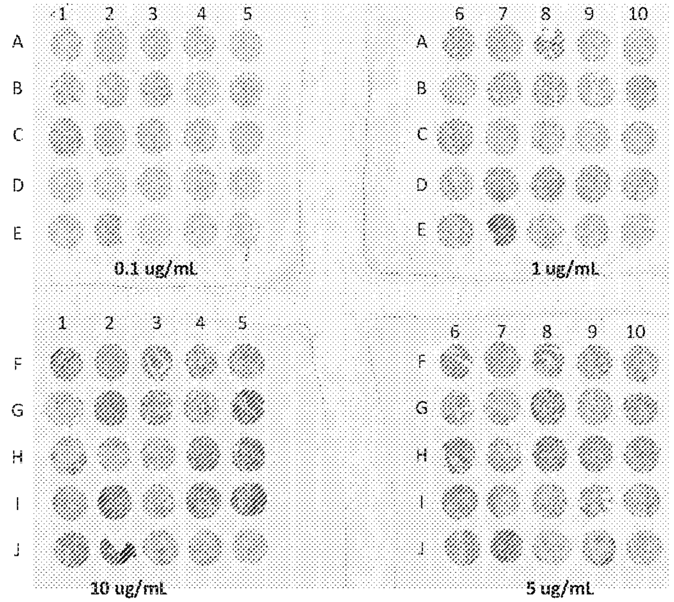


Fig. 171B

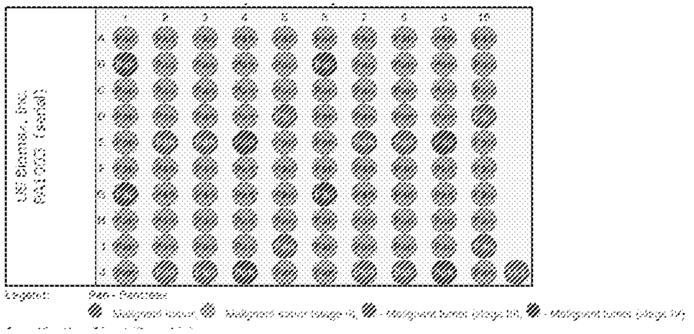
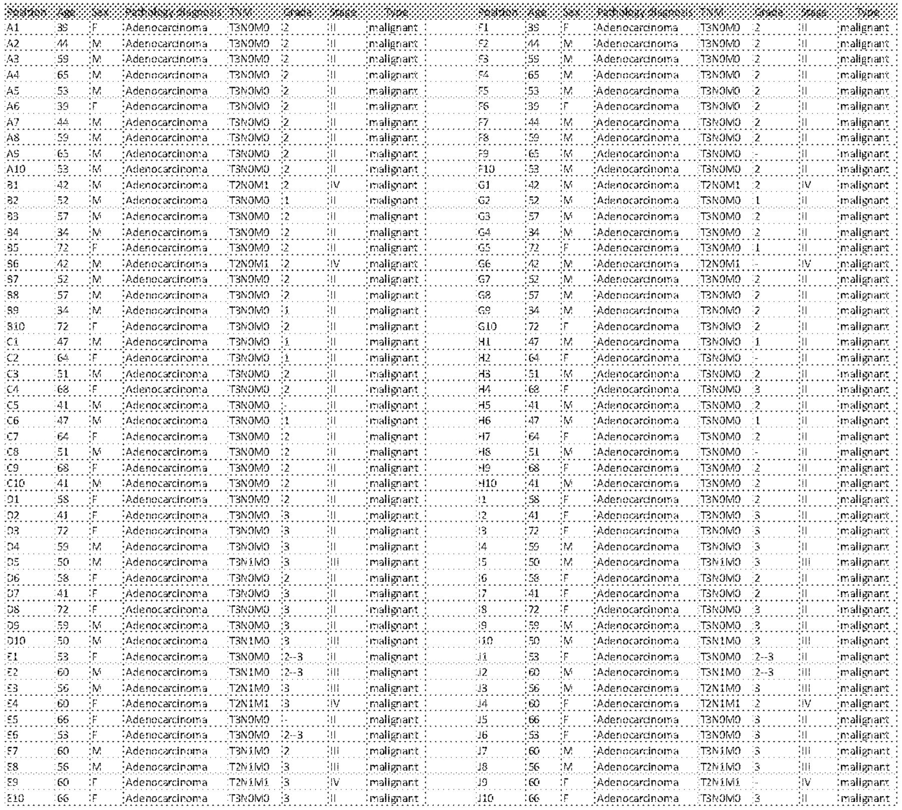


Fig. 171C



Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type	Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type
A1	39	F	Adenocarcinoma	T3N0M0	2	II	malignant	F1	39	F	Adenocarcinoma	T3N0M0	2	II	malignant
A2	44	M	Adenocarcinoma	T3N0M0	2	II	malignant	F2	44	M	Adenocarcinoma	T3N0M0	2	II	malignant
A3	59	M	Adenocarcinoma	T3N0M0	2	II	malignant	F3	59	M	Adenocarcinoma	T3N0M0	2	II	malignant
A4	65	M	Adenocarcinoma	T3N0M0	2	II	malignant	F4	65	M	Adenocarcinoma	T3N0M0	2	II	malignant
A5	53	M	Adenocarcinoma	T3N0M0	2	II	malignant	F5	53	M	Adenocarcinoma	T3N0M0	2	II	malignant
A6	39	F	Adenocarcinoma	T3N0M0	2	II	malignant	F6	39	F	Adenocarcinoma	T3N0M0	2	II	malignant
A7	44	M	Adenocarcinoma	T3N0M0	2	II	malignant	F7	44	M	Adenocarcinoma	T3N0M0	2	II	malignant
A8	59	M	Adenocarcinoma	T3N0M0	2	II	malignant	F8	59	M	Adenocarcinoma	T3N0M0	2	II	malignant
A9	65	M	Adenocarcinoma	T3N0M0	2	II	malignant	F9	65	M	Adenocarcinoma	T3N0M0	-	II	malignant
A10	53	M	Adenocarcinoma	T3N0M0	2	II	malignant	F10	53	M	Adenocarcinoma	T3N0M0	2	II	malignant
B1	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant	G1	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant
B2	52	M	Adenocarcinoma	T3N0M0	1	II	malignant	G2	52	M	Adenocarcinoma	T3N0M0	1	II	malignant
B3	57	M	Adenocarcinoma	T3N0M0	2	II	malignant	G3	57	M	Adenocarcinoma	T3N0M0	2	II	malignant
B4	34	M	Adenocarcinoma	T3N0M0	2	II	malignant	G4	34	M	Adenocarcinoma	T3N0M0	2	II	malignant
B5	72	F	Adenocarcinoma	T3N0M0	2	II	malignant	G5	72	F	Adenocarcinoma	T3N0M0	1	II	malignant
B6	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant	G6	42	M	Adenocarcinoma	T2N0M1	-	IV	malignant
B7	52	M	Adenocarcinoma	T3N0M0	2	II	malignant	G7	52	M	Adenocarcinoma	T3N0M0	2	II	malignant
B8	57	M	Adenocarcinoma	T3N0M0	2	II	malignant	G8	57	M	Adenocarcinoma	T3N0M0	2	II	malignant
B9	34	M	Adenocarcinoma	T3N0M0	1	II	malignant	G9	34	M	Adenocarcinoma	T3N0M0	2	II	malignant
B10	72	F	Adenocarcinoma	T3N0M0	2	II	malignant	G10	72	F	Adenocarcinoma	T3N0M0	2	II	malignant
C1	47	M	Adenocarcinoma	T3N0M0	1	II	malignant	H1	47	M	Adenocarcinoma	T3N0M0	1	II	malignant
C2	64	F	Adenocarcinoma	T3N0M0	1	II	malignant	H2	64	F	Adenocarcinoma	T3N0M0	-	II	malignant
C3	51	M	Adenocarcinoma	T3N0M0	2	II	malignant	H3	51	M	Adenocarcinoma	T3N0M0	2	II	malignant
C4	68	F	Adenocarcinoma	T3N0M0	2	II	malignant	H4	68	F	Adenocarcinoma	T3N0M0	3	II	malignant
C5	41	M	Adenocarcinoma	T3N0M0	-	II	malignant	H5	41	M	Adenocarcinoma	T3N0M0	2	II	malignant
C6	47	M	Adenocarcinoma	T3N0M0	1	II	malignant	H6	47	M	Adenocarcinoma	T3N0M0	1	II	malignant
C7	64	F	Adenocarcinoma	T3N0M0	2	II	malignant	H7	64	F	Adenocarcinoma	T3N0M0	2	II	malignant
C8	51	M	Adenocarcinoma	T3N0M0	2	II	malignant	H8	51	M	Adenocarcinoma	T3N0M0	-	II	malignant
C9	68	F	Adenocarcinoma	T3N0M0	2	II	malignant	H9	68	F	Adenocarcinoma	T3N0M0	2	II	malignant
C10	41	M	Adenocarcinoma	T3N0M0	2	II	malignant	H10	41	M	Adenocarcinoma	T3N0M0	2	II	malignant
D1	58	F	Adenocarcinoma	T3N0M0	2	II	malignant	I1	58	F	Adenocarcinoma	T3N0M0	2	II	malignant
D2	41	F	Adenocarcinoma	T3N0M0	3	II	malignant	I2	41	F	Adenocarcinoma	T3N0M0	3	II	malignant
D3	72	F	Adenocarcinoma	T3N0M0	3	II	malignant	I3	72	F	Adenocarcinoma	T3N0M0	3	II	malignant
D4	59	M	Adenocarcinoma	T3N0M0	3	II	malignant	I4	59	M	Adenocarcinoma	T3N0M0	3	II	malignant
D5	50	M	Adenocarcinoma	T3N1M0	3	III	malignant	I5	50	M	Adenocarcinoma	T3N1M0	3	III	malignant
D6	58	F	Adenocarcinoma	T3N0M0	2	II	malignant	I6	58	F	Adenocarcinoma	T3N0M0	2	II	malignant
D7	41	F	Adenocarcinoma	T3N0M0	3	II	malignant	I7	41	F	Adenocarcinoma	T3N0M0	2	II	malignant
D8	72	F	Adenocarcinoma	T3N0M0	3	II	malignant	I8	72	F	Adenocarcinoma	T3N0M0	3	II	malignant
D9	59	M	Adenocarcinoma	T3N0M0	3	II	malignant	I9	59	M	Adenocarcinoma	T3N0M0	3	II	malignant
D10	50	M	Adenocarcinoma	T3N1M0	3	III	malignant	I10	50	M	Adenocarcinoma	T3N1M0	3	III	malignant
E1	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant	J1	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant
E2	60	M	Adenocarcinoma	T3N1M0	2--3	III	malignant	J2	60	M	Adenocarcinoma	T3N1M0	2--3	III	malignant
E3	56	M	Adenocarcinoma	T2N1M0	3	III	malignant	J3	56	M	Adenocarcinoma	T2N1M0	3	III	malignant
E4	60	F	Adenocarcinoma	T2N1M1	3	IV	malignant	J4	60	F	Adenocarcinoma	T2N1M1	2	IV	malignant
E5	66	F	Adenocarcinoma	T3N0M0	-	II	malignant	J5	66	F	Adenocarcinoma	T3N0M0	3	II	malignant
E6	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant	J6	53	F	Adenocarcinoma	T3N0M0	3	II	malignant
E7	60	M	Adenocarcinoma	T3N1M0	2	III	malignant	J7	60	M	Adenocarcinoma	T3N1M0	3	III	malignant
E8	56	M	Adenocarcinoma	T2N1M0	3	III	malignant	J8	56	M	Adenocarcinoma	T2N1M0	3	III	malignant
E9	60	F	Adenocarcinoma	T2N1M1	3	IV	malignant	J9	60	F	Adenocarcinoma	T2N1M1	-	IV	malignant
E10	66	F	Adenocarcinoma	T3N0M0	3	II	malignant	J10	66	F	Adenocarcinoma	T3N0M0	3	II	malignant

Fig. 171A-171C

N+20/C-27-antibody 31A1 1 ug/mL

Pancreatic cancer tissue array PA1003

Fig. 172A

Position: B7
Cell Type: Adenocarcinoma
Tumor Grade: 1
TNM: T3N0M0

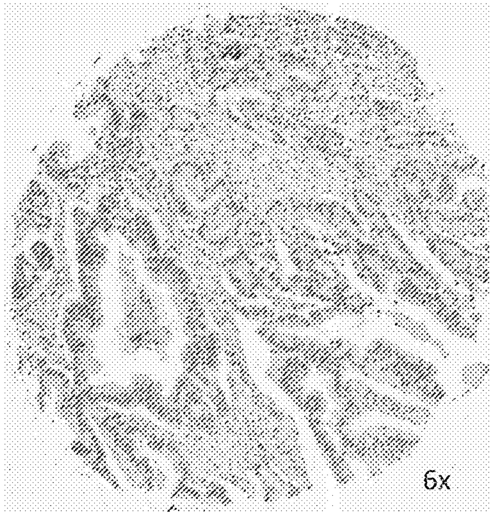


Fig. 172B

Position: B10
Cell Type: Adenocarcinoma
Tumor Grade: 2
TNM: T3N0M0

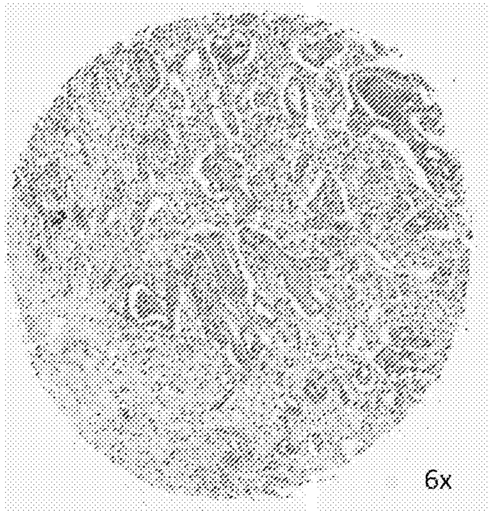


Fig. 172C

Position: D8
Cell Type: Adenocarcinoma
Tumor Grade: 3
TNM: T3N0M0

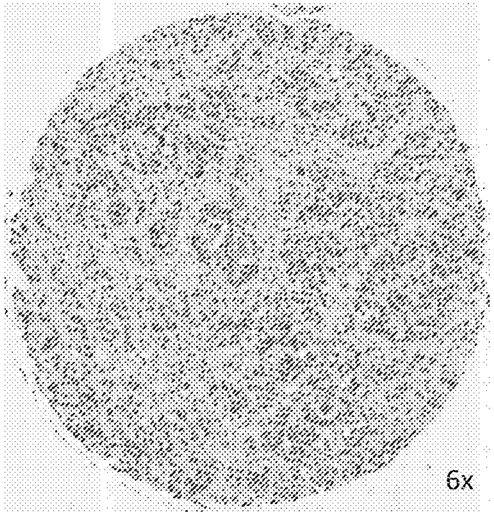


Fig. 172D

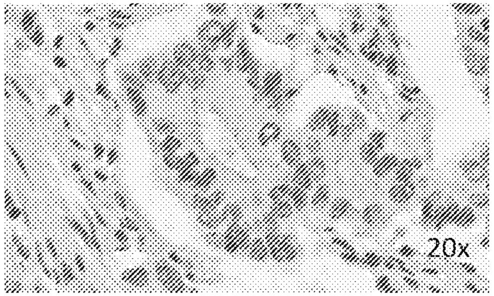


Fig. 172E

Fig. 172F

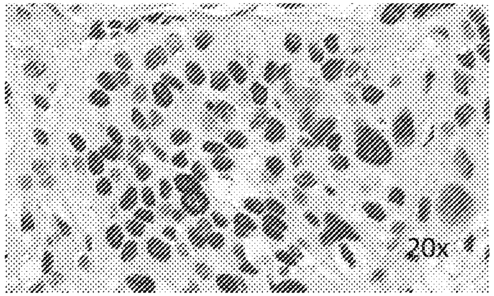


Fig. 172A–172F

N+20/C-27 antibody 32C1 IgG 0.25 ug/mL

FDA Normal tissue array MNO1021

Fig. 173A

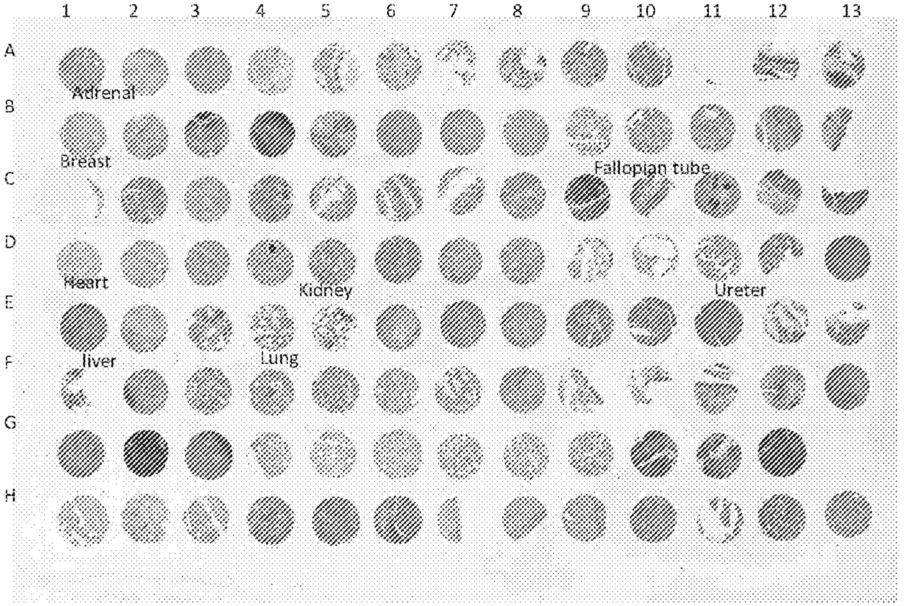


Fig. 173B

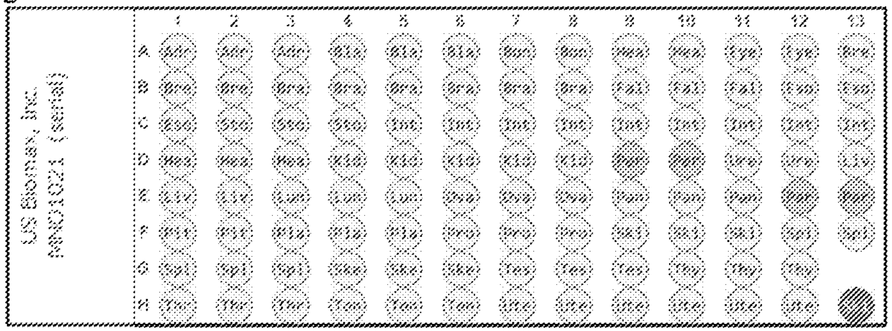


Fig. 173C

Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis	Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis
A1	F	31	Adrenal gland	Normal	E1	M	59	Liver	Normal
A2	M	51	Adrenal gland	Normal	E2	F	27	Liver	Normal
A3	M	53	Adrenal gland	Normal	E3	M	72	Lung	Normal
A4	M	75	Bladder, umary	Normal	E4	F	55	Lung	Normal
A5	M	72	Bladder, umary	Normal	E5	M	43	Lung	Normal
A6	M	52	Bladder, umary	Normal	E6	F	47	Ovary	Normal
A7	M	53	Bone, bone marrow	Normal	E7	F	46	Ovary	Normal
A8	M	43	Bone, bone marrow	Normal	E8	F	40	Ovary	Normal
A9	F	44	Head and neck, salivary gland	Normal	E9	M	42	Pancreas	Normal
A10	M	18	Head and neck, salivary gland	Normal	E10	F	26	Pancreas	Normal
A11	M	55	Eye	Normal	E11	F	59	Pancreas	Normal
A12	M	50	Eye	Normal	E12	M	17	Parathyroid	Adenoma
A13	F	35	Breast	Normal	E13	M	72	Parathyroid	Adenoma
B1	F	38	Breast	Normal	F1	F	3	Pituitary gland	Normal
B2	F	33	Breast	Normal	F2	F		Pituitary gland	Normal
B3	M	58	Brain, cerebellum	Normal	F3	F	32	Placenta	Normal
B4	M	65	Brain, cerebellum	Normal	F4	F	30	Placenta	Normal
B5	F		Brain, cerebellum	Normal	F5	F	27	Placenta	Normal
B6	M	56	Brain, cerebral cortex	Normal	F6	M	64	Prostate	Normal
B7	M	65	Brain, cerebral cortex	Normal	F7	M	65	Prostate	Normal
B8	F		Brain, cerebral cortex	Normal	F8	M	65	Prostate	Normal
B9	F	42	Fallopian tube	Normal	F9	F	32	Skin	Normal
B10	F	32	Fallopian tube	Normal	F10	F	68	Skin	Normal
B11	F	24	Fallopian tube	Normal	F11	M	26	Skin	Normal
B12	M	45	Esophagus	Normal	F12	M	47	Spinal cord	Normal
B13	F	68	Esophagus	Normal	F13	M	58	Spinal cord	Normal
C1	M	54	Esophagus	Normal	G1	M	27	Spleen	Normal
C2	M	45	Stomach	Normal	G2	M	60	Spleen	Normal
C3	M	49	Stomach	Normal	G3	M	31	Spleen	Normal
C4	M	77	Stomach	Normal	G4	F	60	Skeletal muscle	Normal
C5	M	45	Intestine, small intestine	Normal	G5	F	49	Skeletal muscle	Normal
C6	F	75	Intestine, small intestine	Normal	G6	M	70	Skeletal muscle	Normal
C7	F	75	Intestine, small intestine	Normal	G7	M	43	Testis	Normal
C8	M	2	Intestine, colon	Normal	G8	M	30	Testis	Normal
C9	M	46	Intestine, colon	Normal	G9	M	77	Testis	Normal
C10	M	74	Intestine, colon	Normal	G10	M	15	Thymus	Normal
C11	F	47	Intestine, rectum	Normal	G11	M	28	Thymus	Normal
C12	F	75	Intestine, rectum	Normal	G12	F	9	Thymus	Normal
C13	M	66	Intestine, rectum	Normal	G13	-	-	-	-
D1	M	58	Heart	Normal	H1	F	26	Thyroid	Normal
D2	M	46	Heart	Normal	H2	F	37	Thyroid	Normal
D3	F	34	Heart	Normal	H3	F	51	Thyroid	Normal
D4	F	52	Kidney, cortex	Normal	H4	M	46	Tonsil	Normal
D5	M	23	Kidney, cortex	Normal	H5	M	37	Tonsil	Normal
D6	M	63	Kidney, cortex	Normal	H6	M	13	Tonsil	Normal
D7	F	52	Kidney, medulla	Normal	H7	F	38	Uterus, cervix	Normal
D8	M	23	Kidney, medulla	Normal	H8	F	35	Uterus, cervix	Normal
D9	M	59	Peripheral nerve	Schwannoma	H9	F	44	Uterus, cervix	Normal
D10	F	29	Peripheral nerve	Schwannoma	H10	F	38	Uterus, endometrium	Normal
D11	F	44	Ureter	Normal	H11	F	41	Uterus, endometrium	Normal
D12	F	42	Ureter	Normal	H12	F	46	Uterus, endometrium	Normal
D13	F	57	Liver	Normal	H13	M	58	Skin	Malignant melanoma (tissue marker)

Figure 173A-173C

N+20/C-27 antibody 32C1 IgG 0.25 ug/mL

FDA Normal tissue array MNO1021

Fig. 174A
Normal Adrenal Gland

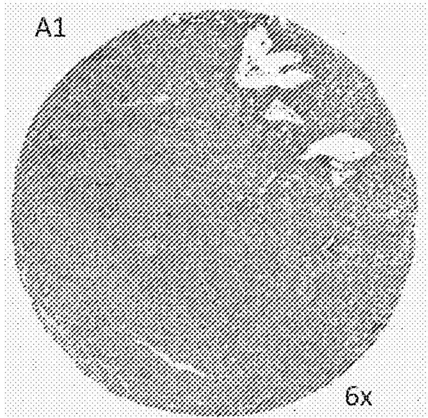


Fig. 174B
Normal Breast

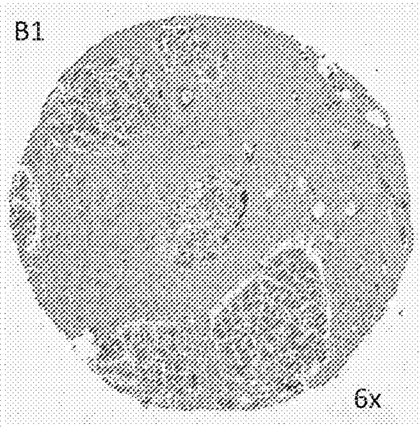


Fig. 174C
Normal Fallopian Tubes

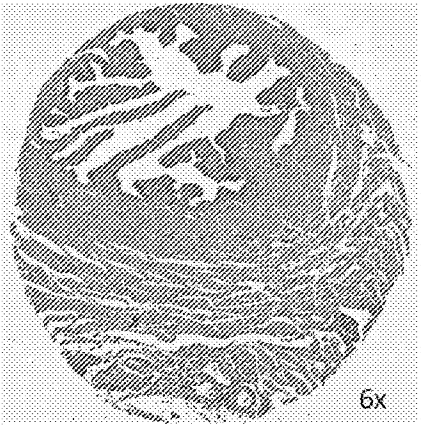


Fig. 174D
Normal Kidney

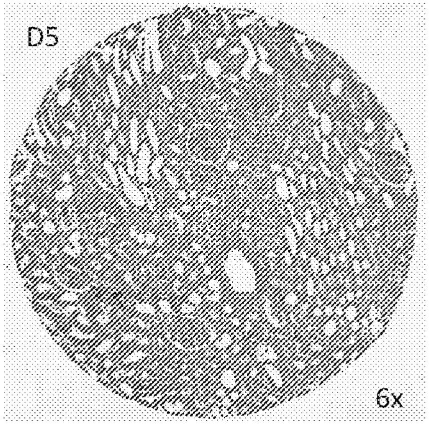


Fig. 174E

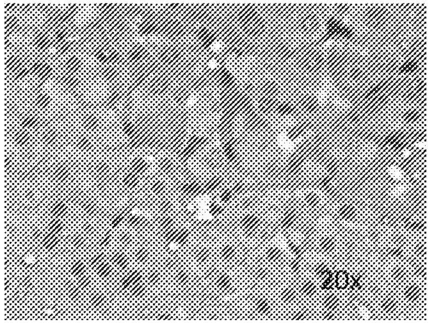


Fig. 174F

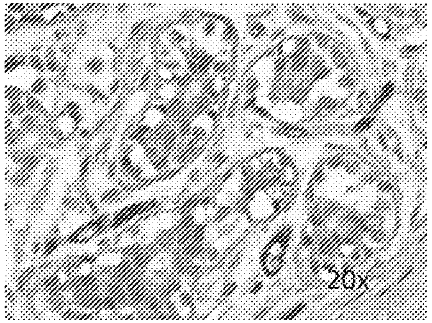


Fig. 174G

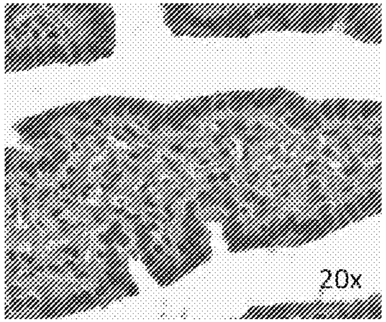


Fig. 174H

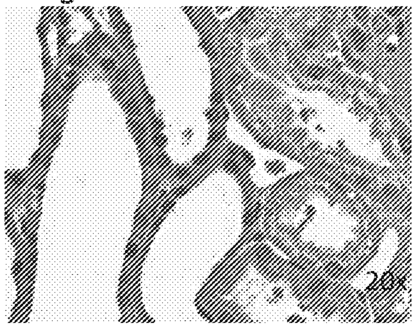


Figure 174A-174H

N+20/C-27 antibody 32C1 IgG 0.25 ug/mL

FDA Normal tissue array MNO1021

Fig. 174I
Normal Heart

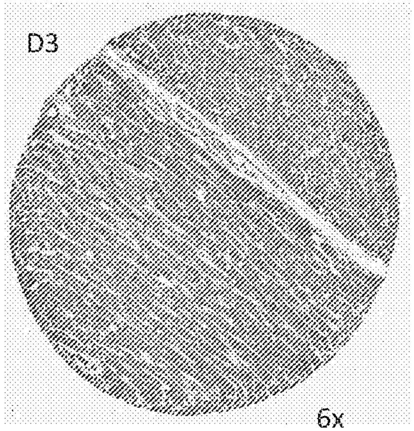


Fig. 174J
Normal Liver

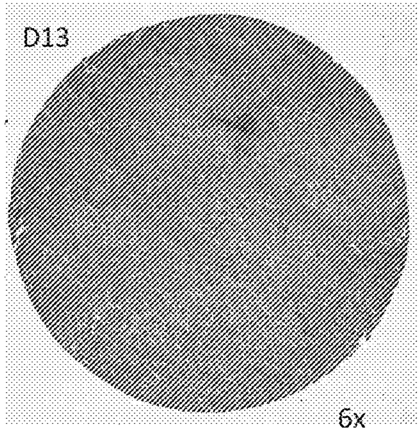


Fig. 174K
Normal Lung

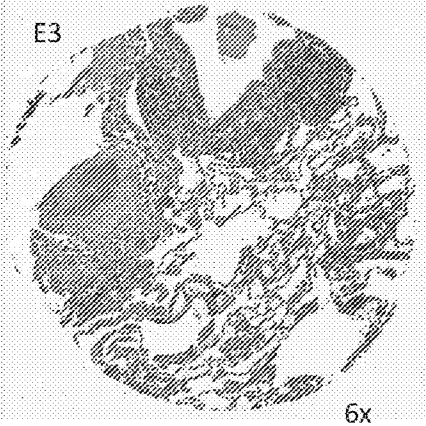


Fig. 174L
Normal Ureter

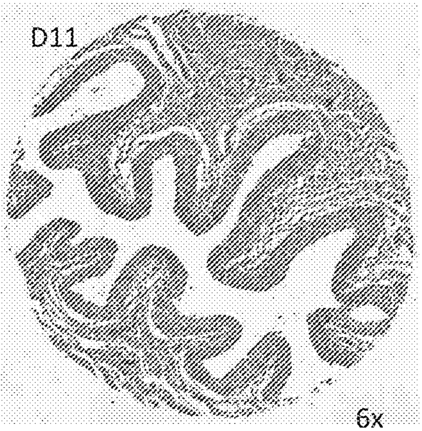


Fig. 174M

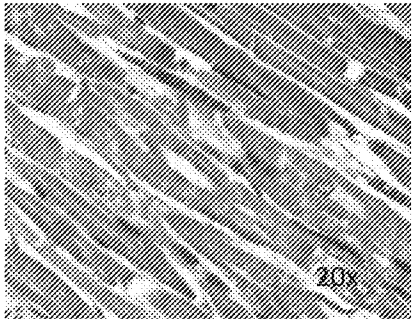


Fig. 174N

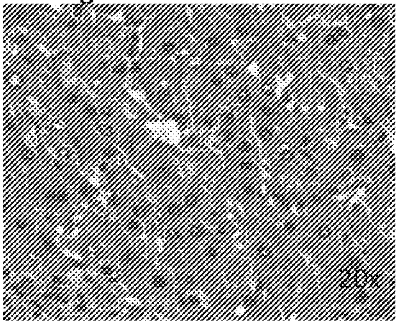


Fig. 174O

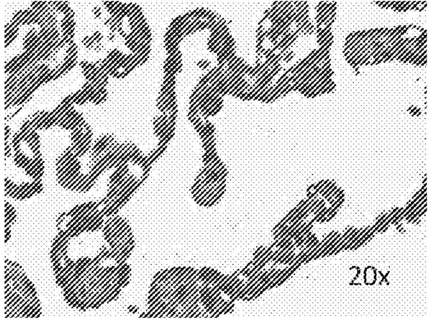


Fig. 174P

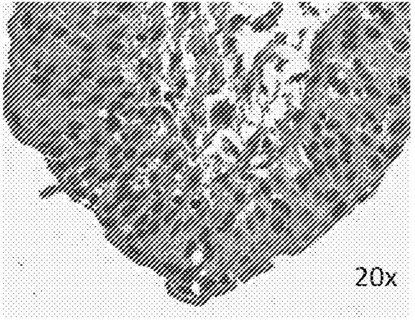


Figure 174I-174P

N+20/C-27 antibody 32C1 IgG 0.25 ug/mL

FDA Normal tissue array MNO1021

Fig. 174Q
Normal eye

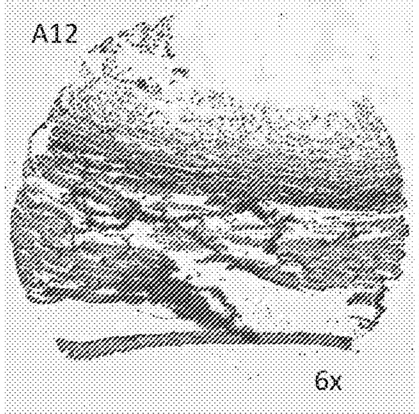


Fig. 174R
Normal Cerebral cortex

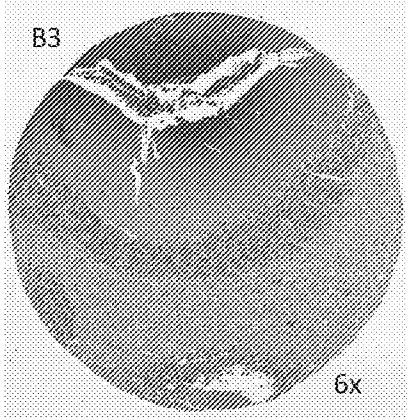


Fig. 174S
Normal Bone marrow

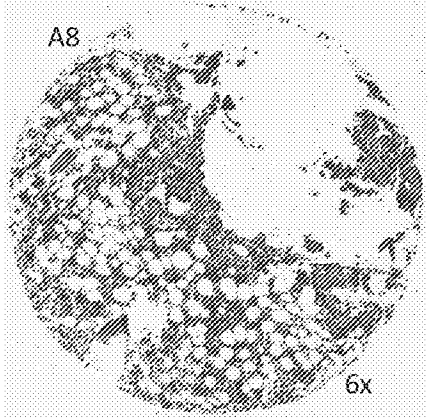


Fig. 174T
Normal Skeletal muscle

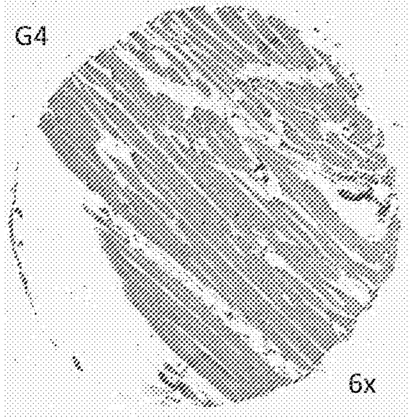


Fig. 174U

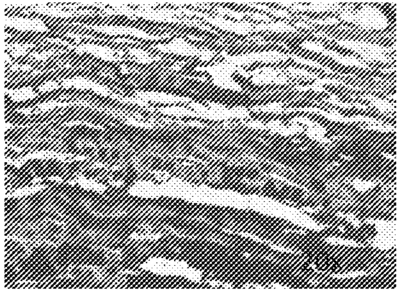


Fig. 174V

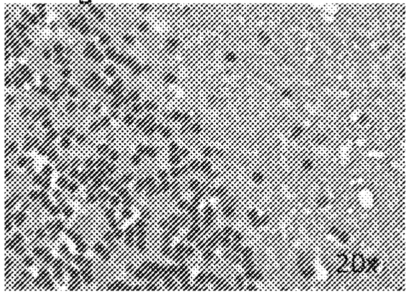


Fig. 174W

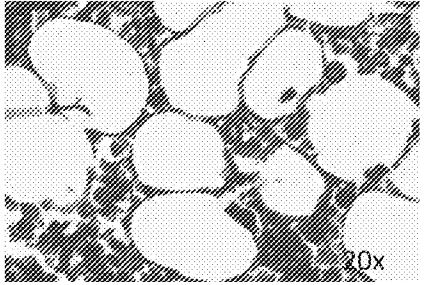


Fig. 174X

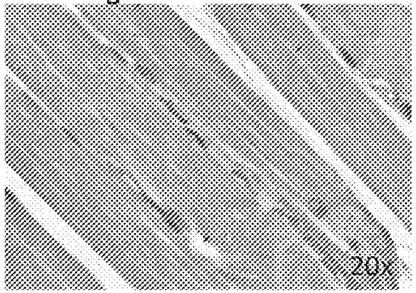


Figure 174Q-174X

N+20/C-27 antibody 32C1 IgG 0.25 ug/mL

Breast cancer tissue array Br1141

Fig. 175A

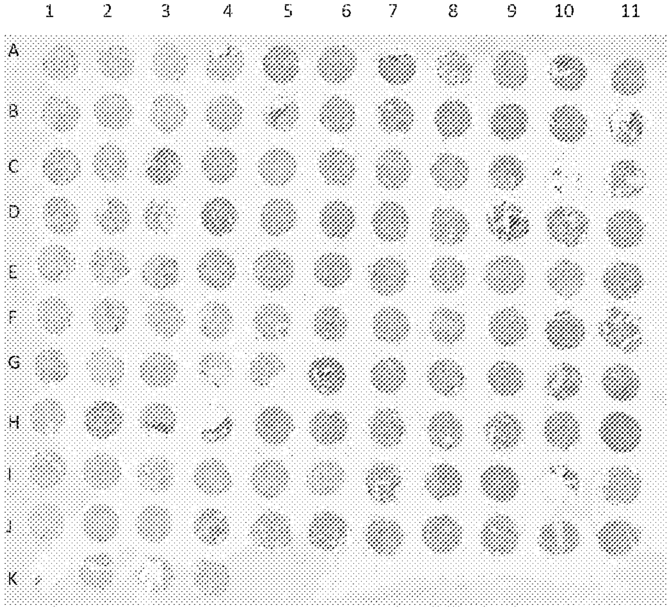


Fig. 175B

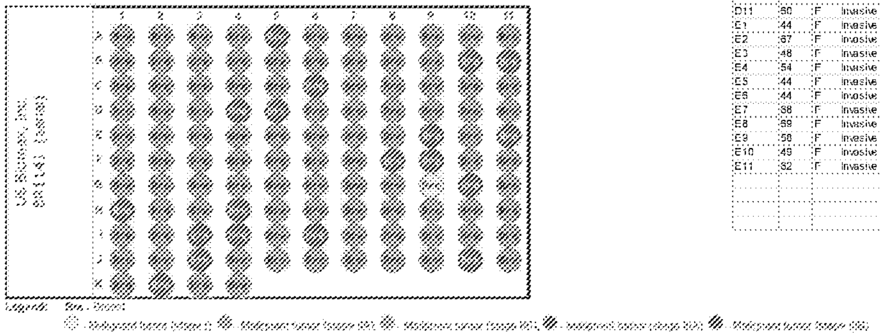


Fig. 175C

Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type
A1	45	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A2	38	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A3	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A4	41	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A5	70	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
A6	46	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
A7	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
A8	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
A9	68	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
A10	62	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
A11	50	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B1	43	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B2	63	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
B3	57	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
B4	77	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B5	56	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B6	46	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B7	48	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B8	40	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B9	53	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
B10	54	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
B11	47	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
C1	48	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
C2	48	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
C3	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C4	41	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C5	56	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C6	41	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
C7	41	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C8	60	F	Invasive ductal carcinoma	T2N1M0	*	IIB	Malignant
C9	40	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
C10	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
C11	57	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D1	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D2	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D3	48	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
D4	46	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
D5	52	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
D6	51	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D7	62	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D8	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
D9	43	F	Invasive ductal carcinoma	T2N1M0	1	IIB	Malignant
D10	44	F	Invasive ductal carcinoma	T2N0M0	*	IIA	Malignant
D11	60	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E1	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E2	67	F	Invasive ductal carcinoma	T2N0M0	3	IIA	Malignant
E3	48	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E4	54	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
E5	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E6	44	F	Invasive ductal carcinoma	T2N0M0	*	IIA	Malignant
E7	38	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E8	59	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E9	58	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
E10	49	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
E11	32	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
F1	52	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F2	44	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F3	53	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F4	64	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
F5	63	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F6	69	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
F7	43	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
F8	45	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
F9	82	F	Invasive ductal carcinoma	T3N1M0	*	IIIA	Malignant
F10	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
F11	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G1	45	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G2	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G3	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G4	45	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
G5	45	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G6	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G7	53	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
G8	42	F	Invasive ductal carcinoma	T2N1M0	2	IIB	Malignant
G9	38	F	Invasive ductal carcinoma	T1N0M0	2	I	Malignant
G10	46	F	Invasive ductal carcinoma	T4N1M0	2	IIIB	Malignant
G11	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H1	49	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
H2	63	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
H3	52	F	Invasive ductal carcinoma	T3N0M0	2	IIB	Malignant
H4	50	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
H5	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H6	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H7	47	F	Invasive ductal carcinoma	T2N0M0	3	IIA	Malignant
H8	48	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H9	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H10	51	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
H11	42	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I1	45	F	Invasive ductal carcinoma	T2N1M0	*	IIB	Malignant
I2	68	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I3	79	F	Invasive ductal carcinoma	T4N1M0	2	IIIB	Malignant
I4	56	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
I5	54	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I6	42	F	Invasive ductal carcinoma	T3N1M0	2	IIIA	Malignant
I7	38	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I8	62	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I9	39	F	Invasive ductal carcinoma	T2N0M0	1	IIA	Malignant
I10	47	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
I11	57	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
J1	73	F	Invasive ductal carcinoma	T2N0M0	2	IIA	Malignant
J2	66	F	Invasive ductal carcinoma	T2N0M0	3	IIA	Malignant
J3	45	F	Invasive ductal carcinoma	T2N2M0	3	IIIA	Malignant
J4	44	F	Invasive ductal carcinoma	T2N1M0	3	IIB	Malignant
J5	46	F	Medullary carcinoma	T3N0M0	-	IIB	Malignant
J6	52	F	Medullary carcinoma	T2N0M0	-	IIA	Malignant
J7	56	F	Medullary carcinoma	T2N0M0	-	IIA	Malignant
J8	42	F	Medullary carcinoma	T2N0M0	-	IIA	Malignant
J9	41	F	Medullary carcinoma	T2N1M0	-	IIB	Malignant
J10	53	F	Mucinous carcinoma	T3N1M0	-	IIIA	Malignant
J11	57	F	Medullary carcinoma	T3N0M0	*	IIB	Malignant
K1	45	F	Invasive lobular carcinoma	T2N0M0	-	IIA	Malignant
K2	48	F	Invasive apocrine carcinor	T3N1M0	-	IIIA	Malignant
K3	48	F	Invasive apocrine carcinor	T2N0M0	*	IIA	Malignant
K4	48	F	Invasive micropapillary ca	T2N1M0	-	IIB	Malignant

Figure 175A-175C

N+20/C-27 antibody 32C1 IgG 0.25 ug/mL

Breast cancer tissue array Br1141

Fig. 176A

Position: B1

Cell Type: Invasive Ductal Carcinoma

Tumor Grade: 2

TNM: T2N0M0

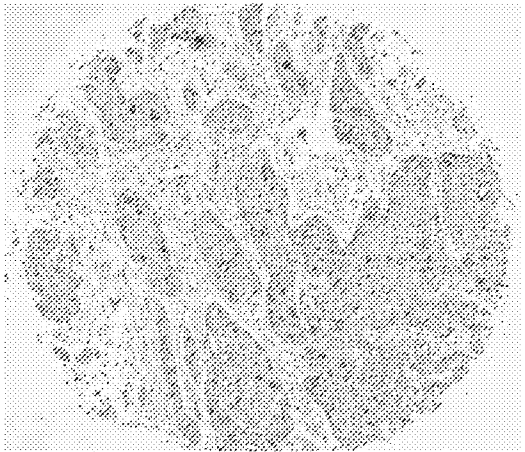


Fig. 176B

Position: B8

Cell Type: Invasive Ductal Carcinoma

Tumor Grade: 2

TNM: T2N0M0

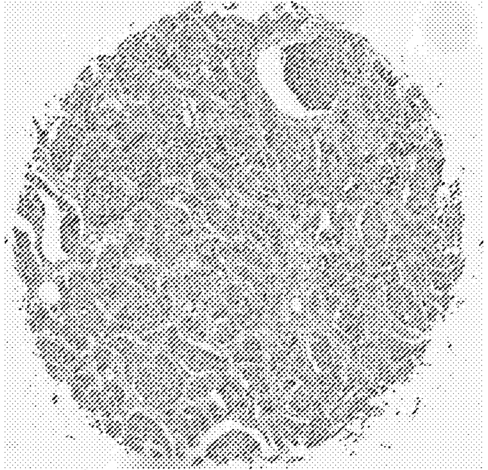


Fig. 176C

Position: G11

Cell Type: Invasive Ductal Carcinoma

Tumor Grade: 2

TNM: T2N0M0

Fig. 176D

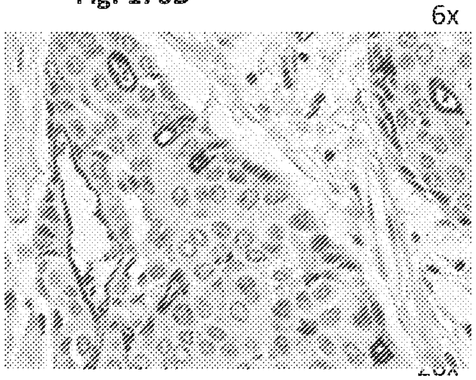


Fig. 176E

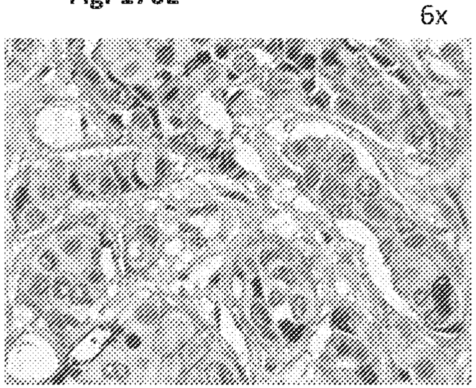


Fig. 176F

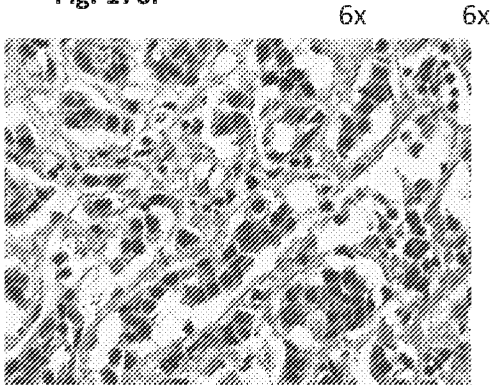


Fig. 176A–176F

N+20/C-27 antibody 32C1 IgG 1-15 ug/mL

Esophageal cancer tissue array ES1001

Fig. 177A

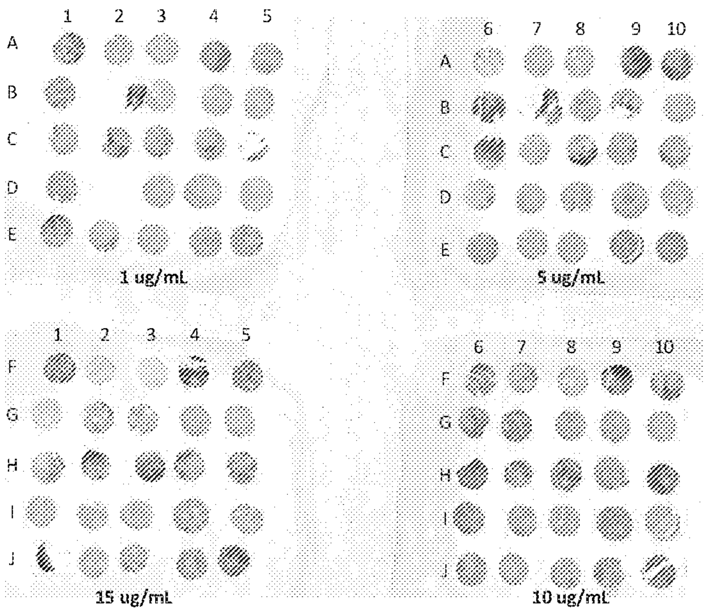


Fig. 177B

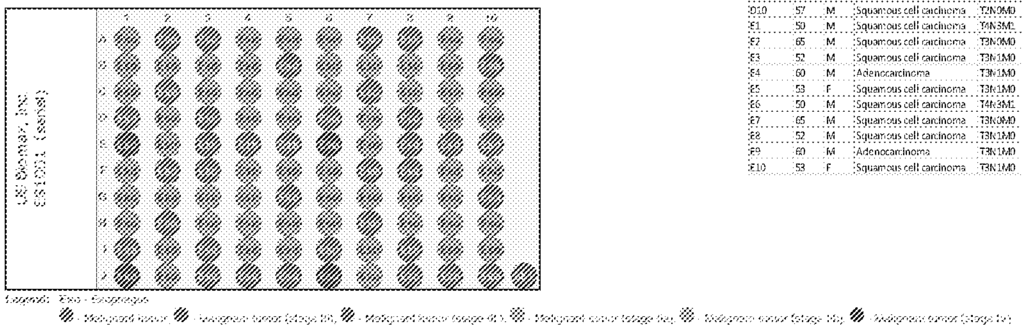


Fig. 177C

Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type	Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type
A1	61	F	Squamous cell carcinoma	T3N0M0	1	IIa	malignant	F1	61	F	Squamous cell carcinoma	T3N0M0	1	IIa	malignant
A2	63	M	Squamous cell carcinoma	T3N2M0	2	III	malignant	F2	63	M	Squamous cell carcinoma	T3N2M0	2	III	malignant
A3	57	F	Squamous cell carcinoma	T3N1M0	1	III	malignant	F3	57	F	Squamous cell carcinoma	T3N1M0	1	III	malignant
A4	60	M	Squamous cell carcinoma	T2N0M0	2	IIa	malignant	F4	60	M	Squamous cell carcinoma	T2N0M0	2	IIa	malignant
A5	50	F	Squamous cell carcinoma	T3N0M0	3	IIa	malignant	F5	50	F	Squamous cell carcinoma	T3N0M0	3	IIa	malignant
A6	61	F	Squamous cell carcinoma	T3N0M0	1	IIa	malignant	F6	61	F	Squamous cell carcinoma	T3N0M0	1	IIa	malignant
A7	63	M	Squamous cell carcinoma	T3N2M0	2	III	malignant	F7	63	M	Squamous cell carcinoma	T3N2M0	2	III	malignant
A8	57	F	Squamous cell carcinoma	T3N1M0	1	III	malignant	F8	57	F	Squamous cell carcinoma	T3N1M0	1	III	malignant
A9	60	M	Squamous cell carcinoma	T2N0M0	2	IIa	malignant	F9	60	M	Squamous cell carcinoma	T2N0M0	2	IIa	malignant
A10	50	F	Squamous cell carcinoma	T3N0M0	3	IIa	malignant	F10	50	F	Squamous cell carcinoma	T3N0M0	-	IIa	malignant
B1	50	M	Squamous cell carcinoma	T2N0M0	2	IIa	malignant	G1	50	M	Squamous cell carcinoma	T2N0M0	2	IIa	malignant
B2	58	M	Squamous cell carcinoma	T2N0M0	3	IIa	malignant	G2	58	M	Squamous cell carcinoma	T2N0M0	3	IIa	malignant
B3	60	M	Squamous cell carcinoma	T2N0M0	2	IIa	malignant	G3	60	M	Squamous cell carcinoma	T2N0M0	2	IIa	malignant
B4	64	M	Squamous cell carcinoma	T3N0M0	2	IIa	malignant	G4	64	M	Squamous cell carcinoma	T3N0M0	2	IIa	malignant
B5	58	F	Squamous cell carcinoma	T3N1M0	2	III	malignant	G5	58	F	Squamous cell carcinoma	T3N1M0	2	III	malignant
B6	50	M	Squamous cell carcinoma	T2N0M0	2	IIa	malignant	G6	50	M	Squamous cell carcinoma	T2N0M0	2	IIa	malignant
B7	58	M	Squamous cell carcinoma	T2N0M0	3	IIa	malignant	G7	58	M	Squamous cell carcinoma	T2N0M0	3	IIa	malignant
B8	60	M	Squamous cell carcinoma	T2N0M0	2	IIa	malignant	G8	60	M	Squamous cell carcinoma	T2N0M0	2	IIa	malignant
B9	64	M	Squamous cell carcinoma	T3N0M0	2	IIa	malignant	G9	64	M	Squamous cell carcinoma	T3N0M0	2	IIa	malignant
B10	58	F	Squamous cell carcinoma	T3N1M0	2	III	malignant	G10	58	F	Squamous cell carcinoma	T3N1M0	2	III	malignant
C1	56	M	Squamous cell carcinoma	T3N0M0	2	IIa	malignant	H1	56	M	Squamous cell carcinoma	T3N0M0	2	IIa	malignant
C2	50	M	Squamous cell carcinoma	T3N1M0	2	III	malignant	H2	50	M	Squamous cell carcinoma	T3N1M0	2	III	malignant
C3	58	M	Squamous cell carcinoma	T2N2M0	-	IIb	malignant	H3	58	M	Squamous cell carcinoma	T2N2M0	-	IIb	malignant
C4	55	M	Squamous cell carcinoma	T2N0M0	2	IIa	malignant	H4	55	M	Squamous cell carcinoma	T2N0M0	2	IIa	malignant
C5	55	M	Squamous cell carcinoma	T2N1M0	2	IIb	malignant	H5	55	M	Squamous cell carcinoma	T2N1M0	2	IIb	malignant
C6	56	M	Squamous cell carcinoma	T3N0M0	2	IIa	malignant	H6	56	M	Squamous cell carcinoma	T3N0M0	2	IIa	malignant
C7	50	M	Squamous cell carcinoma	T3N1M0	2	III	malignant	H7	50	M	Squamous cell carcinoma	T3N1M0	2	III	malignant
C8	58	M	Squamous cell carcinoma	T2N2M0	2	IIb	malignant	H8	58	M	Squamous cell carcinoma	T2N2M0	2	IIb	malignant
C9	55	M	Squamous cell carcinoma	T2N0M0	2	IIa	malignant	H9	55	M	Squamous cell carcinoma	T2N0M0	2	IIa	malignant
C10	55	M	Squamous cell carcinoma	T2N1M0	2	IIb	malignant	H10	55	M	Squamous cell carcinoma	T2N1M0	2	IIb	malignant
D1	47	M	Squamous cell carcinoma	T3N1M0	2	III	malignant	I1	47	M	Squamous cell carcinoma	T3N1M0	2	III	malignant
D2	52	M	Squamous cell carcinoma	T2N1M0	2	IIb	malignant	I2	52	M	Squamous cell carcinoma	T2N1M0	2	IIb	malignant
D3	60	M	Squamous cell carcinoma	T3N1M0	2	III	malignant	I3	60	M	Squamous cell carcinoma	T3N1M0	2	III	malignant
D4	56	M	Squamous cell carcinoma	T3N0M0	2--3	IIa	malignant	I4	56	M	Squamous cell carcinoma	T3N0M0	2--3	IIa	malignant
D5	57	M	Squamous cell carcinoma	T2N0M0	2	IIa	malignant	I5	57	M	Squamous cell carcinoma	T2N0M0	2	IIa	malignant
D6	47	M	Squamous cell carcinoma	T3N1M0	2	III	malignant	I6	47	M	Squamous cell carcinoma	T3N1M0	2	III	malignant
D7	52	M	Squamous cell carcinoma	T2N1M0	2	IIb	malignant	I7	52	M	Squamous cell carcinoma	T2N1M0	2	IIb	malignant
D8	60	M	Squamous cell carcinoma	T3N1M0	2	III	malignant	I8	60	M	Squamous cell carcinoma	T3N1M0	2	III	malignant
D9	56	M	Squamous cell carcinoma	T3N0M0	2--3	IIa	malignant	I9	56	M	Squamous cell carcinoma	T3N0M0	2--3	IIa	malignant
D10	57	M	Squamous cell carcinoma	T2N0M0	-	IIa	malignant	I10	57	M	Squamous cell carcinoma	T2N0M0	2	IIa	malignant
E1	50	M	Squamous cell carcinoma	T4N3M1	3	IV	malignant	J1	50	M	Squamous cell carcinoma	T4N3M1	3	IV	malignant
E2	65	M	Squamous cell carcinoma	T3N0M0	2	IIa	malignant	J2	65	M	Squamous cell carcinoma	T3N0M0	2	IIa	malignant
E3	52	M	Squamous cell carcinoma	T3N1M0	2	III	malignant	J3	52	M	Squamous cell carcinoma	T3N1M0	2	III	malignant
E4	60	M	Adenocarcinoma	T3N1M0	2	III	malignant	J4	60	M	Adenocarcinoma	T3N1M0	2	III	malignant
E5	53	F	Squamous cell carcinoma	T3N1M0	3	III	malignant	J5	53	F	Squamous cell carcinoma	T3N1M0	3	III	malignant
E6	50	M	Squamous cell carcinoma	T4N3M1	3	IV	malignant	J6	50	M	Squamous cell carcinoma	T4N3M1	3	IV	malignant
E7	65	M	Squamous cell carcinoma	T3N0M0	2	IIa	malignant	J7	65	M	Squamous cell carcinoma	T3N0M0	2	IIa	malignant
E8	52	M	Squamous cell carcinoma	T3N1M0	2	III	malignant	J8	52	M	Squamous cell carcinoma	T3N1M0	2	III	malignant
E9	60	M	Adenocarcinoma	T3N1M0	2	III	malignant	J9	60	M	Adenocarcinoma	T3N1M0	2	III	malignant
E10	53	F	Squamous cell carcinoma	T3N1M0	3	III	malignant	J10	53	F	Squamous cell carcinoma	T3N1M0	3	III	malignant

Fig. 177A–177C

N+20/C-27 antibody 32C1 IgG 1 ug/mL

Esophageal cancer tissue array ES1001

Fig. 178A

Position: D1

Cell Type: Squamous cell carcinoma
Tumor Grade: 2
TNM: T3N1M0

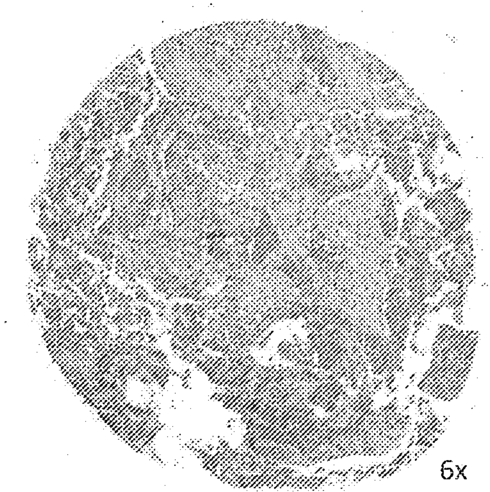


Fig. 178B

Position: E4

Cell Type: Adenocarcinoma
Tumor Grade: 2
TNM: T3N1M0

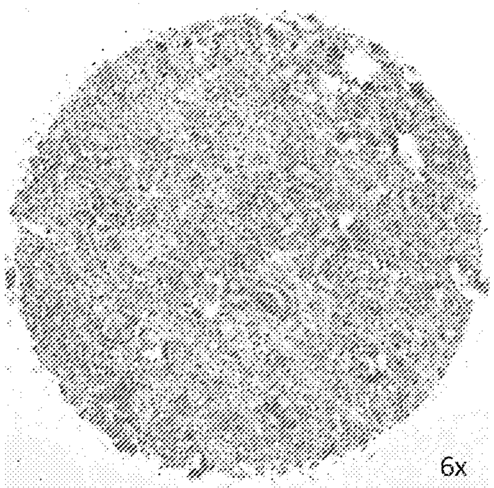


Fig. 178C

Position: E5

Cell Type: Squamous cell carcinoma
Tumor Grade: 3
TNM: T3N1M0

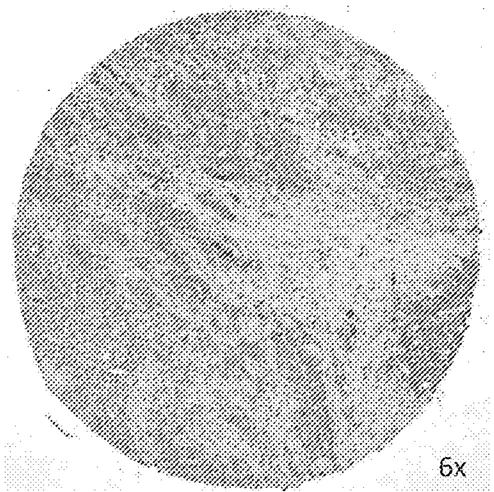


Fig. 178D

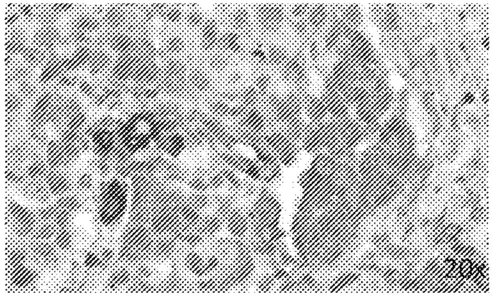


Fig. 178E

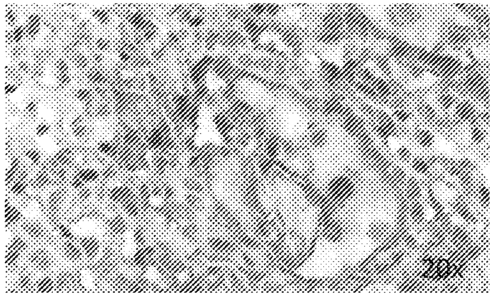


Fig. 178F

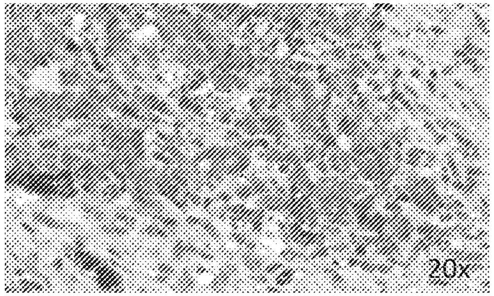


Fig. 178A–178F

N+20/C-27 antibody 45C11 IgG 12.5 ug/mL

FDA Normal tissue array MNO1021

Fig. 179A

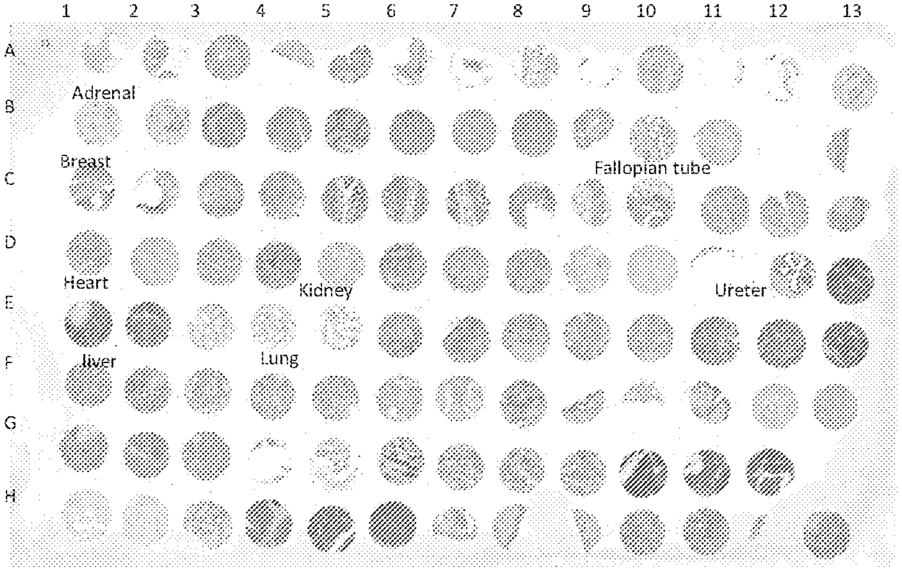


Fig. 179B

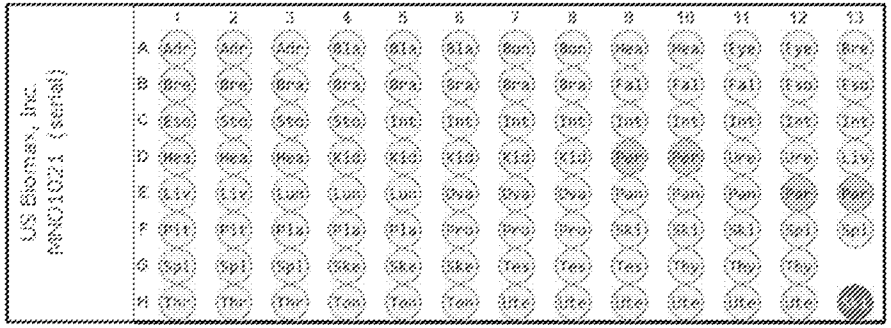


Fig. 179C

Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis	Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis
A1	F	31	Adrenal gland	Normal	E1	M	59	Liver	Normal
A2	M	51	Adrenal gland	Normal	E2	F	27	Liver	Normal
A3	M	53	Adrenal gland	Normal	E3	M	72	Lung	Normal
A4	M	75	Bladder, umary	Normal	E4	F	55	Lung	Normal
A5	M	72	Bladder, umary	Normal	E5	M	43	Lung	Normal
A6	M	52	Bladder, umary	Normal	E6	F	47	Ovary	Normal
A7	M	53	Bone, bone marrow	Normal	E7	F	46	Ovary	Normal
A8	M	43	Bone, bone marrow	Normal	E8	F	40	Ovary	Normal
A9	F	44	Head and neck, salivary gland	Normal	E9	M	42	Pancreas	Normal
A10	M	18	Head and neck, salivary gland	Normal	E10	F	26	Pancreas	Normal
A11	M	55	Eye	Normal	E11	F	59	Pancreas	Normal
A12	M	50	Eye	Normal	E12	M	17	Parathyroid	Adenoma
A13	F	35	Breast	Normal	E13	M	72	Parathyroid	Adenoma
B1	F	38	Breast	Normal	F1	F	3	Pituitary gland	Normal
B2	F	33	Breast	Normal	F2	F		Pituitary gland	Normal
B3	M	58	Brain, cerebellum	Normal	F3	F	32	Placenta	Normal
B4	M	65	Brain, cerebellum	Normal	F4	F	30	Placenta	Normal
B5	F		Brain, cerebellum	Normal	F5	F	27	Placenta	Normal
B6	M	56	Brain, cerebral cortex	Normal	F6	M	64	Prostate	Normal
B7	M	65	Brain, cerebral cortex	Normal	F7	M	65	Prostate	Normal
B8	F		Brain, cerebral cortex	Normal	F8	M	65	Prostate	Normal
B9	F	42	Fallopian tube	Normal	F9	F	32	Skin	Normal
B10	F	32	Fallopian tube	Normal	F10	F	68	Skin	Normal
B11	F	24	Fallopian tube	Normal	F11	M	26	Skin	Normal
B12	M	45	Esophagus	Normal	F12	M	47	Spinal cord	Normal
B13	F	68	Esophagus	Normal	F13	M	58	Spinal cord	Normal
C1	M	54	Esophagus	Normal	G1	M	27	Spleen	Normal
C2	M	45	Stomach	Normal	G2	M	60	Spleen	Normal
C3	M	49	Stomach	Normal	G3	M	31	Spleen	Normal
C4	M	77	Stomach	Normal	G4	F	60	Skeletal muscle	Normal
C5	M	45	Intestine, small intestine	Normal	G5	F	49	Skeletal muscle	Normal
C6	F	75	Intestine, small intestine	Normal	G6	M	70	Skeletal muscle	Normal
C7	F	75	Intestine, small intestine	Normal	G7	M	43	Testis	Normal
C8	M	2	Intestine, colon	Normal	G8	M	30	Testis	Normal
C9	M	46	Intestine, colon	Normal	G9	M	77	Testis	Normal
C10	M	74	Intestine, colon	Normal	G10	M	15	Thymus	Normal
C11	F	47	Intestine, rectum	Normal	G11	M	28	Thymus	Normal
C12	F	75	Intestine, rectum	Normal	G12	F	9	Thymus	Normal
C13	M	66	Intestine, rectum	Normal	G13	-	-	-	-
D1	M	58	Heart	Normal	H1	F	26	Thyroid	Normal
D2	M	46	Heart	Normal	H2	F	37	Thyroid	Normal
D3	F	34	Heart	Normal	H3	F	51	Thyroid	Normal
D4	F	52	Kidney, cortex	Normal	H4	M	46	Tonsil	Normal
D5	M	23	Kidney, cortex	Normal	H5	M	37	Tonsil	Normal
D6	M	63	Kidney, cortex	Normal	H6	M	13	Tonsil	Normal
D7	F	52	Kidney, medulla	Normal	H7	F	38	Uterus, cervix	Normal
D8	M	23	Kidney, medulla	Normal	H8	F	35	Uterus, cervix	Normal
D9	M	59	Peripheral nerve	Schwannoma	H9	F	44	Uterus, cervix	Normal
D10	F	29	Peripheral nerve	Schwannoma	H10	F	38	Uterus, endometrium	Normal
D11	F	44	Ureter	Normal	H11	F	41	Uterus, endometrium	Normal
D12	F	42	Ureter	Normal	H12	F	46	Uterus, endometrium	Normal
D13	F	57	Liver	Normal	H13	M	58	Skin	Malignant melanoma (tissue marker)

Figure 179A-179C

N+20/C-27 antibody 45C11 IgG 12.5 ug/mL

FDA Normal tissue array MNO1021

Fig. 180A
Normal Adrenal Gland

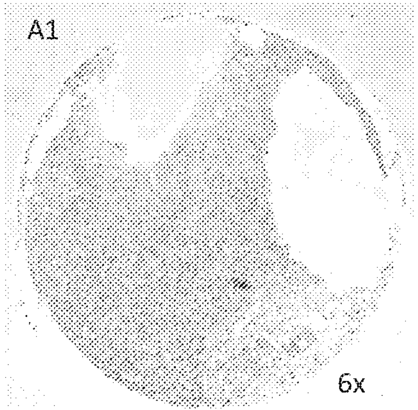


Fig. 180B
Normal Breast

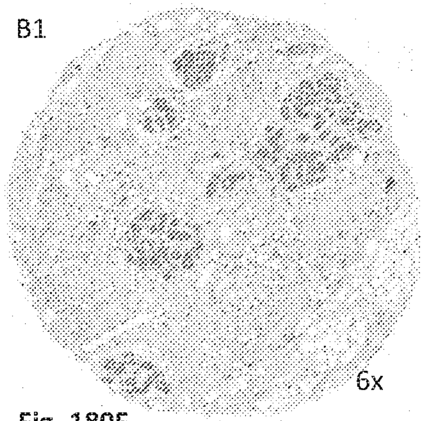


Fig. 180C
Normal Fallopian Tubes

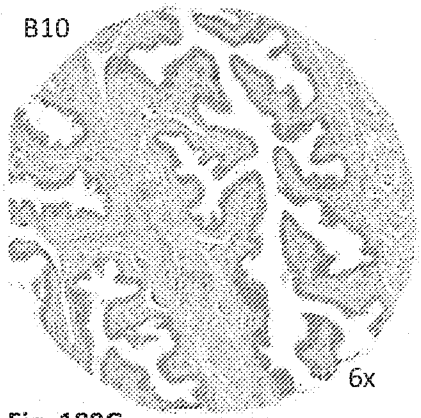


Fig. 180D
Normal Kidney

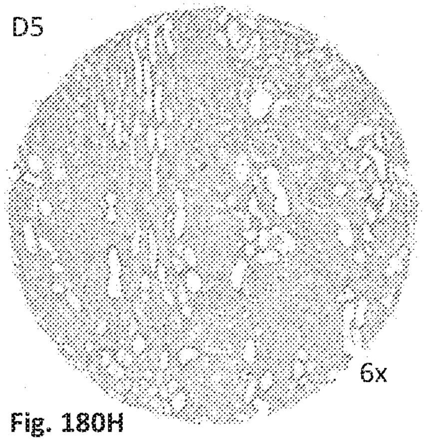


Fig. 180E

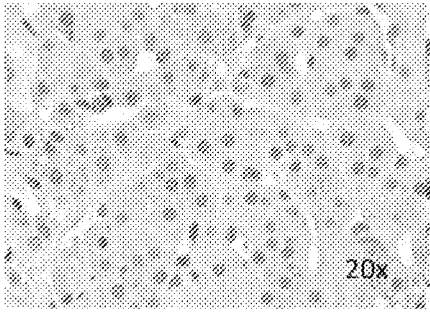


Fig. 180F

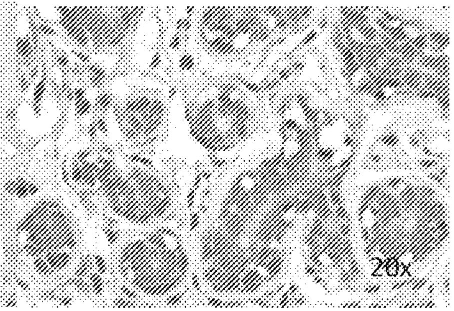


Fig. 180G

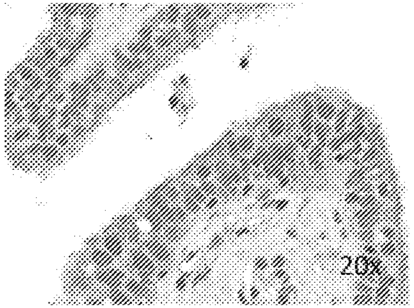


Fig. 180H

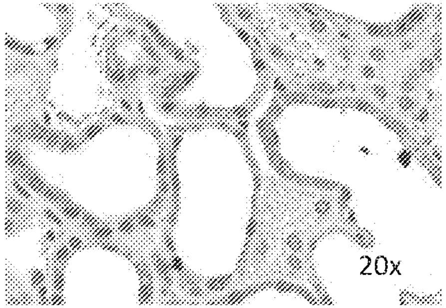


Figure 180A-180H

N+20/C-27 antibody 45C11 IgG 12.5 ug/mL

FDA Normal tissue array MNO1021

Fig. 180I
Normal Heart

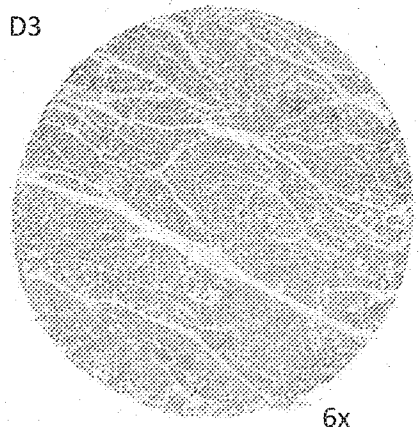


Fig. 180J
Normal Liver

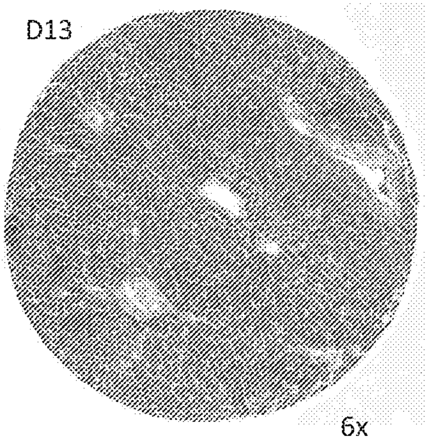


Fig. 180K
Normal Lung

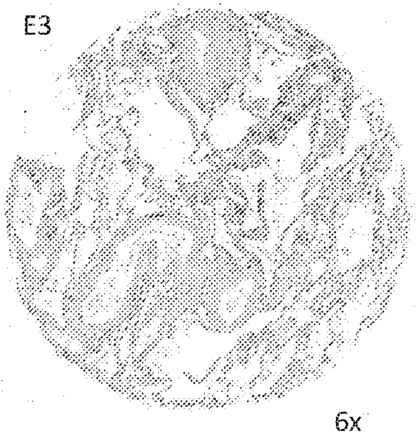


Fig. 180L
Normal Ureter

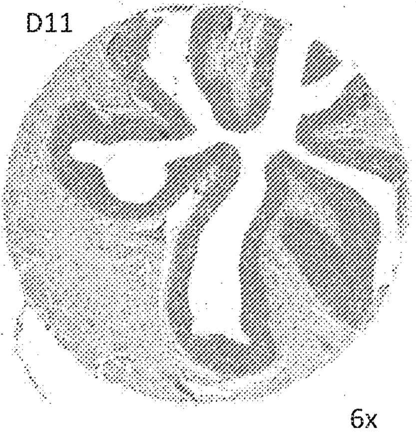


Fig. 180M

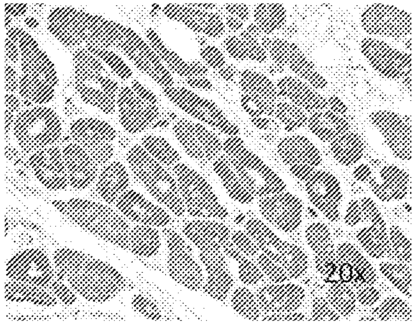


Fig. 180N

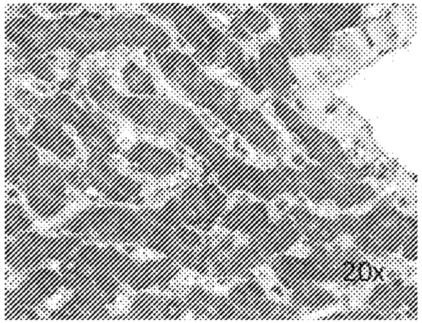


Fig. 180O

Fig. 180P

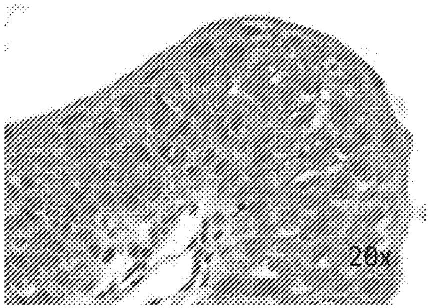


Figure 180I-180P

N+20/C-27 antibody 45C11 IgG 12.5 ug/mL

FDA Normal tissue array MNO1021

Fig. 180Q
Normal eye

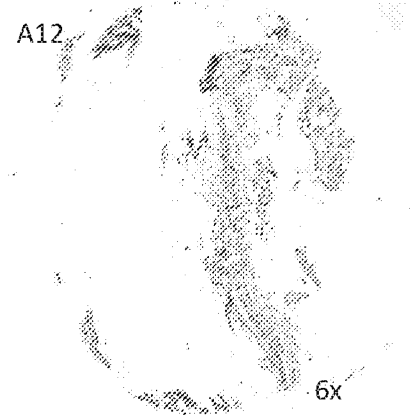


Fig. 180R
Normal Cerebral cortex

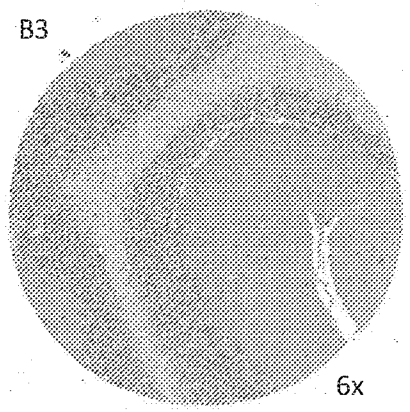


Fig. 180S
Normal Bone marrow

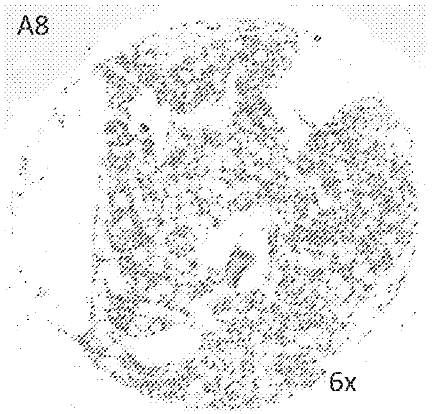


Fig. 180T
Normal Skeletal muscle

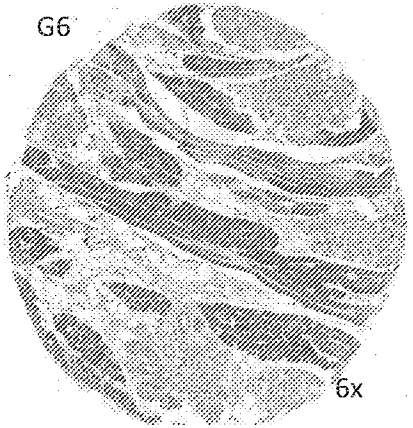


Fig. 180U

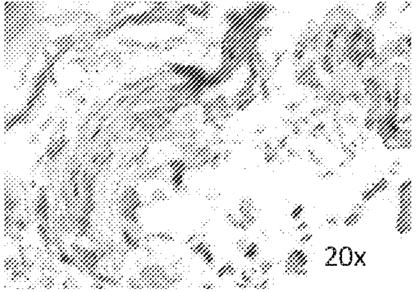


Fig. 180V

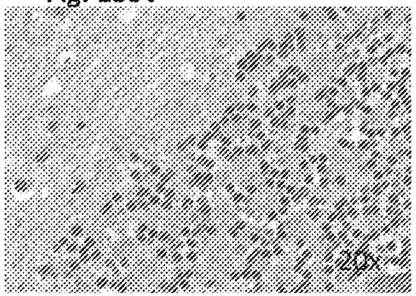


Fig. 180W

Fig. 180X

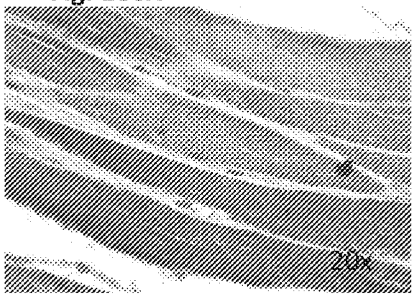


Figure 180Q-180X

N+20/C-27 antibody 45C11 IgG 10 ug/mL

Breast cancer tissue array BR1007

Fig. 181A

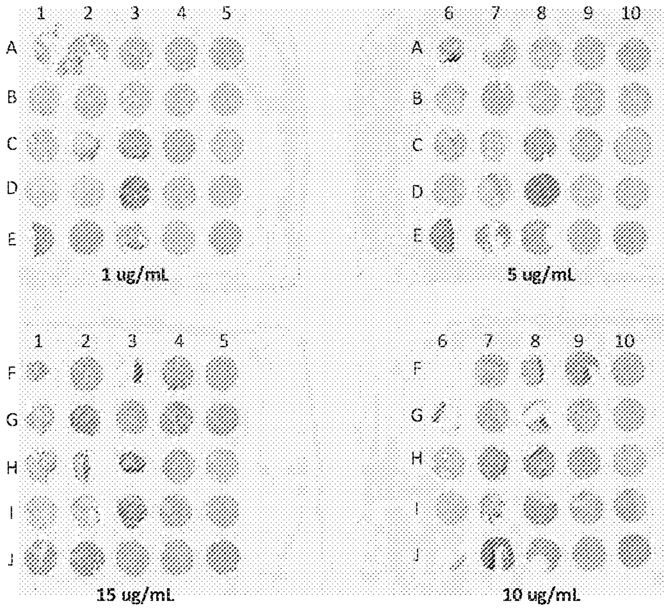


Fig. 181B

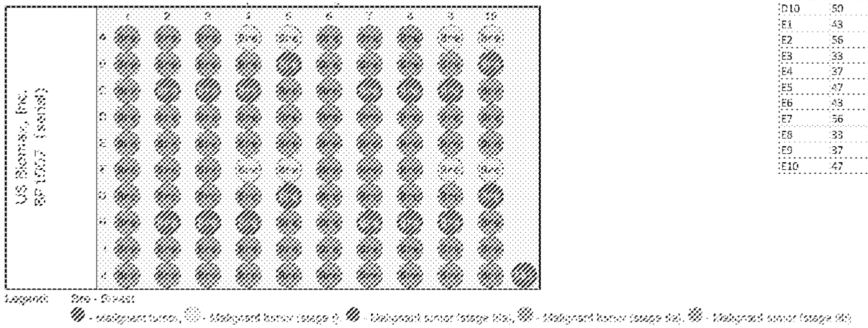


Fig. 181C

Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type		Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type
A1	63	F	Invasive ductal carcinoma	T3N1M0	2	IIb	malignant		F1	63	F	Invasive ductal carcinoma	T3N1M0	2	IIb	malignant
A2	43	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant		F2	43	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
A3	52	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant		F3	52	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
A4	52	F	Invasive ductal carcinoma	T1N0M0	2	I	malignant		F4	52	F	Invasive ductal carcinoma	T1N0M0	2	I	malignant
A5	34	F	Invasive ductal carcinoma	T1N0M0	2	I	malignant		F5	34	F	Invasive ductal carcinoma	T1N0M0	2	I	malignant
A6	63	F	Invasive ductal carcinoma	T3N1M0	2	IIb	malignant		F6	63	F	Invasive ductal carcinoma	T3N1M0	2	IIb	malignant
A7	43	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant		F7	43	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
A8	52	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant		F8	52	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
A9	52	F	Invasive ductal carcinoma	T1N0M0	2	I	malignant		F9	52	F	Invasive ductal carcinoma	T1N0M0	2	I	malignant
A10	34	F	Invasive ductal carcinoma	T1N0M0	2	I	malignant		F10	34	F	Invasive ductal carcinoma	T1N0M0	2	I	malignant
B1	47	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant		G1	47	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
B2	45	F	Invasive ductal carcinoma	T2N0M0	2	IIa	malignant		G2	45	F	Invasive ductal carcinoma	T2N0M0	2	IIa	malignant
B3	55	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant		G3	55	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
B4	64	F	Invasive ductal carcinoma	T1N1M0	2	IIa	malignant		G4	64	F	Invasive ductal carcinoma	T1N1M0	2	IIa	malignant
B5	39	F	Invasive ductal carcinoma	T2N2M0	2	IIIa	malignant		G5	39	F	Invasive ductal carcinoma	T2N2M0	2	IIIa	malignant
B6	47	F	Invasive ductal carcinoma	T2N1M0	-	IIb	malignant		G6	47	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
B7	45	F	Invasive ductal carcinoma	T2N0M0	2	IIa	malignant		G7	45	F	Invasive ductal carcinoma	T2N0M0	2	IIa	malignant
B8	55	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant		G8	55	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
B9	64	F	Invasive ductal carcinoma	T1N1M0	2	IIa	malignant		G9	64	F	Invasive ductal carcinoma	T1N1M0	2	IIa	malignant
B10	39	F	Invasive ductal carcinoma	T2N2M0	2	IIIa	malignant		G10	39	F	Invasive ductal carcinoma	T2N2M0	2	IIIa	malignant
C1	49	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant		H1	49	F	Invasive ductal carcinoma	T2N1M0	-	IIb	malignant
C2	61	F	Invasive ductal carcinoma	T2N2M0	2	IIIa	malignant		H2	61	F	Invasive ductal carcinoma	T2N2M0	2	IIIa	malignant
C3	52	F	Invasive ductal carcinoma	T2N2M0	2	IIIa	malignant		H3	52	F	Invasive ductal carcinoma	T2N2M0	2	IIIa	malignant
C4	48	F	Invasive ductal carcinoma	T4N0M0	2	IIIa	malignant		H4	48	F	Invasive ductal carcinoma	T4N0M0	2	IIIa	malignant
C5	57	F	Invasive ductal carcinoma	T2N0M0	2	IIa	malignant		H5	57	F	Invasive ductal carcinoma	T2N0M0	2	IIa	malignant
C6	49	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant		H6	49	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
C7	61	F	Invasive ductal carcinoma	T2N2M0	-	IIIa	malignant		H7	61	F	Invasive ductal carcinoma	T2N2M0	2	IIIa	malignant
C8	52	F	Invasive ductal carcinoma	T2N2M0	2	IIIa	malignant		H8	52	F	Invasive ductal carcinoma	T2N2M0	2	IIIa	malignant
C9	48	F	Invasive ductal carcinoma	T4N0M0	2	IIIa	malignant		H9	48	F	Invasive ductal carcinoma	T4N0M0	2	IIIa	malignant
C10	57	F	Invasive ductal carcinoma	T2N0M0	2	IIa	malignant		H10	57	F	Invasive ductal carcinoma	T2N0M0	2	IIa	malignant
D1	50	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant		I1	50	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
D2	33	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant		I2	33	F	Invasive ductal carcinoma	T2N1M0	-	IIb	malignant
D3	54	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant		I3	54	F	Invasive ductal carcinoma	T2N1M0	3	IIb	malignant
D4	46	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant		I4	46	F	Invasive ductal carcinoma	T2N1M0	3	IIb	malignant
D5	50	F	Invasive ductal carcinoma	T2N0M0	2	IIa	malignant		I5	50	F	Invasive ductal carcinoma	T2N0M0	2	IIa	malignant
D6	50	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant		I6	50	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
D7	33	F	Invasive ductal carcinoma	T2N1M0	-	IIb	malignant		I7	33	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
D8	54	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant		I8	54	F	Invasive ductal carcinoma	T2N1M0	2	IIb	malignant
D9	46	F	Invasive ductal carcinoma	T2N1M0	3	IIb	malignant		I9	46	F	Invasive ductal carcinoma	T2N1M0	3	IIb	malignant
D10	50	F	Invasive ductal carcinoma	T2N0M0	2	IIa	malignant		I10	50	F	Invasive ductal carcinoma	T2N0M0	2	IIa	malignant
E1	43	F	Invasive ductal carcinoma	T2N1M0	3	IIb	malignant		J1	43	F	Invasive ductal carcinoma	T2N1M0	3	IIb	malignant
E2	56	F	Invasive ductal carcinoma	T2N0M0	3	IIa	malignant		J2	56	F	Invasive ductal carcinoma	T2N0M0	3	IIa	malignant
E3	33	F	Invasive ductal carcinoma	T2N0M0	3	IIa	malignant		J3	33	F	Invasive ductal carcinoma	T2N0M0	3	IIa	malignant
E4	37	F	Invasive ductal carcinoma	T2N1M0	3	IIb	malignant		J4	37	F	Invasive ductal carcinoma	T2N1M0	3	IIb	malignant
E5	47	F	Invasive ductal carcinoma	T3N1M0	3	IIb	malignant		J5	47	F	Invasive ductal carcinoma	T3N1M0	3	IIb	malignant
E6	43	F	Invasive ductal carcinoma	T2N1M0	3	IIb	malignant		J6	43	F	Invasive ductal carcinoma	T2N1M0	3	IIb	malignant
E7	56	F	Invasive ductal carcinoma	T2N0M0	3	IIa	malignant		J7	56	F	Invasive ductal carcinoma	T2N0M0	3	IIa	malignant
E8	33	F	Invasive ductal carcinoma	T2N0M0	3	IIa	malignant		J8	33	F	Invasive ductal carcinoma	T2N0M0	3	IIa	malignant
E9	37	F	Invasive ductal carcinoma	T2N1M0	3	IIb	malignant		J9	37	F	Invasive ductal carcinoma	T2N1M0	3	IIb	malignant
E10	47	F	Invasive ductal carcinoma	T3N1M0	3	IIb	malignant		J10	47	F	Invasive ductal carcinoma	T3N1M0	3	IIb	malignant

Fig. 181A–181C

N+20/C-27 antibody 45C11 IgG 10 ug/mL

Breast cancer tissue array BR1007

Fig. 182A

Position: B4
Cell Type: Invasive Ductal Carcinoma
Tumor Grade: 2
TNM: T1N1M0

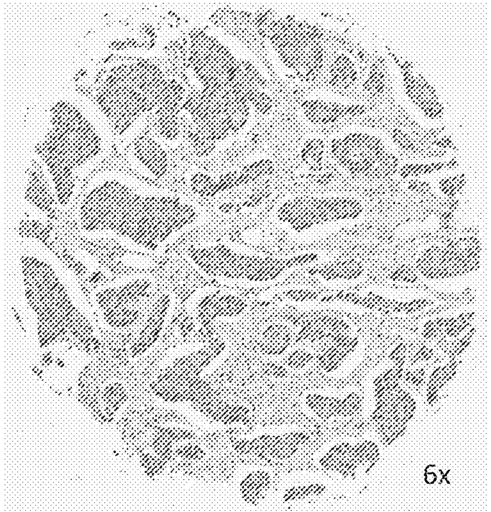


Fig. 182B

Position: B5
Cell Type: Invasive Ductal Carcinoma
Tumor Grade: 2
TNM: T2N2M0

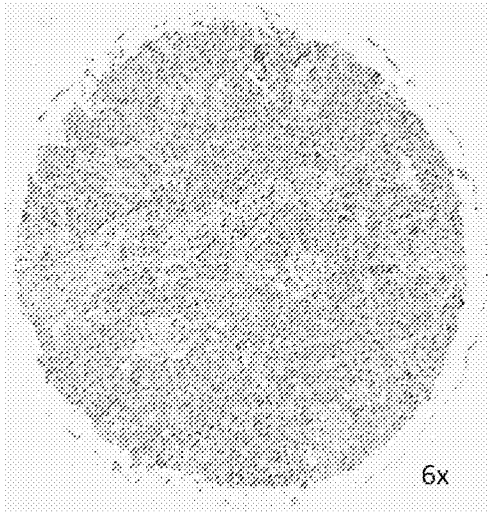


Fig. 182C

Position: D5
Cell Type: Invasive Ductal Carcinoma
Tumor Grade: 2
TNM: T2N0M0

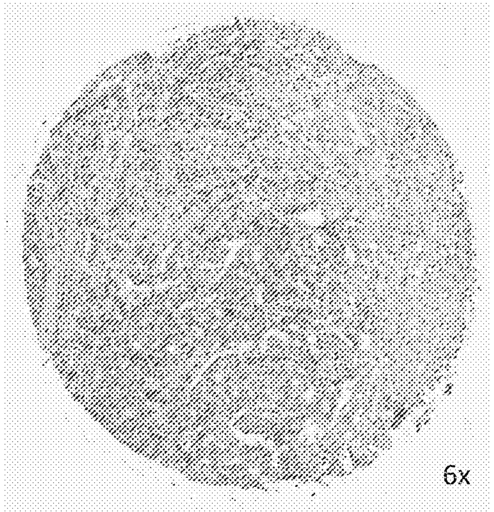


Fig. 182D

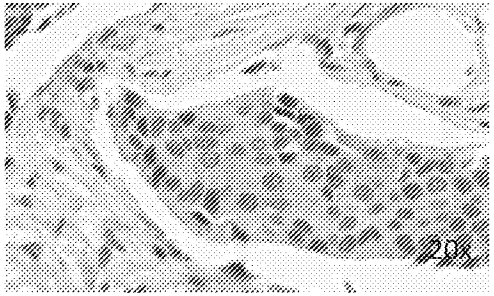


Fig. 182E

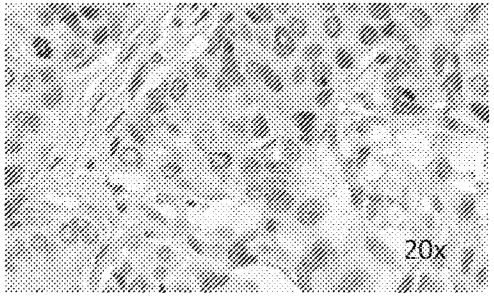


Fig. 182F

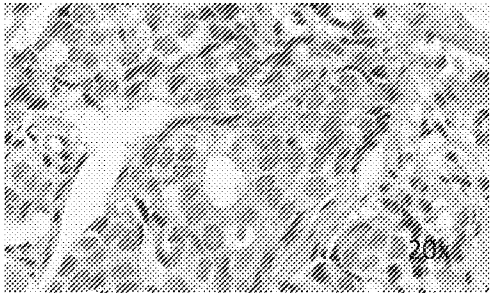


Fig. 182A–182F

N+20/C-27 antibody 45C11 5-15 ug/mL
Pancreatic cancer tissue array PA1003

Fig. 183A

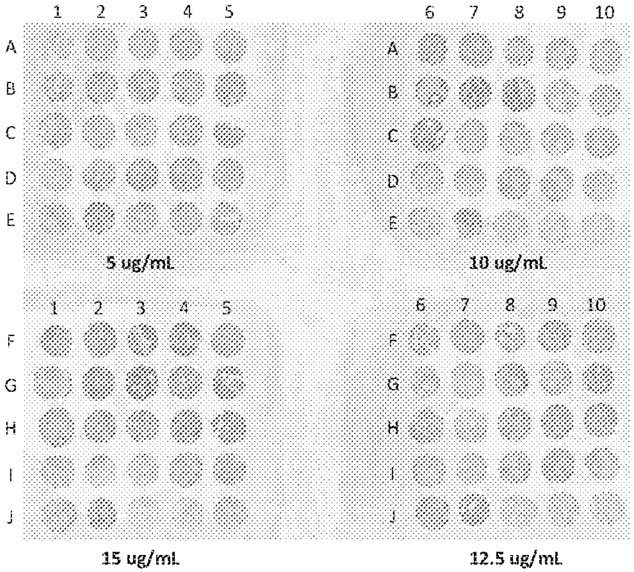


Fig. 183B

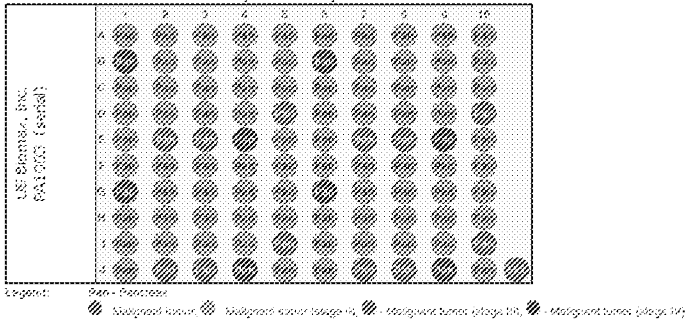


Fig. 183C

Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type	Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type
A1	39	F	Adenocarcinoma	T3N0M0	2	II	malignant	F1	39	F	Adenocarcinoma	T3N0M0	2	II	malignant
A2	44	M	Adenocarcinoma	T3N0M0	2	II	malignant	F2	44	M	Adenocarcinoma	T3N0M0	2	II	malignant
A3	59	M	Adenocarcinoma	T3N0M0	2	II	malignant	F3	59	M	Adenocarcinoma	T3N0M0	2	II	malignant
A4	65	M	Adenocarcinoma	T3N0M0	2	II	malignant	F4	65	M	Adenocarcinoma	T3N0M0	2	II	malignant
A5	53	M	Adenocarcinoma	T3N0M0	2	II	malignant	F5	53	M	Adenocarcinoma	T3N0M0	2	II	malignant
A6	39	F	Adenocarcinoma	T3N0M0	2	II	malignant	F6	39	F	Adenocarcinoma	T3N0M0	2	II	malignant
A7	44	M	Adenocarcinoma	T3N0M0	2	II	malignant	F7	44	M	Adenocarcinoma	T3N0M0	2	II	malignant
A8	59	M	Adenocarcinoma	T3N0M0	2	II	malignant	F8	59	M	Adenocarcinoma	T3N0M0	2	II	malignant
A9	65	M	Adenocarcinoma	T3N0M0	2	II	malignant	F9	65	M	Adenocarcinoma	T3N0M0	-	II	malignant
A10	53	M	Adenocarcinoma	T3N0M0	2	II	malignant	F10	53	M	Adenocarcinoma	T3N0M0	2	II	malignant
B1	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant	G1	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant
B2	52	M	Adenocarcinoma	T3N0M0	1	II	malignant	G2	52	M	Adenocarcinoma	T3N0M0	1	II	malignant
B3	57	M	Adenocarcinoma	T3N0M0	2	II	malignant	G3	57	M	Adenocarcinoma	T3N0M0	2	II	malignant
B4	34	M	Adenocarcinoma	T3N0M0	2	II	malignant	G4	34	M	Adenocarcinoma	T3N0M0	2	II	malignant
B5	72	F	Adenocarcinoma	T3N0M0	2	II	malignant	G5	72	F	Adenocarcinoma	T3N0M0	1	II	malignant
B6	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant	G6	42	M	Adenocarcinoma	T2N0M1	-	IV	malignant
B7	52	M	Adenocarcinoma	T3N0M0	2	II	malignant	G7	52	M	Adenocarcinoma	T3N0M0	2	II	malignant
B8	57	M	Adenocarcinoma	T3N0M0	2	II	malignant	G8	57	M	Adenocarcinoma	T3N0M0	2	II	malignant
B9	34	M	Adenocarcinoma	T3N0M0	1	II	malignant	G9	34	M	Adenocarcinoma	T3N0M0	2	II	malignant
B10	72	F	Adenocarcinoma	T3N0M0	2	II	malignant	G10	72	F	Adenocarcinoma	T3N0M0	2	II	malignant
C1	47	M	Adenocarcinoma	T3N0M0	1	II	malignant	H1	47	M	Adenocarcinoma	T3N0M0	1	II	malignant
C2	64	F	Adenocarcinoma	T3N0M0	1	II	malignant	H2	64	F	Adenocarcinoma	T3N0M0	-	II	malignant
C3	51	M	Adenocarcinoma	T3N0M0	2	II	malignant	H3	51	M	Adenocarcinoma	T3N0M0	2	II	malignant
C4	68	F	Adenocarcinoma	T3N0M0	2	II	malignant	H4	68	F	Adenocarcinoma	T3N0M0	3	II	malignant
C5	41	M	Adenocarcinoma	T3N0M0	-	II	malignant	H5	41	M	Adenocarcinoma	T3N0M0	2	II	malignant
C6	47	M	Adenocarcinoma	T3N0M0	1	II	malignant	H6	47	M	Adenocarcinoma	T3N0M0	1	II	malignant
C7	64	F	Adenocarcinoma	T3N0M0	2	II	malignant	H7	64	F	Adenocarcinoma	T3N0M0	2	II	malignant
C8	51	M	Adenocarcinoma	T3N0M0	2	II	malignant	H8	51	M	Adenocarcinoma	T3N0M0	-	II	malignant
C9	68	F	Adenocarcinoma	T3N0M0	2	II	malignant	H9	68	F	Adenocarcinoma	T3N0M0	2	II	malignant
C10	41	M	Adenocarcinoma	T3N0M0	2	II	malignant	H10	41	M	Adenocarcinoma	T3N0M0	2	II	malignant
D1	58	F	Adenocarcinoma	T3N0M0	2	II	malignant	I1	58	F	Adenocarcinoma	T3N0M0	2	II	malignant
D2	41	F	Adenocarcinoma	T3N0M0	3	II	malignant	I2	41	F	Adenocarcinoma	T3N0M0	3	II	malignant
D3	72	F	Adenocarcinoma	T3N0M0	3	II	malignant	I3	72	F	Adenocarcinoma	T3N0M0	3	II	malignant
D4	59	M	Adenocarcinoma	T3N0M0	3	II	malignant	I4	59	M	Adenocarcinoma	T3N0M0	3	II	malignant
D5	50	M	Adenocarcinoma	T3N1M0	3	III	malignant	I5	50	M	Adenocarcinoma	T3N1M0	3	III	malignant
D6	58	F	Adenocarcinoma	T3N0M0	2	II	malignant	I6	58	F	Adenocarcinoma	T3N0M0	2	II	malignant
D7	41	F	Adenocarcinoma	T3N0M0	3	II	malignant	I7	41	F	Adenocarcinoma	T3N0M0	2	II	malignant
D8	72	F	Adenocarcinoma	T3N0M0	3	II	malignant	I8	72	F	Adenocarcinoma	T3N0M0	3	II	malignant
D9	59	M	Adenocarcinoma	T3N0M0	3	II	malignant	I9	59	M	Adenocarcinoma	T3N0M0	3	II	malignant
D10	50	M	Adenocarcinoma	T3N1M0	3	III	malignant	I10	50	M	Adenocarcinoma	T3N1M0	3	III	malignant
E1	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant	J1	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant
E2	60	M	Adenocarcinoma	T3N1M0	2--3	III	malignant	J2	60	M	Adenocarcinoma	T3N1M0	2--3	III	malignant
E3	56	M	Adenocarcinoma	T2N1M0	3	III	malignant	J3	56	M	Adenocarcinoma	T2N1M0	3	III	malignant
E4	60	F	Adenocarcinoma	T2N1M1	3	IV	malignant	J4	60	F	Adenocarcinoma	T2N1M1	2	IV	malignant
E5	66	F	Adenocarcinoma	T3N0M0	-	II	malignant	J5	66	F	Adenocarcinoma	T3N0M0	3	II	malignant
E6	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant	J6	53	F	Adenocarcinoma	T3N0M0	3	II	malignant
E7	60	M	Adenocarcinoma	T3N1M0	2	III	malignant	J7	60	M	Adenocarcinoma	T3N1M0	3	III	malignant
E8	56	M	Adenocarcinoma	T2N1M0	3	III	malignant	J8	56	M	Adenocarcinoma	T2N1M0	3	III	malignant
E9	60	F	Adenocarcinoma	T2N1M1	3	IV	malignant	J9	60	F	Adenocarcinoma	T2N1M1	-	IV	malignant
E10	66	F	Adenocarcinoma	T3N0M0	3	II	malignant	J10	66	F	Adenocarcinoma	T3N0M0	3	II	malignant

Fig. 183A–183C

N+20/C-27 antibody 45C11 12.5 ug/mL

Pancreatic cancer tissue array PA805c

Fig. 184A

Position: F6
Cell Type: Invasive ductal carcinoma
Tumor Grade: 2
TNM: T3N1M0

Fig. 184B

Position: H8
Cell Type: Invasive ductal carcinoma
Tumor Grade: 2
TNM: T2N2M0

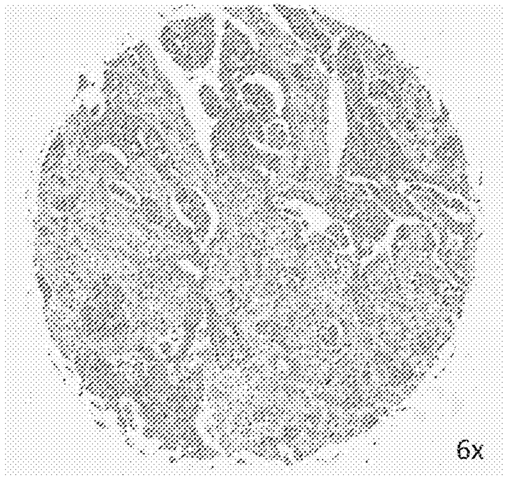


Fig. 184C

Position: I9
Cell Type: Invasive ductal carcinoma
Tumor Grade: 3
TNM: T2N1M0

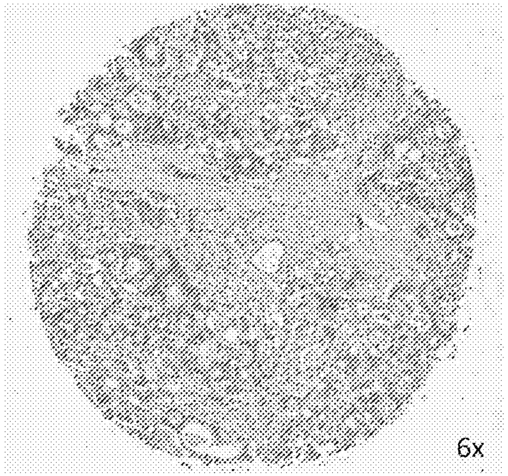


Fig. 184D

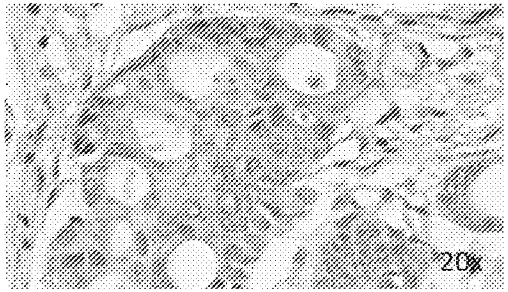


Fig. 184E

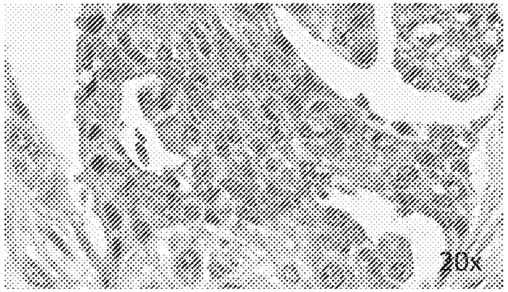


Fig. 184F

Fig. 184A–184F

N+9/C-9 antibody 3C5 IgG 10 ug/mL

FDA Normal tissue array MNO1021

Fig. 185A

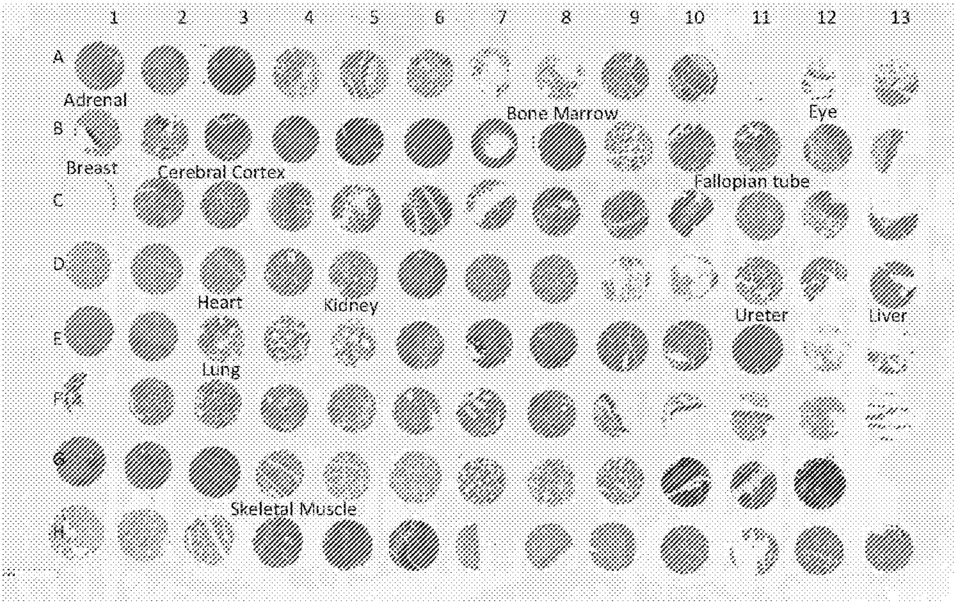


Fig. 185B

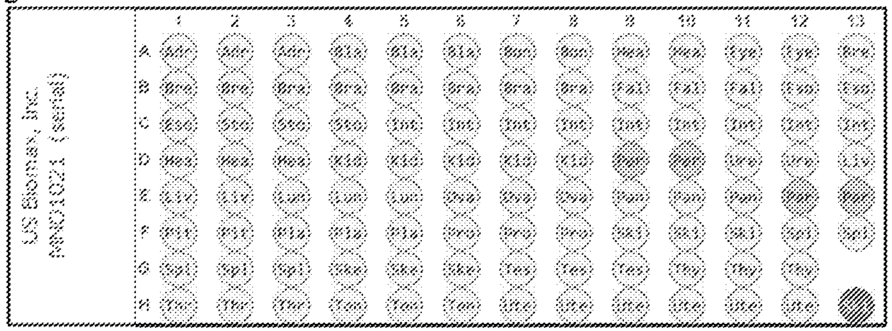


Fig. 185C

Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis	Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis
A1	F	31	Adrenal gland	Normal	E1	M	59	Liver	Normal
A2	M	51	Adrenal gland	Normal	E2	F	27	Liver	Normal
A3	M	53	Adrenal gland	Normal	E3	M	72	Lung	Normal
A4	M	75	Bladder, umary	Normal	E4	F	55	Lung	Normal
A5	M	72	Bladder, umary	Normal	E5	M	43	Lung	Normal
A6	M	52	Bladder, umary	Normal	E6	F	47	Ovary	Normal
A7	M	53	Bone, bone marrow	Normal	E7	F	46	Ovary	Normal
A8	M	43	Bone, bone marrow	Normal	E8	F	40	Ovary	Normal
A9	F	44	Head and neck, salivary gland	Normal	E9	M	42	Pancreas	Normal
A10	M	18	Head and neck, salivary gland	Normal	E10	F	26	Pancreas	Normal
A11	M	55	Eye	Normal	E11	F	59	Pancreas	Normal
A12	M	50	Eye	Normal	E12	M	17	Parathyroid	Adenoma
A13	F	35	Breast	Normal	E13	M	72	Parathyroid	Adenoma
B1	F	38	Breast	Normal	F1	F	3	Pituitary gland	Normal
B2	F	33	Breast	Normal	F2	F		Pituitary gland	Normal
B3	M	58	Brain, cerebellum	Normal	F3	F	32	Placenta	Normal
B4	M	65	Brain, cerebellum	Normal	F4	F	30	Placenta	Normal
B5	F		Brain, cerebellum	Normal	F5	F	27	Placenta	Normal
B6	M	56	Brain, cerebral cortex	Normal	F6	M	64	Prostate	Normal
B7	M	65	Brain, cerebral cortex	Normal	F7	M	65	Prostate	Normal
B8	F		Brain, cerebral cortex	Normal	F8	M	65	Prostate	Normal
B9	F	42	Fallopian tube	Normal	F9	F	32	Skin	Normal
B10	F	32	Fallopian tube	Normal	F10	F	68	Skin	Normal
B11	F	24	Fallopian tube	Normal	F11	M	26	Skin	Normal
B12	M	45	Esophagus	Normal	F12	M	47	Spinal cord	Normal
B13	F	68	Esophagus	Normal	F13	M	58	Spinal cord	Normal
C1	M	54	Esophagus	Normal	G1	M	27	Spleen	Normal
C2	M	45	Stomach	Normal	G2	M	60	Spleen	Normal
C3	M	49	Stomach	Normal	G3	M	31	Spleen	Normal
C4	M	77	Stomach	Normal	G4	F	60	Skeletal muscle	Normal
C5	M	45	Intestine, small intestine	Normal	G5	F	49	Skeletal muscle	Normal
C6	F	75	Intestine, small intestine	Normal	G6	M	70	Skeletal muscle	Normal
C7	F	75	Intestine, small intestine	Normal	G7	M	43	Testis	Normal
C8	M	2	Intestine, colon	Normal	G8	M	30	Testis	Normal
C9	M	46	Intestine, colon	Normal	G9	M	77	Testis	Normal
C10	M	74	Intestine, colon	Normal	G10	M	15	Thymus	Normal
C11	F	47	Intestine, rectum	Normal	G11	M	28	Thymus	Normal
C12	F	75	Intestine, rectum	Normal	G12	F	9	Thymus	Normal
C13	M	66	Intestine, rectum	Normal	G13	-	-	-	-
D1	M	58	Heart	Normal	H1	F	26	Thyroid	Normal
D2	M	46	Heart	Normal	H2	F	37	Thyroid	Normal
D3	F	34	Heart	Normal	H3	F	51	Thyroid	Normal
D4	F	52	Kidney, cortex	Normal	H4	M	46	Tonsil	Normal
D5	M	23	Kidney, cortex	Normal	H5	M	37	Tonsil	Normal
D6	M	63	Kidney, cortex	Normal	H6	M	13	Tonsil	Normal
D7	F	52	Kidney, medulla	Normal	H7	F	38	Uterus, cervix	Normal
D8	M	23	Kidney, medulla	Normal	H8	F	35	Uterus, cervix	Normal
D9	M	59	Peripheral nerve	Schwannoma	H9	F	44	Uterus, cervix	Normal
D10	F	29	Peripheral nerve	Schwannoma	H10	F	38	Uterus, endometrium	Normal
D11	F	44	Ureter	Normal	H11	F	41	Uterus, endometrium	Normal
D12	F	42	Ureter	Normal	H12	F	46	Uterus, endometrium	Normal
D13	F	57	Liver	Normal	H13	M	58	Skin	Malignant melanoma (tissue marker)

Figure 185A-185C

N+9/C-9 antibody 3C5 IgG 10 ug/mL

FDA Normal tissue array MNO1021

Fig. 186A
Normal Adrenal Gland

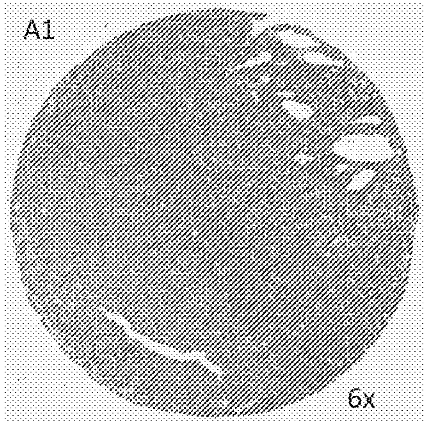


Fig. 186B
Normal Breast

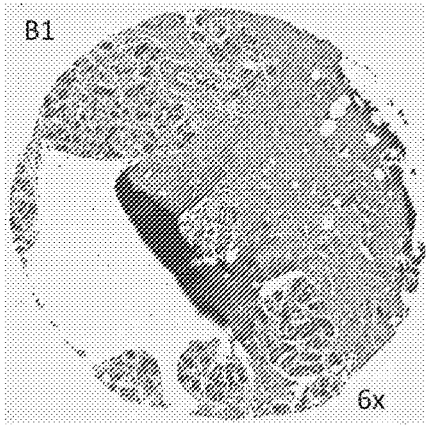


Fig. 186C
Normal Fallopian Tubes

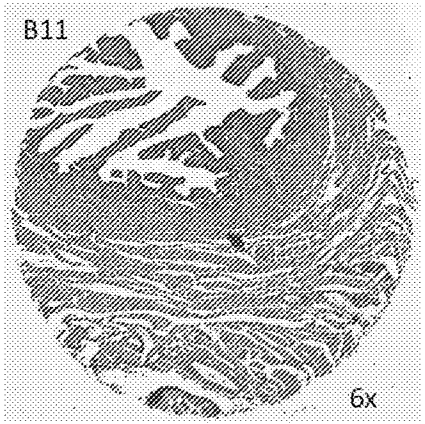


Fig. 186D
Normal Kidney

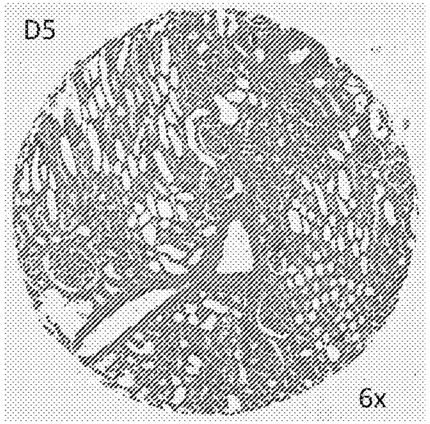


Fig. 186E

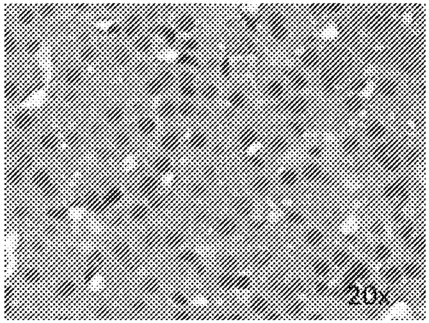


Fig. 186F

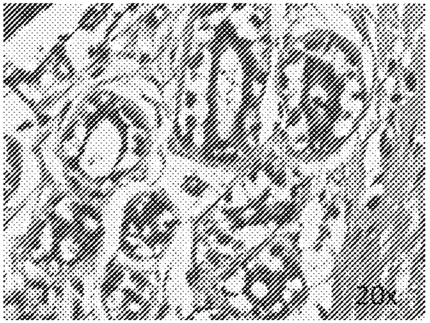


Fig. 186G

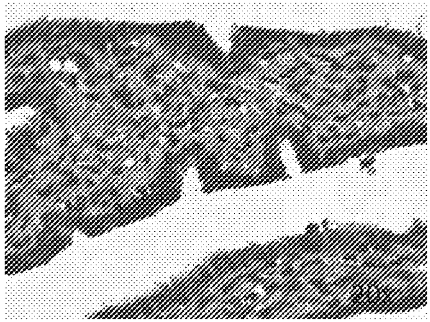


Fig. 186H

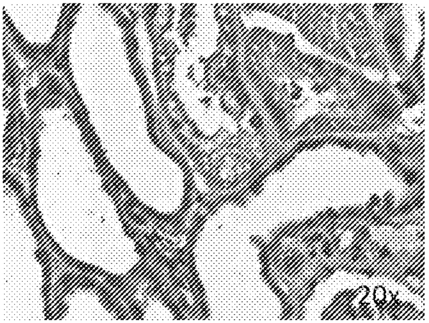


Figure 186A-186H

N+9/C-9 antibody 3C5 IgG 10 ug/mL

FDA Normal tissue array MNO1021

Fig. 186I
Normal Heart

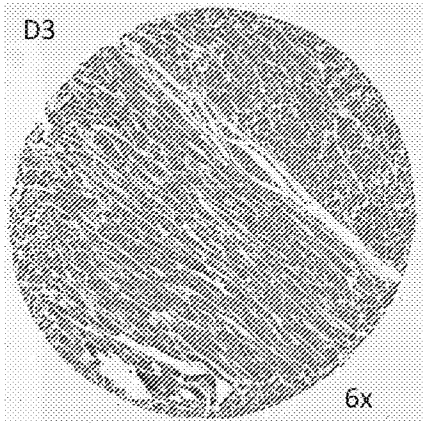


Fig. 186J
Normal Liver

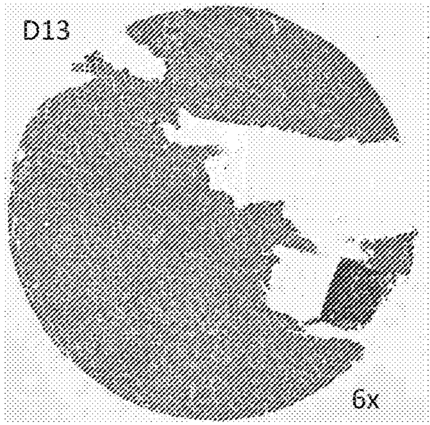


Fig. 186K
Normal Lung

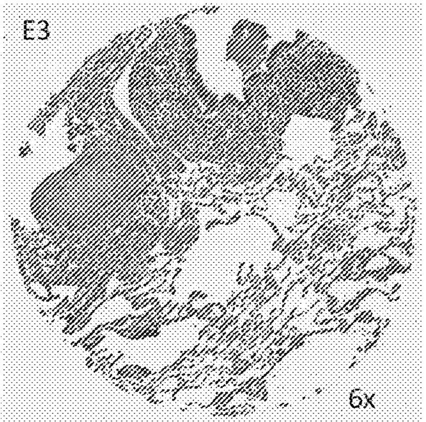


Fig. 186L
Normal Ureter

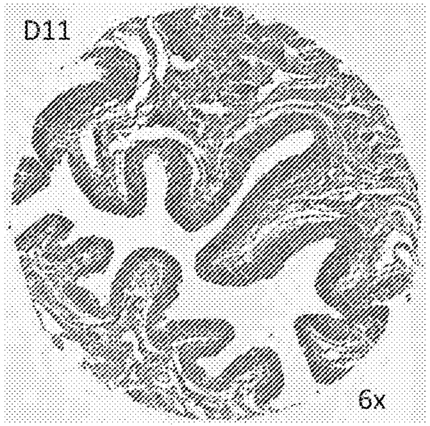


Fig. 186M

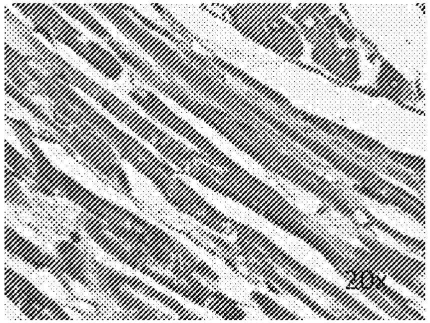


Fig. 186N

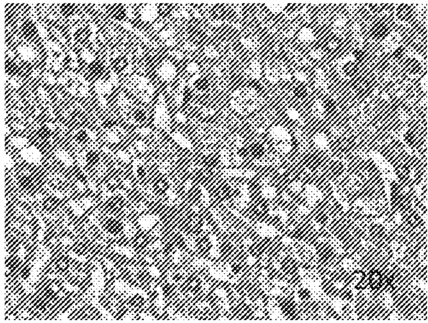


Fig. 186O

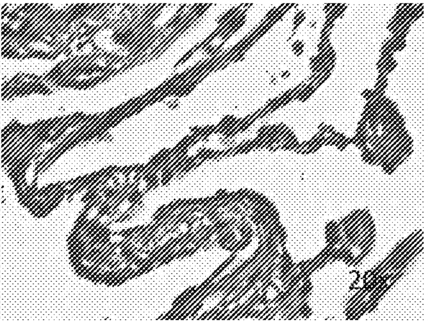


Fig. 186P

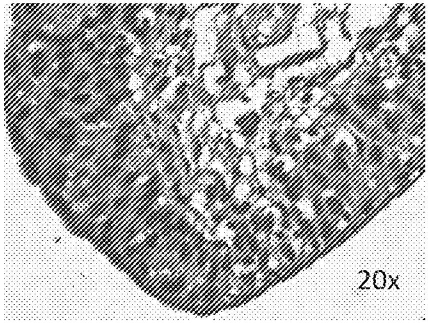


Figure 186I-186P

N+9/C-9 antibody 3C5 IgG 10 ug/mL

FDA Normal tissue array MNO1021

Fig. 186Q
Normal Eye

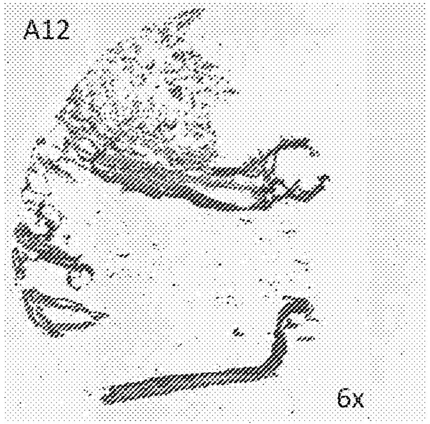


Fig. 186R
Normal Cerebral Cortex

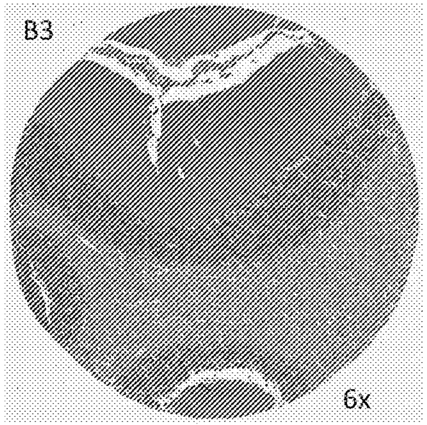


Fig. 186S
Normal Bone Marrow

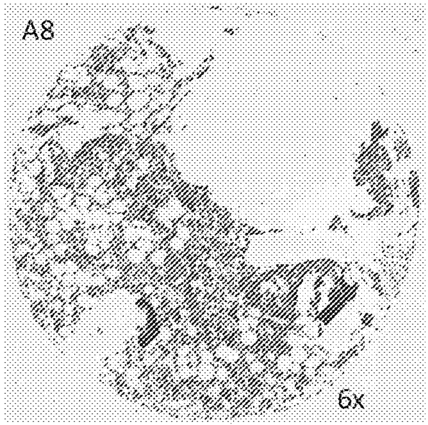


Fig. 186T
Normal Skeletal Muscle

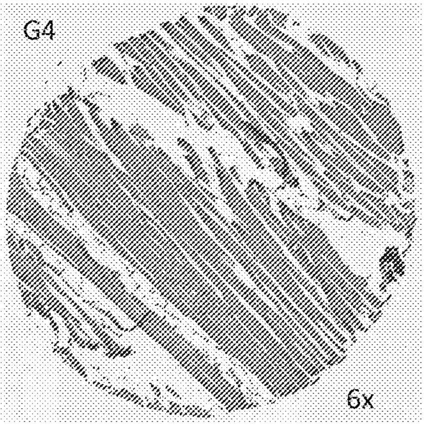


Fig. 186U

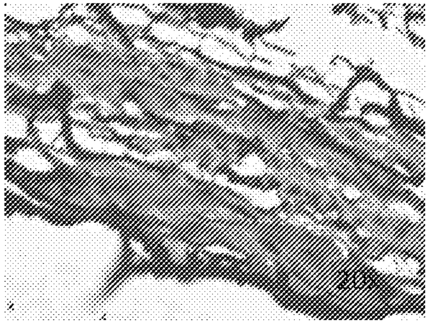


Fig. 186V

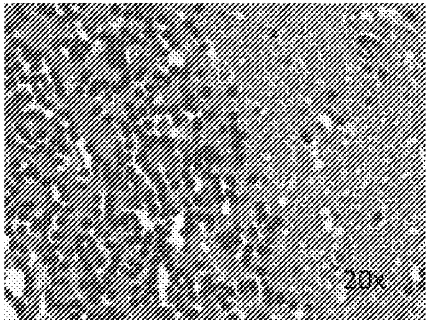


Fig. 186W

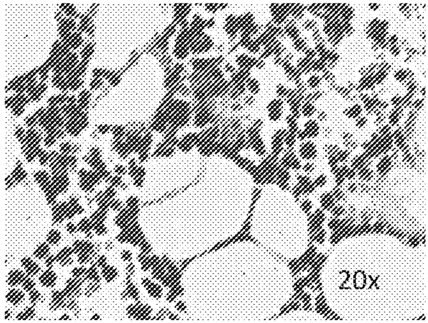


Fig. 186X

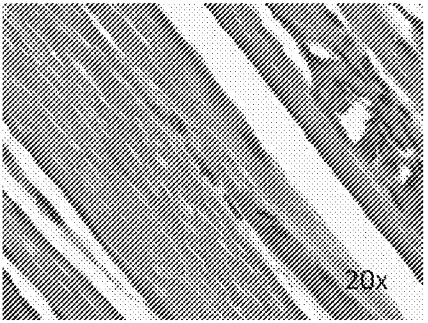


Figure 186Q-186X

N+9/C-9 antibody 3C5 10 ug/mL

Pancreatic cancer tissue array PA1003

Fig. 187A

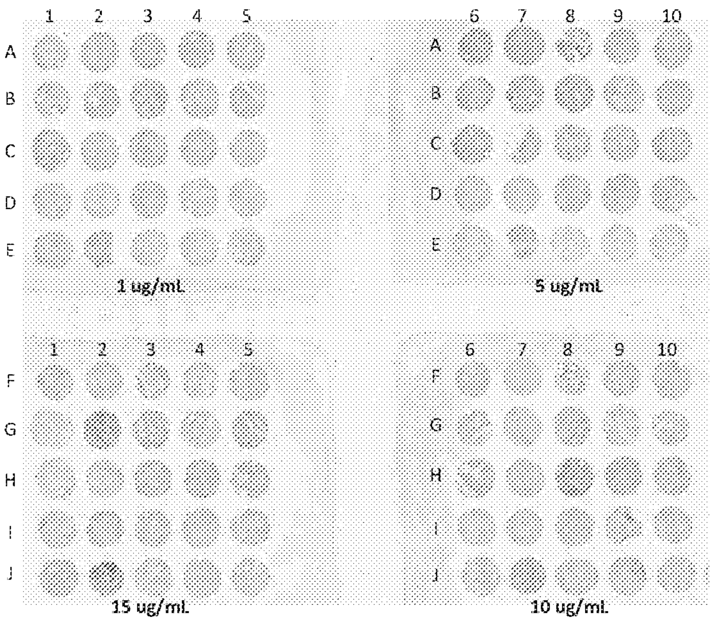


Fig. 187B

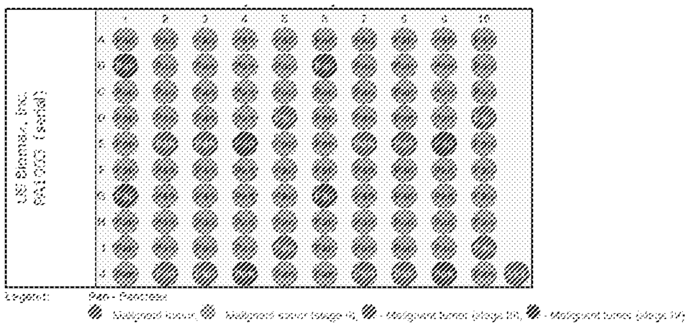


Fig. 187C

Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type	Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type
A1	39	F	Adenocarcinoma	T3N0M0	2	II	malignant	F1	39	F	Adenocarcinoma	T3N0M0	2	II	malignant
A2	44	M	Adenocarcinoma	T3N0M0	2	II	malignant	F2	44	M	Adenocarcinoma	T3N0M0	2	II	malignant
A3	59	M	Adenocarcinoma	T3N0M0	2	II	malignant	F3	59	M	Adenocarcinoma	T3N0M0	2	II	malignant
A4	65	M	Adenocarcinoma	T3N0M0	2	II	malignant	F4	65	M	Adenocarcinoma	T3N0M0	2	II	malignant
A5	53	M	Adenocarcinoma	T3N0M0	2	II	malignant	F5	53	M	Adenocarcinoma	T3N0M0	2	II	malignant
A6	39	F	Adenocarcinoma	T3N0M0	2	II	malignant	F6	39	F	Adenocarcinoma	T3N0M0	2	II	malignant
A7	44	M	Adenocarcinoma	T3N0M0	2	II	malignant	F7	44	M	Adenocarcinoma	T3N0M0	2	II	malignant
A8	59	M	Adenocarcinoma	T3N0M0	2	II	malignant	F8	59	M	Adenocarcinoma	T3N0M0	2	II	malignant
A9	65	M	Adenocarcinoma	T3N0M0	2	II	malignant	F9	65	M	Adenocarcinoma	T3N0M0	-	II	malignant
A10	53	M	Adenocarcinoma	T3N0M0	2	II	malignant	F10	53	M	Adenocarcinoma	T3N0M0	2	II	malignant
B1	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant	G1	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant
B2	52	M	Adenocarcinoma	T3N0M0	1	II	malignant	G2	52	M	Adenocarcinoma	T3N0M0	1	II	malignant
B3	57	M	Adenocarcinoma	T3N0M0	2	II	malignant	G3	57	M	Adenocarcinoma	T3N0M0	2	II	malignant
B4	34	M	Adenocarcinoma	T3N0M0	2	II	malignant	G4	34	M	Adenocarcinoma	T3N0M0	2	II	malignant
B5	72	F	Adenocarcinoma	T3N0M0	2	II	malignant	G5	72	F	Adenocarcinoma	T3N0M0	1	II	malignant
B6	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant	G6	42	M	Adenocarcinoma	T2N0M1	-	IV	malignant
B7	52	M	Adenocarcinoma	T3N0M0	2	II	malignant	G7	52	M	Adenocarcinoma	T3N0M0	2	II	malignant
B8	57	M	Adenocarcinoma	T3N0M0	2	II	malignant	G8	57	M	Adenocarcinoma	T3N0M0	2	II	malignant
B9	34	M	Adenocarcinoma	T3N0M0	1	II	malignant	G9	34	M	Adenocarcinoma	T3N0M0	2	II	malignant
B10	72	F	Adenocarcinoma	T3N0M0	2	II	malignant	G10	72	F	Adenocarcinoma	T3N0M0	2	II	malignant
C1	47	M	Adenocarcinoma	T3N0M0	1	II	malignant	H1	47	M	Adenocarcinoma	T3N0M0	1	II	malignant
C2	64	F	Adenocarcinoma	T3N0M0	1	II	malignant	H2	64	F	Adenocarcinoma	T3N0M0	-	II	malignant
C3	51	M	Adenocarcinoma	T3N0M0	2	II	malignant	H3	51	M	Adenocarcinoma	T3N0M0	2	II	malignant
C4	68	F	Adenocarcinoma	T3N0M0	2	II	malignant	H4	68	F	Adenocarcinoma	T3N0M0	3	II	malignant
C5	41	M	Adenocarcinoma	T3N0M0	-	II	malignant	H5	41	M	Adenocarcinoma	T3N0M0	2	II	malignant
C6	47	M	Adenocarcinoma	T3N0M0	1	II	malignant	H6	47	M	Adenocarcinoma	T3N0M0	1	II	malignant
C7	64	F	Adenocarcinoma	T3N0M0	2	II	malignant	H7	64	F	Adenocarcinoma	T3N0M0	2	II	malignant
C8	51	M	Adenocarcinoma	T3N0M0	2	II	malignant	H8	51	M	Adenocarcinoma	T3N0M0	-	II	malignant
C9	68	F	Adenocarcinoma	T3N0M0	2	II	malignant	H9	68	F	Adenocarcinoma	T3N0M0	2	II	malignant
C10	41	M	Adenocarcinoma	T3N0M0	2	II	malignant	H10	41	M	Adenocarcinoma	T3N0M0	2	II	malignant
D1	58	F	Adenocarcinoma	T3N0M0	2	II	malignant	I1	58	F	Adenocarcinoma	T3N0M0	2	II	malignant
D2	41	F	Adenocarcinoma	T3N0M0	3	II	malignant	I2	41	F	Adenocarcinoma	T3N0M0	3	II	malignant
D3	72	F	Adenocarcinoma	T3N0M0	3	II	malignant	I3	72	F	Adenocarcinoma	T3N0M0	3	II	malignant
D4	59	M	Adenocarcinoma	T3N0M0	3	II	malignant	I4	59	M	Adenocarcinoma	T3N0M0	3	II	malignant
D5	50	M	Adenocarcinoma	T3N1M0	3	III	malignant	I5	50	M	Adenocarcinoma	T3N1M0	3	III	malignant
D6	58	F	Adenocarcinoma	T3N0M0	2	II	malignant	I6	58	F	Adenocarcinoma	T3N0M0	2	II	malignant
D7	41	F	Adenocarcinoma	T3N0M0	3	II	malignant	I7	41	F	Adenocarcinoma	T3N0M0	2	II	malignant
D8	72	F	Adenocarcinoma	T3N0M0	3	II	malignant	I8	72	F	Adenocarcinoma	T3N0M0	3	II	malignant
D9	59	M	Adenocarcinoma	T3N0M0	3	II	malignant	I9	59	M	Adenocarcinoma	T3N0M0	3	II	malignant
D10	50	M	Adenocarcinoma	T3N1M0	3	III	malignant	I10	50	M	Adenocarcinoma	T3N1M0	3	III	malignant
E1	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant	J1	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant
E2	60	M	Adenocarcinoma	T3N1M0	2--3	III	malignant	J2	60	M	Adenocarcinoma	T3N1M0	2--3	III	malignant
E3	56	M	Adenocarcinoma	T2N1M0	3	III	malignant	J3	56	M	Adenocarcinoma	T2N1M0	3	III	malignant
E4	60	F	Adenocarcinoma	T2N1M1	3	IV	malignant	J4	60	F	Adenocarcinoma	T2N1M1	2	IV	malignant
E5	66	F	Adenocarcinoma	T3N0M0	-	II	malignant	J5	66	F	Adenocarcinoma	T3N0M0	3	II	malignant
E6	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant	J6	53	F	Adenocarcinoma	T3N0M0	3	II	malignant
E7	60	M	Adenocarcinoma	T3N1M0	2	III	malignant	J7	60	M	Adenocarcinoma	T3N1M0	3	III	malignant
E8	56	M	Adenocarcinoma	T2N1M0	3	III	malignant	J8	56	M	Adenocarcinoma	T2N1M0	3	III	malignant
E9	60	F	Adenocarcinoma	T2N1M1	3	IV	malignant	J9	60	F	Adenocarcinoma	T2N1M1	-	IV	malignant
E10	66	F	Adenocarcinoma	T3N0M0	3	II	malignant	J10	66	F	Adenocarcinoma	T3N0M0	3	II	malignant

Fig. 187A–187C

N+9/C-9 antibody 3C5 10 ug/mL

Pancreatic cancer tissue array PA1003

Fig. 188A

Position: C3
Cell Type: Adenocarcinoma
Tumor Grade: 2
TNM: T3N0M0

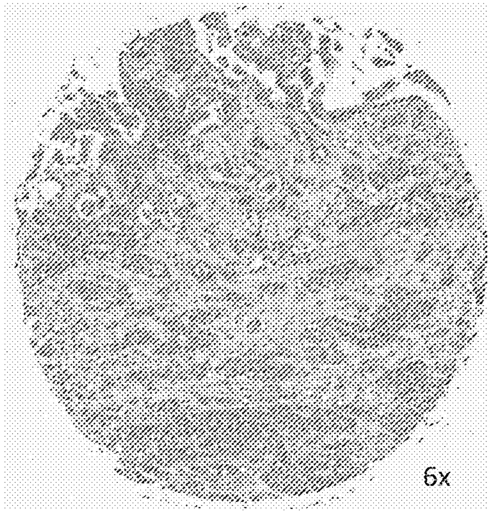


Fig. 188B

Position: C4
Cell Type: Adenocarcinoma
Tumor Grade: 2
TNM: T3N0M0

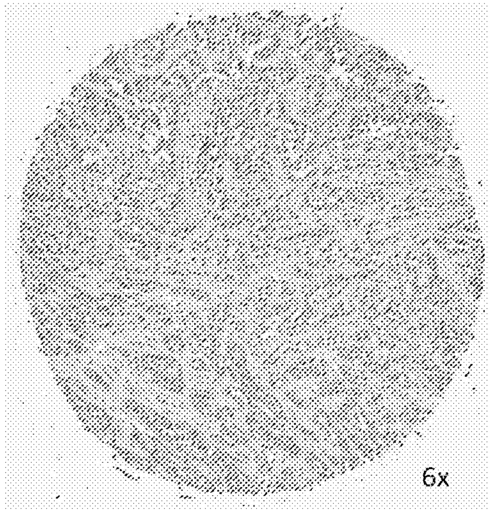


Fig. 188C

Position: E2
Cell Type: Adenocarcinoma
Tumor Grade: 2-3
TNM: T3N1M0

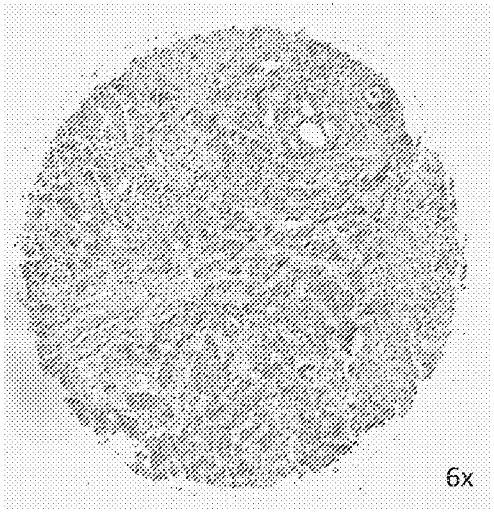


Fig. 188D

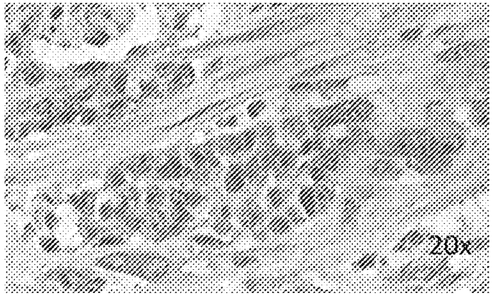


Fig. 188E

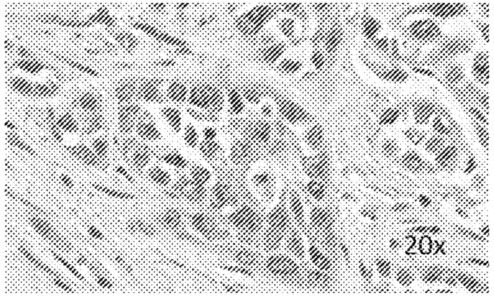


Fig. 188F

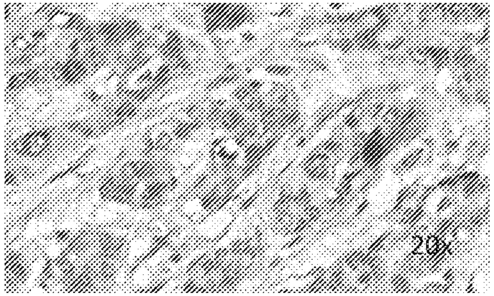


Fig. 188A–188F

N+9/C-9 antibody 8A9 IgG 15 ug/mL

FDA Normal tissue array MNO1021

Fig. 189A

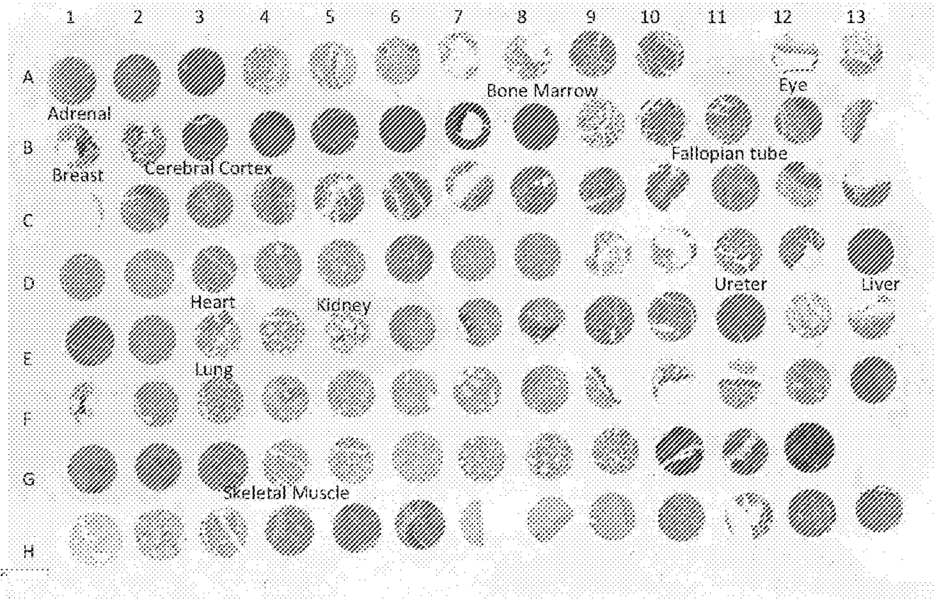


Fig. 189B

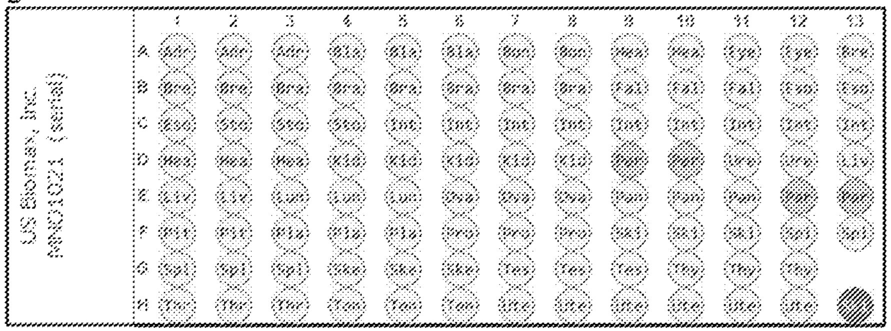


Figure 189A-189C

Fig. 189C

Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis	Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis
A1	F	31	Adrenal gland	Normal	E1	M	59	Liver	Normal
A2	M	51	Adrenal gland	Normal	E2	F	27	Liver	Normal
A3	M	53	Adrenal gland	Normal	E3	M	72	Lung	Normal
A4	M	75	Bladder, umary	Normal	E4	F	55	Lung	Normal
A5	M	72	Bladder, umary	Normal	E5	M	43	Lung	Normal
A6	M	52	Bladder, umary	Normal	E6	F	47	Ovary	Normal
A7	M	53	Bone, bone marrow	Normal	E7	F	46	Ovary	Normal
A8	M	43	Bone, bone marrow	Normal	E8	F	40	Ovary	Normal
A9	F	44	Head and neck, salivary gland	Normal	E9	M	42	Pancreas	Normal
A10	M	18	Head and neck, salivary gland	Normal	E10	F	26	Pancreas	Normal
A11	M	55	Eye	Normal	E11	F	59	Pancreas	Normal
A12	M	50	Eye	Normal	E12	M	17	Parathyroid	Adenoma
A13	F	35	Breast	Normal	E13	M	72	Parathyroid	Adenoma
B1	F	38	Breast	Normal	F1	F	3	Pituitary gland	Normal
B2	F	33	Breast	Normal	F2	F		Pituitary gland	Normal
B3	M	58	Brain, cerebellum	Normal	F3	F	32	Placenta	Normal
B4	M	65	Brain, cerebellum	Normal	F4	F	30	Placenta	Normal
B5	F		Brain, cerebellum	Normal	F5	F	27	Placenta	Normal
B6	M	56	Brain, cerebral cortex	Normal	F6	M	64	Prostate	Normal
B7	M	65	Brain, cerebral cortex	Normal	F7	M	65	Prostate	Normal
B8	F		Brain, cerebral cortex	Normal	F8	M	65	Prostate	Normal
B9	F	42	Fallopian tube	Normal	F9	F	32	Skin	Normal
B10	F	32	Fallopian tube	Normal	F10	F	68	Skin	Normal
B11	F	24	Fallopian tube	Normal	F11	M	26	Skin	Normal
B12	M	45	Esophagus	Normal	F12	M	47	Spinal cord	Normal
B13	F	68	Esophagus	Normal	F13	M	58	Spinal cord	Normal
C1	M	54	Esophagus	Normal	G1	M	27	Spleen	Normal
C2	M	45	Stomach	Normal	G2	M	60	Spleen	Normal
C3	M	49	Stomach	Normal	G3	M	31	Spleen	Normal
C4	M	77	Stomach	Normal	G4	F	60	Skeletal muscle	Normal
C5	M	45	Intestine, small intestine	Normal	G5	F	49	Skeletal muscle	Normal
C6	F	75	Intestine, small intestine	Normal	G6	M	70	Skeletal muscle	Normal
C7	F	75	Intestine, small intestine	Normal	G7	M	43	Testis	Normal
C8	M	2	Intestine, colon	Normal	G8	M	30	Testis	Normal
C9	M	46	Intestine, colon	Normal	G9	M	77	Testis	Normal
C10	M	74	Intestine, colon	Normal	G10	M	15	Thymus	Normal
C11	F	47	Intestine, rectum	Normal	G11	M	28	Thymus	Normal
C12	F	75	Intestine, rectum	Normal	G12	F	9	Thymus	Normal
C13	M	66	Intestine, rectum	Normal	G13	-	-	-	-
D1	M	58	Heart	Normal	H1	F	26	Thyroid	Normal
D2	M	46	Heart	Normal	H2	F	37	Thyroid	Normal
D3	F	34	Heart	Normal	H3	F	51	Thyroid	Normal
D4	F	52	Kidney, cortex	Normal	H4	M	46	Tonsil	Normal
D5	M	23	Kidney, cortex	Normal	H5	M	37	Tonsil	Normal
D6	M	63	Kidney, cortex	Normal	H6	M	13	Tonsil	Normal
D7	F	52	Kidney, medulla	Normal	H7	F	38	Uterus, cervl65	Normal
D8	M	23	Kidney, medulla	Normal	H8	F	35	Uterus, cervl65	Normal
D9	M	59	Peripheral nerve	Schwannoma	H9	F	44	Uterus, cervl65	Normal
D10	F	29	Peripheral nerve	Schwannoma	H10	F	38	Uterus, endometrium	Normal
D11	F	44	Ureter	Normal	H11	F	41	Uterus, endometrium	Normal
D12	F	42	Ureter	Normal	H12	F	46	Uterus, endometrium	Normal
D13	F	57	Liver	Normal	H13	M	58	Skin	Malignant melanoma (tissue marker)

N+9/C-9 antibody 8A9 IgG 15 ug/mL

FDA Normal tissue array MNO1021

Fig. 190A
Normal Adrenal Gland

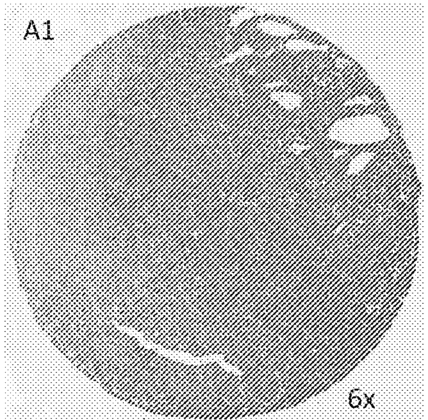


Fig. 190B
Normal Breast

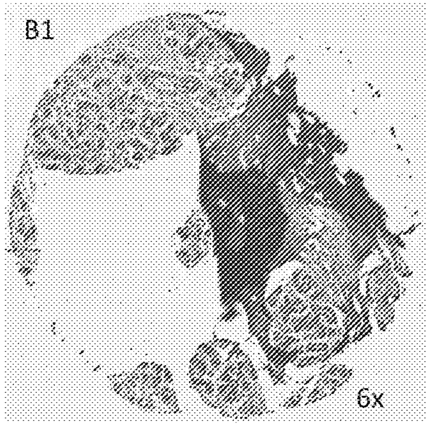


Fig. 190C
Normal Fallopian Tubes

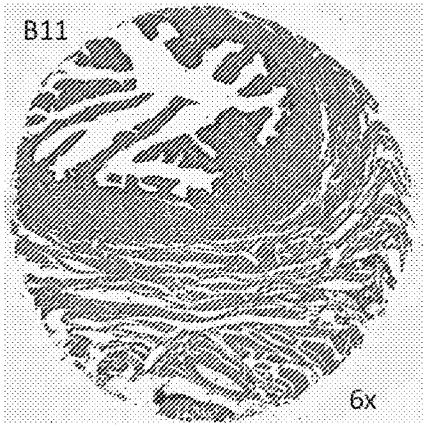


Fig. 190D
Normal Kidney

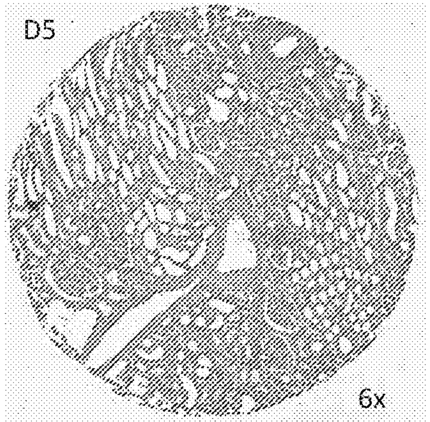


Fig. 190E

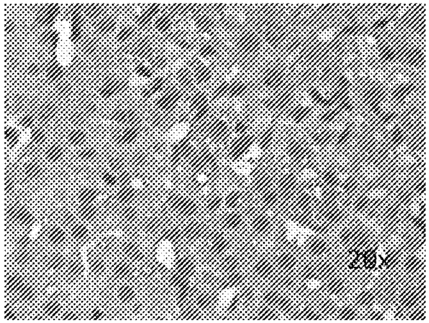


Fig. 190F

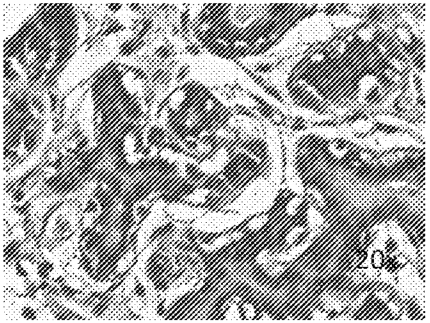


Fig. 190G

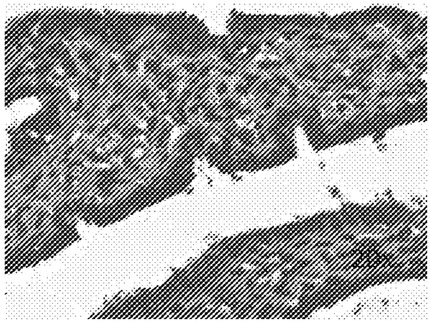


Fig. 190H

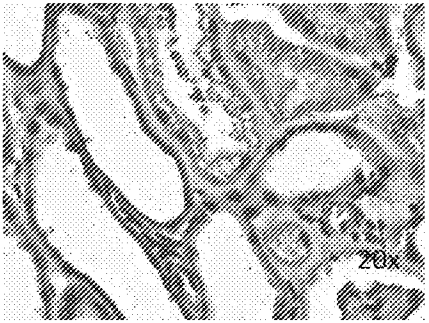


Figure 190A-190H

N+9/C-9 antibody 8A9 IgG 15 ug/mL

FDA Normal tissue array MNO1021

Fig. 190I
Normal Heart

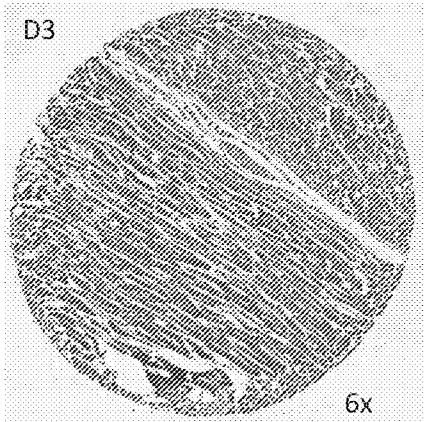


Fig. 190J
Normal Liver

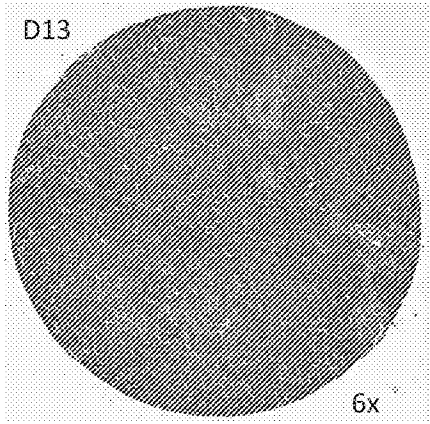


Fig. 190K
Normal Lung

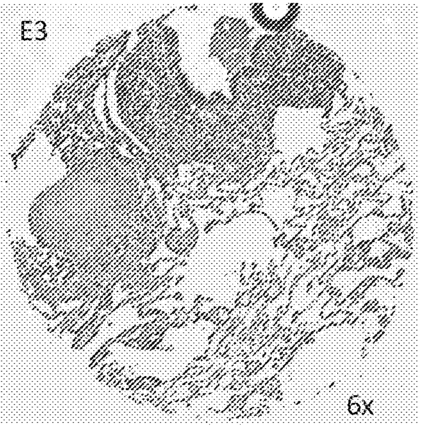


Fig. 190L
Normal Ureter

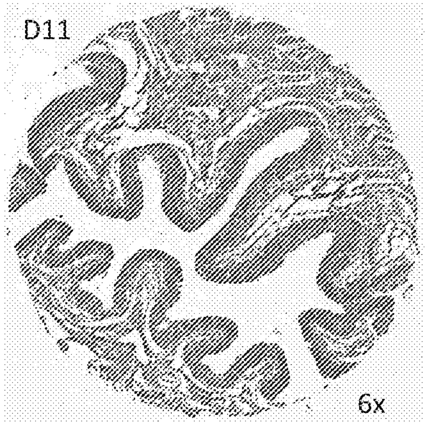


Fig. 190M

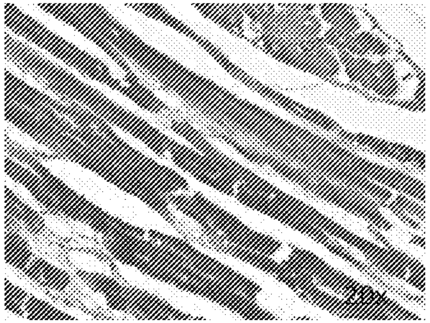


Fig. 190N

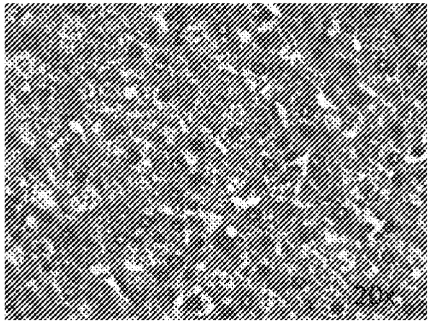


Fig. 190O

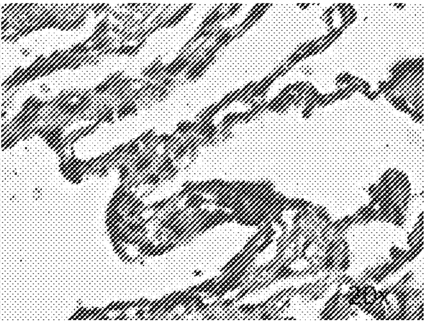


Fig. 190P

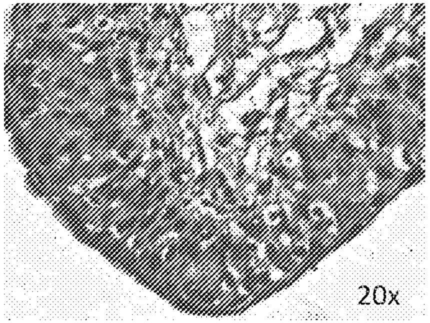


Figure 190I-190P

N+9/C-9 antibody 8A9 IgG 15 ug/mL

FDA Normal tissue array MNO1021

Fig. 190Q
Normal Eye

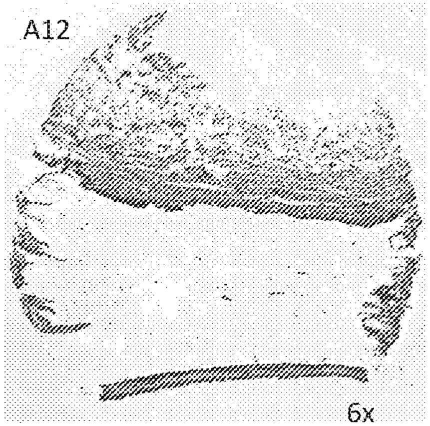


Fig. 190R
Normal Cerebral Cortex

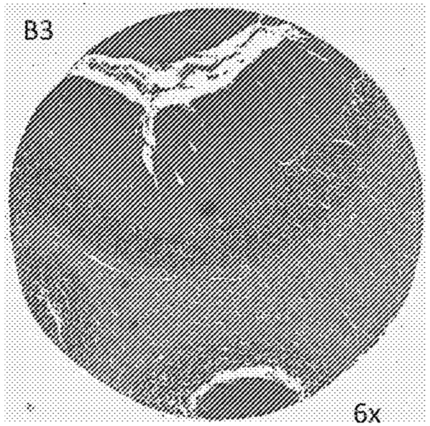


Fig. 190S
Normal Bone Marrow

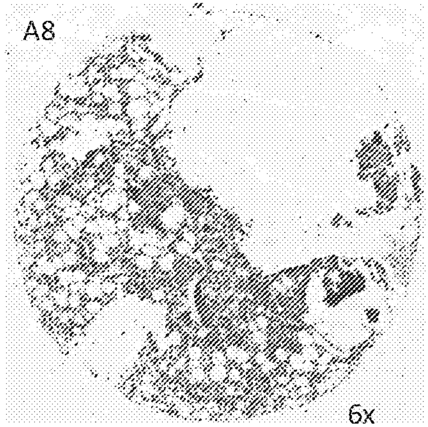


Fig. 190T
Normal Skeletal Muscle

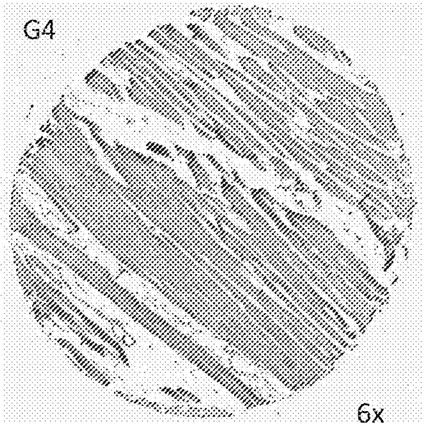


Fig. 190U

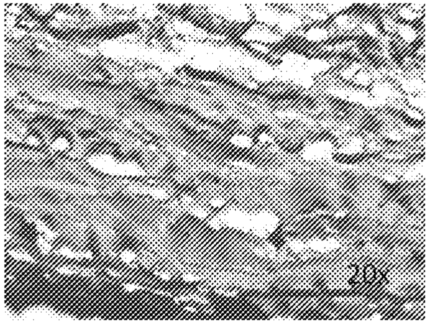


Fig. 190V

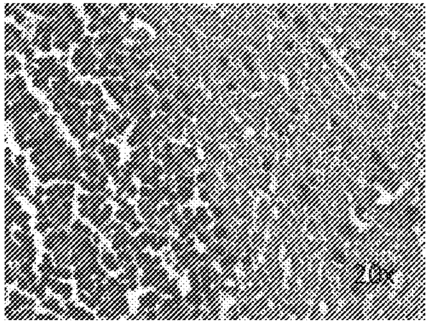


Fig.

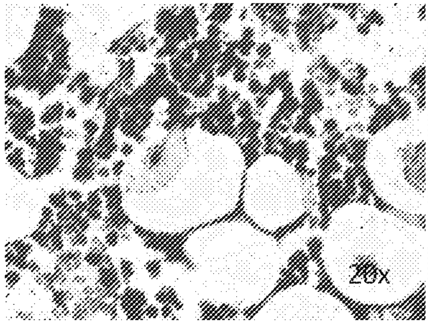


Fig. 190X

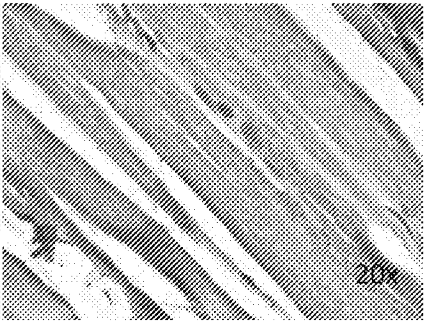


Figure 190Q-190X

N+9/C-9 antibody 8A9 15 ug/mL

Pancreatic cancer tissue array PA1003

Fig. 191A

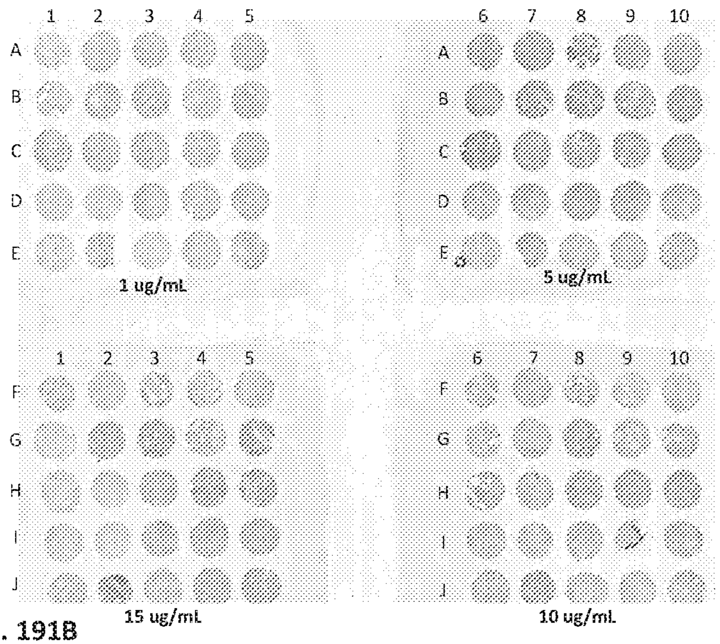


Fig. 191B

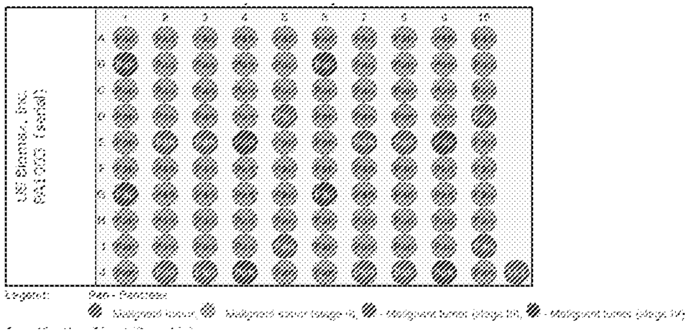


Fig. 191C

Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type	Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type
A1	39	F	Adenocarcinoma	T3N0M0	2	II	malignant	F1	39	F	Adenocarcinoma	T3N0M0	2	II	malignant
A2	44	M	Adenocarcinoma	T3N0M0	2	II	malignant	F2	44	M	Adenocarcinoma	T3N0M0	2	II	malignant
A3	59	M	Adenocarcinoma	T3N0M0	2	II	malignant	F3	59	M	Adenocarcinoma	T3N0M0	2	II	malignant
A4	65	M	Adenocarcinoma	T3N0M0	2	II	malignant	F4	65	M	Adenocarcinoma	T3N0M0	2	II	malignant
A5	53	M	Adenocarcinoma	T3N0M0	2	II	malignant	F5	53	M	Adenocarcinoma	T3N0M0	2	II	malignant
A6	39	F	Adenocarcinoma	T3N0M0	2	II	malignant	F6	39	F	Adenocarcinoma	T3N0M0	2	II	malignant
A7	44	M	Adenocarcinoma	T3N0M0	2	II	malignant	F7	44	M	Adenocarcinoma	T3N0M0	2	II	malignant
A8	59	M	Adenocarcinoma	T3N0M0	2	II	malignant	F8	59	M	Adenocarcinoma	T3N0M0	2	II	malignant
A9	65	M	Adenocarcinoma	T3N0M0	2	II	malignant	F9	65	M	Adenocarcinoma	T3N0M0	-	II	malignant
A10	53	M	Adenocarcinoma	T3N0M0	2	II	malignant	F10	53	M	Adenocarcinoma	T3N0M0	2	II	malignant
B1	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant	G1	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant
B2	52	M	Adenocarcinoma	T3N0M0	1	II	malignant	G2	52	M	Adenocarcinoma	T3N0M0	1	II	malignant
B3	57	M	Adenocarcinoma	T3N0M0	2	II	malignant	G3	57	M	Adenocarcinoma	T3N0M0	2	II	malignant
B4	34	M	Adenocarcinoma	T3N0M0	2	II	malignant	G4	34	M	Adenocarcinoma	T3N0M0	2	II	malignant
B5	72	F	Adenocarcinoma	T3N0M0	2	II	malignant	G5	72	F	Adenocarcinoma	T3N0M0	1	II	malignant
B6	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant	G6	42	M	Adenocarcinoma	T2N0M1	-	IV	malignant
B7	52	M	Adenocarcinoma	T3N0M0	2	II	malignant	G7	52	M	Adenocarcinoma	T3N0M0	2	II	malignant
B8	57	M	Adenocarcinoma	T3N0M0	2	II	malignant	G8	57	M	Adenocarcinoma	T3N0M0	2	II	malignant
B9	34	M	Adenocarcinoma	T3N0M0	1	II	malignant	G9	34	M	Adenocarcinoma	T3N0M0	2	II	malignant
B10	72	F	Adenocarcinoma	T3N0M0	2	II	malignant	G10	72	F	Adenocarcinoma	T3N0M0	2	II	malignant
C1	47	M	Adenocarcinoma	T3N0M0	1	II	malignant	H1	47	M	Adenocarcinoma	T3N0M0	1	II	malignant
C2	64	F	Adenocarcinoma	T3N0M0	1	II	malignant	H2	64	F	Adenocarcinoma	T3N0M0	-	II	malignant
C3	51	M	Adenocarcinoma	T3N0M0	2	II	malignant	H3	51	M	Adenocarcinoma	T3N0M0	2	II	malignant
C4	68	F	Adenocarcinoma	T3N0M0	2	II	malignant	H4	68	F	Adenocarcinoma	T3N0M0	3	II	malignant
C5	41	M	Adenocarcinoma	T3N0M0	-	II	malignant	H5	41	M	Adenocarcinoma	T3N0M0	2	II	malignant
C6	47	M	Adenocarcinoma	T3N0M0	1	II	malignant	H6	47	M	Adenocarcinoma	T3N0M0	1	II	malignant
C7	64	F	Adenocarcinoma	T3N0M0	2	II	malignant	H7	64	F	Adenocarcinoma	T3N0M0	2	II	malignant
C8	51	M	Adenocarcinoma	T3N0M0	2	II	malignant	H8	51	M	Adenocarcinoma	T3N0M0	-	II	malignant
C9	68	F	Adenocarcinoma	T3N0M0	2	II	malignant	H9	68	F	Adenocarcinoma	T3N0M0	2	II	malignant
C10	41	M	Adenocarcinoma	T3N0M0	2	II	malignant	H10	41	M	Adenocarcinoma	T3N0M0	2	II	malignant
D1	58	F	Adenocarcinoma	T3N0M0	2	II	malignant	I1	58	F	Adenocarcinoma	T3N0M0	2	II	malignant
D2	41	F	Adenocarcinoma	T3N0M0	3	II	malignant	I2	41	F	Adenocarcinoma	T3N0M0	3	II	malignant
D3	72	F	Adenocarcinoma	T3N0M0	3	II	malignant	I3	72	F	Adenocarcinoma	T3N0M0	3	II	malignant
D4	59	M	Adenocarcinoma	T3N0M0	3	II	malignant	I4	59	M	Adenocarcinoma	T3N0M0	3	II	malignant
D5	50	M	Adenocarcinoma	T3N1M0	3	III	malignant	I5	50	M	Adenocarcinoma	T3N1M0	3	III	malignant
D6	58	F	Adenocarcinoma	T3N0M0	2	II	malignant	I6	58	F	Adenocarcinoma	T3N0M0	2	II	malignant
D7	41	F	Adenocarcinoma	T3N0M0	3	II	malignant	I7	41	F	Adenocarcinoma	T3N0M0	2	II	malignant
D8	72	F	Adenocarcinoma	T3N0M0	3	II	malignant	I8	72	F	Adenocarcinoma	T3N0M0	3	II	malignant
D9	59	M	Adenocarcinoma	T3N0M0	3	II	malignant	I9	59	M	Adenocarcinoma	T3N0M0	3	II	malignant
D10	50	M	Adenocarcinoma	T3N1M0	3	III	malignant	I10	50	M	Adenocarcinoma	T3N1M0	3	III	malignant
E1	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant	J1	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant
E2	60	M	Adenocarcinoma	T3N1M0	2--3	III	malignant	J2	60	M	Adenocarcinoma	T3N1M0	2--3	III	malignant
E3	56	M	Adenocarcinoma	T2N1M0	3	III	malignant	J3	56	M	Adenocarcinoma	T2N1M0	3	III	malignant
E4	60	F	Adenocarcinoma	T2N1M1	3	IV	malignant	J4	60	F	Adenocarcinoma	T2N1M1	2	IV	malignant
E5	66	F	Adenocarcinoma	T3N0M0	-	II	malignant	J5	66	F	Adenocarcinoma	T3N0M0	3	II	malignant
E6	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant	J6	53	F	Adenocarcinoma	T3N0M0	3	II	malignant
E7	60	M	Adenocarcinoma	T3N1M0	2	III	malignant	J7	60	M	Adenocarcinoma	T3N1M0	3	III	malignant
E8	56	M	Adenocarcinoma	T2N1M0	3	III	malignant	J8	56	M	Adenocarcinoma	T2N1M0	3	III	malignant
E9	60	F	Adenocarcinoma	T2N1M1	3	IV	malignant	J9	60	F	Adenocarcinoma	T2N1M1	-	IV	malignant
E10	66	F	Adenocarcinoma	T3N0M0	3	II	malignant	J10	66	F	Adenocarcinoma	T3N0M0	3	II	malignant

Fig. 191A–191C

N+9/C-9 antibody 8A9 15 ug/mL

Pancreatic cancer tissue array PA1003

Fig. 192A

Position: A1
Cell Type: Adenocarcinoma
Tumor Grade: 2
TNM: T3N0M0

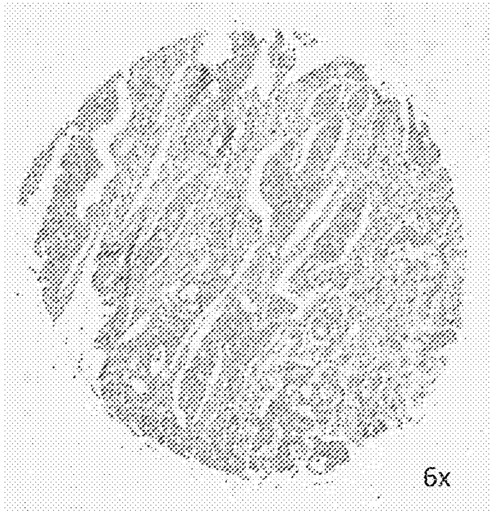


Fig. 192B

Position: B3
Cell Type: Adenocarcinoma
Tumor Grade: 2
TNM: T3N0M0

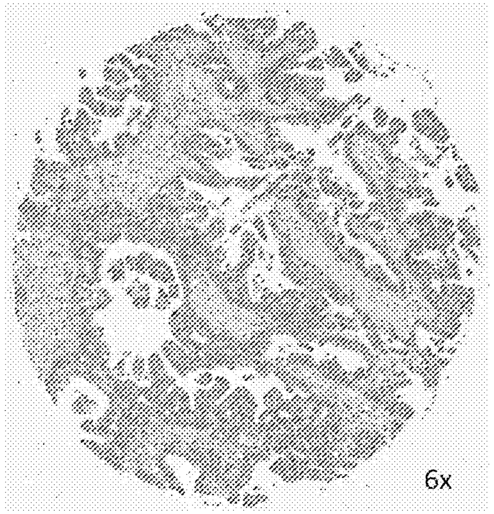


Fig. 192C

Position: C4
Cell Type: Adenocarcinoma
Tumor Grade: 2
TNM: T3N0M0

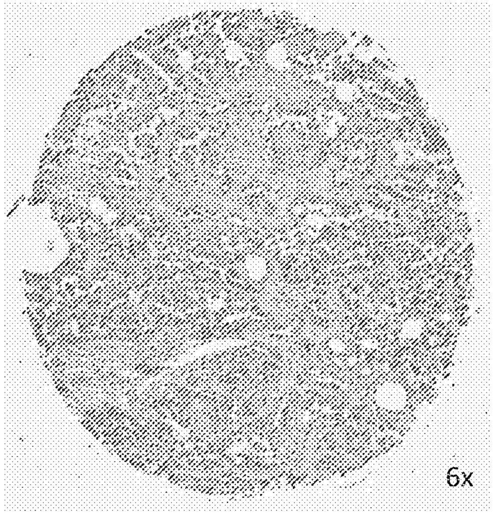


Fig. 192D

Fig. 192E

Fig. 192F

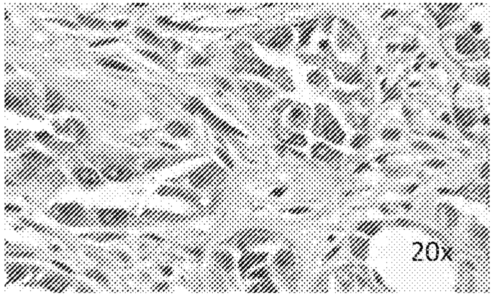


Fig. 192A–192F

N+9/C-9 antibody 17H6 30 ug/mL

FDA Normal tissue array MNO1021

Fig. 193A

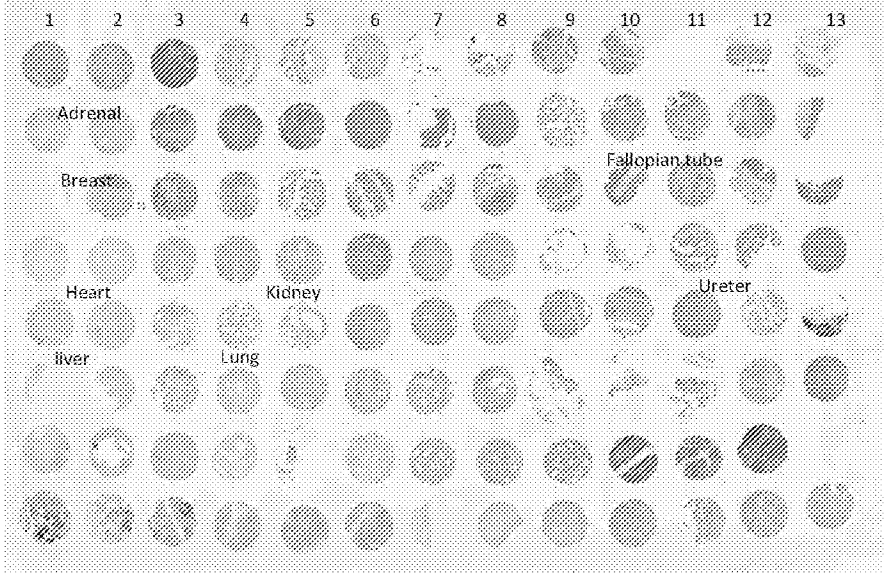


Fig. 193B

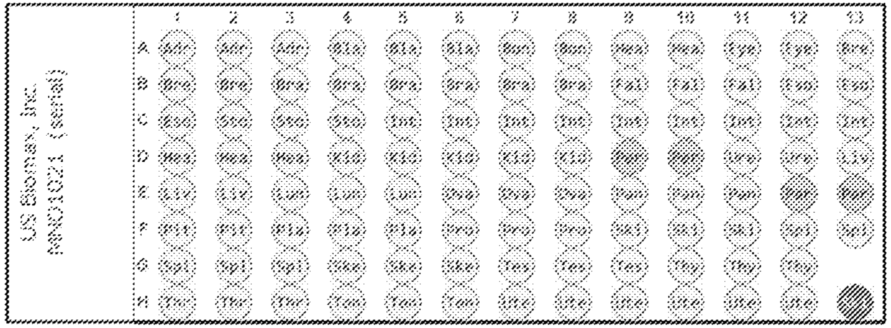


Fig. 193C

Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis	Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis
A1	F	31	Adrenal gland	Normal	E1	M	59	Liver	Normal
A2	M	51	Adrenal gland	Normal	E2	F	27	Liver	Normal
A3	M	53	Adrenal gland	Normal	E3	M	72	Lung	Normal
A4	M	75	Bladder, urinary	Normal	E4	F	55	Lung	Normal
A5	M	72	Bladder, urinary	Normal	E5	M	43	Lung	Normal
A6	M	52	Bladder, urinary	Normal	E6	F	47	Ovary	Normal
A7	M	53	Bone, bone marrow	Normal	E7	F	46	Ovary	Normal
A8	M	43	Bone, bone marrow	Normal	E8	F	40	Ovary	Normal
A9	F	44	Head and neck, salivary gland	Normal	E9	M	42	Pancreas	Normal
A10	M	18	Head and neck, salivary gland	Normal	E10	F	26	Pancreas	Normal
A11	M	55	Eye	Normal	E11	F	59	Pancreas	Normal
A12	M	50	Eye	Normal	E12	M	17	Parathyroid	Adenoma
A13	F	35	Breast	Normal	E13	M	72	Parathyroid	Adenoma
B1	F	36	Breast	Normal	F1	F	3	Pituitary gland	Normal
B2	F	33	Breast	Normal	F2	F		Pituitary gland	Normal
B3	M	58	Brain, cerebellum	Normal	F3	F	32	Placenta	Normal
B4	M	65	Brain, cerebellum	Normal	F4	F	30	Placenta	Normal
B5	F		Brain, cerebellum	Normal	F5	F	27	Placenta	Normal
B6	M	58	Brain, cerebral cortex	Normal	F6	M	64	Prostate	Normal
B7	M	65	Brain, cerebral cortex	Normal	F7	M	65	Prostate	Normal
B8	F		Brain, cerebral cortex	Normal	F8	M	65	Prostate	Normal
B9	F	42	Fallopian tube	Normal	F9	F	32	Skin	Normal
B10	F	32	Fallopian tube	Normal	F10	F	68	Skin	Normal
B11	F	24	Fallopian tube	Normal	F11	M	28	Skin	Normal
B12	M	45	Esophagus	Normal	F12	M	47	Spinal cord	Normal
B13	F	68	Esophagus	Normal	F13	M	58	Spinal cord	Normal
C1	M	54	Esophagus	Normal	G1	M	27	Spleen	Normal
C2	M	45	Stomach	Normal	G2	M	60	Spleen	Normal
C3	M	49	Stomach	Normal	G3	M	31	Spleen	Normal
C4	M	77	Stomach	Normal	G4	F	60	Skeletal muscle	Normal
C5	M	45	Intestine, small intestine	Normal	G5	F	49	Skeletal muscle	Normal
C6	F	75	Intestine, small intestine	Normal	G6	M	70	Skeletal muscle	Normal
C7	F	75	Intestine, small intestine	Normal	G7	M	43	Testis	Normal
C8	M	2	Intestine, colon	Normal	G8	M	30	Testis	Normal
C9	M	46	Intestine, colon	Normal	G9	M	77	Testis	Normal
C10	M	74	Intestine, colon	Normal	G10	M	15	Thymus	Normal
C11	F	47	Intestine, rectum	Normal	G11	M	28	Thymus	Normal
C12	F	75	Intestine, rectum	Normal	G12	F	9	Thymus	Normal
C13	M	66	Intestine, rectum	Normal	G13	-	-	-	-
D1	M	58	Heart	Normal	H1	F	26	Thyroid	Normal
D2	M	48	Heart	Normal	H2	F	37	Thyroid	Normal
D3	F	34	Heart	Normal	H3	F	51	Thyroid	Normal
D4	F	52	Kidney, cortex	Normal	H4	M	46	Tonsil	Normal
D5	M	23	Kidney, cortex	Normal	H5	M	37	Tonsil	Normal
D6	M	63	Kidney, cortex	Normal	H6	M	13	Tonsil	Normal
D7	F	52	Kidney, medulla	Normal	H7	F	38	Uterus, cervl69	Normal
D8	M	23	Kidney, medulla	Normal	H8	F	35	Uterus, cervl69	Normal
D9	M	59	Peripheral nerve	Schwannoma	H9	F	44	Uterus, cervl69	Normal
D10	F	29	Peripheral nerve	Schwannoma	H10	F	38	Uterus, endometrium	Normal
D11	F	44	Ureter	Normal	H11	F	41	Uterus, endometrium	Normal
D12	F	42	Ureter	Normal	H12	F	46	Uterus, endometrium	Normal
D13	F	57	Liver	Normal	H13	M	58	Skin	Malignant melanoma (tissue marker)

Figure 193A-193C

N+9/C-9 antibody 17H6 30 ug/mL

FDA Normal tissue array MNO1021

Fig. 194A
Normal Adrenal Gland

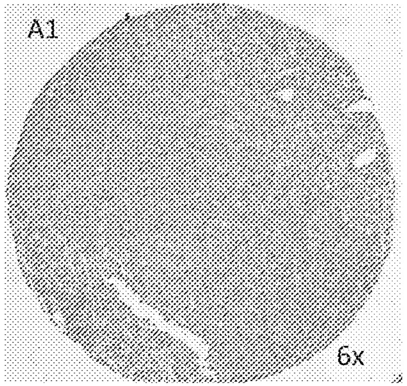


Fig. 194B
Normal Breast

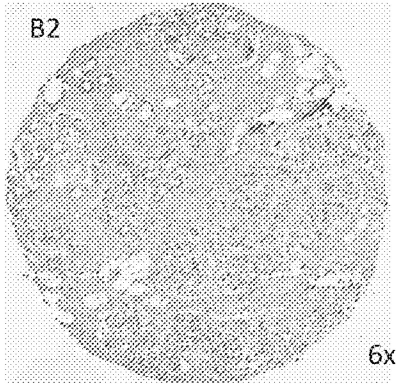


Fig. 194C
Normal Fallopian Tubes

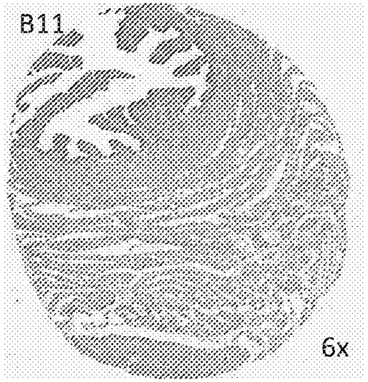


Fig. 194D
Normal Kidney

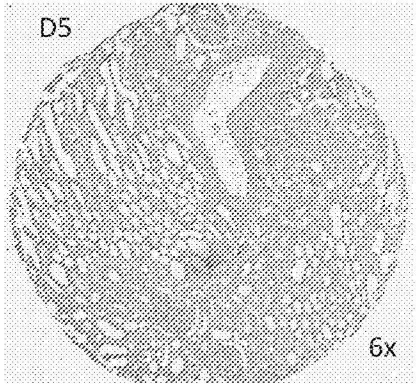


Fig. 194E

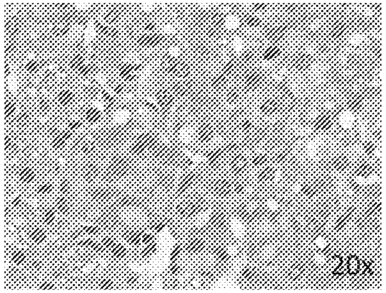


Fig. 194F

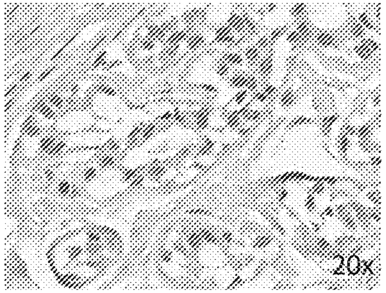


Fig. 194G

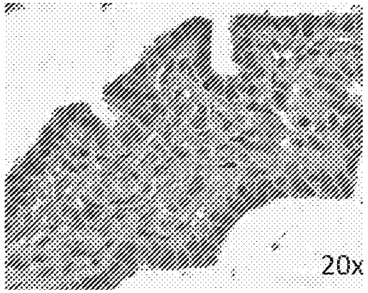


Fig. 194H

Figure 194A-194H

N+9/C-9 antibody 17H6 30 ug/mL
FDA Normal tissue array MNO1021

Fig. 194I
Normal Heart

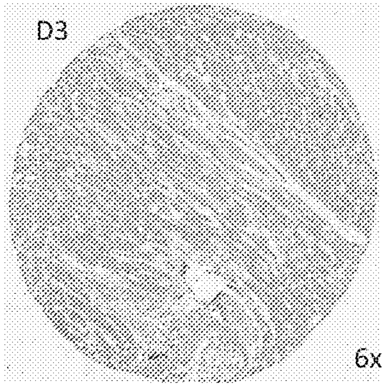


Fig. 194J
Normal Liver

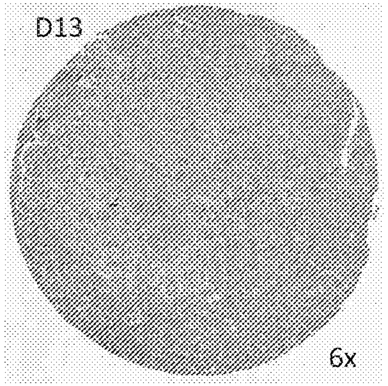


Fig. 194K
Normal Lung

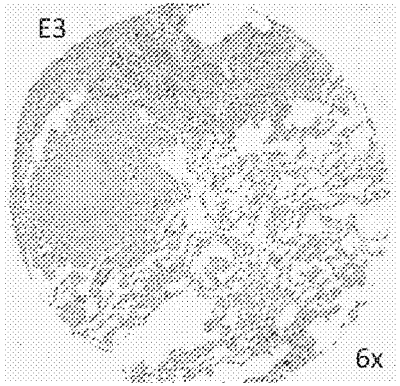


Fig. 194L
Normal Ureter

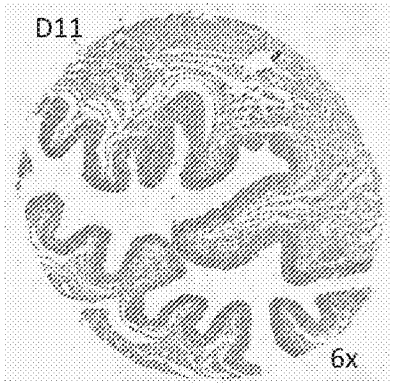


Fig. 194M

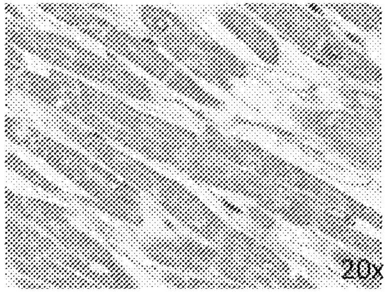


Fig. 194N

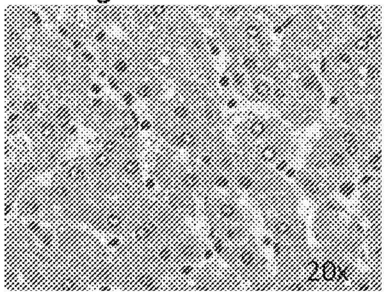


Fig. 194O

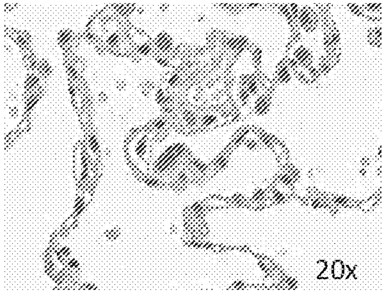


Fig. 194P

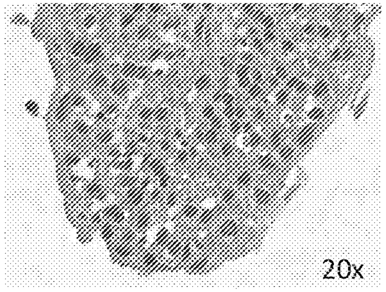


Figure 194I-194P

N+9/C-9 antibody 17H6 30 ug/mL

FDA Normal tissue array MNO1021

Fig. 194Q
Normal eye

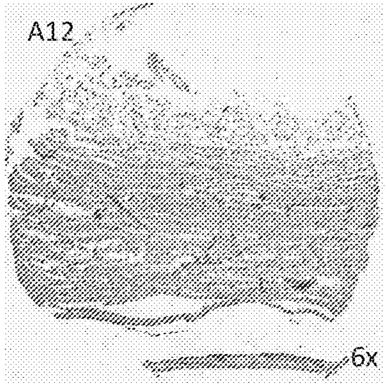


Fig. 194R
Normal Cerebral cortex

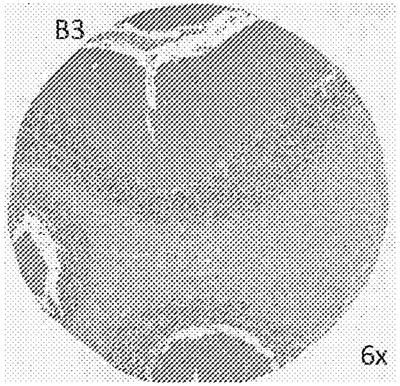


Fig. 194S
Normal Bone marrow

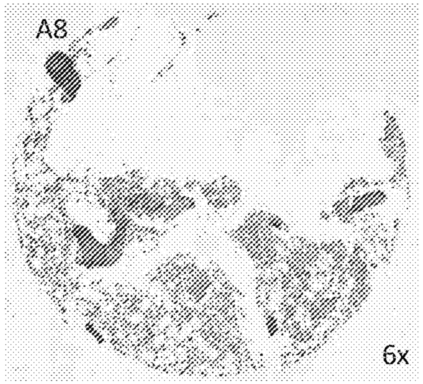


Fig. 194T
Normal Skeletal muscle

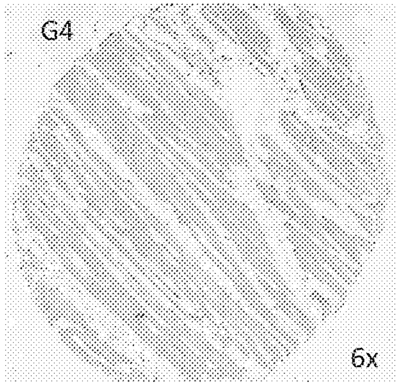


Fig. 194U

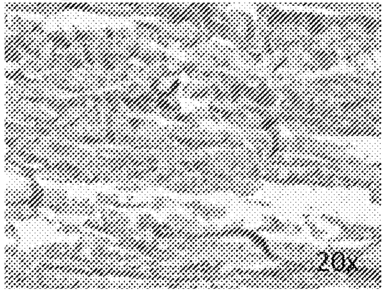


Fig. 194V

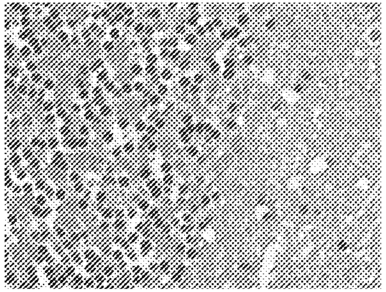


Fig. 194W

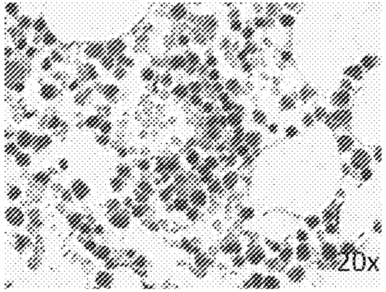


Fig. 194X

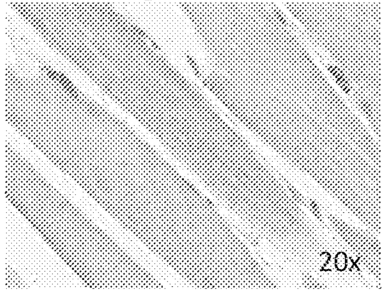


Figure 194Q-194X

N+9/C-9 antibody 17H6 IgG 30 ug/mL

Pancreatic cancer tissue array PA805c

Fig. 195A

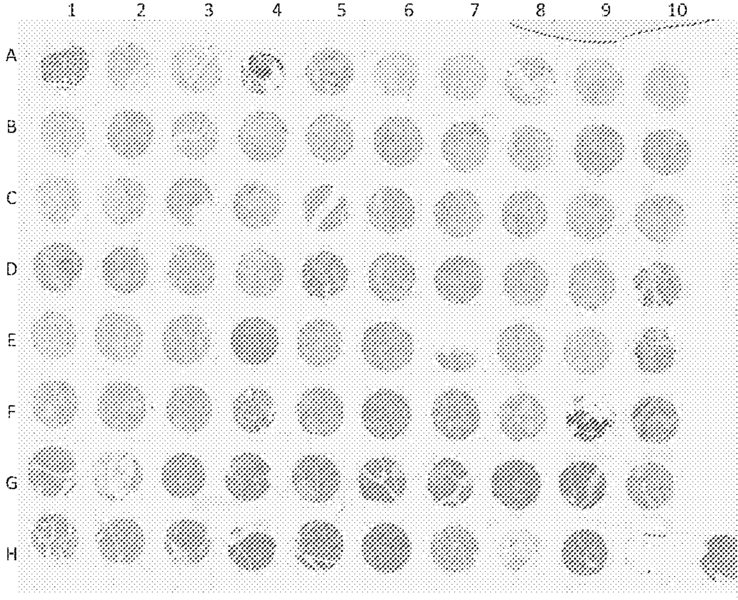


Fig. 195B

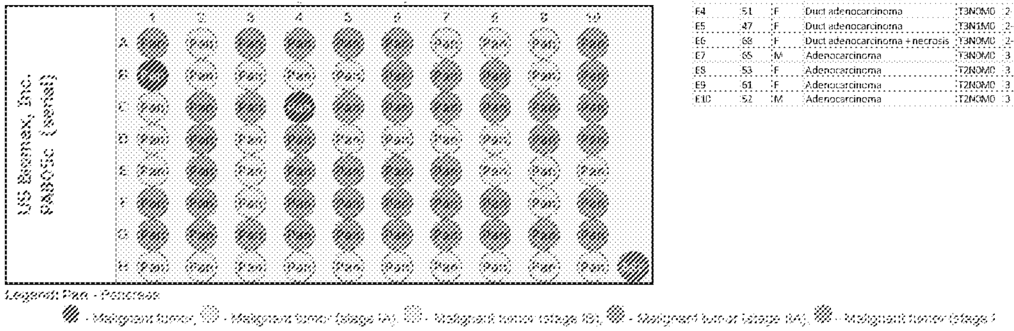


Fig. 195C

Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type	Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type
A1	42	F	Duct adenocarcinoma	T3N0M0	2	IIA	Malignant	F1	51	M	Adenocarcinoma	T3N0M0	3	IIA	Malignant
A2	47	M	Duct adenocarcinoma	T2N0M0	1	IB	Malignant	F2	23	F	Adenocarcinoma	T3N0M0	3	IIA	Malignant
A3	51	F	Duct adenocarcinoma	T3N0M0	1	IIA	Malignant	F3	55	F	Adenocarcinoma	T2N0M0	3	IB	Malignant
A4	56	M	Duct adenocarcinoma	T2N1M0	1	IIB	Malignant	F4	61	M	Adenocarcinoma	T3N0M0	3	IIA	Malignant
A5	58	M	Mucinous adenocarcinoma	T3N0M0	1	IIA	Malignant	F5	62	F	Adenocarcinoma	T3N0M0	3	IIA	Malignant
A6	60	M	Duct adenocarcinoma	T3N0M0	1	IIA	Malignant	F6	64	M	Adenocarcinoma	T3N0M0	3	IIA	Malignant
A7	61	M	Duct adenocarcinoma	T2N0M0	*	IB	Malignant	F7	62	M	Adenocarcinoma	T3N0M0	3	IIA	Malignant
A8	56	F	Duct adenocarcinoma	T2N0M0	1	IB	Malignant	F8	66	F	Adenocarcinoma	T2N1M0	3	IIB	Malignant
A9	42	M	Duct adenocarcinoma	T2N0M0	1	IB	Malignant	F9	40	M	Acinic cell carcinoma	T1N0M0	-	IA	Malignant
A10	51	M	Duct adenocarcinoma	T3N1M0	3	IIB	Malignant	F10	62	M	Squamous cell carcinoma	T3N0M0	2--3	IIA	Malignant
B1	66	M	Adenocarcinoma	T2N0M1	*	IV	Malignant	G1	52	M	Adjacent normal pancreas tissue	-	-	-	NAT
B2	80	M	Duct adenocarcinoma	T2N0M0	1	IB	Malignant	G2	51	F	Adjacent normal pancreas tissue	-	-	-	NAT
B3	64	F	Duct adenocarcinoma	T2N0M0	2	IB	Malignant	G3	51	M	Adjacent normal pancreas tissue	-	-	-	NAT
B4	77	M	Duct adenocarcinoma	T1N0M0	2	IA	Malignant	G4	48	F	Adjacent normal pancreas tissue	-	-	-	NAT
B5	58	M	Adenocarcinoma	T2N0M0	1--2	IB	Malignant	G5	56	F	Adjacent normal pancreas tissue	-	-	-	NAT
B6	54	F	Duct adenocarcinoma	T3N0M0	2	IIA	Malignant	G6	75	M	Adjacent normal pancreas tissue	-	-	-	NAT
B7	51	F	Duct adenocarcinoma	T3N0M0	1	IIA	Malignant	G7	60	M	Adjacent normal pancreas tissue	-	-	-	NAT
B8	44	M	Duct adenocarcinoma	T3N0M0	2	IIA	Malignant	G8	52	M	Adjacent normal pancreas tissue	-	-	-	NAT
B9	54	M	Duct adenocarcinoma	T2N0M0	2	IB	Malignant	G9	38	M	Adjacent normal pancreas tissue	-	-	-	NAT
B10	40	M	Duct adenocarcinoma	T2N1M0	2	IIB	Malignant	G10	60	F	Adjacent normal pancreas tissue	-	-	-	NAT
C1	54	M	Duct adenocarcinoma	T2N0M0	2	IB	Malignant	H1	49	F	Pancreas tissue	-	-	-	Normal
C2	56	F	Mucinous adenocarcinoma	T3N1M0	2	IIB	Malignant	H2	40	M	Pancreas tissue	-	-	-	Normal
C3	44	M	Mucinous adenocarcinoma	T3N1M0	2	IIB	Malignant	H3	47	M	Pancreas tissue	-	-	-	Normal
C4	62	F	Duct adenocarcinoma	T3N1M1	2	IV	Malignant	H4	25	M	Pancreas tissue	-	-	-	Normal
C5	58	F	Duct adenocarcinoma	T3N1M0	2	IIB	Malignant	H5	42	M	Pancreas tissue	-	-	-	Normal
C6	54	M	Papillary adenocarcinoma	T3N0M0	2	IIA	Malignant	H6	29	M	Pancreas tissue	-	-	-	Normal
C7	60	M	Duct adenocarcinoma	T3N0M0	2	IIA	Malignant	H7	50	M	Head of pancreas tissue	-	-	-	Normal
C8	59	M	Duct adenocarcinoma	T3N0M0	2	IIA	Malignant	H8	39	F	Pancreas tissue	-	-	-	Normal
C9	56	M	Duct adenocarcinoma	T3N1M0	2	IIB	Malignant	H9	35	M	Pancreas tissue	-	-	-	Normal
C10	67	F	Duct adenocarcinoma	T3N1M0	2	IIB	Malignant	H10	21	F	Pancreas tissue	-	*	-	Normal
D1	60	M	Duct adenocarcinoma	T2N0M0	1	IB	Malignant								
D2	48	F	Duct adenocarcinoma	T3N0M0	2	IIA	Malignant								
D3	53	M	Duct adenocarcinoma	T2N0M0	2	IB	Malignant								
D4	64	M	Duct adenocarcinoma	T3N0M0	2	IIA	Malignant								
D5	71	F	Duct adenocarcinoma	T2N0M0	2--3	IB	Malignant								
D6	44	F	Duct adenocarcinoma	T2N0M0	2--3	IB	Malignant								
D7	46	F	Papillary adenocarcinoma	T2N0M0	2	IB	Malignant								
D8	68	F	Mucinous adenocarcinoma	T2N0M0	3	IB	Malignant								
D9	57	M	Duct adenocarcinoma	T3N0M0	*	IIA	Malignant								
D10	60	M	Adenocarcinoma	T2N1M0	3	IIB	Malignant								
E1	56	M	Adenocarcinoma	T2N0M0	2	IB	Malignant								
E2	41	M	Duct adenocarcinoma	T3N0M0	2--3	IIA	Malignant								
E3	56	M	Duct adenocarcinoma	T2N0M0	2--3	IB	Malignant								
E4	51	F	Duct adenocarcinoma	T3N0M0	2--3	IIA	Malignant								
E5	47	F	Duct adenocarcinoma	T3N1M0	2--3	IIB	Malignant								
E6	68	F	Duct adenocarcinoma + necrosis	T3N0M0	2--3	IIA	Malignant								
E7	65	M	Adenocarcinoma	T3N0M0	3	IIA	Malignant								
E8	53	F	Adenocarcinoma	T2N0M0	3	IB	Malignant								
E9	61	F	Adenocarcinoma	T2N0M0	3	IB	Malignant								
E10	52	M	Adenocarcinoma	T2N0M0	3	IB	Malignant								

Fig. 195A–195C

N+9/C-9 antibody 17H6 IgG 30 ug/mL

Pancreatic cancer tissue array PA805c

Fig. 196A

Position: D7
Cell Type: Papillary Adenocarcinoma
Tumor Grade: 2
TNM: T2N0M0

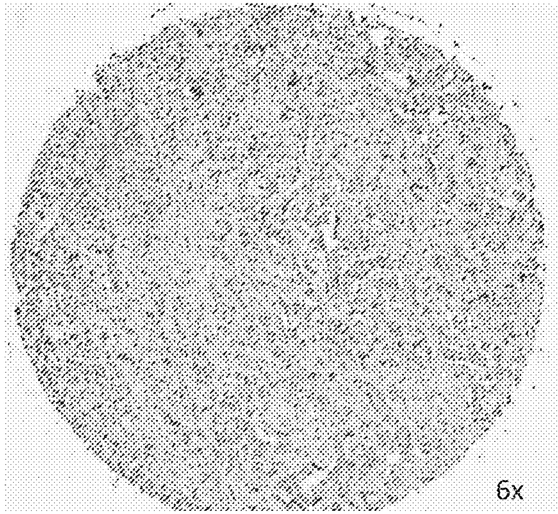


Fig. 196B

Position: E5
Cell Type: Ductal Carcinoma
Tumor Grade: 2-3
TNM: T3N1M0

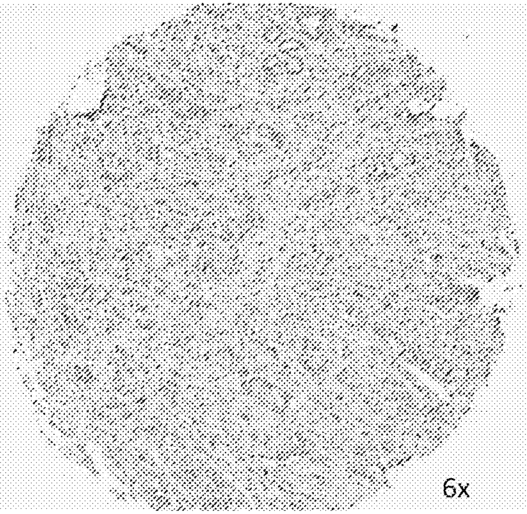


Fig. 196C

Position: F1
Cell Type: Adenocarcinoma
Tumor Grade: 3
TNM: T3N0M0

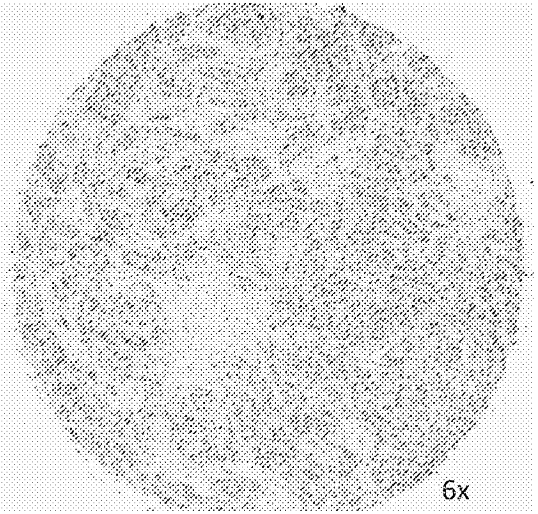


Fig. 196D

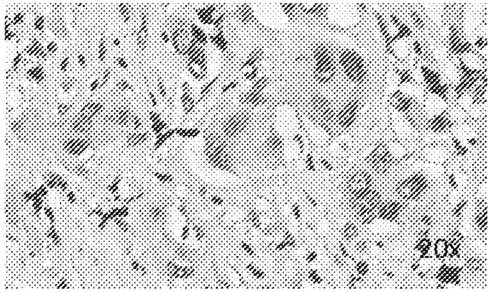


Fig. 196E

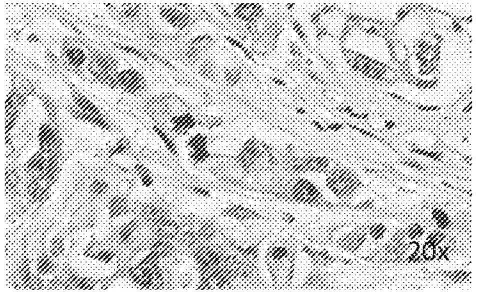


Fig. 196F

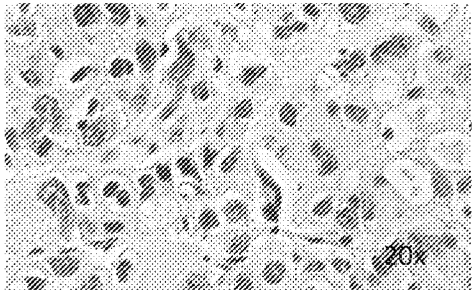


Fig. 196A–196F

N+9/C-9 antibody 39H5 5 ug/mL

FDA Normal tissue array MNO1021

Fig. 197A

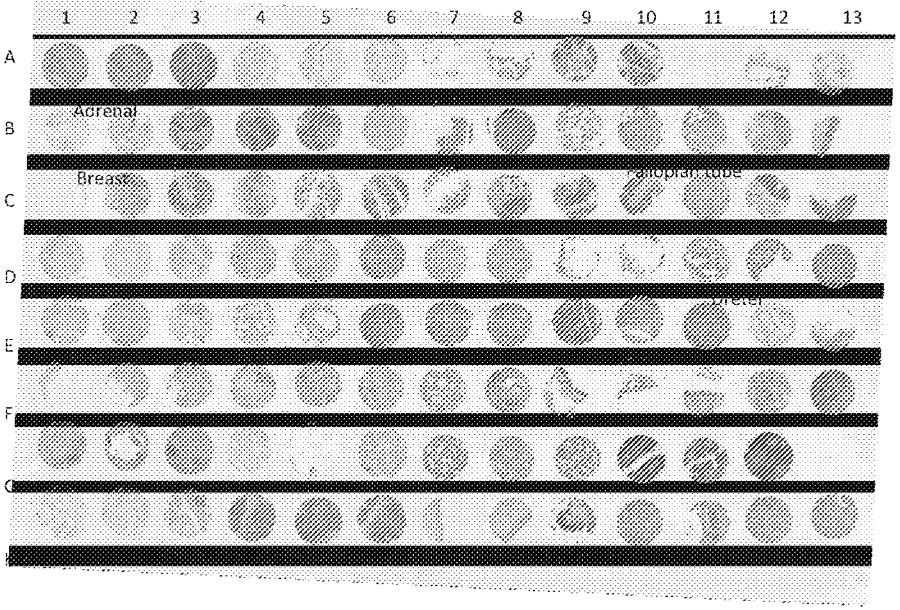


Fig. 197B

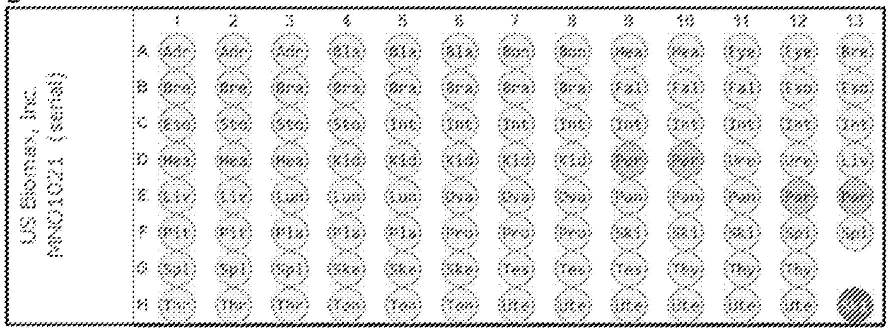


Fig. 197C

Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis	Position	Age	Sex	Organ/Anatomic Site	Pathology diagnosis
A1	F	31	Adrenal gland	Normal	E1	M	59	Liver	Normal
A2	M	51	Adrenal gland	Normal	E2	F	27	Liver	Normal
A3	M	53	Adrenal gland	Normal	E3	M	72	Lung	Normal
A4	M	75	Bladder, urinary	Normal	E4	F	55	Lung	Normal
A5	M	72	Bladder, urinary	Normal	E5	M	43	Lung	Normal
A6	M	52	Bladder, urinary	Normal	E6	F	47	Ovary	Normal
A7	M	53	Bone, bone marrow	Normal	E7	F	46	Ovary	Normal
A8	M	43	Bone, bone marrow	Normal	E8	F	40	Ovary	Normal
A9	F	44	Head and neck, salivary gland	Normal	E9	M	42	Pancreas	Normal
A10	M	18	Head and neck, salivary gland	Normal	E10	F	26	Pancreas	Normal
A11	M	55	Eye	Normal	E11	F	59	Pancreas	Normal
A12	M	50	Eye	Normal	E12	M	17	Parathyroid	Adenoma
A13	F	35	Breast	Normal	E13	M	72	Parathyroid	Adenoma
B1	F	36	Breast	Normal	F1	F	3	Pituitary gland	Normal
B2	F	33	Breast	Normal	F2	F		Pituitary gland	Normal
B3	M	58	Brain, cerebellum	Normal	F3	F	32	Placenta	Normal
B4	M	65	Brain, cerebellum	Normal	F4	F	30	Placenta	Normal
B5	F		Brain, cerebellum	Normal	F5	F	27	Placenta	Normal
B6	M	58	Brain, cerebral cortex	Normal	F6	M	64	Prostate	Normal
B7	M	65	Brain, cerebral cortex	Normal	F7	M	65	Prostate	Normal
B8	F		Brain, cerebral cortex	Normal	F8	M	65	Prostate	Normal
B9	F	42	Fallopian tube	Normal	F9	F	32	Skin	Normal
B10	F	32	Fallopian tube	Normal	F10	F	68	Skin	Normal
B11	F	24	Fallopian tube	Normal	F11	M	28	Skin	Normal
B12	M	45	Esophagus	Normal	F12	M	47	Spinal cord	Normal
B13	F	68	Esophagus	Normal	F13	M	58	Spinal cord	Normal
C1	M	54	Esophagus	Normal	G1	M	27	Spleen	Normal
C2	M	45	Stomach	Normal	G2	M	60	Spleen	Normal
C3	M	49	Stomach	Normal	G3	M	31	Spleen	Normal
C4	M	77	Stomach	Normal	G4	F	60	Skeletal muscle	Normal
C5	M	45	Intestine, small intestine	Normal	G5	F	49	Skeletal muscle	Normal
C6	F	75	Intestine, small intestine	Normal	G6	M	70	Skeletal muscle	Normal
C7	F	75	Intestine, small intestine	Normal	G7	M	43	Testis	Normal
C8	M	2	Intestine, colon	Normal	G8	M	30	Testis	Normal
C9	M	46	Intestine, colon	Normal	G9	M	77	Testis	Normal
C10	M	74	Intestine, colon	Normal	G10	M	15	Thymus	Normal
C11	F	47	Intestine, rectum	Normal	G11	M	28	Thymus	Normal
C12	F	75	Intestine, rectum	Normal	G12	F	9	Thymus	Normal
C13	M	66	Intestine, rectum	Normal	G13	-	-	-	-
D1	M	58	Heart	Normal	H1	F	26	Thyroid	Normal
D2	M	46	Heart	Normal	H2	F	37	Thyroid	Normal
D3	F	34	Heart	Normal	H3	F	51	Thyroid	Normal
D4	F	52	Kidney, cortex	Normal	H4	M	46	Tonsil	Normal
D5	M	23	Kidney, cortex	Normal	H5	M	37	Tonsil	Normal
D6	M	63	Kidney, cortex	Normal	H6	M	13	Tonsil	Normal
D7	F	52	Kidney, medulla	Normal	H7	F	38	Uterus, cervl73	Normal
D8	M	23	Kidney, medulla	Normal	H8	F	35	Uterus, cervl73	Normal
D9	M	59	Peripheral nerve	Schwannoma	H9	F	44	Uterus, cervl73	Normal
D10	F	29	Peripheral nerve	Schwannoma	H10	F	38	Uterus, endometrium	Normal
D11	F	44	Ureter	Normal	H11	F	41	Uterus, endometrium	Normal
D12	F	42	Ureter	Normal	H12	F	46	Uterus, endometrium	Normal
D13	F	57	Liver	Normal	H13	M	58	Skin	Malignant melanoma (tissue marker)

Figure 197A-197C

N+9/C-9 antibody 39H5 5 ug/mL

FDA Normal tissue array MNO1021

Fig. 198A
Normal Adrenal Gland

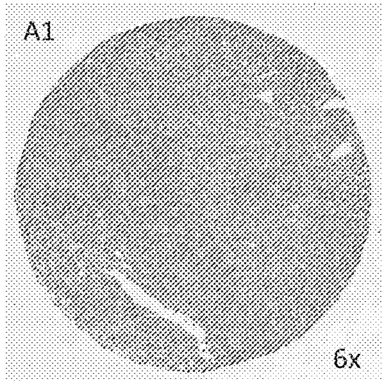


Fig. 198B
Normal Breast

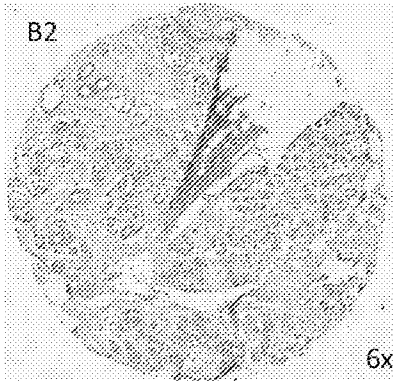


Fig. 198C
Normal Fallopian Tubes

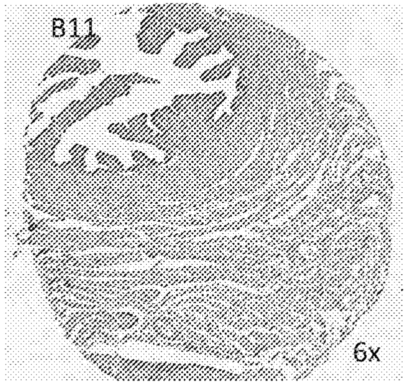


Fig. 198D
Normal Kidney

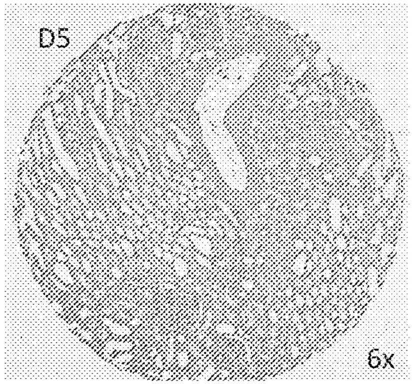


Fig. 198E

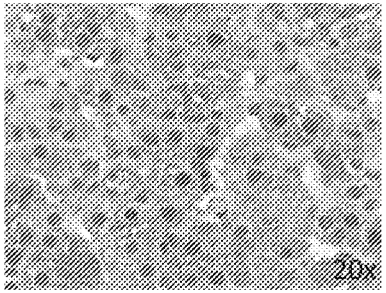


Fig. 198F

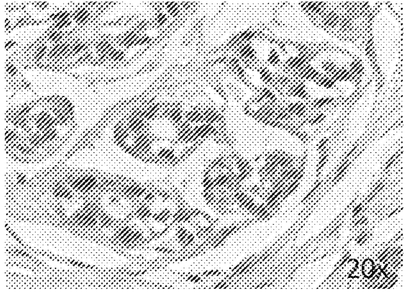


Fig. 198G

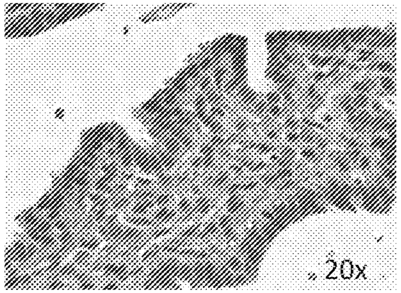


Fig. 198H

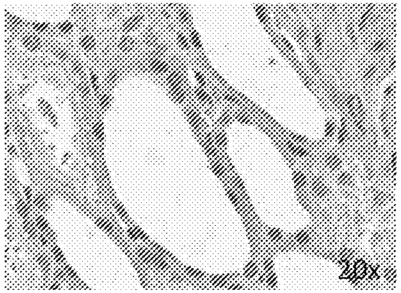


Figure 198A-198H

N+9/C-9 antibody 39H5 5 ug/mL

FDA Normal tissue array MNO1021

Fig. 198I
Normal Heart

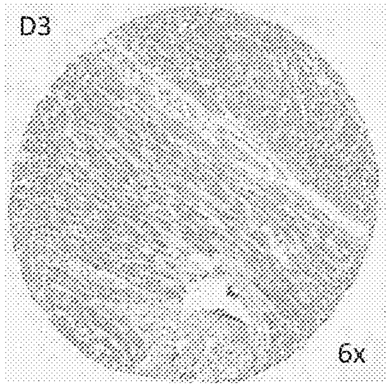


Fig. 198J
Normal Liver

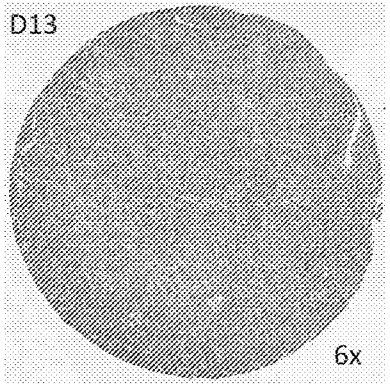


Fig. 198K
Normal Lung

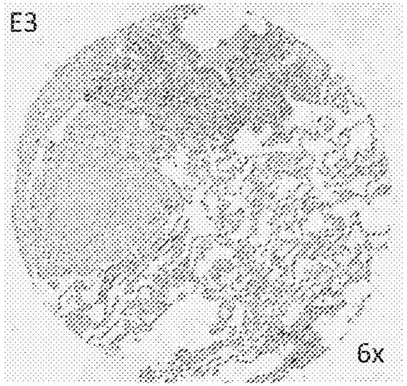


Fig. 198L
Normal Ureter

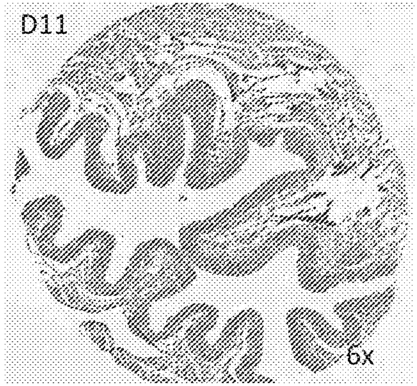


Fig. 198M

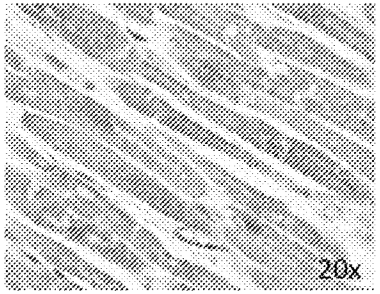


Fig. 198N

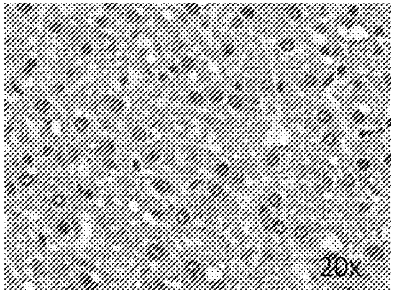


Fig. 198O

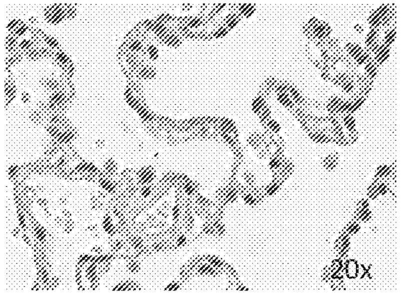


Fig. 198P

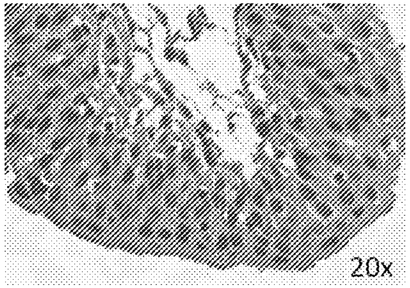


Figure 198I-198P

N+9/C-9 antibody 39H5 5 ug/mL

FDA Normal tissue array MNO1021

Fig. 198Q
Normal eye

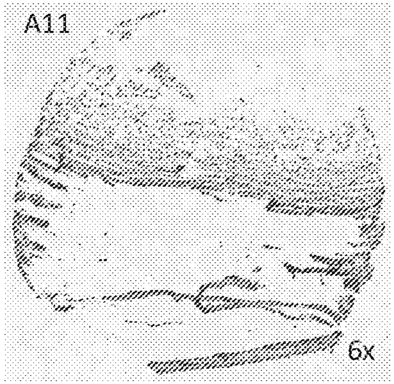


Fig. 198R
Normal Cerebral cortex

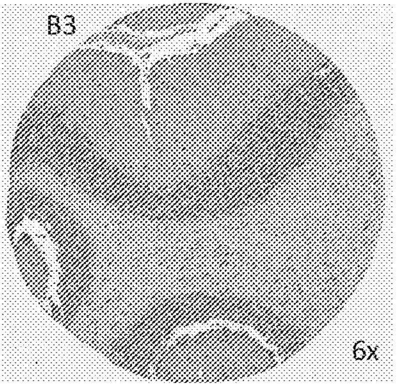


Fig. 198S
Normal Bone marrow

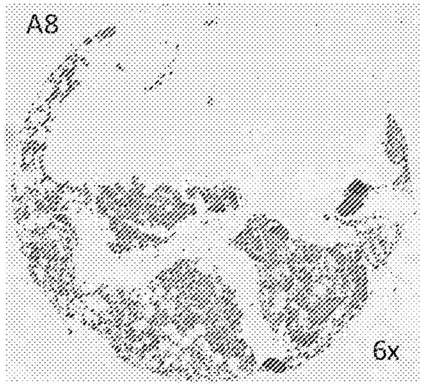


Fig. 198T
Normal Skeletal muscle

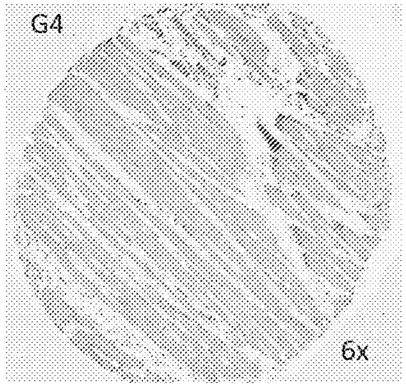


Fig. 198U

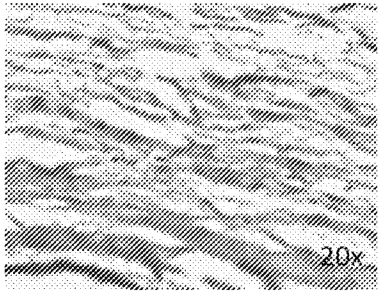


Fig. 198V

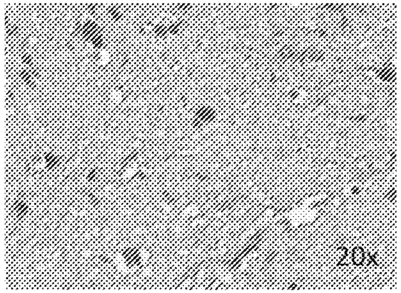


Fig. 198W

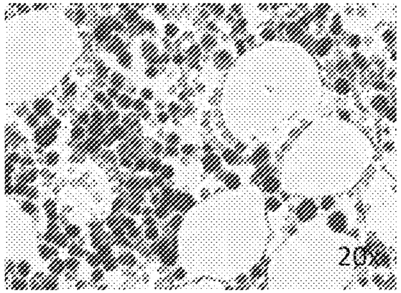


Fig. 198X

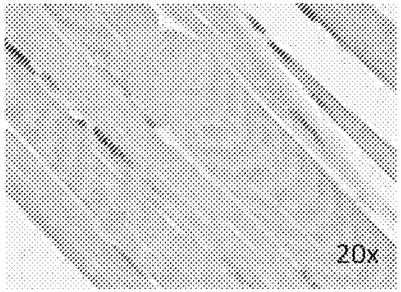


Figure 198Q-198X

N+9/C-9 antibody 39H5 5 ug/mL

Pancreatic cancer tissue array PA1003

Fig. 199A

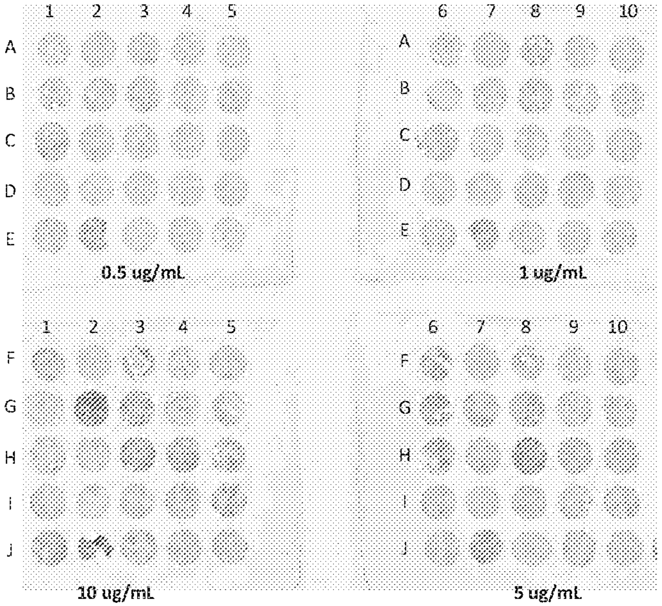


Fig. 199B

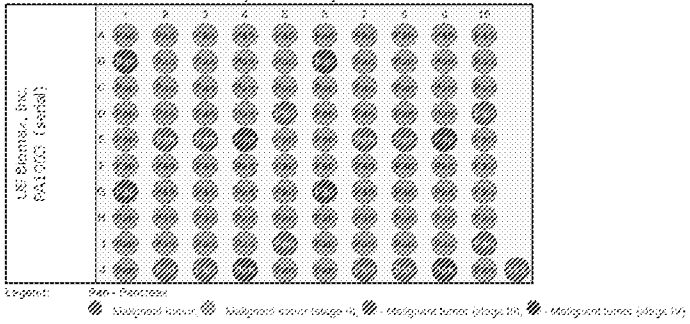
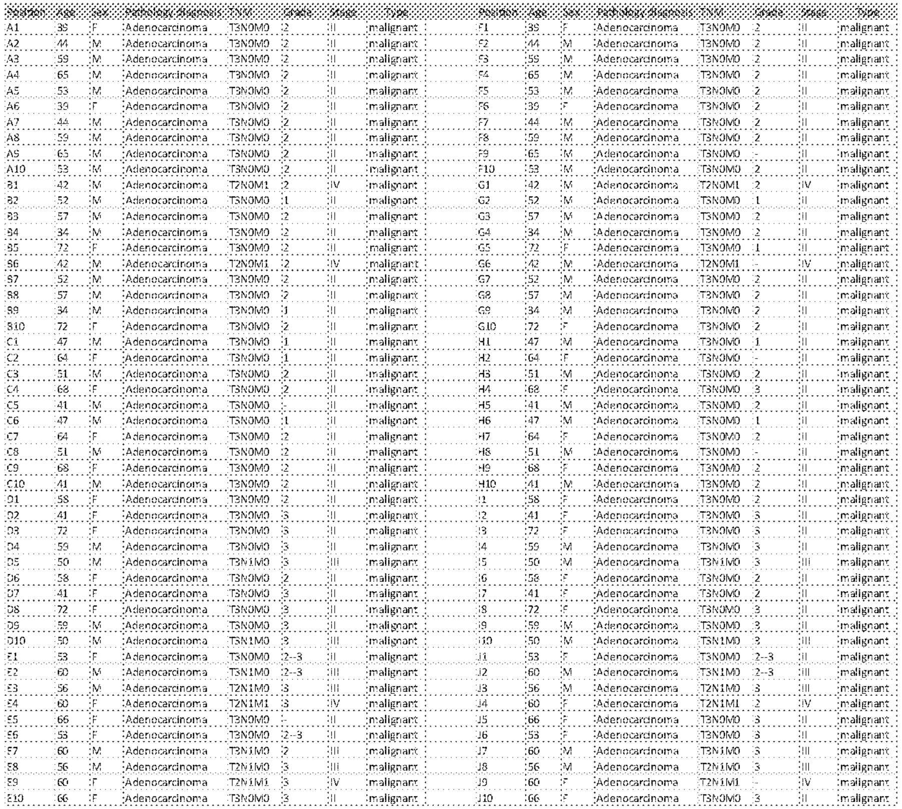


Fig. 199C



Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type	Position	Age	Sex	Pathology diagnosis	TNM	Grade	Stage	Type
A1	39	F	Adenocarcinoma	T3N0M0	2	II	malignant	F1	39	F	Adenocarcinoma	T3N0M0	2	II	malignant
A2	44	M	Adenocarcinoma	T3N0M0	2	II	malignant	F2	44	M	Adenocarcinoma	T3N0M0	2	II	malignant
A3	59	M	Adenocarcinoma	T3N0M0	2	II	malignant	F3	59	M	Adenocarcinoma	T3N0M0	2	II	malignant
A4	65	M	Adenocarcinoma	T3N0M0	2	II	malignant	F4	65	M	Adenocarcinoma	T3N0M0	2	II	malignant
A5	53	M	Adenocarcinoma	T3N0M0	2	II	malignant	F5	53	M	Adenocarcinoma	T3N0M0	2	II	malignant
A6	39	F	Adenocarcinoma	T3N0M0	2	II	malignant	F6	39	F	Adenocarcinoma	T3N0M0	2	II	malignant
A7	44	M	Adenocarcinoma	T3N0M0	2	II	malignant	F7	44	M	Adenocarcinoma	T3N0M0	2	II	malignant
A8	59	M	Adenocarcinoma	T3N0M0	2	II	malignant	F8	59	M	Adenocarcinoma	T3N0M0	2	II	malignant
A9	65	M	Adenocarcinoma	T3N0M0	2	II	malignant	F9	65	M	Adenocarcinoma	T3N0M0	-	II	malignant
A10	53	M	Adenocarcinoma	T3N0M0	2	II	malignant	F10	53	M	Adenocarcinoma	T3N0M0	2	II	malignant
B1	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant	G1	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant
B2	52	M	Adenocarcinoma	T3N0M0	1	II	malignant	G2	52	M	Adenocarcinoma	T3N0M0	1	II	malignant
B3	57	M	Adenocarcinoma	T3N0M0	2	II	malignant	G3	57	M	Adenocarcinoma	T3N0M0	2	II	malignant
B4	34	M	Adenocarcinoma	T3N0M0	2	II	malignant	G4	34	M	Adenocarcinoma	T3N0M0	2	II	malignant
B5	72	F	Adenocarcinoma	T3N0M0	2	II	malignant	G5	72	F	Adenocarcinoma	T3N0M0	1	II	malignant
B6	42	M	Adenocarcinoma	T2N0M1	2	IV	malignant	G6	42	M	Adenocarcinoma	T2N0M1	-	IV	malignant
B7	52	M	Adenocarcinoma	T3N0M0	2	II	malignant	G7	52	M	Adenocarcinoma	T3N0M0	2	II	malignant
B8	57	M	Adenocarcinoma	T3N0M0	2	II	malignant	G8	57	M	Adenocarcinoma	T3N0M0	2	II	malignant
B9	34	M	Adenocarcinoma	T3N0M0	1	II	malignant	G9	34	M	Adenocarcinoma	T3N0M0	2	II	malignant
B10	72	F	Adenocarcinoma	T3N0M0	2	II	malignant	G10	72	F	Adenocarcinoma	T3N0M0	2	II	malignant
C1	47	M	Adenocarcinoma	T3N0M0	1	II	malignant	H1	47	M	Adenocarcinoma	T3N0M0	1	II	malignant
C2	64	F	Adenocarcinoma	T3N0M0	1	II	malignant	H2	64	F	Adenocarcinoma	T3N0M0	-	II	malignant
C3	51	M	Adenocarcinoma	T3N0M0	2	II	malignant	H3	51	M	Adenocarcinoma	T3N0M0	2	II	malignant
C4	68	F	Adenocarcinoma	T3N0M0	2	II	malignant	H4	68	F	Adenocarcinoma	T3N0M0	3	II	malignant
C5	41	M	Adenocarcinoma	T3N0M0	-	II	malignant	H5	41	M	Adenocarcinoma	T3N0M0	2	II	malignant
C6	47	M	Adenocarcinoma	T3N0M0	1	II	malignant	H6	47	M	Adenocarcinoma	T3N0M0	1	II	malignant
C7	64	F	Adenocarcinoma	T3N0M0	2	II	malignant	H7	64	F	Adenocarcinoma	T3N0M0	2	II	malignant
C8	51	M	Adenocarcinoma	T3N0M0	2	II	malignant	H8	51	M	Adenocarcinoma	T3N0M0	-	II	malignant
C9	68	F	Adenocarcinoma	T3N0M0	2	II	malignant	H9	68	F	Adenocarcinoma	T3N0M0	2	II	malignant
C10	41	M	Adenocarcinoma	T3N0M0	2	II	malignant	H10	41	M	Adenocarcinoma	T3N0M0	2	II	malignant
D1	58	F	Adenocarcinoma	T3N0M0	2	II	malignant	I1	58	F	Adenocarcinoma	T3N0M0	2	II	malignant
D2	41	F	Adenocarcinoma	T3N0M0	3	II	malignant	I2	41	F	Adenocarcinoma	T3N0M0	3	II	malignant
D3	72	F	Adenocarcinoma	T3N0M0	3	II	malignant	I3	72	F	Adenocarcinoma	T3N0M0	3	II	malignant
D4	59	M	Adenocarcinoma	T3N0M0	3	II	malignant	I4	59	M	Adenocarcinoma	T3N0M0	3	II	malignant
D5	50	M	Adenocarcinoma	T3N1M0	3	III	malignant	I5	50	M	Adenocarcinoma	T3N1M0	3	III	malignant
D6	58	F	Adenocarcinoma	T3N0M0	2	II	malignant	I6	58	F	Adenocarcinoma	T3N0M0	2	II	malignant
D7	41	F	Adenocarcinoma	T3N0M0	3	II	malignant	I7	41	F	Adenocarcinoma	T3N0M0	2	II	malignant
D8	72	F	Adenocarcinoma	T3N0M0	3	II	malignant	I8	72	F	Adenocarcinoma	T3N0M0	3	II	malignant
D9	59	M	Adenocarcinoma	T3N0M0	3	II	malignant	I9	59	M	Adenocarcinoma	T3N0M0	3	II	malignant
D10	50	M	Adenocarcinoma	T3N1M0	3	III	malignant	I10	50	M	Adenocarcinoma	T3N1M0	3	III	malignant
E1	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant	J1	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant
E2	60	M	Adenocarcinoma	T3N1M0	2--3	III	malignant	J2	60	M	Adenocarcinoma	T3N1M0	2--3	III	malignant
E3	56	M	Adenocarcinoma	T2N1M0	3	III	malignant	J3	56	M	Adenocarcinoma	T2N1M0	3	III	malignant
E4	60	F	Adenocarcinoma	T2N1M1	3	IV	malignant	J4	60	F	Adenocarcinoma	T2N1M1	2	IV	malignant
E5	66	F	Adenocarcinoma	T3N0M0	-	II	malignant	J5	66	F	Adenocarcinoma	T3N0M0	3	II	malignant
E6	53	F	Adenocarcinoma	T3N0M0	2--3	II	malignant	J6	53	F	Adenocarcinoma	T3N0M0	3	II	malignant
E7	60	M	Adenocarcinoma	T3N1M0	2	III	malignant	J7	60	M	Adenocarcinoma	T3N1M0	3	III	malignant
E8	56	M	Adenocarcinoma	T2N1M0	3	III	malignant	J8	56	M	Adenocarcinoma	T2N1M0	3	III	malignant
E9	60	F	Adenocarcinoma	T2N1M1	3	IV	malignant	J9	60	F	Adenocarcinoma	T2N1M1	-	IV	malignant
E10	66	F	Adenocarcinoma	T3N0M0	3	II	malignant	J10	66	F	Adenocarcinoma	T3N0M0	3	II	malignant

Fig. 199A–199C

N+9/C-9 antibody 39H5 5 ug/mL

Pancreatic cancer tissue array PA1003

Fig. 200A

Position: F6
Cell Type: Adenocarcinoma
Tumor Grade: 2
TNM: T3N0M0

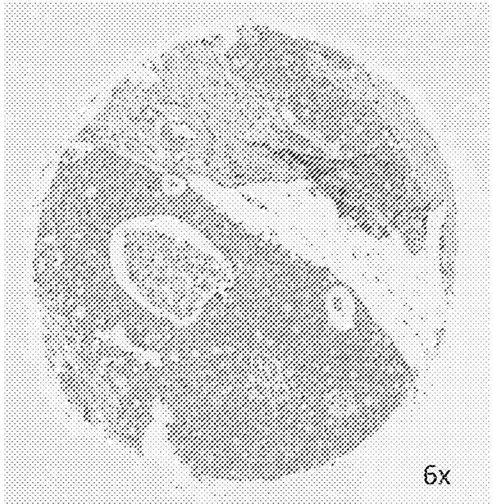


Fig. 200B

Position: F7
Cell Type: Adenocarcinoma
Tumor Grade: 2
TNM: T3N0M0

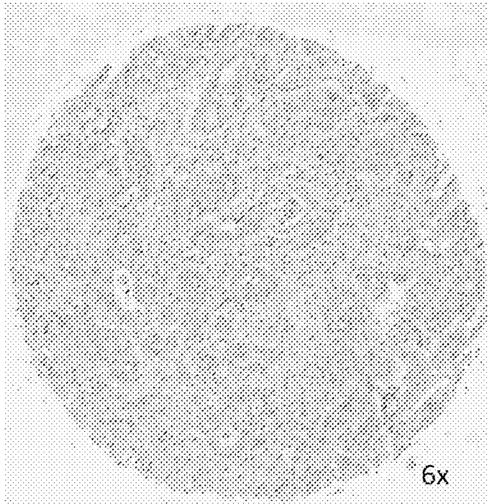
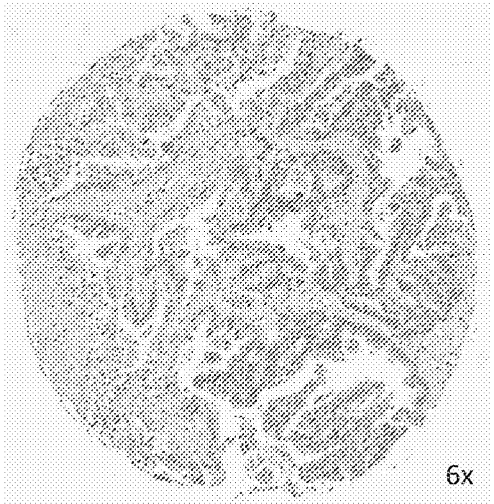


Fig. 200C

Position: G8
Cell Type: Adenocarcinoma
Tumor Grade: 2
TNM: T3N0M0



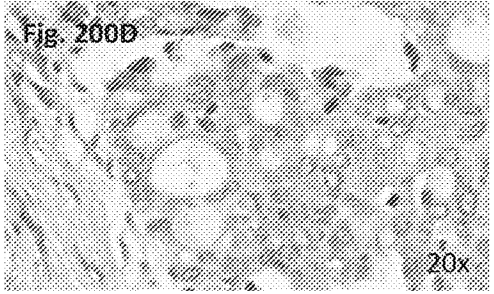


Fig. 200D

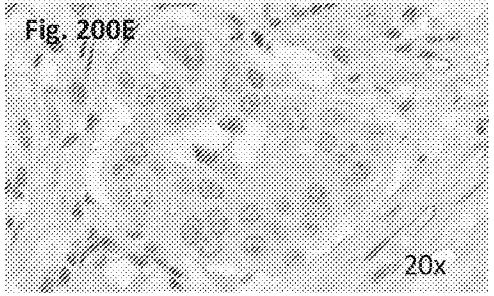


Fig. 200E

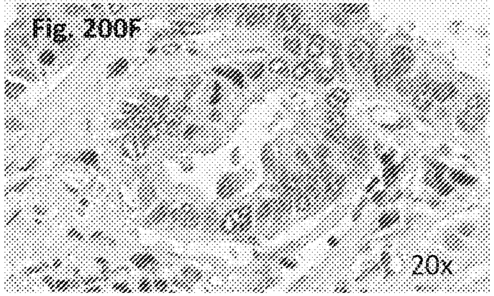


Fig. 200F

Fig. 200A–200F

ELISA – binding of antibodies raised against PSMGFR

Fig. 201A

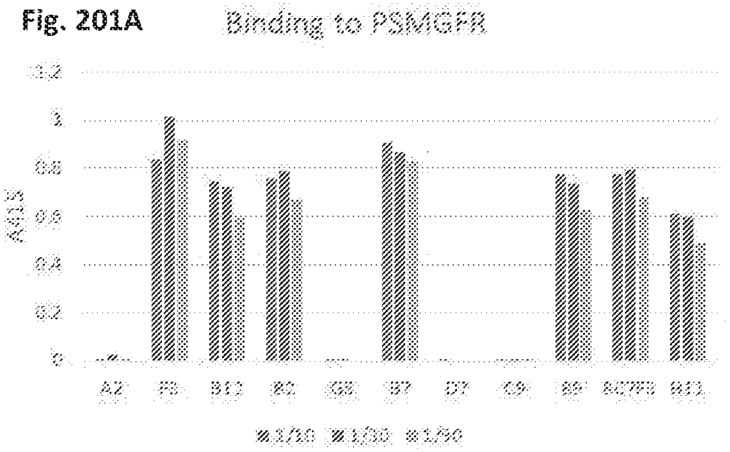


Fig. 201B

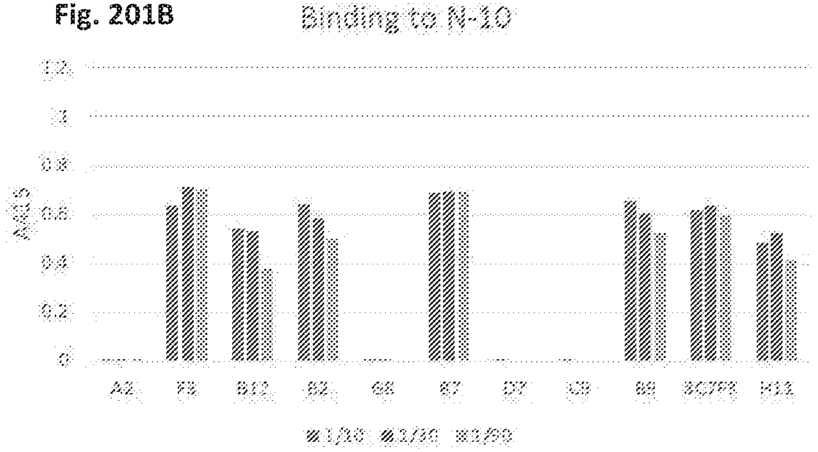


Fig. 201C

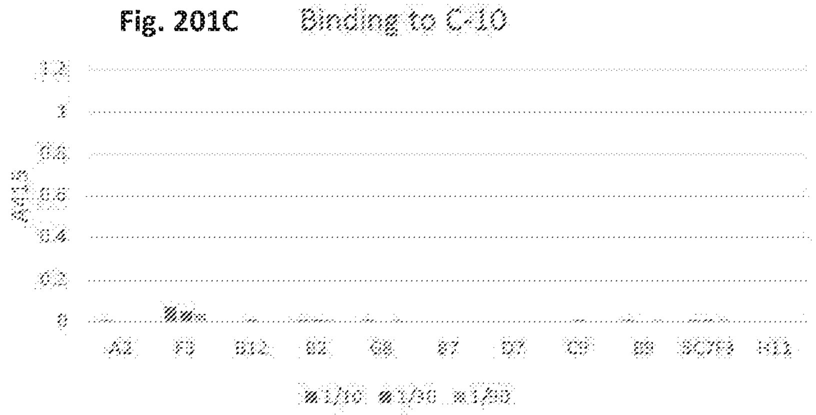


Figure 201A-201C

Pancreatic Array PA1003:

Fig. 202A

10 ug/mL 1E4 (N+20/C-27)

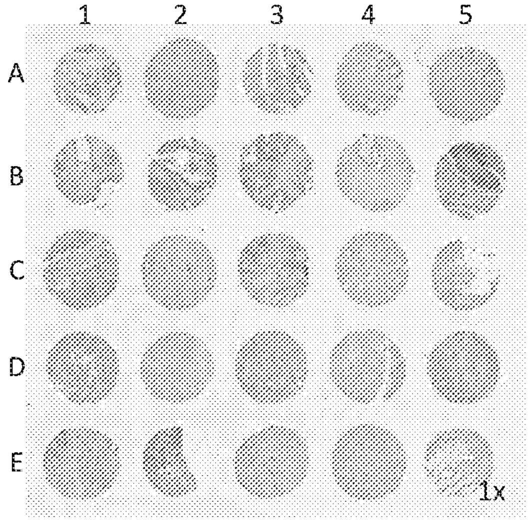


Fig. 202B

10 ug/mL 18B4 (PSMGFR)

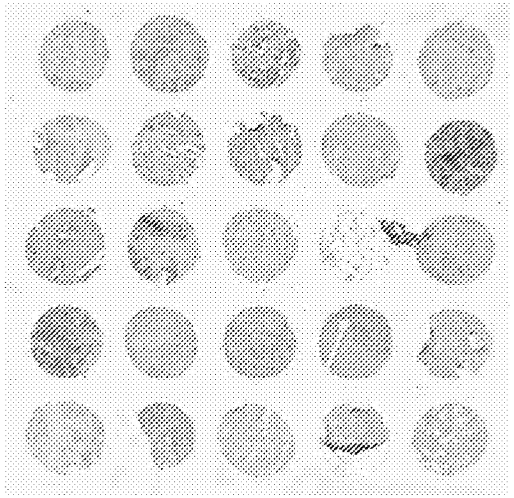


Fig. 202C

1 ug/mL SDIX (PSMGFR)

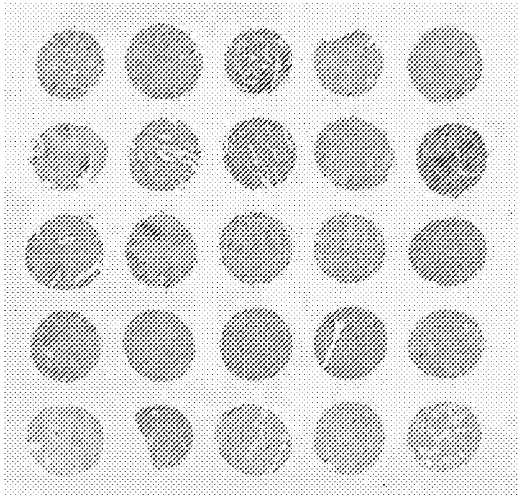
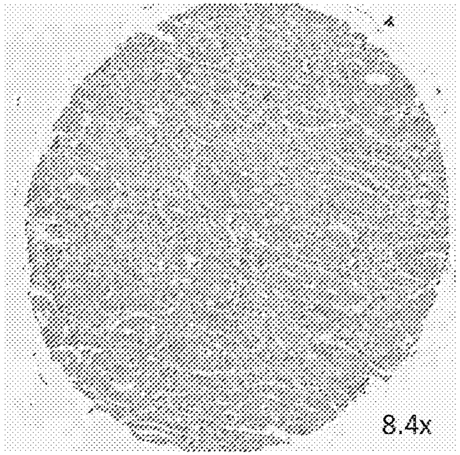


Figure 202A-202C

Pancreatic Array PA1003: Donor A2

Fig. 203A
10 ug/mL 1E4 (N+20/C-27)



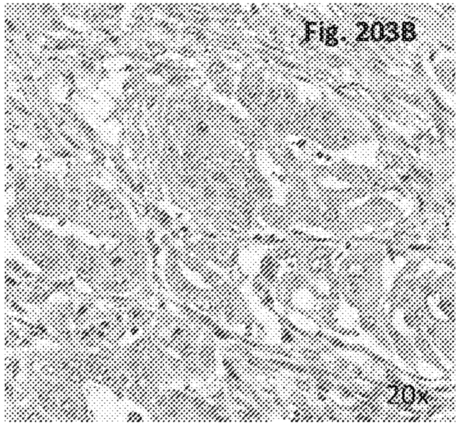
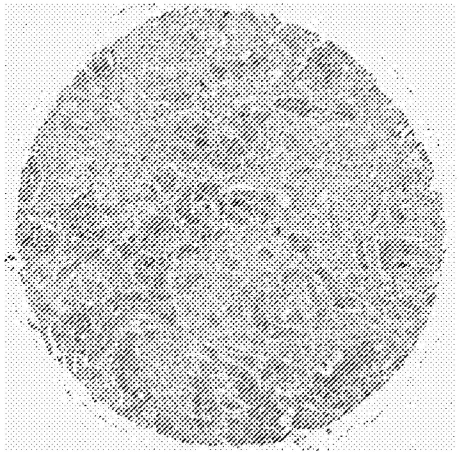


Fig. 203B

Fig. 203C
10 ug/mL 18B4 (PSMGFR)



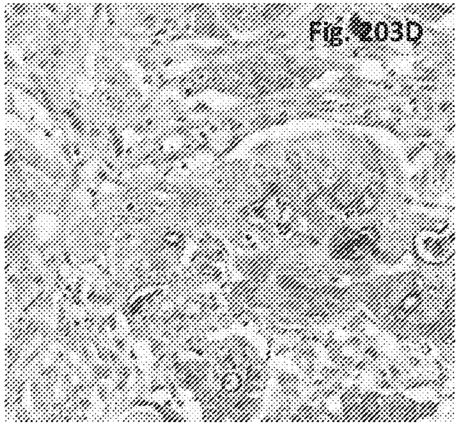
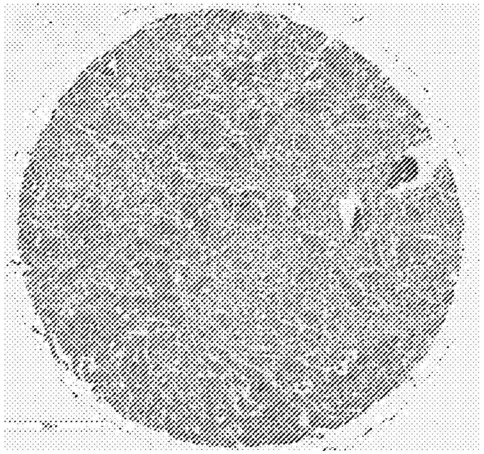


Fig. 203D

Fig. 203E
1 ug/mL SDIX (PSMGFR)



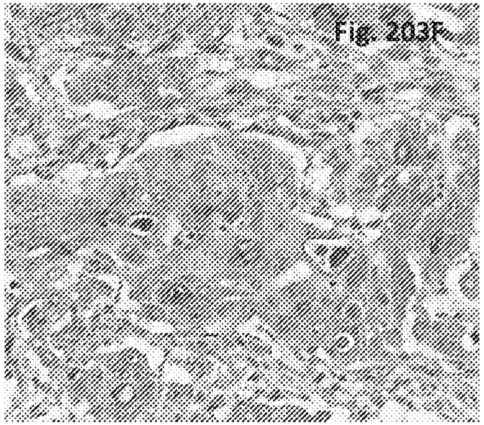


Fig. 203F

Figure 203A-203F

Pancreatic Array PA1003: Donor D4

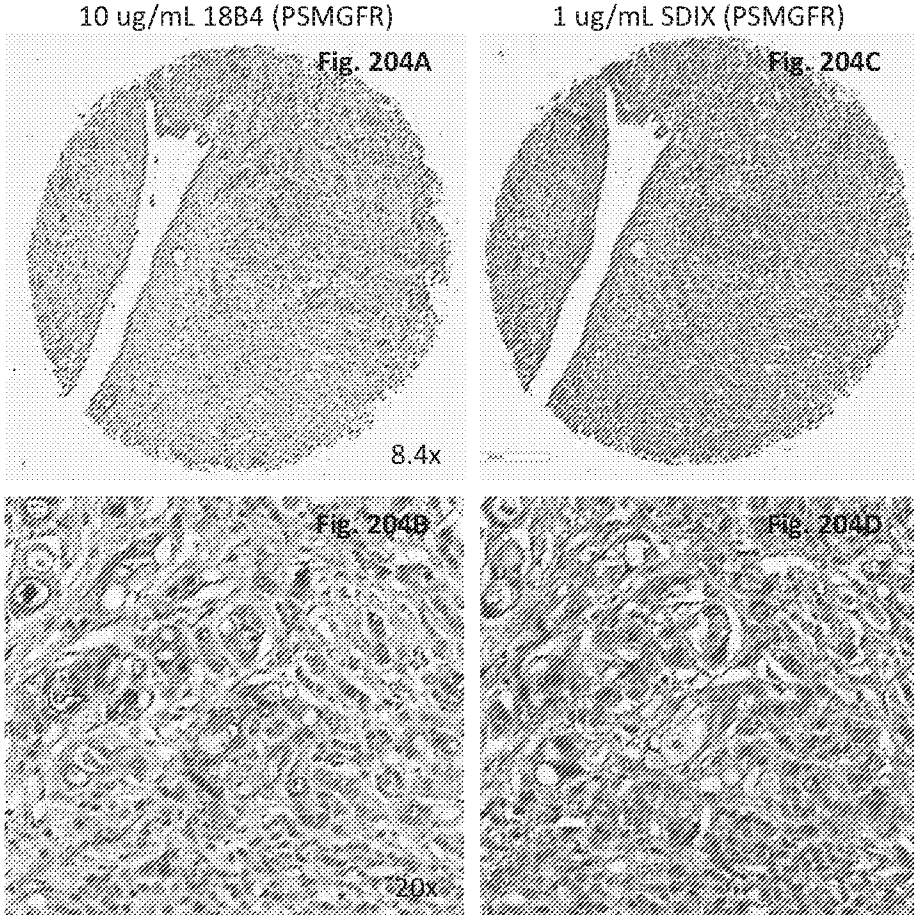


Figure 204A-204D

Pancreatic Array PA1003: Donor E1

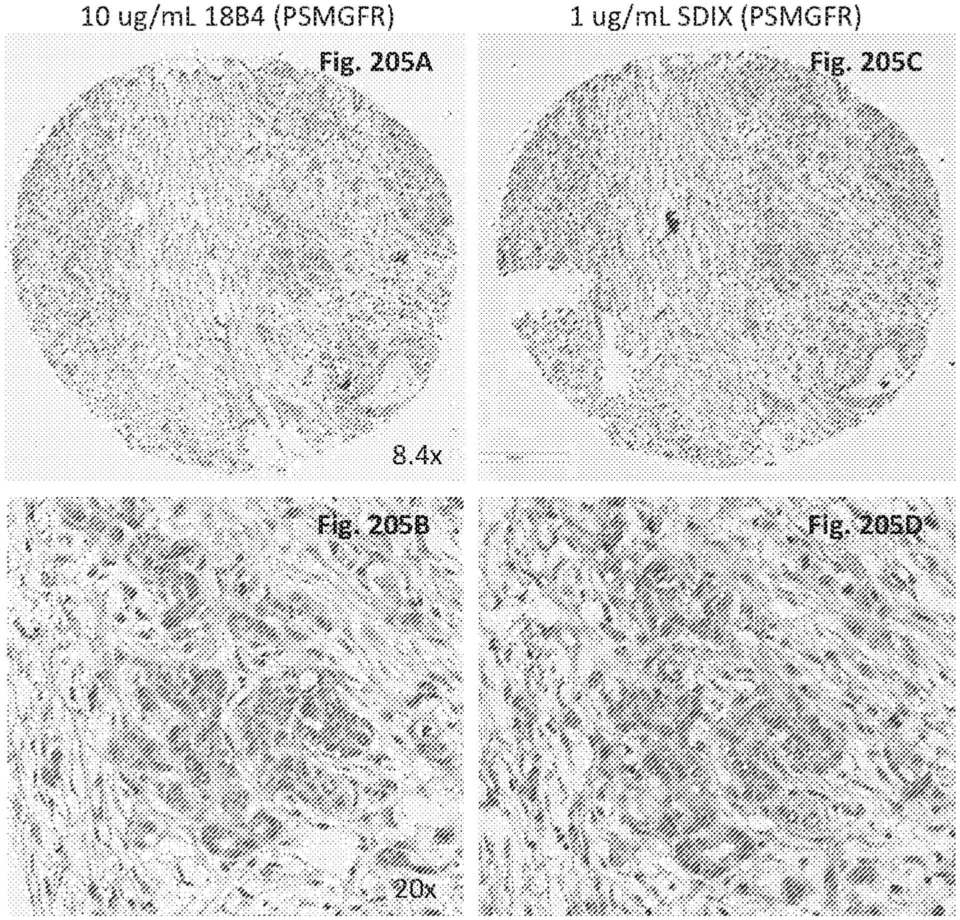


Figure 205A-205D

Pancreatic Array PA1003: Donor C3

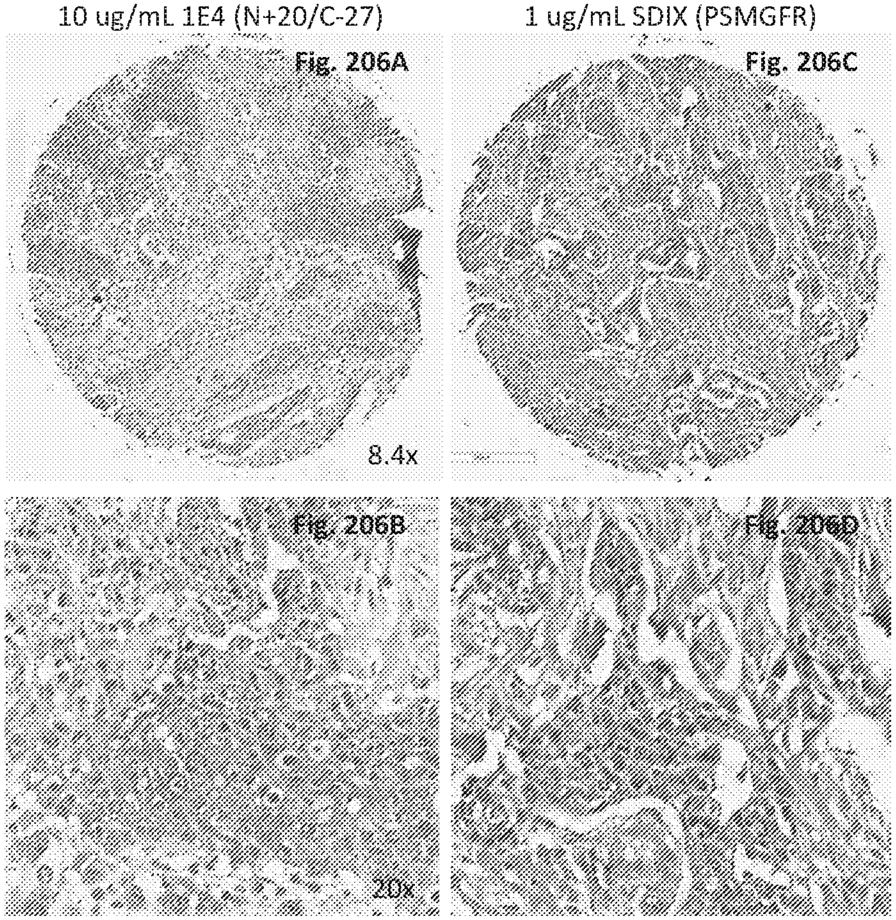


Figure 206A-206D

Pancreatic Array PA1003: Donor D1

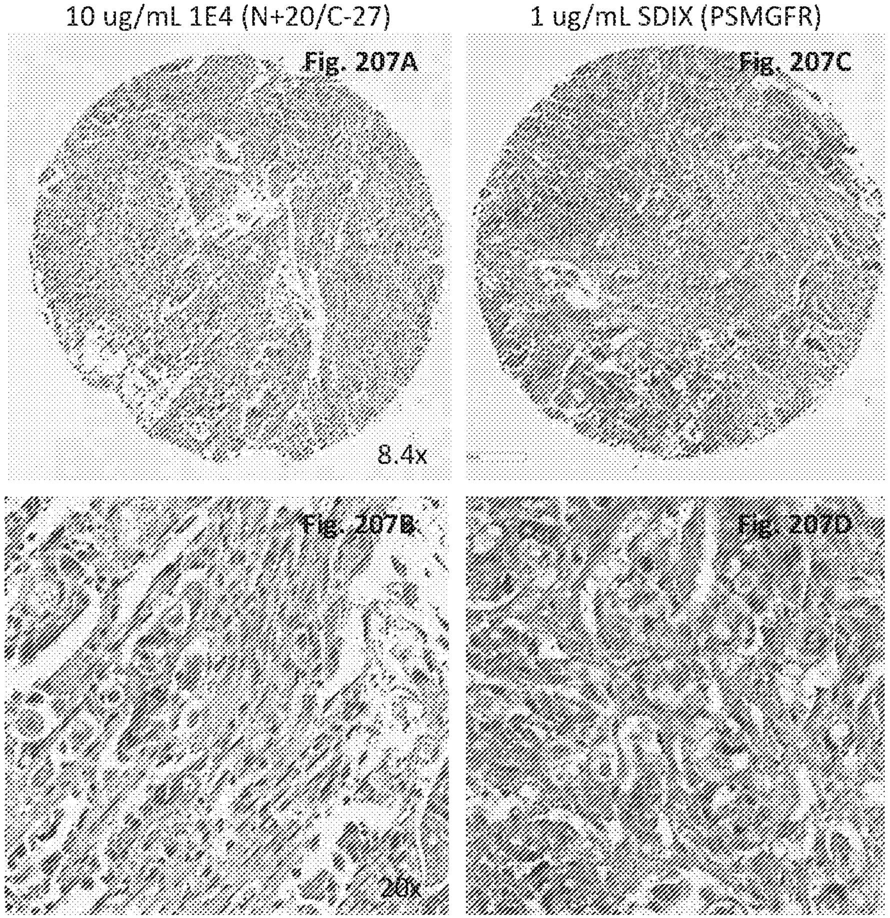


Figure 207A-207D

Pancreatic Array PA1003:

1 ug/mL SDIX (PSMGFR)

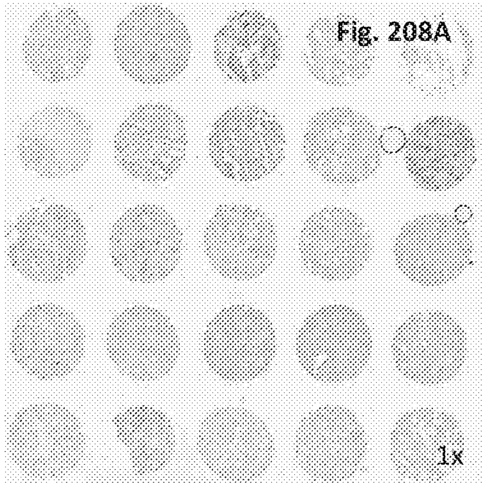


Fig. 208A

0.5 ug/mL 20A10 (PSMGFR)

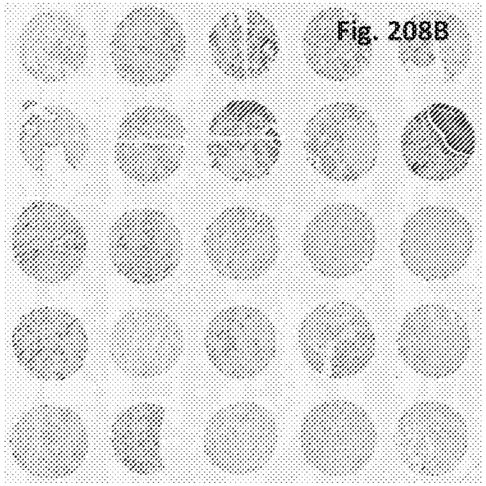


Fig. 208B

4 ug/mL 29H1 (N+20/C-27)

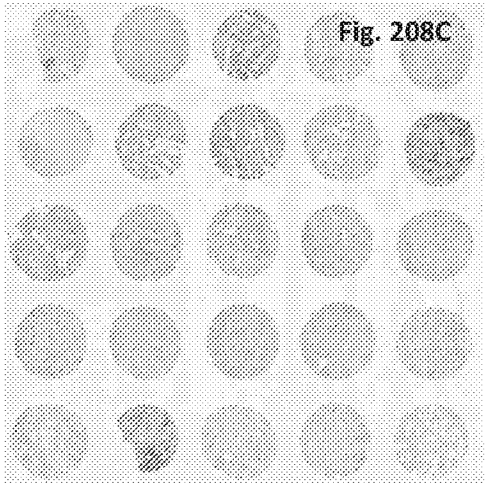


Fig. 208C

Figure 208A-208C

Esophageal Cancer Array ES1001: overview of MUC1* monoclonal staining

1 ug/mL SDIX (PSMGFR)

0.5 ug/mL 20A10 (PSMGFR)

4 ug/mL 29H1 (N+20/C-27)

5.9 ug/mL 31A1 (N+20/C-27)

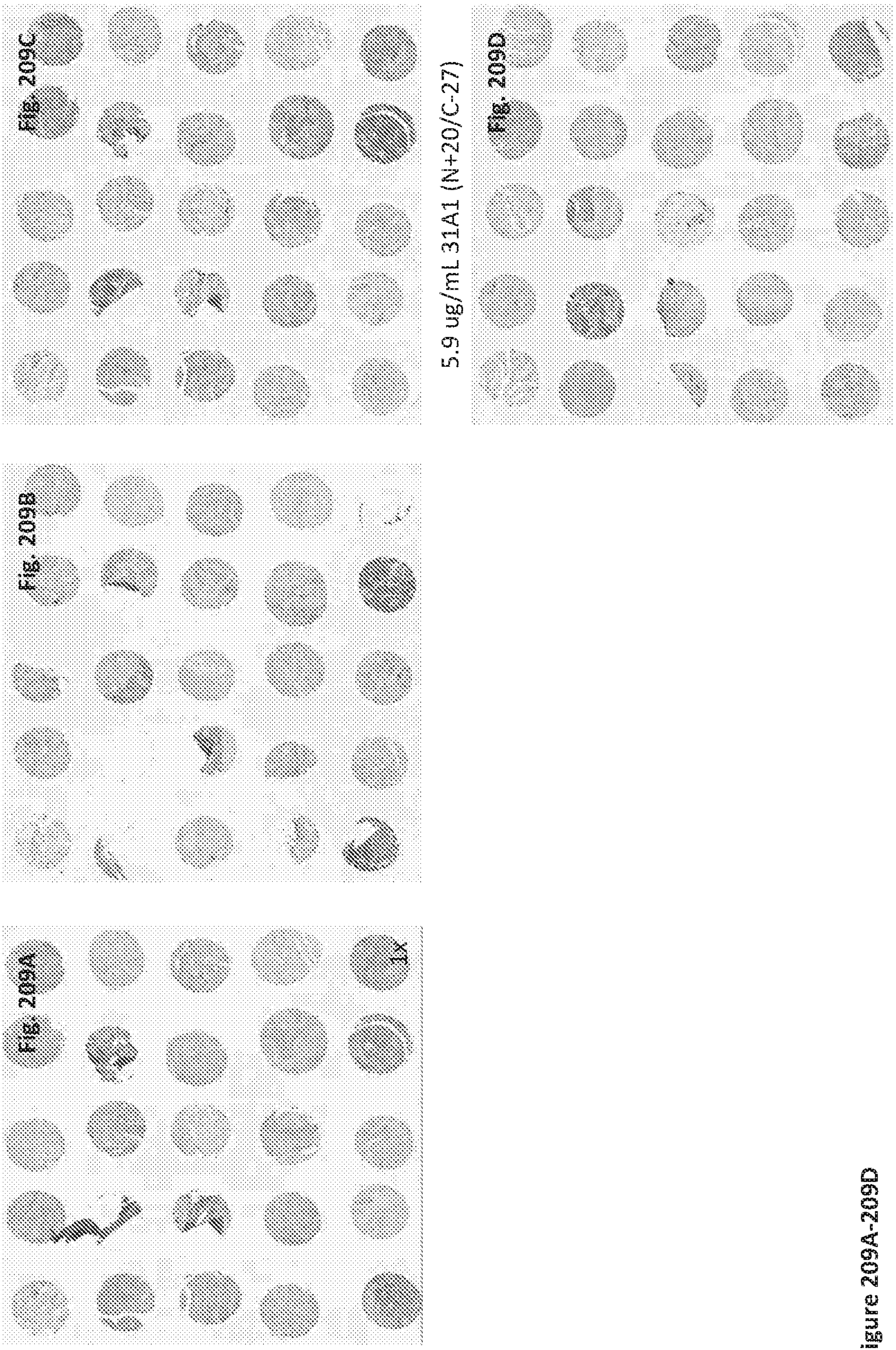


Figure 209A-209D

Prostate Cancer Array PR1001: overview of MUC1* monoclonal staining

1 ug/mL SDIX (PSMGFR)

0.5 ug/mL 20A10 (PSMGFR)

4 ug/mL 29H1 (N+20/C-27)

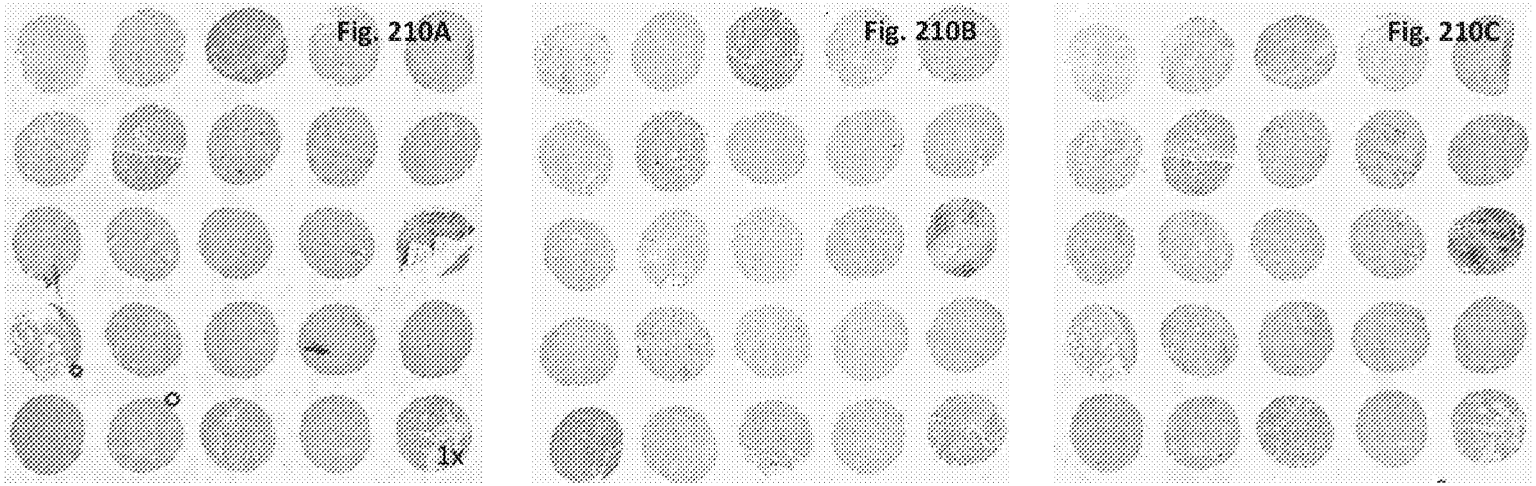


Figure 210A-210C

huMNC2-CAR44 with NFAT inducible IL-18 for increased persistence

Fig. 211A

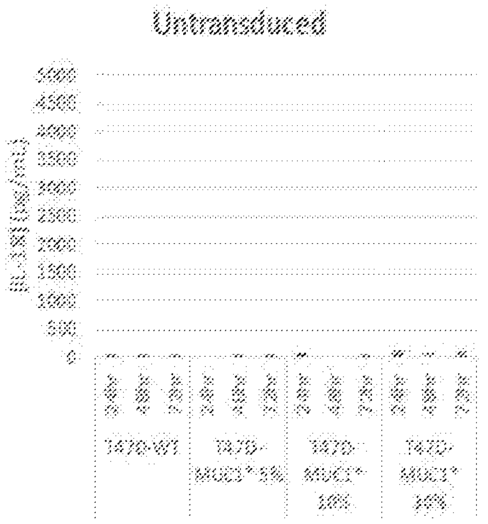


Fig. 211B

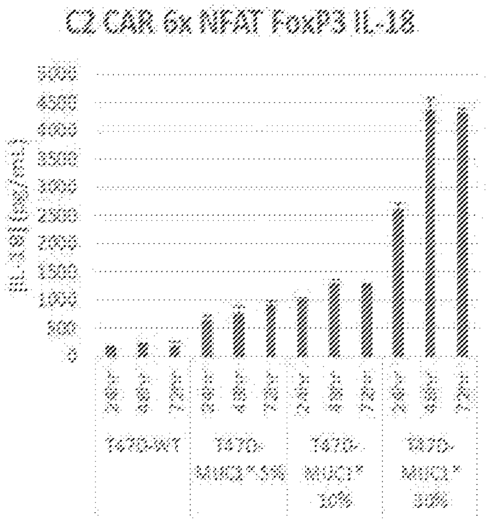
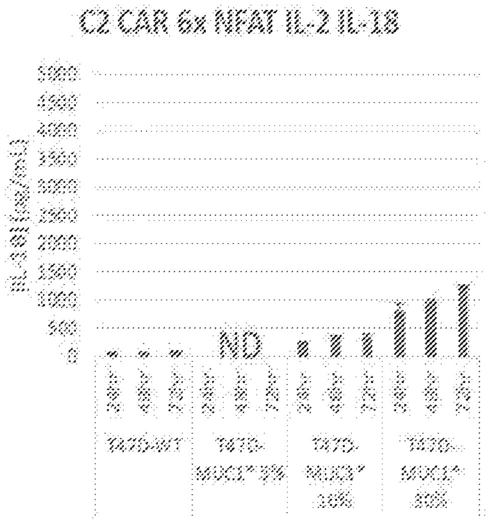


Fig. 211C



T47D breast cancer cells low – med antigen density; doped with increasing percentages of high antigen density cells

Figure 211A-211C

IL-18 also increases killing of low antigen density cells in a concentration dependent manner

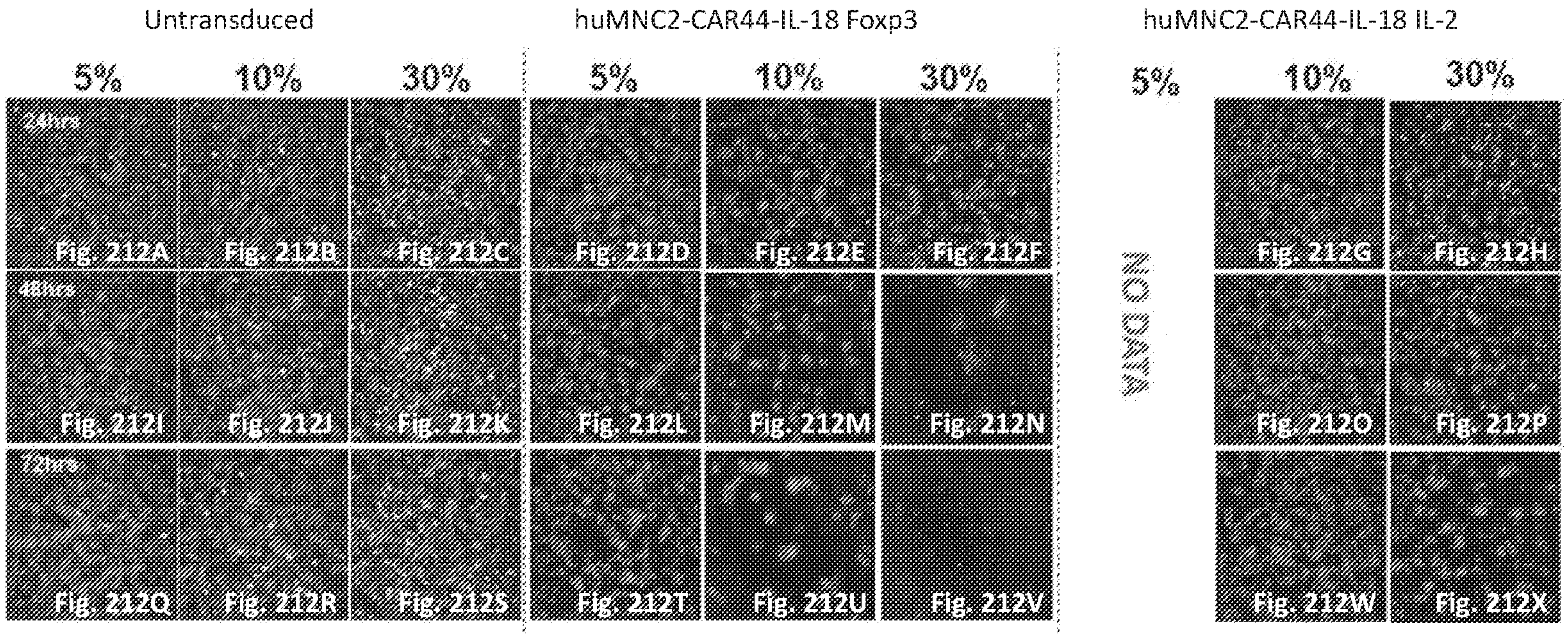


Figure 212A-212X

huMNC2-CAR44-IL-18 does not increase killing of normal cells

Fig. 213A

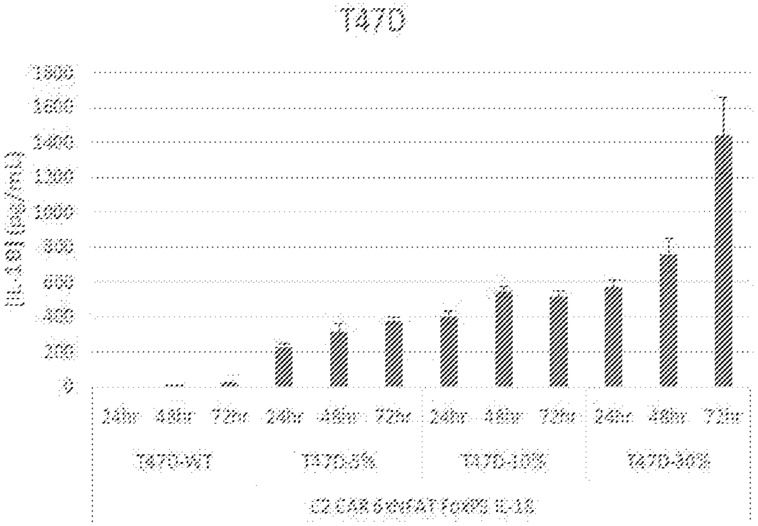


Fig. 213B

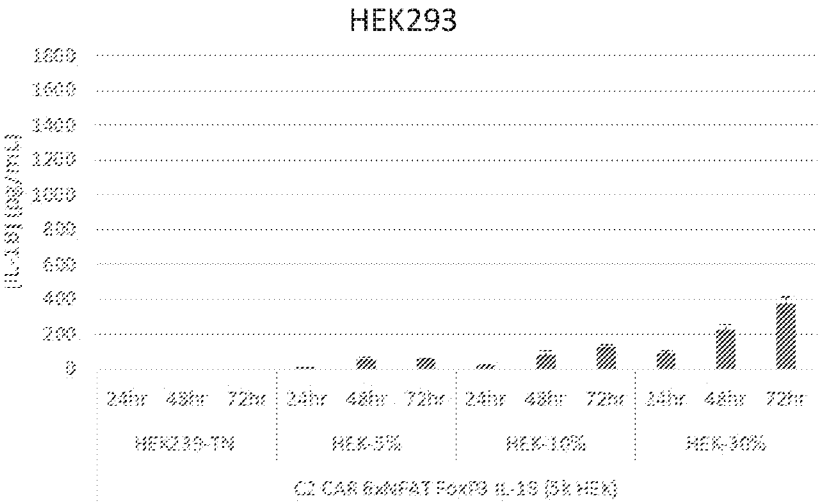


Figure 213A-213B

At 72 hrs still no killing of non-target cells, but all high density cells gone

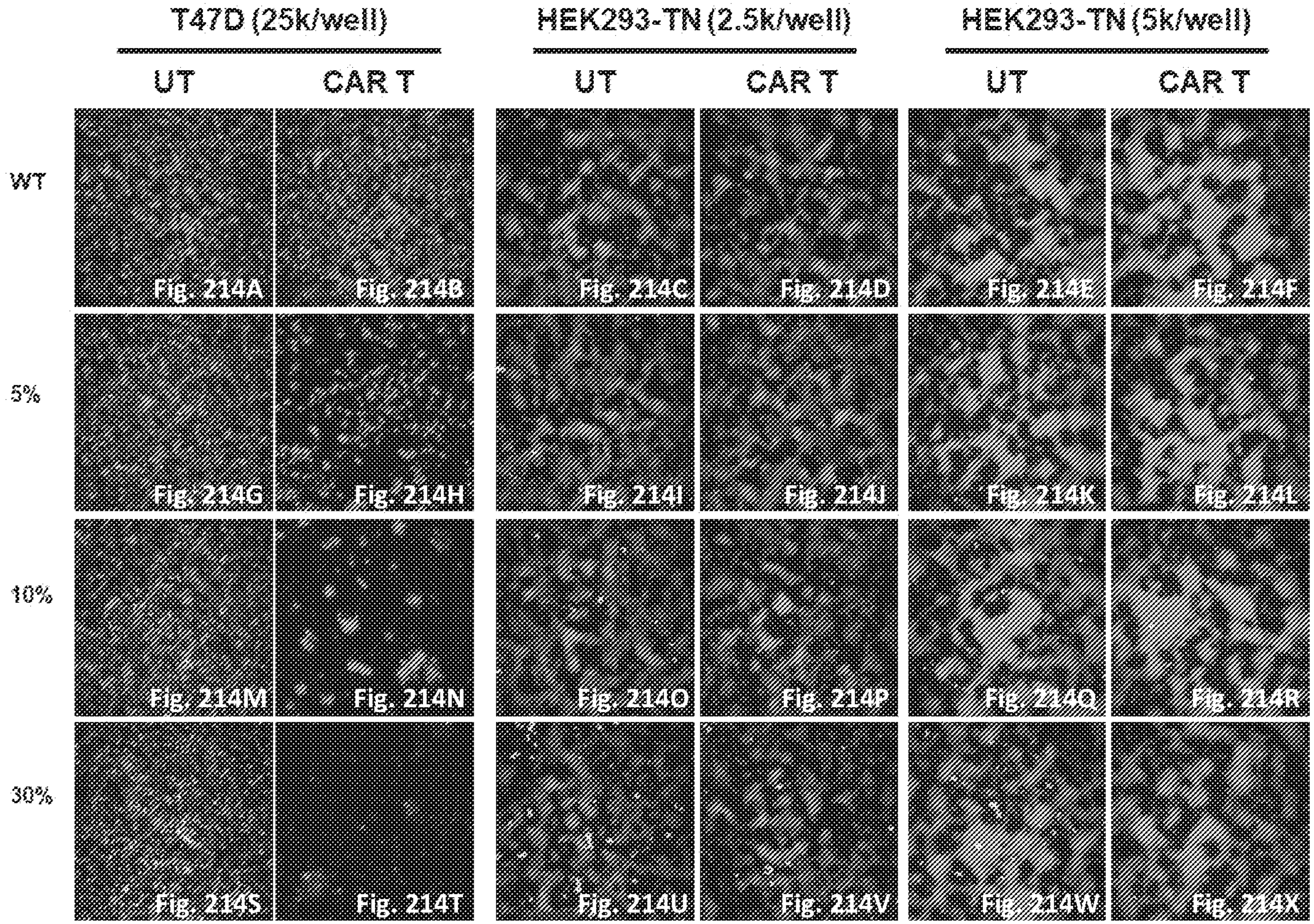


Figure 214A-214X

Heavy Chain Consensus Sequences

Fig. 215A

CDR1

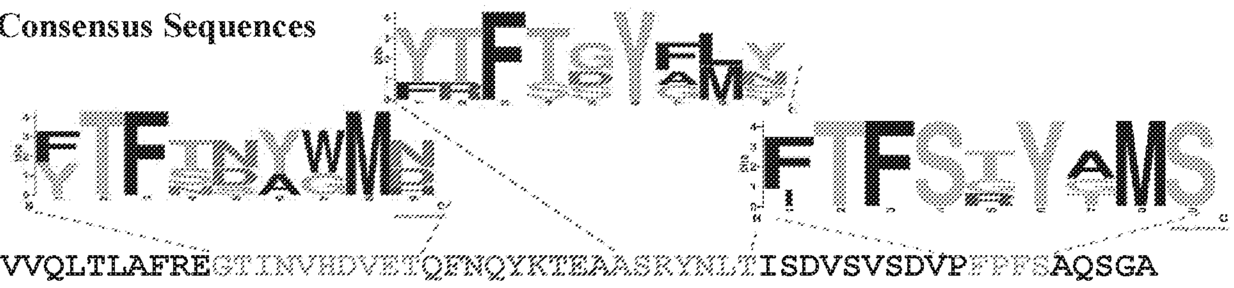


Fig. 215B

CDR2

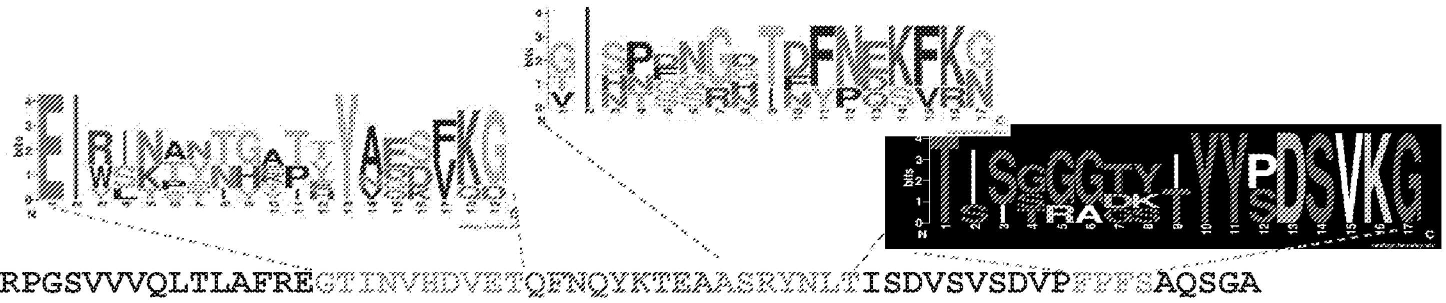


Fig. 215C

CDR3

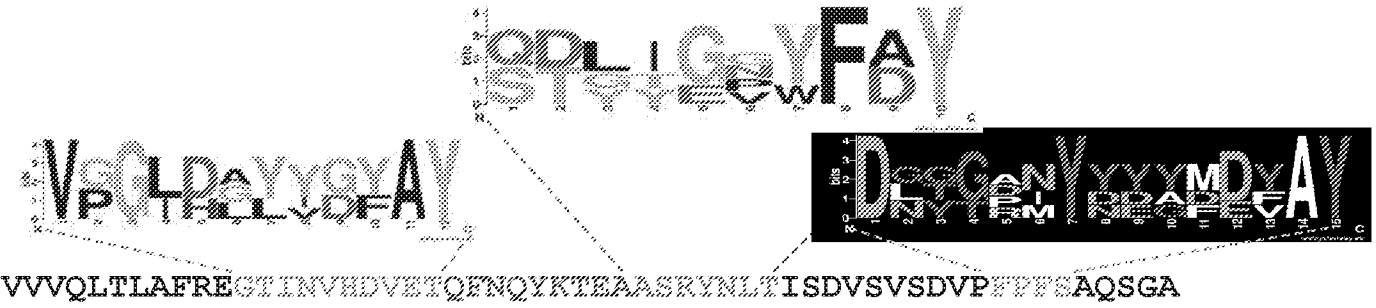


Figure 215A-215C

Light Chain Consensus Sequences

Fig. 216A

CDR1

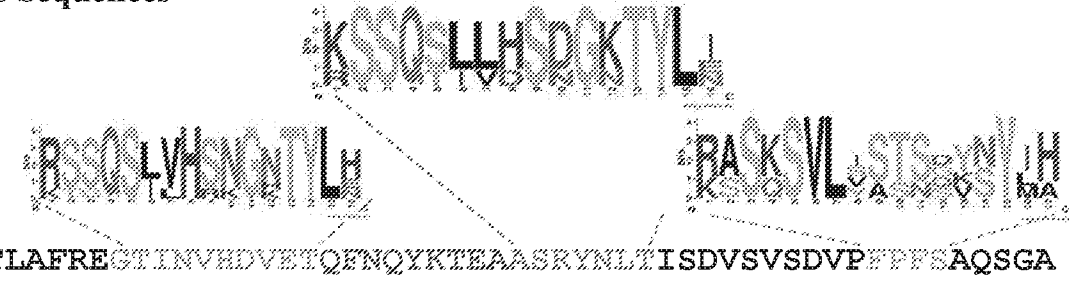


Fig. 216B

CDR2

Fig. 216C

CDR3

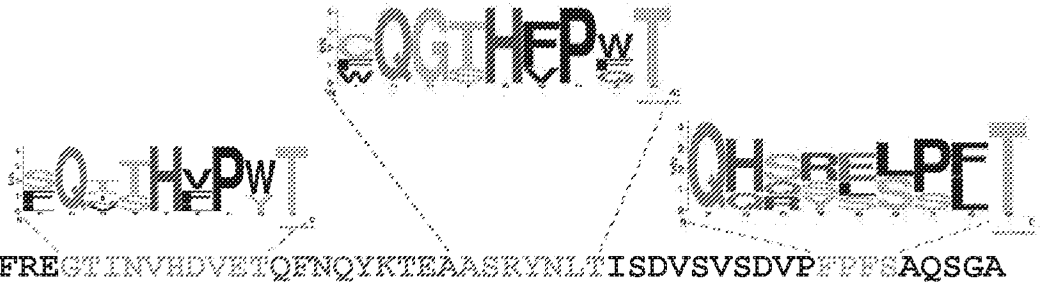


Figure 216A-216C

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<110>  MINERVA BIOTECHNOLOGIES CORPORATION

<120>  ANTI-VARIABLE MUC1* ANTIBODIES AND USES THEREOF

<130>  6977-5801

<140>  PCT/US2020/013410
<141>  2020-01-13

<160>  1790

<170>  PatentIn version 3.5

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<213>  Homo sapiens

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            20                  25                  30


Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
        35                  40                  45


Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
    50                  55                  60


Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
65                  70                  75                  80


Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
                85                  90                  95


Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
            100                 105                 110


Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro
        115                 120                 125


Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
    130                 135                 140


Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
145                 150                 155                 160


Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
                165                 170                 175


Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
            180                 185                 190
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Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
        195                 200                 205

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
    210                 215                 220

Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
225                 230                 235                 240

Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
                245                 250                 255

Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
            260                 265                 270

Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
        275                 280                 285

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
    290                 295                 300

Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
305                 310                 315                 320

Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
                325                 330                 335

Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
            340                 345                 350

Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
        355                 360                 365

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
    370                 375                 380

Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
385                 390                 395                 400

Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
                405                 410                 415

Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
            420                 425                 430

Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
        435                 440                 445

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
    450                 455                 460
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Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
465                 470                 475                 480

Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
                485                 490                 495

Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
            500                 505                 510

Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
        515                 520                 525

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
    530                 535                 540

Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
545                 550                 555                 560

Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
                565                 570                 575

Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
            580                 585                 590

Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
        595                 600                 605

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
    610                 615                 620

Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
625                 630                 635                 640

Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
                645                 650                 655

Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
            660                 665                 670

Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
        675                 680                 685

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
    690                 695                 700

Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
705                 710                 715                 720

Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
                725                 730                 735
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Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
            740   745   750

Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
        755   760   765

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
    770   775   780

Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
785   790   795   800

Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
                805   810   815

Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
            820   825   830

Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
        835   840   845

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
    850   855   860

Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
865   870   875   880

Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
                885   890   895

Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
            900   905   910

Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
        915   920   925

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Asn
    930   935   940

Arg Pro Ala Leu Gly Ser Thr Ala Pro Pro Val His Asn Val Thr Ser
945   950   955   960

Ala Ser Gly Ser Ala Ser Gly Ser Ala Ser Thr Leu Val His Asn Gly
                965   970   975

Thr Ser Ala Arg Ala Thr Thr Thr Pro Ala Ser Lys Ser Thr Pro Phe
            980   985   990

Ser Ile Pro Ser His His Ser Asp Thr Pro Thr Thr Leu Ala Ser His
        995   1000   1005

Ser Thr Lys Thr Asp Ala Ser Ser Thr His His Ser Ser Val Pro

1010 1015 1020

Pro Leu Thr Ser Ser Asn His Ser Thr Ser Pro Gln Leu Ser Thr
1025 1030 1035

Gly Val Ser Phe Phe Phe Leu Ser Phe His Ile Ser Asn Leu Gln
1040 1045 1050

Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln Glu
1055 1060 1065

Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln
1070 1075 1080

Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser
1085 1090 1095

Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn
1100 1105 1110

Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala
1115 1120 1125

Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp
1130 1135 1140

Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly Val Pro Gly
1145 1150 1155

Trp Gly Ile Ala Leu Leu Val Leu Val Cys Val Leu Val Ala Leu
1160 1165 1170

Ala Ile Val Tyr Leu Ile Ala Leu Ala Val Cys Gln Cys Arg Arg
1175 1180 1185

Lys Asn Tyr Gly Gln Leu Asp Ile Phe Pro Ala Arg Asp Thr Tyr
1190 1195 1200

His Pro Met Ser Glu Tyr Pro Thr Tyr His Thr His Gly Arg Tyr
1205 1210 1215

Val Pro Pro Ser Ser Thr Asp Arg Ser Pro Tyr Glu Lys Val Ser
1220 1225 1230

Ala Gly Asn Gly Gly Ser Ser Leu Ser Tyr Thr Asn Pro Ala Val
1235 1240 1245

Ala Ala Ala Ser Ala Asn Leu
1250 1255

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Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val
            20                  25                  30


Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala
        35                  40                  45


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<220>
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<400>  3

Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr
1               5                   10                  15


Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln
            20                  25                  30


Ser Gly Ala
        35


<210>  4
<211>  26
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-19 peptide

<400>  4

Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val
1               5                   10                  15


Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala
            20                  25


<210>  5
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<220>
<223>  N-23 peptide

<400>  5
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Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe
1               5                   10                  15


Ser Ala Gln Ser Gly Ala
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<212>  PRT
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Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln
1               5                   10                  15


Ser Gly Ala



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<400>  7

Ser Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala
1               5                   10                  15


<210>  8
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<220>
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1               5                   10                  15


Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser
            20                  25                  30


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1               5                   10                  15


Pro Phe Pro Phe Ser
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<210>  12
<211>  366
<212>  DNA
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<220>
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tcctgtgtag tctctggatt cactttcagt agatatggca tgtcttgggt tcgccagact      120

ccaggcaaga ggctggagtg ggtcgcaacc attagtggtg gcggtactta catctactat      180

ccagacagtg tgaaggggcg attcaccatc tccagagaca atgccaagaa caccctgtac      240

ctgcaaatga gcagtctgaa gtctgaggac acagccatgt atcactgtac aagggataac      300

tacggtagga actacgacta cggtatggac tactggggtc aaggaacctc agtcaccgtc      360

tcctca                                                                 366


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<400>  13

Glu Val Lys Val Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Lys Leu Ser Cys Val Val Ser Gly Phe Thr Phe Ser Arg Tyr
            20                  25                  30
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Gly Met Ser Trp Val Arg Gln Thr Pro Gly Lys Arg Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Gly Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr His Cys
85 90 95

Thr Arg Asp Asn Tyr Gly Arg Asn Tyr Asp Tyr Gly Met Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Ser Val Thr Val Ser Ser
115 120

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tcctgtgtag tctct 75

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1 5 10 15

Ser Leu Lys Leu Ser Cys Val Val Ser Gly Phe Thr Phe Ser
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1 (CDR1) sequence

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<400> 17

Arg Tyr Gly Met Ser
1   5

<210> 18
<211> 42
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<210> 19
<211> 14
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<400> 19

Trp Val Arg Gln Thr Pro Gly Lys Arg Leu Glu Trp Val Ala
1   5   10

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       2 (CDR2) sequence

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<210> 21
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       2 (CDR2) sequence

<400> 21

Thr Ile Ser Gly Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val Lys
1   5   10   15

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Gly



<210>  22
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<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse E6 heavy chain variable framework region 3 (FWR3) acid
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aagtctgagg acacagccat gtatcactgt acaagg                                 96


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Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln
1               5                   10                  15


Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr His Cys Thr Arg
            20                  25                  30


<210>  24
<211>  39
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<220>
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<210>  25
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<213>  Artificial Sequence

<220>
<223>  Mouse E6 heavy chain variable complementarity determining regions
       3 (CDR3) sequence:

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1               5                   10


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<400>  26
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<210> 38
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       IGHV3-21*03

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tcctgtgcag cctctggatt caccttcagt aggtatggca tgagctgggt ccgccaggct 120

ccagggaaga ggctggagtg ggtctcaacc attagtggcg gaggcaccta catatactac 180

ccagactcag tgaagggccg attcaccatc tccagagaca acgccaagaa caccctgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtac cagagataac 300

tatggccgca actatgatta tggcatggat tattggggcc agggcaccct ggtgaccgtg 360

agcagc 366

<210> 39
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized E6 heavy chain variable region sequence from
IGHV3-21*03

<400> 39

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Arg Leu Glu Trp Val
35 40 45

Ser Thr Ile Ser Gly Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Asp Asn Tyr Gly Arg Asn Tyr Asp Tyr Gly Met Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 40
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized E6 heavy chain variable framework region 1 (FWR1) acid
sequence

<400> 40
gaggtgcagc tggtggagtc tgggggaggc ctggtcaagc ctggggggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt 90

<210> 41
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized E6 heavy chain variable framework region 1 (FWR1) acid sequence

<400> 41

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            20                  25                  30
```

<210> 42
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized E6 heavy chain variable complementarity determining regions 1 (CDR1) sequence

<400> 42

```
aggtatggca tgagc                                                        15
```

<210> 43
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized E6 heavy chain variable complementarity determining regions 1 (CDR1) sequence

<400> 43

```
Arg Tyr Gly Met Ser
1               5
```

<210> 44
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized E6 heavy chain variable framework region 2 (FWR2) acid sequence

<400> 44

```
tgggtccgcc aggctccagg gaagaggctg gagtgggtct ca                          42
```

<210> 45
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized E6 heavy chain variable framework region 2 (FWR2) acid

```
       sequence

<400>  45

Trp Val Arg Gln Ala Pro Gly Lys Arg Leu Glu Trp Val Ser
1               5                   10


<210>  46
<211>  51
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized E6 heavy chain variable complementarity determining
       regions 2 (CDR2) sequence

<400>  46
accattagtg gcggaggcac ctacatatac tacccagact cagtgaaggg c                51


<210>  47
<211>  17
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized E6 heavy chain variable complementarity determining
       regions 2 (CDR2) sequence

<400>  47

Thr Ile Ser Gly Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val Lys
1               5                   10                  15


Gly



<210>  48
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized E6 heavy chain variable framework region 3 (FWR3) acid
       sequence

<400>  48
cgattcacca tctccagaga caacgccaag aacaccctgt atctgcaaat gaacagcctg       60

agagccgagg acacggctgt gtattactgt accaga                                 96


<210>  49
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized E6 heavy chain variable framework region 3 (FWR3) acid
       sequence

<400>  49

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln
1               5                   10                  15
```

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Arg
20 25 30

<210> 50
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized E6 heavy chain variable complementarity determining regions 3 (CDR3) sequence

<400> 50
gataactatg gccgcaacta tgattatggc atggattat 39

<210> 51
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized E6 heavy chain variable complementarity determining regions 3 (CDR3) sequence

<400> 51

Asp Asn Tyr Gly Arg Asn Tyr Asp Tyr Gly Met Asp Tyr
1 5 10

<210> 52
<211> 1442
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized E6 IgG2 heavy chain synthesized by Genescript

<400> 52
gaattctaag cttgggccac catggaactg gggctccgct gggttttcct tgttgctatt 60

ttagaaggtg tccagtgtga ggtgcagctg gtggagtctg gggggaggcct ggtcaagcct 120

ggggggtccc tgagactctc ctgtgcagcc tctggattca ccttcagtag gtatggcatg 180

agctgggtcc gccaggctcc agggaagagg ctggagtggg tctcaaccat tagtggcgga 240

ggcacctaca tatactaccc agactcagtg aagggccgat tcaccatctc cagagacaac 300

gccaagaaca ccctgtatct gcaaatgaac agcctgagag ccgaggacac ggctgtgtat 360

tactgtacca gagataacta tggccgcaac tatgattatg gcatggatta ttggggccag 420

ggcaccctgg tgaccgtgag cagcgcctcc accaagggcc catcggtctt ccccctggcg 480

ccctgctcca ggagcacctc cgagagcaca gccgccctgg gctgcctggt caaggactac 540

ttccccgaac cggtgacggt gtcgtggaac tcaggcgctc tgaccagcgg cgtgcacacc 600

ttcccagctg tcctacagtc ctcaggactc tactccctca gcagcgtggt gaccgtgccc 660

tccagcaact tcggcaccca gacctacacc tgcaacgtag atcacaagcc cagcaacacc 720

aaggtggaca agacagttga gcgcaaatgt tgtgtcgagt gcccaccgtg cccagcacca 780

cctgtggcag gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 840 tcccggaccc ctgaggtcac gtgcgtggtg gtggacgtga gccacgaaga ccccgaggtc 900

cagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccacgggag 960

gagcagttca acagcacgtt ccgtgtggtc agcgtcctca ccgttgtgca ccaggactgg 1020

ctgaacggca aggagtacaa gtgcaaggtc tccaacaaag gcctcccagc ccccatcgag 1080

aaaaccatct ccaaaaccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 1140

tcccgggagg agatgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctac 1200

cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1260

acacctccca tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac 1320

aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1380

aaccactaca cgcagaagag cctctccctg tctccgggta aatagtaagt ttaaactcta 1440

ga 1442

<210> 53
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized E6 IgG2 heavy chain synthesized by Genescript

<220>
<221> misc_feature
<222> (477)..(477)
<223> Xaa can be any naturally occurring amino acid

<400> 53

Glu Phe Ala Trp Ala Thr Met Glu Leu Gly Leu Arg Trp Val Phe Leu
1 5 10 15

Val Ala Ile Leu Glu Gly Val Gln Cys Glu Val Gln Leu Val Glu Ser
20 25 30

Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
35 40 45

Ala Ser Gly Phe Thr Phe Ser Arg Tyr Gly Met Ser Trp Val Arg Gln
50 55 60

Ala Pro Gly Lys Arg Leu Glu Trp Val Ser Thr Ile Ser Gly Gly Gly
65 70 75 80

Thr Tyr Ile Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
85 90 95

Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
100 105 110

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Arg Asp Asn Tyr Gly Arg

```
        115                 120                 125


Asn Tyr Asp Tyr Gly Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
    130                 135                 140


Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
145                 150                 155                 160


Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val
                165                 170                 175


Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
            180                 185                 190


Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
        195                 200                 205


Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly
    210                 215                 220


Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys
225                 230                 235                 240


Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys
                245                 250                 255


Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
            260                 265                 270


Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        275                 280                 285


Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
    290                 295                 300


Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
305                 310                 315                 320


Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His
                325                 330                 335


Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            340                 345                 350


Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
        355                 360                 365


Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
    370                 375                 380


Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
385                 390                 395                 400
```

```
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                405                 410                 415


Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
            420                 425                 430


Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        435                 440                 445


Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    450                 455                 460


Lys Ser Leu Ser Leu Ser Pro Gly Lys Val Thr Leu Xaa
465                 470                 475
```

<210> 54
<211> 981
<212> DNA
<213> Artificial Sequence

<220>
<223> Human IgG2 heavy chain constant region sequence

<400> 54

```
gcctccacca agggcccatc ggtcttcccc ctggcgccct gctccaggag cacctccgag       60

agcacagccg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg      120

tggaactcag gcgctctgac cagcggcgtg cacaccttcc cagctgtcct acagtcctca      180

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcaacttcgg cacccagacc      240

tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagac agttgagcgc      300

aaatgttgtg tcgagtgccc accgtgccca gcaccacctg tggcaggacc gtcagtcttc      360

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacgtgc      420

gtggtggtgg acgtgagcca cgaagacccc gaggtccagt tcaactggta cgtggacggc      480

gtggaggtgc ataatgccaa gacaaagcca cgggaggagc agttcaacag cacgttccgt      540

gtggtcagcg tcctcaccgt tgtgcaccag gactggctga acggcaagga gtacaagtgc      600

aaggtctcca acaaaggcct cccagccccc atcgagaaaa ccatctccaa aaccaaaggg      660

cagccccgag aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac      720

caggtcagcc tgacctgcct ggtcaaaggc ttctacccca gcgacatcgc cgtggagtgg      780

gagagcaatg ggcagccgga gaacaactac aagaccacac ctcccatgct ggactccgac      840

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac      900

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc      960

tccctgtctc cgggtaaata g                                                981
```

<210> 55
<211> 326
<212> PRT

```
<213>  Artificial Sequence

<220>
<223>  Human IgG2 heavy chain constant region sequence

<400>  55

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1               5                   10                  15


Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30


Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45


Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60


Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
65                  70                  75                  80


Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95


Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
            100                 105                 110


Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
        115                 120                 125


Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
    130                 135                 140


Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
145                 150                 155                 160


Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
                165                 170                 175


Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
            180                 185                 190


Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
        195                 200                 205


Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
    210                 215                 220


Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
225                 230                 235                 240


Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
                245                 250                 255
```

```
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
            260                 265                 270


Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
        275                 280                 285


Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
    290                 295                 300


Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305                 310                 315                 320


Ser Leu Ser Pro Gly Lys
                325


<210>  56
<211>  1362
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized E6 IgG1 heavy chain sequence

<400>  56
gaggtgcagc tggtggagtc tgggggaggc ctggtcaagc ctgggggtc cctgagactc       60

tcctgtgcag cctctggatt caccttcagt aggtatggca tgagctgggt ccgccaggct      120

ccagggaaga ggctggagtg ggtctcaacc attagtggcg gaggcaccta catatactac      180

ccagactcag tgaagggccg attcaccatc tccagagaca acgccaagaa cccactgtat      240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtcc cagagataac      300

tatggccgca actatgatta tggcatggat tattggggcc agggcaccct ggtgaccgtg      360

agcagcgcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc      420

tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg      480

gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag      540

tcctcaggac tctactccct cagcagcgtg gtgacagtgc cctccagcag cttgggcacc      600

cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt      660

gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg      720

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg      780

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      840

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag      900

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      960

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc     1020

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg     1080

gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc     1140
```

```
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct     1200

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc     1260

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac     1320

tacacgcaga agagcctctc cctgtctccg ggtaaatgat aa                        1362
```

<210> 57
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized E6 IgG1 heavy chain sequence

<400> 57

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
            20                  25                  30


Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Arg Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Gly Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Pro Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Pro Arg Asp Asn Tyr Gly Arg Asn Tyr Asp Tyr Gly Met Asp Tyr Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
        115                 120                 125


Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
    130                 135                 140


Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145                 150                 155                 160


Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                165                 170                 175


Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180                 185                 190


Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
        195                 200                 205
```

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
    210   215   220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
225   230   235   240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                245   250   255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            260   265   270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        275   280   285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    290   295   300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305   310   315   320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                325   330   335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            340   345   350

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
        355   360   365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    370   375   380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385   390   395   400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                405   410   415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            420   425   430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        435   440   445

Ser Pro Gly Lys
    450

<210> 58
<211> 996
<212> DNA

<213> Artificial Sequence

<220>
<223> Human IgG1 heavy chain constant region sequence

<400> 58
gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg   60

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg   120

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca   180

ggactctact ccctcagcag cgtggtgaca gtgccctcca gcagcttggg cacccagacc   240

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc   300

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga   360

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct   420

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg   480

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac   540

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag   600

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc   660

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag   720

atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc   780

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg   840

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg   900

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg   960

cagaagagcc tctccctgtc tccgggtaaa tgataa   996

<210> 59
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG1 heavy chain constant region sequence

<400> 59

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1   5   10   15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20   25   30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35   40   45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50   55   60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65   70   75   80

```
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100                 105                 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
        115                 120                 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    130                 135                 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145                 150                 155                 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225                 230                 235                 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
        275                 280                 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    290                 295                 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305                 310                 315                 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330

<210>  60

<400>  60
```

```
000

<210>  61

<400>  61
000

<210>  62

<400>  62
000

<210>  63

<400>  63
000

<210>  64

<400>  64
000

<210>  65
<211>  318
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse E6 Light Chain variable region sequence

<400>  65
caaattgttc tcacccagtc tccagcaatc atgtctgcat ctccagggga ggaggtcacc       60

ctaacctgca gtgccacctc aagtgtaagt tacatacact ggttccagca gaggccaggc      120

acttctccca aactctggat ttatagcaca tccaacctgg cttctggagt ccctgttcgc      180

ttcagtggca gtggatatgg gacctcttac tctctcacaa tcagccgaat ggaggctgaa      240

gatgctgcca cttattactg ccagcaaagg agtagttccc cattcacgtt cggctcgggg      300

acaaagttgg aaataaaa                                                    318


<210>  66
<211>  106
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse E6 Light Chain variable region sequence

<400>  66

Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
1               5                   10                  15


Glu Glu Val Thr Leu Thr Cys Ser Ala Thr Ser Ser Val Ser Tyr Ile
            20                  25                  30


His Trp Phe Gln Gln Arg Pro Gly Thr Ser Pro Lys Leu Trp Ile Tyr
        35                  40                  45


Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Val Arg Phe Ser Gly Ser
    50                  55                  60
```

Gly Tyr Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
65   70   75   80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Ser Pro Phe Thr
                85   90   95

Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 67
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse E6 light chain variable framework region 1 (FWR1) sequence

<400> 67
caaattgttc tcacccagtc tccagcaatc atgtctgcat ctccagggga ggaggtcacc   60

ctaacctgc   69

<210> 68
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse E6 light chain variable framework region 1 (FWR1) sequence

<400> 68

Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
1   5   10   15

Glu Glu Val Thr Leu Thr Cys
            20

<210> 69
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse E6 light chain variable complementarity determining regions
       1 (CDR1) sequence

<400> 69
agtgccacct caagtgtaag ttacatacac   30

<210> 70
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse E6 light chain variable complementarity determining regions
       1 (CDR1) sequence

<400> 70

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Ser Ala Thr Ser Ser Val Ser Tyr Ile His
1               5                   10


<210>  71
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse E6 light chain variable framework region 2 (FWR2) sequence

<400>  71
tggttccagc agaggccagg cacttctccc aaactctgga tttat                       45


<210>  72
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse E6 light chain variable framework region 2 (FWR2) sequence

<400>  72

Trp Phe Gln Gln Arg Pro Gly Thr Ser Pro Lys Leu Trp Ile Tyr
1               5                   10                  15


<210>  73
<211>  21
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse E6 light chain variable complementarity determining regions
       2 (CDR2) sequence

<400>  73
agcacatcca acctggcttc t                                                 21


<210>  74
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse E6 light chain variable complementarity determining regions
       2 (CDR2) sequence

<400>  74

Ser Thr Ser Asn Leu Ala Ser
1               5


<210>  75
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse E6 light chain variable framework region 3 (FWR3) sequence

<400>  75
ggagtccctg ttcgcttcag tggcagtgga tatgggacct cttactctct cacaatcagc       60
```

cgaatggagg ctgaagatgc tgccacttat tactgc 96

<210> 76
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse E6 light chain variable framework region 3 (FWR3) sequence

<400> 76

Gly Val Pro Val Arg Phe Ser Gly Ser Gly Tyr Gly Thr Ser Tyr Ser
1   5   10   15

Leu Thr Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
            20   25   30

<210> 77
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse E6 light chain variable complementarity determining regions
3 (CDR3) sequence

<400> 77
cagcaaagga gtagttcccc attcacg 27

<210> 78
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse E6 light chain variable complementarity determining regions
3 (CDR3) sequence

<400> 78

Gln Gln Arg Ser Ser Ser Pro Phe Thr
1   5

<210> 79

<400> 79
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<210> 80

<400> 80
000

<210> 81

<400> 81
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<210> 82

<400> 82
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<210> 83

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<210> 84

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<210> 85

<400> 85
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<210> 86

<400> 86
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<210> 87

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<210> 88

<400> 88
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<210> 89

<400> 89
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<210> 90

<400> 90
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<210> 91

<400> 91
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<210> 92

<400> 92
000

<210> 93
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized E6 light chain variable region sequence from
IGKV3-11*02

<400> 93
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctcacctgca gcgccaccag cagtgttagc tacatccact ggtaccaaca gaggcctggc 120

cagagcccca ggctcctcat ctatagcacc tccaacctgg ccagcggcat cccagccagg 180

ttcagtggca gtgggtctgg gagcgactac actctcacca tcagcagcct agagcctgaa 240

gattttgcag tttattactg tcagcagcgt agcagctccc ctttcacctt tggcagcggc 300 accaaagtgg aaattaaa 318

<210> 94
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized E6 light chain variable region sequence from
IGKV3-11*02

<400> 94

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Thr Cys Ser Ala Thr Ser Ser Val Ser Tyr Ile
20 25 30

His Trp Tyr Gln Gln Arg Pro Gly Gln Ser Pro Arg Leu Leu Ile Tyr
35 40 45

Ser Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Ser Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Ser Ser Pro Phe Thr
85 90 95

Phe Gly Ser Gly Thr Lys Val Glu Ile Lys
100 105

<210> 95
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized E6 light chain variable framework region 1 (FWR1) acid
sequence

<400> 95
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctcacctgc 69

<210> 96
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized E6 light chain variable framework region 1 (FWR1) acid
sequence

<400> 96

```
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15


Glu Arg Ala Thr Leu Thr Cys
            20


<210>  97
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized E6 light chain variable complementarity determining
       regions 1 (CDR1) sequence

<400>  97
agcgccacca gcagtgttag ctacatccac                                        30


<210>  98
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized E6 light chain variable complementarity determining
       regions 1 (CDR1) sequence

<400>  98

Ser Ala Thr Ser Ser Val Ser Tyr Ile His
1               5                   10


<210>  99
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized E6 heavy light variable framework region 2 (FWR2) acid
       sequence

<400>  99
tggtaccaac agaggcctgg ccagagcccc aggctcctca tctat                       45


<210>  100
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized E6 heavy light variable framework region 2 (FWR2) acid
       sequence

<400>  100

Trp Tyr Gln Gln Arg Pro Gly Gln Ser Pro Arg Leu Leu Ile Tyr
1               5                   10                  15


<210>  101
<211>  21
<212>  DNA
<213>  Artificial Sequence
```

<220>
<223> Humanized E6 light chain variable complementarity determining
      regions 2 (CDR2) sequence

<400> 101
agcacctcca acctggccag c   21

<210> 102
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized E6 light chain variable complementarity determining
      regions 2 (CDR2) sequence

<400> 102

Ser Thr Ser Asn Leu Ala Ser
1   5

<210> 103
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized E6 light chain variable framework region 3 (FWR3) acid
      sequence

<400> 103
ggcatcccag ccaggttcag tggcagtggg tctgggagcg actacactct caccatcagc   60

agcctagagc ctgaagattt tgcagtttat tactgt   96

<210> 104
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized E6 light chain variable framework region 3 (FWR3) acid
      sequence

<400> 104

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Tyr Thr
1   5   10   15

Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
            20   25   30

<210> 105
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized E6 light chain variable complementarity determining
      regions 3 (CDR3) sequence

<400> 105
cagcagcgta gcagctcccc tttcacc   27

<210> 106
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized E6 light chain variable complementarity determining
regions 3 (CDR3) sequence

<400> 106

Gln Gln Arg Ser Ser Ser Pro Phe Thr
1 5

<210> 107
<211> 740
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized E6 Kappa light chain synthesized by Genescript

<400> 107
gaattctaag cttgggccac catggaagcc ccagcgcagc ttctcttcct cctgctactc 60

tggctcccag ataccactgg agaaattgtg ttgacacagt ctccagccac cctgtctttg 120

tctccagggg aaagagccac cctcacctgc agcgccacca gcagtgttag ctacatccac 180

tggtaccaac agaggcctgg ccagagcccc aggctcctca tctatagcac ctccaacctg 240

gccagcggca tcccagccag gttcagtggc agtgggtctg ggagcgacta cactctcacc 300

atcagcagcc tagagcctga agattttgca gtttattact gtcagcagcg tagcagctcc 360

cctttcacct ttggcagcgg caccaaagtg gaaattaaaa ggacggtggc tgcaccatct 420

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 480

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 540

caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 600

ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 660

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 720

tagtaagttt aaactctaga 740

<210> 108
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized E6 Kappa light chain synthesized by Genescript

<220>
<221> misc_feature
<222> (243)..(243)
<223> Xaa can be any naturally occurring amino acid

<400> 108

Glu Phe Ala Trp Ala Thr Met Glu Ala Pro Ala Gln Leu Leu Phe Leu

1   5   10   15

Leu Leu Leu Trp Leu Pro Asp Thr Thr Gly Glu Ile Val Leu Thr Gln
            20   25   30

Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr
        35   40   45

Cys Ser Ala Thr Ser Ser Val Ser Tyr Ile His Trp Tyr Gln Gln Arg
    50   55   60

Pro Gly Gln Ser Pro Arg Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala
65   70   75   80

Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Tyr
                85   90   95

Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
            100   105   110

Cys Gln Gln Arg Ser Ser Ser Pro Phe Thr Phe Gly Ser Gly Thr Lys
        115   120   125

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    130   135   140

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
145   150   155   160

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                165   170   175

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            180   185   190

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        195   200   205

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    210   215   220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Val
225   230   235   240

Thr Leu Xaa

<210> 109
<211> 324
<212> DNA
<213> Artificial Sequence

<220>

<223> Human Kappa light chain constant region sequence

<400> 109
aggacggtgg ctgcaccatc tgtcttcatc ttcccgccat ctgatgagca gttgaaatct   60

ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag   120

tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac   180

agcaaggaca gcacctacag cctcagcagc accctgacgc tgagcaaagc agactacgag   240

aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag   300

agcttcaaca ggggagagtg ttag   324

<210> 110
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Human Kappa light chain constant region sequence

<400> 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1   5   10   15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
            20   25   30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
        35   40   45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
    50   55   60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65   70   75   80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
                85   90   95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
            100   105

<210> 111
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized E6 lambda light chain sequence

<400> 111
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc   60

ctcacctgca gcgccaccag cagtgttagc tacatccact ggtaccaaca gaggcctggc   120

cagagcccca ggctcctcat ctatagcacc tccaacctgg ccagcggcat cccagccagg   180 ttcagtggca gtgggtctgg gagcgactac actctcacca tcagcagcct agagcctgaa 240

gattttgcag tttattactg tcagcagcgt agcagctccc ctttcacctt tggcagcggc 300

accaaagtgg aaattaaagg tcagcccaag gctgcccccct cggtcactct gttcccgccc 360

tcctctgagg agcttcaagc caacaaggcc acactggtgt gtctcataag tgacttctac 420

ccgggagccg tgacagtggc ctggaaggca gatagcagcc ccgtcaaggc gggagtggag 480

accaccacac cctccaaaca aagcaacaac aagtacgcgg ccagcagcta tctgagcctg 540

acgcctgagc agtggaagtc ccacagaagc tacagctgcc aggtcacgca tgaagggagc 600

accgtggaga agacagtggc ccctacagaa tgttcatagt aa 642

<210> 112
<211> 212
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized E6 lambda light chain sequence

<400> 112

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Thr Cys Ser Ala Thr Ser Ser Val Ser Tyr Ile
20 25 30

His Trp Tyr Gln Gln Arg Pro Gly Gln Ser Pro Arg Leu Leu Ile Tyr
35 40 45

Ser Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Ser Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Ser Ser Pro Phe Thr
85 90 95

Phe Gly Ser Gly Thr Lys Val Glu Ile Lys Gly Gln Pro Lys Ala Ala
100 105 110

Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn
115 120 125

Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val
130 135 140

Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu
145 150 155 160

Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser
165 170 175

```
Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser
            180                 185                 190


Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro
        195                 200                 205


Thr Glu Cys Ser
    210


<210>  113
<211>  324
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized lambda light chain constant region sequence

<400>  113
ggtcagccca aggctgcccc ctcggtcact ctgttcccgc cctcctctga ggagcttcaa       60

gccaacaagg ccacactggt gtgtctcata agtgacttct acccgggagc cgtgacagtg      120

gcctggaagg cagatagcag ccccgtcaag gcgggagtgg agaccaccac accctccaaa      180

caaagcaaca acaagtacgc ggccagcagc tatctgagcc tgacgcctga gcagtggaag      240

tcccacagaa gctacagctg ccaggtcacg catgaaggga gcaccgtgga gaagacagtg      300

gcccctacag aatgttcata gtaa                                             324


<210>  114
<211>  106
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized lambda light chain constant region sequence

<400>  114

Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
1               5                   10                  15


Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
            20                  25                  30


Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
        35                  40                  45


Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
    50                  55                  60


Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
65                  70                  75                  80


Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
                85                  90                  95
```

```
Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
            100                 105


<210>  115

<400>  115
000

<210>  116

<400>  116
000

<210>  117

<400>  117
000

<210>  118
<211>  390
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse C2 heavy chain variable region sequence

<400>  118
gaggtccagc tggaggagtc agggggaggc ttagtgaagc ctggagggtc cctgaaactc       60

tcctgtgcag cctctggatt cactttcagt ggctatgcca tgtcttgggt tcgccagact      120

ccggagaaga ggctggagtg ggtcgcaacc attagtagtg gtggtactta tatctactat      180

ccagacagtg tgaaggggcg attcaccatc tccagagaca atgccaagaa caccctgtac      240

ctgcaaatga gcagtctgag gtctgaggac acggccatgt attactgtgc aagacttggg      300

ggggataatt actacgaata cttcgatgtc tggggcgcag ggaccacggt caccgtctcc      360

tccgccaaaa cgacaccccc atctgtctat                                       390


<210>  119
<211>  130
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse C2 heavy chain variable region sequence

<400>  119

Glu Val Gln Leu Glu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
        35                  40                  45


Ala Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val
    50                  55                  60
```

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
                85   90   95

Ala Arg Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr Phe Asp Val Trp Gly
            100   105   110

Ala Gly Thr Thr Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser
        115   120   125

Val Tyr
    130

<210> 120
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse C2 heavy chain variable framework region 1 (FWR1) sequence

<400> 120
gaggtccagc tggaggagtc agggggaggc ttagtgaagc ctggagggtc cctgaaactc   60

tcctgtgcag cctctggatt cactttcagt   90

<210> 121
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse C2 heavy chain variable framework region 1 (FWR1) sequence

<400> 121

Glu Val Gln Leu Glu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1   5   10   15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            20   25   30

<210> 122
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse C2 heavy chain variable complementarity determining regions
       1 (CDR1) sequence

<400> 122
ggctatgcca tgtct   15

<210> 123
<211> 5
<212> PRT

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<213>  Artificial Sequence

<220>
<223>  Mouse C2 heavy chain variable complementarity determining regions
       1 (CDR1) sequence

<400>  123

Gly Tyr Ala Met Ser
1               5


<210>  124
<211>  42
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse C2 heavy chain variable framework region 2 (FWR2) sequence

<400>  124
tgggttcgcc agactccgga gaagaggctg gagtgggtcg ca                          42


<210>  125
<211>  14
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse C2 heavy chain variable framework region 2 (FWR2) sequence

<400>  125

Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val Ala
1               5                   10


<210>  126
<211>  51
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse C2 heavy chain variable complementarity determining regions
       2 (CDR2) sequence

<400>  126
accattagta gtggtggtac ttatatctac tatccagaca gtgtgaaggg g                51


<210>  127
<211>  17
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse C2 heavy chain variable complementarity determining regions
       2 (CDR2) sequence

<400>  127

Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val Lys
1               5                   10                  15


Gly
```

<210> 128
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse C2 heavy chain variable framework region 3 (FWR3) sequence

<400> 128
cgattcacca tctccagaga caatgccaag aacaccctgt acctgcaaat gagcagtctg   60

aggtctgagg acacggccat gtattactgt gcaaga   96

<210> 129
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse C2 heavy chain variable framework region 3 (FWR3) sequence

<400> 129

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln
1   5   10   15

Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys Ala Arg
            20   25   30

<210> 130
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse C2 heavy chain variable complementarity determining regions
       3 (CDR3) sequence

<400> 130
cttggggggg ataattacta cgaatacttc gatgtc   36

<210> 131
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse C2 heavy chain variable complementarity determining regions
       3 (CDR3) sequence

<400> 131

Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr Phe Asp Val
1   5   10

<210> 132

<400> 132
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<210> 133

<400> 133

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000

<210>  134

<400>  134
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<210>  135

<400>  135
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<210>  136

<400>  136
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<210>  137

<400>  137
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<210>  138

<400>  138
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<210>  139

<400>  139
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<210>  140

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<210>  141

<400>  141
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<210>  142

<400>  142
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<210>  143

<400>  143
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<210>  144
<211>  363
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized derived from IGHV3-21*04 - Humanized C2 heavy chain
       variable region sequence

<400>  144
gaggtgcagc tggtggagtc tgggggaggc ctggtcaagc ctgggggtc cctgagactc       60

tcctgtgcag cctctggatt caccttcagt ggctatgcca tgagctgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtctcaacc attagtagtg gcggaaccta catatactac      180

cccgactcag tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat      240
```

ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagacttggg   300

ggggataatt actacgaata cttcgatgtc tggggcaaag ggaccacggt caccgtctcc   360

tcc   363

<210> 145
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized C2 heavy chain variable region sequence

<400> 145

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
            20   25   30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr Phe Asp Val Trp Gly
            100   105   110

Lys Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 146
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized C2 heavy chain variable framework region 1 (FWR1)
       sequence

<400> 146
gaggtgcagc tggtggagtc tgggggaggc ctggtcaagc ctggggggtc cctgagactc   60

tcctgtgcag cctctggatt caccttcagt   90

<210> 147
<211> 30
<212> PRT
<213> Artificial Sequence

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<220>
<223>  Humanized C2 heavy chain variable framework region 1 (FWR1)
       sequence

<400>  147

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            20                  25                  30


<210>  148
<211>  15
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C2 heavy chain variable complementarity determining
       regions 1 (CDR1) sequence

<400>  148
ggctatgcca tgagc                                                        15


<210>  149
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C2 heavy chain variable complementarity determining
       regions 1 (CDR1) sequence

<400>  149

Gly Tyr Ala Met Ser
1               5


<210>  150
<211>  43
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C2 heavy chain variable framework region 2 (FWR2)
       sequence

<400>  150
tgggtccgcc aggctccagg gaaggggctg gagtgggtct caa                         43


<210>  151
<211>  14
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C2 heavy chain variable framework region 2 (FWR2)
       sequence

<400>  151

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
1               5                   10
```

```
<210>  152
<211>  51
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C2 heavy chain variable complementarity determining
       regions 2 (CDR2) sequence

<400>  152
accattagta gtggcggaac ctacatatac taccccgact cagtgaaggg c                51


<210>  153
<211>  17
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C2 heavy chain variable complementarity determining
       regions 2 (CDR2) sequence

<400>  153

Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val Lys
1               5                   10                  15


Gly



<210>  154
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C2 heavy chain variable framework region 3 (FWR3)
       sequence

<400>  154
cgattcacca tctccagaga caacgccaag aactcactgt atctgcaaat gaacagcctg       60

agagccgagg acacggccgt gtattactgt gcgaga                                 96


<210>  155
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C2 heavy chain variable framework region 3 (FWR3)
       sequence

<400>  155

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
1               5                   10                  15


Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
            20                  25                  30


<210>  156
```

```
<211>  36
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C2 heavy chain variable complementarity determining
       regions 3 (CDR3) sequence

<400>  156
cttggggggg ataattacta cgaatacttc gatgtc                                 36


<210>  157
<211>  12
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C2 heavy chain variable complementarity determining
       regions 3 (CDR3) sequence

<400>  157

Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr Phe Asp Val
1               5                   10


<210>  158
<211>  451
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C2 IgG1 heavy chain sequence

<400>  158

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr Phe Asp Val Trp Gly
            100                 105                 110


Lys Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125
```

```
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
```

405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 159

<400> 159
000

<210> 160

<400> 160
000

<210> 161

<400> 161
000

<210> 162

<400> 162
000

<210> 163
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized C2 IgG2 heavy chain sequence

<400> 163
gaggtgcagc tggtggagtc tgggggaggc ctggtcaagc ctggggggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt ggctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcaacc attagtagtg gcggaaccta catatactac 180

cccgactcag tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagacttggg 300

ggggataatt actacgaata cttcgatgtc tggggcaaag ggaccacggt caccgtctcc 360

tccgcctcca ccaagggccc atcggtcttc cccctggcgc cctgctccag gagcacctcc 420

gagagcacag ccgccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgctct gaccagcggc gtgcacacct tcccagctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcaactt cggcacccag 600

acctacacct gcaacgtaga tcacaagccc agcaacacca aggtggacaa gacagttgag 660

cgcaaatgtt gtgtcgagtg cccaccgtgc ccagcaccac ctgtggcagg accgtcagtc 720

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcacg 780 tgcgtggtgg tggacgtgag ccacgaagac cccgaggtcc agttcaactg gtacgtggac   840

ggcgtggagg tgcataatgc caagacaaag ccacgggagg agcagttcaa cagcacgttc   900

cgtgtggtca gcgtcctcac cgttgtgcac caggactggc tgaacggcaa ggagtacaag   960

tgcaaggtct ccaacaaagg cctcccagcc cccatcgaga aaaccatctc caaaaccaaa   1020

gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag   1080

aaccaggtca gcctgacctg cctggtcaaa ggcttctacc ccagcgacat cgccgtggag   1140

tgggagagca atgggcagcc ggagaacaac tacaagacca cacctcccat gctggactcc   1200

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg   1260

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc   1320

ctctccctgt ctccgggtaa atagtaa   1347

<210> 164
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized C2 IgG2 heavy chain sequence

<400> 164

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr Phe Asp Val Trp Gly
            100                 105                 110


Lys Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125


Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
    130                 135                 140


Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
```

```
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys
    210                 215                 220

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
            260                 265                 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
                325                 330                 335

Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
385                 390                 395                 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430
```

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435   440   445

<210> 165

<400> 165
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<210> 166

<400> 166
000

<210> 167

<400> 167
000

<210> 168
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse C2 light chain variable region sequence

<400> 168
gacattgtga tcacacagtc tacagcttcc ttaggtgtat ctctggggca gagggccacc   60

atctcatgca gggccagcaa aagtgtcagt acatctggct atagttatat gcactggtac   120

caacagagac caggacagcc acccaaactc ctcatctatc ttgcatccaa cctagaatct   180

ggggtccctg ccaggttcag tggcagtggg tctgggacag acttcaccct caacatccat   240

cctgtggagg aggaggatgc tgcaacctat tactgtcagc acagtaggga gcttccgttc   300

acgttcggag gggggaccaa gctggagata aaacgggctg atgctgcacc aactgtatcc   360

<210> 169
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse C2 light chain variable region sequence

<400> 169

Asp Ile Val Ile Thr Gln Ser Thr Ala Ser Leu Gly Val Ser Leu Gly
1   5   10   15

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30

Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Arg Pro Gly Gln Pro Pro
        35   40   45

Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
    50   55   60

```
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80


Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg
                85                  90                  95


Glu Leu Pro Phe Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105                 110


Ala Asp Ala Ala Pro Thr Val Ser
        115                 120


<210>  170
<211>  69
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse C2 light chain variable framework region 1 (FWR1) sequence

<400>  170
gacattgtga tcacacagtc tacagcttcc ttaggtgtat ctctggggca gagggccacc       60

atctcatgc                                                               69


<210>  171
<211>  23
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse C2 light chain variable framework region 1 (FWR1) sequence

<400>  171

Asp Ile Val Ile Thr Gln Ser Thr Ala Ser Leu Gly Val Ser Leu Gly
1               5                   10                  15


Gln Arg Ala Thr Ile Ser Cys
            20


<210>  172
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse C2 light chain variable complementarity determining regions
       1 (CDR1) sequence

<400>  172
agggccagca aaagtgtcag tacatctggc tatagttata tgcac                       45


<210>  173
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse C2 light chain variable complementarity determining regions
       1 (CDR1) sequence
```

<400> 173

Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr Met His
1   5   10   15

<210> 174
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse C2 light chain variable framework region 2 (FWR2) sequence

<400> 174
tggtaccaac agagaccagg acagccaccc aaactcctca tctat   45

<210> 175
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse C2 light chain variable framework region 2 (FWR2) sequence

<400> 175

Trp Tyr Gln Gln Arg Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
1   5   10   15

<210> 176
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse C2 light chain variable complementarity determining regions
       2 (CDR2) sequence

<400> 176
cttgcatcca acctagaatc   20

<210> 177
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse C2 light chain variable complementarity determining regions
       2 (CDR2) sequence

<400> 177

Leu Ala Ser Asn Leu Glu Ser
1   5

<210> 178
<211> 97
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse C2 light chain variable framework region 3 (FWR3) sequence

```
<400>  178
tggggtccct gccaggttca gtggcagtgg gtctgggaca gacttcaccc tcaacatcca       60

tcctgtggag gaggaggatg ctgcaaccta ttactgt                                97


<210>  179
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse C2 light chain variable framework region 3 (FWR3) sequence

<400>  179

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1               5                   10                  15


Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys
            20                  25                  30


<210>  180
<211>  27
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse C2 light chain variable complementarity determining regions
       3 (CDR3) sequence

<400>  180
cagcacagta gggagcttcc gttcacg                                           27


<210>  181
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse C2 light chain variable complementarity determining regions
       3 (CDR3) sequence

<400>  181

Gln His Ser Arg Glu Leu Pro Phe Thr
1               5


<210>  182

<400>  182
000

<210>  183

<400>  183
000

<210>  184

<400>  184
000

<210>  185
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<400> 185
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<210> 186

<400> 186
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<210> 187

<400> 187
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<210> 188

<400> 188
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<210> 189

<400> 189
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<210> 190

<400> 190
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<210> 191

<400> 191
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<210> 192

<400> 192
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<210> 193

<400> 193
000

<210> 194
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized derived from IGKV73*01 - Humanized C2 light chain
       variable region sequence

<400> 194
```
gacattgtgc tgacccagtc tccagcctcc ttggccgtgt ctccaggaca gagggccacc       60

atcacctgca gagccagtaa gagtgtcagt accagcggat actcctacat gcactggtat      120

cagcagaaac caggacaacc tcctaaactc ctgatttacc tggcatccaa tctggagagc      180

ggggtcccag ccaggttcag cggcagtggg tctgggaccg atttcaccct cacaattaat      240

cctgtggaag ctaatgatac tgcaaattat tactgtcagc acagtaggga gctgcctttc      300

acattcggcg gagggaccaa ggtggagatc aaacgaact                             339
```

<210> 195
<211> 113
<212> PRT

<213> Artificial Sequence

<220>
<223> Humanized derived from IGKV73*01 - Humanized C2 light chain
variable region sequence

<400> 195

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Pro Gly
1   5   10   15

Gln Arg Ala Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30

Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45

Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
    50   55   60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn
65   70   75   80

Pro Val Glu Ala Asn Asp Thr Ala Asn Tyr Tyr Cys Gln His Ser Arg
                85   90   95

Glu Leu Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
            100   105   110

Thr

<210> 196
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized C2 light chain variable framework region 1 (FWR1) acid
sequence

<400> 196
gacattgtgc tgacccagtc tccagcctcc ttggccgtgt ctccaggaca gagggccacc   60

atcacctgc   69

<210> 197
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized C2 light chain variable framework region 1 (FWR1) acid
sequence

<400> 197

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Pro Gly
1   5   10   15

```
Gln Arg Ala Thr Ile Thr Cys
            20


<210>  198
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C2 light chain variable complementarity determining
       regions 1 (CDR1) sequence

<400>  198
agagccagta agagtgtcag taccagcgga tactcctaca tgcac                       45


<210>  199
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C2 light chain variable complementarity determining
       regions 1 (CDR1) sequence

<400>  199

Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr Met His
1               5                   10                  15


<210>  200
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C2 heavy light variable framework region 2 (FWR2) acid
       sequence

<400>  200
tggtatcagc agaaaccagg acaacctcct aaactcctga tttac                       45


<210>  201
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C2 heavy light variable framework region 2 (FWR2) acid
       sequence

<400>  201

Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
1               5                   10                  15


<210>  202
<211>  21
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C2 light chain variable complementarity determining
       regions 2 (CDR2) sequence
```

```
<400>  202
ctggcatcca atctggagag c                                                21


<210>  203
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C2 light chain variable complementarity determining
       regions 2 (CDR2) sequence

<400>  203

Leu Ala Ser Asn Leu Glu Ser
1               5


<210>  204
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C2 light chain variable framework region 3 (FWR3) acid
       sequence

<400>  204
ggggtcccag ccaggttcag cggcagtggg tctgggaccg atttcaccct cacaattaat      60

cctgtggaag ctaatgatac tgcaaattat tactgt                                96


<210>  205
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C2 light chain variable framework region 3 (FWR3) acid
       sequence

<400>  205

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1               5                   10                  15


Leu Thr Ile Asn Pro Val Glu Ala Asn Asp Thr Ala Asn Tyr Tyr Cys
            20                  25                  30


<210>  206
<211>  27
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C2 light chain variable complementarity determining
       regions 3 (CDR3) sequence

<400>  206
cagcacagta gggagctgcc tttcaca                                          27


<210>  207
<211>  9
```

<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized C2 light chain variable complementarity determining
regions 3 (CDR3) sequence

<400> 207

Gln His Ser Arg Glu Leu Pro Phe Thr
1   5

<210> 208
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized C2 light chain variable complementarity determining
regions 3 (CDR3) sequence

<400> 208
ctgcagagta agaattttcc tcccaca   27

<210> 209
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized C2 light chain variable complementarity determining
regions 3 (CDR3) sequence

<400> 209

Leu Gln Ser Lys Asn Phe Pro Pro Thr
1   5

<210> 210

<400> 210
000

<210> 211

<400> 211
000

<210> 212

<400> 212
000

<210> 213

<400> 213
000

<210> 214

<400> 214
000

<210> 215

<400> 215

```
000

<210>  216

<400>  216
000

<210>  217

<400>  217
000

<210>  218

<400>  218
000

<210>  219

<400>  219
000

<210>  220

<400>  220
000

<210>  221

<400>  221
000

<210>  222
<211>  63
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Murine Ig kappa chain leader sequence

<400>  222
atggagacag acacactcct gctatgggta ctgctgctct gggttccagg ttccactggt       60

gac                                                                     63


<210>  223
<211>  21
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Murine Ig kappa chain leader sequence

<400>  223

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1               5                   10                  15


Gly Ser Thr Gly Asp
            20


<210>  224
<211>  60
<212>  DNA
<213>  Artificial Sequence
```

<220>
<223> Interleukin2 (IL2) leader sequence

<400> 224
atgtacagga tgcaactcct gtcttgcatt gcactaagtc ttgcacttgt cacaaacagt   60

<210> 225
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Interleukin2 (IL2) leader sequence

<400> 225

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
1   5   10   15

Val Thr Asn Ser
            20

<210> 226
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> CD33 leader sequence

<400> 226
atgcctcttc tgcttctgct tcctctgctt tgggctggag ctcttgct   48

<210> 227
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33 leader sequence

<400> 227

Met Pro Leu Leu Leu Leu Leu Pro Leu Leu Trp Ala Gly Ala Leu Ala
1   5   10   15

<210> 228
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> IGHV321*03 leader sequence

<400> 228
atggaactgg ggctccgctg ggttttcctt gttgctattt tagaaggtgt ccagtgt   57

<210> 229
<211> 19
<212> PRT
<213> Artificial Sequence

<220>

<223> IGHV321*03 leader sequence

<400> 229

```
Met Glu Leu Gly Leu Arg Trp Val Phe Leu Val Ala Ile Leu Glu Gly
1               5                   10                  15


Val Gln Cys
```

<210> 230
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> IGHV311*02 leader sequence

<400> 230

```
atggaagccc cagcgcagct tctcttcctc ctgctactct ggctcccaga taccactgga       60
```

<210> 231
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> IGHV311*02 leader sequence

<400> 231

```
Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1               5                   10                  15


Asp Thr Thr Gly
            20
```

<210> 232
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized E6 single chain GS3

<400> 232

```
gaggtgcagc tggtggagtc tgggggaggc ctggtcaagc ctggggggtc cctgagactc       60

tcctgtgcag cctctggatt caccttcagt aggtatggca tgagctgggt ccgccaggct      120

ccagggaaga ggctggagtg ggtctcaacc attagtggcg gaggcaccta catatactac      180

ccagactcag tgaagggccg attcaccatc tccagagaca acgccaagaa caccctgtat      240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtac cagagataac      300

tatggccgca actatgatta tggcatggat tattggggcc agggcaccct ggtgaccgtg      360

agcagcggcg gtggcggatc cggcggtggc ggatccggcg gtggcggatc cgaaattgtg      420

ttgacacagt ctccagccac cctgtctttg tctccagggg aaagagccac cctcacctgc      480

agcgccacca gcagtgttag ctacatccac tggtaccaac agaggcctgg ccagagcccc      540
```

aggctcctca tctatagcac ctccaacctg gccagcggca tcccagccag gttcagtggc 600

agtgggtctg ggagcgacta cactctcacc atcagcagcc tagagcctga agattttgca 660

gtttattact gtcagcagcg tagcagctcc cctttcacct ttggcagcgg caccaaagtg 720

gaaattaaa 729

<210> 233
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized E6 single chain GS3

<400> 233

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Arg Leu Glu Trp Val
35 40 45

Ser Thr Ile Ser Gly Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Asp Asn Tyr Gly Arg Asn Tyr Asp Tyr Gly Met Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
145 150 155 160

Ser Ala Thr Ser Ser Val Ser Tyr Ile His Trp Tyr Gln Gln Arg Pro
165 170 175

Gly Gln Ser Pro Arg Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala Ser
180 185 190

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Tyr Thr
195 200 205

```
Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
    210                 215                 220


Gln Gln Arg Ser Ser Ser Pro Phe Thr Phe Gly Ser Gly Thr Lys Val
225                 230                 235                 240


Glu Ile Lys




<210>  234
<211>  747
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized E6 single chain IgG1noC

<400>  234
gaggtgcagc tggtggagtc tgggggaggc ctggtcaagc ctgggggtc cctgagactc       60

tcctgtgcag cctctggatt caccttcagt aggtatggca tgagctgggt ccgccaggct      120

ccagggaaga ggctggagtg ggtctcaacc attagtggcg gaggcaccta catatactac      180

ccagactcag tgaagggccg attcaccatc tccagagaca acgccaagaa caccctgtat      240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtac cagagataac      300

tatggccgca actatgatta tggcatggat tattggggcc agggcaccct ggtgaccgtg      360

agcagcgata aaacccatac taaaccgcca aaaccggcgc cggaactgct gggtggtcct      420

ggtaccggtg aaattgtgtt gacacagtct ccagccaccc tgtctttgtc tccaggggaa      480

agagccaccc tcacctgcag cgccaccagc agtgttagct acatccactg gtaccaacag      540

aggcctggcc agagccccag gctcctcatc tatagcacct ccaacctggc cagcggcatc      600

ccagccaggt tcagtggcag tgggtctggg agcgactaca ctctcaccat cagcagccta      660

gagcctgaag attttgcagt ttattactgt cagcagcgta gcagctcccc tttcaccttt      720

ggcagcggca ccaaagtgga aattaaa                                          747


<210>  235
<211>  249
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized E6 single chain IgG1noC

<400>  235

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
            20                  25                  30


Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Arg Leu Glu Trp Val
```

```
        35                  40                  45

Ser Thr Ile Ser Gly Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Thr Arg Asp Asn Tyr Gly Arg Asn Tyr Asp Tyr Gly Met Asp Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Asp Lys Thr His Thr Lys
        115                 120                 125

Pro Pro Lys Pro Ala Pro Glu Leu Leu Gly Gly Pro Gly Thr Gly Glu
    130                 135                 140

Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu
145                 150                 155                 160

Arg Ala Thr Leu Thr Cys Ser Ala Thr Ser Ser Val Ser Tyr Ile His
                165                 170                 175

Trp Tyr Gln Gln Arg Pro Gly Gln Ser Pro Arg Leu Leu Ile Tyr Ser
            180                 185                 190

Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly
        195                 200                 205

Ser Gly Ser Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp
    210                 215                 220

Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Ser Ser Pro Phe Thr Phe
225                 230                 235                 240

Gly Ser Gly Thr Lys Val Glu Ile Lys
                245


<210>  236
<211>  813
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized E6 single chain X4 (linker is IgG1 and IgG2 modified
       hinge region

<400>  236
gaggtgcagc tggtggagtc tgggggaggc ctggtcaagc ctggggggtc cctgagactc       60

tcctgtgcag cctctggatt caccttcagt aggtatggca tgagctgggt ccgccaggct      120
```

ccagggaaga ggctggagtg ggtctcaacc attagtggcg gaggcaccta catatactac 180

ccagactcag tgaagggccg attcaccatc tccagagaca acgccaagaa caccctgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtac cagagataac 300

tatggccgca actatgatta tggcatggat tattggggcc agggcaccct ggtgaccgtg 360

agcagcgata aaacccatac taaaccgcca aaaccggcgc cggaactgct gggtggtcct 420

ggtaccggta ctggtggtcc gactattaaa cctccgaaac ctccgaaacc tgctccgaac 480

ctgctgggtg gtccggaaat tgtgttgaca cagtctccag ccaccctgtc tttgtctcca 540

ggggaaagag ccaccctcac ctgcagcgcc accagcagtg ttagctacat ccactggtac 600

caacagaggc ctggccagag ccccaggctc ctcatctata gcacctccaa cctggccagc 660

ggcatcccag ccaggttcag tggcagtggg tctgggagcg actacactct caccatcagc 720

agcctagagc ctgaagattt tgcagtttat tactgtcagc agcgtagcag ctcccctttc 780

acctttggca gcggcaccaa agtggaaatt aaa 813

<210> 237
<211> 271
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized E6 single chain X4 (linker is IgG1 and IgG2 modified hinge region

<400> 237

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Arg Leu Glu Trp Val
35 40 45

Ser Thr Ile Ser Gly Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Asp Asn Tyr Gly Arg Asn Tyr Asp Tyr Gly Met Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Asp Lys Thr His Thr Lys
115 120 125

Pro Pro Lys Pro Ala Pro Glu Leu Leu Gly Gly Pro Gly Thr Gly Thr

130 135 140

Gly Gly Pro Thr Ile Lys Pro Pro Lys Pro Pro Lys Pro Ala Pro Asn
145 150 155 160

Leu Leu Gly Gly Pro Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu
165 170 175

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys Ser Ala Thr Ser
180 185 190

Ser Val Ser Tyr Ile His Trp Tyr Gln Gln Arg Pro Gly Gln Ser Pro
195 200 205

Arg Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala
210 215 220

Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Tyr Thr Leu Thr Ile Ser
225 230 235 240

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser
245 250 255

Ser Ser Pro Phe Thr Phe Gly Ser Gly Thr Lys Val Glu Ile Lys
260 265 270

<210> 238
<211> 747
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized C2 single chain GS3

<400> 238
gaggtgcagc tggtggagtc tgggggaggc ctggtcaagc ctggggggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt ggctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcaacc attagtagtg gcggaaccta catatactac 180

cccgactcag tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagacttggg 300

ggggataatt actacgaata cttcgatgtc tggggcaaag ggaccacggt caccgtctcc 360

tccggcggtg gcggatccgg cggtggcgga tccggcggtg gcggatccga cattgtgctg 420

acccagtctc cagcctcctt ggccgtgtct ccaggacaga gggccaccat cacctgcaga 480

gccagtaaga gtgtcagtac cagcggatac tcctacatgc actggtatca gcagaaacca 540

ggacaacctc ctaaactcct gatttacctg gcatccaatc tggagagcgg ggtcccagcc 600

aggttcagcg gcagtgggtc tgggaccgat ttcaccctca caattaatcc tgtggaagct 660

aatgatactg caaattatta ctgtcagcac agtagggagc tgcctttcac attcggcgga 720

gggaccaagg tggagatcaa acgaact 747

```
<210>  239
<211>  249
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C2 single chain GS3

<400>  239

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr Phe Asp Val Trp Gly
            100                 105                 110


Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125


Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro
    130                 135                 140


Ala Ser Leu Ala Val Ser Pro Gly Gln Arg Ala Thr Ile Thr Cys Arg
145                 150                 155                 160


Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr Met His Trp Tyr
                165                 170                 175


Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser
            180                 185                 190


Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205


Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asn Asp Thr Ala
    210                 215                 220


Asn Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Phe Thr Phe Gly Gly
```

225   230   235   240

Gly Thr Lys Val Glu Ile Lys Arg Thr
                245

<210> 240

<400> 240
000

<210> 241

<400> 241
000

<210> 242
<211> 831
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized C2 single chain X4 (linker is IgG1 and IgG2 modified
       hinge region

<400> 242
gaggtgcagc tggtggagtc tgggggaggc ctggtcaagc ctgggggtc cctgagactc   60

tcctgtgcag cctctggatt caccttcagt ggctatgcca tgagctgggt ccgccaggct   120

ccagggaagg ggctggagtg ggtctcaacc attagtagtg gcggaaccta catatactac   180

cccgactcag tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat   240

ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagacttggg   300

ggggataatt actacgaata cttcgatgtc tggggcaaag ggaccacggt caccgtctcc   360

tccgataaaa cccatactaa accgccaaaa ccggcgccgg aactgctggg tggtcctggt   420

accggtactg gtggtccgac tattaaacct ccgaaacctc cgaaacctgc tccgaacctg   480

ctgggtggtc cggacattgt gctgacccag tctccagcct ccttggccgt gtctccagga   540

cagagggcca ccatcacctg cagagccagt aagagtgtca gtaccagcgg atactcctac   600

atgcactggt atcagcagaa accaggacaa cctcctaaac tcctgattta cctggcatcc   660

aatctggaga gcggggtccc agccaggttc agcggcagtg ggtctgggac cgatttcacc   720

ctcacaatta atcctgtgga agctaatgat actgcaaatt attactgtca gcacagtagg   780

gagctgcctt tcacattcgg cggagggacc aaggtggaga tcaaacgaac t   831

<210> 243
<211> 277
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized C2 single chain X4 (linker is IgG1 and IgG2 modified
       hinge region

<400> 243

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1   5   10   15

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr Phe Asp Val Trp Gly
            100                 105                 110

Lys Gly Thr Thr Val Thr Val Ser Ser Asp Lys Thr His Thr Lys Pro
        115                 120                 125

Pro Lys Pro Ala Pro Glu Leu Leu Gly Gly Pro Gly Thr Gly Thr Gly
    130                 135                 140

Gly Pro Thr Ile Lys Pro Pro Lys Pro Pro Lys Pro Ala Pro Asn Leu
145                 150                 155                 160

Leu Gly Gly Pro Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
                165                 170                 175

Val Ser Pro Gly Gln Arg Ala Thr Ile Thr Cys Arg Ala Ser Lys Ser
            180                 185                 190

Val Ser Thr Ser Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro
        195                 200                 205

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser
    210                 215                 220

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
225                 230                 235                 240

Leu Thr Ile Asn Pro Val Glu Ala Asn Asp Thr Ala Asn Tyr Tyr Cys
                245                 250                 255

Gln His Ser Arg Glu Leu Pro Phe Thr Phe Gly Gly Gly Thr Lys Val
            260                 265                 270

Glu Ile Lys Arg Thr
        275
```

<210> 244
<211> 744
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized C3 single chain GS3

<400> 244
caggttcagc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc   60

tcctgcaagg cttctggtta cacctttacc gactacgcca tgaactgggt gcgacaggcc   120

cctggacaag ggcttgagtg gatgggagtg atcagcacct tcagcggtaa cacaaacttc   180

aaccagaagt tcaagggcag agtcaccatg accacagaca catccacgag cacagcctac   240

atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagaagcgac   300

tactacggcc catacttcga ctactggggc cagggcacca ccctgaccgt gtccagcggc   360

ggtggcggat ccggcggtgg cggatccggc ggtggcggat ccgatattgt gatgacccag   420

actccactct ctctgtccgt cacccctgga cagccggcct ccatctcctg caggtctagt   480

cagaccattg tccatagtaa tggaaacacc tatttggagt ggtacctgca gaagccaggc   540

cagtctccac agctcctgat ctataaggtt tccaaccggt tctctggagt gccagatagg   600

ttcagtggca gcgggtcagg gacagatttc acactgaaaa tcagccgggt ggaggctgag   660

gatgttgggg tttattactg cttccaaggt agccacgtgc ctttcacctt cggcggaggg   720

accaaggtgg agatcaaacg aact   744

<210> 245
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized C3 single chain GS3

<400> 245

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20   25   30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Val Ile Ser Thr Phe Ser Gly Asn Thr Asn Phe Asn Gln Lys Phe
    50   55   60

Lys Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Ser Asp Tyr Tyr Gly Pro Tyr Phe Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115   120   125

Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Thr Pro Leu Ser
    130   135   140

Leu Ser Val Thr Pro Gly Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser
145   150   155   160

Gln Thr Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu
                165   170   175

Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn
            180   185   190

Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195   200   205

Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val
    210   215   220

Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Phe Thr Phe Gly Gly Gly
225   230   235   240

Thr Lys Val Glu Ile Lys Arg Thr
                245

<210> 246

<400> 246
000

<210> 247

<400> 247
000

<210> 248
<211> 828
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized C3 single chain X4 (linker is IgG1 and IgG2 modified
hinge region

<400> 248
caggttcagc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggtta cacctttacc gactacgcca tgaactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggagtg atcagcacct tcagcggtaa cacaaacttc 180

aaccagaagt tcaagggcag agtcaccatg accacagaca catccacgag cacagcctac 240 atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagaagcgac   300

tactacggcc catacttcga ctactggggc cagggcacca ccctgaccgt gtccagcgat   360

aaaacccata ctaaaccgcc aaaaccggcg ccggaactgc tgggtggtcc tggtaccggt   420

actggtggtc cgactattaa acctccgaaa cctccgaaac ctgctccgaa cctgctgggt   480

ggtccggata ttgtgatgac ccagactcca ctctctctgt ccgtcacccc tggacagccg   540

gcctccatct cctgcaggtc tagtcagacc attgtccata gtaatggaaa cacctatttg   600

gagtggtacc tgcagaagcc aggccagtct ccacagctcc tgatctataa ggtttccaac   660

cggttctctg gagtgccaga taggttcagt ggcagcgggt cagggacaga tttcacactg   720

aaaatcagcc gggtggaggc tgaggatgtt ggggtttatt actgcttcca aggtagccac   780

gtgcctttca ccttcggcgg agggaccaag gtggagatca aacgaact   828

<210> 249
<211> 276
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized C3 single chain X4 (linker is IgG1 and IgG2 modified
       hinge region

<400> 249

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20   25   30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Val Ile Ser Thr Phe Ser Gly Asn Thr Asn Phe Asn Gln Lys Phe
    50   55   60

Lys Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Ser Asp Tyr Tyr Gly Pro Tyr Phe Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Thr Leu Thr Val Ser Ser Asp Lys Thr His Thr Lys Pro Pro Lys
        115   120   125

Pro Ala Pro Glu Leu Leu Gly Gly Pro Gly Thr Gly Thr Gly Gly Pro
    130   135   140

Thr Ile Lys Pro Pro Lys Pro Pro Lys Pro Ala Pro Asn Leu Leu Gly
145   150   155   160

Gly Pro Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr
                165   170   175

Pro Gly Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Thr Ile Val
            180   185   190

His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly
        195   200   205

Gln Ser Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly
    210   215   220

Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
225   230   235   240

Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe
                245   250   255

Gln Gly Ser His Val Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu
            260   265   270

Ile Lys Arg Thr
        275

<210> 250
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized C8 single chain GS3 (linker is [Gly4Ser1]3

<400> 250
gaggtgcagc tggtggagtc tgggggaggc ctggtcaagc ctggggggtc cctgagactc   60

tcctgtgcag cctctggatt caccttcagt ggctatgcca tgagctgggt ccgccaggct   120

ccagggaagg ggctggagtg ggtctcaacc attagtagtg gcggaaccta catatactac   180

cctgactcag tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat   240

ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagactgggc   300

ggcgataact attatgaata ttggggcaaa gggaccacgg tcaccgtctc ctccggcggt   360

ggcggatccg gcggtggcgg atccggcggt ggcggatccg acatcgtgat gacccagtct   420

ccagactccc tggctgtgtc tctgggcgag agggccacca tcaactgcag ggccagcaag   480

agtgttagca ccagcggcta cagctacatg cactggtacc agcagaaacc aggacagcct   540

cctaagctgc tcatttacct ggtgtctaac ctggaatccg gggtccctga ccgattcagt   600

ggcagcgggt ctgggacaga tttcactctc accatcagca gcctgcaggc tgaagatgtg   660

gcagtttatt actgtcaaca cattcgggaa ctgaccagga gtgaattcgg cggagggacc   720

```
aaggtggaga tcaaacgaac t                                                741


<210>  251
<211>  247
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C8 single chain GS3 (linker is [Gly4Ser1]3

<400>  251

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr Trp Gly Lys Gly Thr
            100                 105                 110


Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125


Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu
    130                 135                 140


Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Lys
145                 150                 155                 160


Ser Val Ser Thr Ser Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys
                165                 170                 175


Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Val Ser Asn Leu Glu
            180                 185                 190


Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205


Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr
    210                 215                 220
```

Cys Gln His Ile Arg Glu Leu Thr Arg Ser Glu Phe Gly Gly Gly Thr
225   230   235   240

Lys Val Glu Ile Lys Arg Thr
                245

<210> 252

<400> 252
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<210> 253

<400> 253
000

<210> 254

<400> 254
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<210> 255

<400> 255
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<210> 256
<211> 1509
<212> DNA
<213> Artificial Sequence

<220>
<223> pSECTag2 E6 scFVFC

<400> 256
atggagacag acacactcct gctatgggta ctgctgctct gggttccagg ttccactggt   60

gacgcggccc agccggccga ggtgcagctg gtggagtctg gggggaggcct ggtcaagcct   120

ggggggtccc tgagactctc ctgtgcagcc tctggattca ccttcagtag gtatggcatg   180

agctgggtcc gccaggctcc agggaagagg ctggagtggg tctcaaccat tagtggcgga   240

ggcacctaca tatactaccc agactcagtg aagggccgat tcaccatctc cagagacaac   300

gccaagaaca ccctgtatct gcaaatgaac agcctgagag ccgaggacac ggctgtgtat   360

tactgtacca gagataacta tggccgcaac tatgattatg gcatggatta ttggggccag   420

ggcaccctgg tgaccgtgag cagcggcggt ggcggatccg gcggtggcgg atccggcggt   480

ggcggatccg aaattgtgtt gacacagtct ccagccaccc tgtctttgtc tccaggggaa   540

agagccaccc tcacctgcag cgccaccagc agtgttagct acatccactg gtaccaacag   600

aggcctggcc agagccccag gctcctcatc tatagcacct ccaacctggc cagcggcatc   660

ccagccaggt tcagtggcag tgggtctggg agcgactaca ctctcaccat cagcagccta   720

gagcctgaag attttgcagt ttattactgt cagcagcgta gcagctcccc tttcaccttt   780

ggcagcggca ccaaagtgga aattaaagag cccaaatctt gtgacaaaac tcacacatgc   840

ccaccgtgcc cagcacctga actcctgggg ggaccgtcag tcttcctctt ccccccaaaa   900

cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg   960

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agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat     1020

gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc     1080

accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa     1140

gccctcccag cccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca     1200

caggtgtaca ccctgccccc atcccgggag gagatgacca agaaccaggt cagcctgacc     1260

tgcctggtca aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggcag     1320

ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc     1380

tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc     1440

gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt     1500

aaatgataa                                                             1509


<210>  257
<211>  501
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  pSECTag2 E6 scFVFC

<400>  257

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1               5                   10                  15


Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Glu Val Gln Leu Val Glu
            20                  25                  30


Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys
        35                  40                  45


Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr Gly Met Ser Trp Val Arg
    50                  55                  60


Gln Ala Pro Gly Lys Arg Leu Glu Trp Val Ser Thr Ile Ser Gly Gly
65                  70                  75                  80


Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile
                85                  90                  95


Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu
            100                 105                 110


Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Arg Asp Asn Tyr Gly
        115                 120                 125


Arg Asn Tyr Asp Tyr Gly Met Asp Tyr Trp Gly Gln Gly Thr Leu Val
    130                 135                 140


Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145                 150                 155                 160
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Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu
                165                 170                 175

Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys Ser Ala Thr Ser Ser Val
            180                 185                 190

Ser Tyr Ile His Trp Tyr Gln Gln Arg Pro Gly Gln Ser Pro Arg Leu
        195                 200                 205

Leu Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe
    210                 215                 220

Ser Gly Ser Gly Ser Gly Ser Asp Tyr Thr Leu Thr Ile Ser Ser Leu
225                 230                 235                 240

Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Ser Ser
                245                 250                 255

Pro Phe Thr Phe Gly Ser Gly Thr Lys Val Glu Ile Lys Glu Pro Lys
            260                 265                 270

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
        275                 280                 285

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
    290                 295                 300

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
305                 310                 315                 320

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
                325                 330                 335

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
            340                 345                 350

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
        355                 360                 365

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
    370                 375                 380

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
385                 390                 395                 400

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
                405                 410                 415

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
            420                 425                 430
```

```
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
        435                 440                 445


Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
    450                 455                 460


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
465                 470                 475                 480


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
                485                 490                 495


Leu Ser Pro Gly Lys
            500


<210>  258

<400>  258
000

<210>  259

<400>  259
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<210>  260

<400>  260
000

<210>  261

<400>  261
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<210>  262

<400>  262
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<210>  263

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<210>  264

<400>  264
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<210>  265

<400>  265
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<210>  266

<400>  266
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<210>  267

<400>  267
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000

<210> 268

<400> 268
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<210> 269

<400> 269
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<210> 270

<400> 270
000

<210> 271

<400> 271
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<210> 272
<211> 702
<212> DNA
<213> Artificial Sequence

<220>
<223> Human IgG1 Fc sequence

<400> 272
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg   60

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg   120

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc   180

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag   240

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat   300

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc   360

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg   420

gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc   480

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct   540

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc   600

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac   660

tacacgcaga agagcctctc cctgtctccg ggtaaatgat aa   702

<210> 273
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG1 Fc sequence

<400> 273

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1   5   10   15

```
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Lys
225                 230


<210>  274
<211>  666
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Human IgG1 CH2CH3 domain sequence

<400>  274
ccgtgcccag cacctgaact cctgggggga ccgtcagtct tcctcttccc cccaaaaccc       60

aaggacaccc tcatgatctc ccggacccct gaggtcacat gcgtggtggt ggacgtgagc      120
```

cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc 180

aagacaaagc cgcgggagga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc 240

gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaaggtctc caacaaagcc 300

ctcccagccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag 360

gtgtacaccc tgcccccatc ccgggaggag atgaccaaga accaggtcag cctgacctgc 420

ctggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg 480

gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac 540

agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg 600

atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggtaaa 660

tgataa 666

<210> 275
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG1 CH2CH3 domain sequence

<400> 275

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
1 5 10 15

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
20 25 30

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
35 40 45

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
50 55 60

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
65 70 75 80

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
85 90 95

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
100 105 110

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
115 120 125

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
130 135 140

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

```
145                 150                 155                 160


Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
                165                 170                 175


Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
            180                 185                 190


Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
        195                 200                 205


Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    210                 215                 220


<210>  276
<211>  327
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Human IgG1 CH3 domain sequence

<400>  276
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag       60

aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag      120

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc      180

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg      240

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc      300

ctctccctgt ctccgggtaa atgataa                                          327


<210>  277
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Human IgG1 CH3 domain sequence

<400>  277

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
1               5                   10                  15


Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
            20                  25                  30


Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
        35                  40                  45


Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
    50                  55                  60


Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65                  70                  75                  80
```

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 278

<400> 278
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<210> 279

<400> 279
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<210> 280

<400> 280
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<210> 281

<400> 281
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<210> 295

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<210> 296

<400> 296
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<210> 297
<211> 1464
<212> DNA
<213> Artificial Sequence

<220>
<223> CART E6 CD8/CD8/CD28/CD3z sequence - NCD8lshuMNE6scFvCD8ecd
fragment CD8 transmembrane CD28 CD3zetaC

<400> 297
atggccctgc ccgtgaccgc tttgctgctc cccctggcgc tgctgctgca cgccgccagg 60

ccagaggtcc agctggttga gagtggcggt gggctggtta agcctggcgg ctccctgcgg 120

ctgagctgcg ccgcgagtgg atttactttc agccgatatg ggatgagttg ggtgcggcaa 180

gctcccggga agaggctgga atgggtctca acaatctccg gggggggcac ttacatctat 240

taccccgact cagtcaaggg gagatttacc atttcacgag acaacgctaa gaataccctg 300

tatttgcaga tgaattctct gagagcagag gacacagctg tttactattg tacccgcgac 360

aactatggca ggaactacga ctacggtatg gactattggg gacaagggac attggttaca 420

gtgagcagtg gcggcggggg cagcggagga ggaggcagcg gtgggggggg cagcgagata 480

gtgctcacgc agtcacccgc gactctcagt ctctcacctg ggaacgagc taccctgacg 540

tgctctgcta cctcctcagt gtcatatatt cactggtatc agcaacggcc cgggcagtcc 600

cctagattgc tcatttatag tacctctaat ctggcctcag gtatccctgc acgattttct 660

ggatctggtt caggttctga ttacaccctc actatctcta gcctggagcc tgaagacttt 720 gccgtttatt actgccagca gaggtctagc tccccattca cctttgggag tgggaccaag   780

gttgaaatta aaacgacaac cccggccccc agaccaccaa cgccagcccc caccatcgcc   840

agccaacccc tgtctctgag accagaagcc tgtaggcctg ccgccggtgg agctgtgcac   900

acaagaggac tggatttcgc ctgtgatatc tacatttggg ccccgctcgc aggcacatgt   960

ggagtgctcc tcctctccct ggtgattacc ctgtactgca gaagcaagcg gtctcggctc   1020

ctgcattctg attacatgaa catgacccca agaagaccag gccccaccag gaaacattac   1080

cagccctacg ctccgccacg cgacttcgct gcctaccggt cccgcgttaa gttctcccga   1140

tcagccgacg cgcctgctta caagcagggc cagaaccaac tgtacaacga gctgaatctc   1200

ggtagacggg aagagtacga cgtgttggac aaacggagag gccgcgaccc agaaatgggc   1260

ggcaagcctc gcaggaaaaa cccccaggag ggactgtaca atgagttgca gaaagataag   1320

atggcagaag cttatagcga gatcggaatg aagggggaaa ggagacgagg gaaaggacac   1380

gacggccttt atcagggcct gtccacagca acaaaagata cgtatgacgc cctccatatg   1440

caggcacttc caccacggtg ataa   1464

<210> 298
<211> 486
<212> PRT
<213> Artificial Sequence

<220>
<223> CART E6 CD8/CD8/CD28/CD3z sequence - NCD8lshuMNE6scFvCD8ecd
       fragment CD8 transmembrane CD28 CD3zetaC

<400> 298

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1   5   10   15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
            20   25   30

Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
        35   40   45

Thr Phe Ser Arg Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys
    50   55   60

Arg Leu Glu Trp Val Ser Thr Ile Ser Gly Gly Gly Thr Tyr Ile Tyr
65   70   75   80

Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
                85   90   95

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
            100   105   110

Ala Val Tyr Tyr Cys Thr Arg Asp Asn Tyr Gly Arg Asn Tyr Asp Tyr
        115   120   125

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Gly Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
    130                 135                 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile
145                 150                 155                 160

Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
                165                 170                 175

Ala Thr Leu Thr Cys Ser Ala Thr Ser Ser Val Ser Tyr Ile His Trp
            180                 185                 190

Tyr Gln Gln Arg Pro Gly Gln Ser Pro Arg Leu Leu Ile Tyr Ser Thr
        195                 200                 205

Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
    210                 215                 220

Gly Ser Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
225                 230                 235                 240

Ala Val Tyr Tyr Cys Gln Gln Arg Ser Ser Ser Pro Phe Thr Phe Gly
                245                 250                 255

Ser Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
            260                 265                 270

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
        275                 280                 285

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
    290                 295                 300

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
305                 310                 315                 320

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys
                325                 330                 335

Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
            340                 345                 350

Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp
        355                 360                 365

Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
    370                 375                 380

Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
385                 390                 395                 400
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Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
405 410 415

Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
420 425 430

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
435 440 445

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
450 455 460

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
465 470 475 480

Gln Ala Leu Pro Pro Arg
485

<210> 299

<400> 299
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<210> 300
<211> 1467
<212> DNA
<213> Artificial Sequence

<220>
<223> CART E6 CD8/CD8/41BB/CD3z sequence - NCD8lshuMNE6scFvCD8ecd
fragment CD8 transmembrane 41BB CD3zetaC

<400> 300
atggccctgc ccgtgaccgc tttgctgctc cccctggcgc tgctgctgca cgccgccagg 60

ccagaggtcc agctggttga gagtggcggt gggctggtta agcctggcgg ctccctgcgg 120

ctgagctgcg ccgcgagtgg atttactttc agccgatatg ggatgagttg ggtgcggcaa 180

gctcccggga agaggctgga atgggtctca acaatctccg gggggggcac ttacatctat 240

taccccgact cagtcaaggg gagatttacc atttcacgag acaacgctaa gaataccctg 300

tatttgcaga tgaattctct gagagcagag gacacagctg tttactattg tacccgcgac 360

aactatggca ggaactacga ctacggtatg gactattggg gacaagggac attggttaca 420

gtgagcagtg gcggcggggg cagcggagga ggaggcagcg gtgggggggg cagcgagata 480

gtgctcacgc agtcacccgc gactctcagt ctctcacctg ggaacgagc taccctgacg 540

tgctctgcta cctcctcagt gtcatatatt cactggtatc agcaacggcc cgggcagtcc 600

cctagattgc tcatttatag tacctctaat ctggcctcag gtatccctgc acgattttct 660

ggatctggtt caggttctga ttacaccctc actatctcta gcctggagcc tgaagacttt 720

gccgtttatt actgccagca gaggtctagc tccccattca cctttgggag tgggaccaag 780

gttgaaatta aaacgacaac cccggccccc agaccaccaa cgccagcccc caccatcgcc 840

agccaacccc tgtctctgag accagaagcc tgtaggcctg ccgccggtgg agctgtgcac 900 acaagaggac tggatttcgc ctgtgatatc tacatttggg ccccgctcgc aggcacatgt 960

ggagtgctcc tcctctccct ggtgattacc ctgtactgca aaggggccg caaaaaactc 1020

ctttacattt ttaagcagcc ttttatgagg ccagtacaga cgactcaaga ggaagacggg 1080

tgctcatgcc gctttcctga ggaggaggaa ggagggtgcg aactgcgcgt taagttctcc 1140

cgatcagccg acgcgcctgc ttacaagcag ggccagaacc aactgtacaa cgagctgaat 1200

ctcggtagac gggaagagta cgacgtgttg gacaaacgga gaggccgcga cccagaaatg 1260

ggcggcaagc ctcgcaggaa aaaccccag gagggactgt acaatgagtt gcagaaagat 1320

aagatggcag aagcttatag cgagatcgga atgaaggggg aaaggagacg agggaaagga 1380

cacgacggcc tttatcaggg cctgtccaca gcaacaaaag atacgtatga cgccctccat 1440

atgcaggcac ttccaccacg gtgataa 1467

<210> 301
<211> 487
<212> PRT
<213> Artificial Sequence

<220>
<223> CART E6 CD8/CD8/41BB/CD3z sequence - NCD8lshuMNE6scFvCD8ecd
fragment CD8 transmembrane 41BB CD3zetaC

<400> 301

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Ser Arg Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Arg Leu Glu Trp Val Ser Thr Ile Ser Gly Gly Gly Thr Tyr Ile Tyr
65 70 75 80

Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Thr Arg Asp Asn Tyr Gly Arg Asn Tyr Asp Tyr
115 120 125

Gly Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
130 135 140

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Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile
145                 150                 155                 160


Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
                165                 170                 175


Ala Thr Leu Thr Cys Ser Ala Thr Ser Ser Val Ser Tyr Ile His Trp
            180                 185                 190


Tyr Gln Gln Arg Pro Gly Gln Ser Pro Arg Leu Leu Ile Tyr Ser Thr
        195                 200                 205


Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
    210                 215                 220


Gly Ser Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
225                 230                 235                 240


Ala Val Tyr Tyr Cys Gln Gln Arg Ser Ser Ser Pro Phe Thr Phe Gly
                245                 250                 255


Ser Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
            260                 265                 270


Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
        275                 280                 285


Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
    290                 295                 300


Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
305                 310                 315                 320


Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly
                325                 330                 335


Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
            340                 345                 350


Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
        355                 360                 365


Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
    370                 375                 380


Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
385                 390                 395                 400


Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
                405                 410                 415


Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
```

420 425 430

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
435 440 445

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
450 455 460

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
465 470 475 480

Met Gln Ala Leu Pro Pro Arg
485

<210> 302

<400> 302
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<210> 303
<211> 1590
<212> DNA
<213> Artificial Sequence

<220>
<223> CART E6 CD8/CD8/CD28/41BB/CD3z sequence - NCD8lshuMNE6scFvCD8ecd
fragment CD8 transmembrane CD28 41BB CD3zetaC

<400> 303
atggccctgc ccgtgaccgc tttgctgctc cccctggcgc tgctgctgca cgccgccagg 60

ccagaggtcc agctggttga gagtggcggt gggctggtta agcctggcgg ctccctgcgg 120

ctgagctgcg ccgcgagtgg atttactttc agccgatatg ggatgagttg ggtgcggcaa 180

gctcccggga agaggctgga atgggtctca acaatctccg gggggggcac ttacatctat 240

taccccgact cagtcaaggg gagatttacc atttcacgag acaacgctaa gaataccctg 300

tatttgcaga tgaattctct gagagcagag gacacagctg tttactattg tacccgcgac 360

aactatggca ggaactacga ctacggtatg gactattggg gacaagggac attggttaca 420

gtgagcagtg gcggcggggg cagcggagga ggaggcagcg gtgggggggg cagcgagata 480

gtgctcacgc agtcacccgc gactctcagt ctctcacctg ggaacgagc taccctgacg 540

tgctctgcta cctcctcagt gtcatatatt cactggtatc agcaacggcc cgggcagtcc 600

cctagattgc tcatttatag tacctctaat ctggcctcag gtatccctgc acgattttct 660

ggatctggtt caggttctga ttacaccctc actatctcta gcctggagcc tgaagacttt 720

gccgtttatt actgccagca gaggtctagc tccccattca cctttgggag tgggaccaag 780

gttgaaatta aaacgacaac ccccggcccc agaccaccaa cgccagcccc caccatcgcc 840

agccaacccc tgtctctgag accagaagcc tgtaggcctg ccgccggtgg agctgtgcac 900

acaagaggac tggatttcgc ctgtgatatc tacatttggg ccccgctcgc aggcacatgt 960

ggagtgctcc tcctctccct ggtgattacc ctgtactgca gaagcaagcg gtctcggctc 1020

ctgcattctg attacatgaa catgacccca agaagaccag gccccaccag gaaacattac 1080 cagccctacg ctccgccacg cgacttcgct gcctaccggt ccaaaagggg ccgcaaaaaa 1140

ctcctttaca tttttaagca gccttttatg aggccagtac agacgactca agaggaagac 1200

gggtgctcat gccgctttcc tgaggaggag gaaggagggt gcgaactgcg cgttaagttc 1260

tcccgatcag ccgacgcgcc tgcttacaag cagggccaga accaactgta caacgagctg 1320

aatctcggta gacgggaaga gtacgacgtg ttggacaaac ggagaggccg cgacccagaa 1380

atgggcggca agcctcgcag gaaaaacccc caggagggac tgtacaatga gttgcagaaa 1440

gataagatgg cagaagctta tagcgagatc ggaatgaagg gggaaaggag acgagggaaa 1500

ggacacgacg gcctttatca gggcctgtcc acagcaacaa aagatacgta tgacgccctc 1560

catatgcagg cacttccacc acggtgataa 1590

<210> 304
<211> 528
<212> PRT
<213> Artificial Sequence

<220>
<223> CART E6 CD8/CD8/CD28/41BB/CD3z sequence - NCD8lshuMNE6scFvCD8ecd
fragment CD8 transmembrane CD28 41BB CD3zetaC

<400> 304

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Ser Arg Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Arg Leu Glu Trp Val Ser Thr Ile Ser Gly Gly Gly Thr Tyr Ile Tyr
65 70 75 80

Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Thr Arg Asp Asn Tyr Gly Arg Asn Tyr Asp Tyr
115 120 125

Gly Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile
145 150 155 160

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Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
                165                 170                 175

Ala Thr Leu Thr Cys Ser Ala Thr Ser Ser Val Ser Tyr Ile His Trp
            180                 185                 190

Tyr Gln Gln Arg Pro Gly Gln Ser Pro Arg Leu Leu Ile Tyr Ser Thr
        195                 200                 205

Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
    210                 215                 220

Gly Ser Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
225                 230                 235                 240

Ala Val Tyr Tyr Cys Gln Gln Arg Ser Ser Ser Pro Phe Thr Phe Gly
                245                 250                 255

Ser Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
            260                 265                 270

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
        275                 280                 285

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
    290                 295                 300

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
305                 310                 315                 320

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys
                325                 330                 335

Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
            340                 345                 350

Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp
        355                 360                 365

Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile
    370                 375                 380

Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp
385                 390                 395                 400

Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
                405                 410                 415

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly
            420                 425                 430
```

```
Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
        435                 440                 445


Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
    450                 455                 460


Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
465                 470                 475                 480


Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
                485                 490                 495


Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
            500                 505                 510


Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
        515                 520                 525


<210>  305

<400>  305
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<210>  306
<211>  1608
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CART C2 CD8/CD8/CD28/41BB/CD3z sequence - NCD8lshuMNC2scFvCD8ecd
       fragment CD8 transmembrane CD28 41BB CD3zetaC

<400>  306
atggccttgc cagtgacggc cctgctgctg ccattggctc ttctgttgca cgctgccagg       60

cctgaagtgc agctcgtaga gagtggcggg ggactggtga agcccggtgg aagcctcaga      120

ctcagttgcg ccgcctcagg tttcactttt tcaggttacg ccatgtcctg ggtaagacag      180

gcaccgggga aaggactcga gtgggtgtct actatcagct caggaggcac ttatatatat      240

tatcctgact ctgtaaaagg ccgatttacg atttctcgcg acaatgcaaa gaactccctc      300

tacctccaaa tgaacagtct tagggcagaa gacactgctg tatactattg tgcacgcctc      360

ggcggcgaca actactacga gtactttgac gtgtgggggа aagggactac cgtgacagtt      420

tcaagcggag gaggtggctc aggtggaggc gggtcagggg ggggaggaag tgatattgtg      480

ctcacacaat ccccagcctc cctggctgtg tctcccggcc aacgcgctac aattacatgt      540

cgggcctcca aaagcgtgag caccagcggc tacagctaca tgcactggta tcaacagaaa      600

ccaggacaac ccccсaaact gttgatttat ctcgcttcaa acttggagtc cggcgtgcct      660

gcgcgctttt cagggagtgg gagcggcaca gattttacgc tgactatcaa ccccgtagaa      720

gcaaacgata cagcgaatta ttattgtcaa cattcccggg aactcccctt tacgttcggc      780

gggggcacaa aggtcgaaat taagagaacc acgacaaccc cggcccccag accaccaacg      840

ccagccccca ccatcgccag ccaacccctg tctctgagac cagaagcctg taggcctgcc      900
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gccggtggag ctgtgcacac aagaggactg gatttcgcct gtgatatcta catttgggcc      960

ccgctcgcag gcacatgtgg agtgctcctc ctctccctgg tgattaccct gtactgcaga     1020

agcaagcggt ctcggctcct gcattctgat tacatgaaca tgaccccaag aagaccaggc     1080

cccaccagga aacattacca gccctacgct ccgccacgcg acttcgctgc ctaccggtcc     1140

aaaaggggcc gcaaaaaact cctttacatt tttaagcagc cttttatgag gccagtacag     1200

acgactcaag aggaagacgg gtgctcatgc cgctttcctg aggaggagga aggagggtgc     1260

gaactgcgcg ttaagttctc ccgatcagcc gacgcgcctg cttacaagca gggccagaac     1320

caactgtaca acgagctgaa tctcggtaga cgggaagagt acgacgtgtt ggacaaacgg     1380

agaggccgcg acccagaaat gggcggcaag cctcgcagga aaaaccccca ggagggactg     1440

tacaatgagt tgcagaaaga taagatggca gaagcttata gcgagatcgg aatgaagggg     1500

gaaaggagac gagggaaagg acacgacggc ctttatcagg gcctgtccac agcaacaaaa     1560

gatacgtatg acgccctcca tatgcaggca cttccaccac ggtgataa                  1608


<210>  307
<211>  513
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CART C2 CD8/CD8/CD28/41BB/CD3z sequence - NCD8lshuMNC2scFvCD8ecd
       fragment CD8 transmembrane CD28 41BB CD3zetaC

<400>  307

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr Phe Asp Val Trp Gly
            100                 105                 110


Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
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Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro
    130                 135                 140

Ala Ser Leu Ala Val Ser Pro Gly Gln Arg Ala Thr Ile Thr Cys Arg
145                 150                 155                 160

Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr Met His Trp Tyr
                165                 170                 175

Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser
            180                 185                 190

Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asn Asp Thr Ala
    210                 215                 220

Asn Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Phe Thr Phe Gly Gly
225                 230                 235                 240

Gly Thr Lys Val Glu Ile Lys Arg Thr Thr Thr Thr Pro Ala Pro Arg
                245                 250                 255

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
            260                 265                 270

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
        275                 280                 285

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
    290                 295                 300

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser
305                 310                 315                 320

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
                325                 330                 335

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
            340                 345                 350

Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr
        355                 360                 365

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
    370                 375                 380

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
385                 390                 395                 400

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln
```

```
                405                 410                 415

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
            420                 425                 430

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
        435                 440                 445

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
    450                 455                 460

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
465                 470                 475                 480

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
                485                 490                 495

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
            500                 505                 510

Arg



<210>  308

<400>  308
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<210>  309

<400>  309
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<210>  310

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<210>  311

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<400>  340
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<210>  341
<211>  729
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized E6 scFV sequence in CAR

<400>  341
gaggtccagc tggttgagag tggcggtggg ctggttaagc ctggcggctc cctgcggctg       60
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agctgcgccg cgagtggatt tactttcagc cgatatggga tgagttgggt gcggcaagct      120

cccgggaaga ggctggaatg ggtctcaaca atctccgggg ggggcactta catctattac      180

cccgactcag tcaaggggag atttaccatt tcacgagaca acgctaagaa taccctgtat      240

ttgcagatga attctctgag agcagaggac acagctgttt actattgtac ccgcgacaac      300

tatggcagga actacgacta cggtatggac tattggggac aagggacatt ggttacagtg      360

agcagtggcg gcgggggcag cggaggagga ggcagcggtg gggggggcag cgagatagtg      420

ctcacgcagt cacccgcgac tctcagtctc tcacctgggg aacgagctac cctgacgtgc      480

tctgctacct cctcagtgtc atatattcac tggtatcagc aacggcccgg gcagtcccct      540

agattgctca tttatagtac ctctaatctg gcctcaggta tccctgcacg attttctgga      600

tctggttcag gttctgatta caccctcact atctctagcc tggagcctga agactttgcc      660

gtttattact gccagcagag gtctagctcc ccattcacct ttgggagtgg gaccaaggtt      720

gaaattaaa                                                              729


<210>  342
<211>  243
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized E6 scFV sequence in CAR

<400>  342

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
            20                  25                  30


Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Arg Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Gly Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Thr Arg Asp Asn Tyr Gly Arg Asn Tyr Asp Tyr Gly Met Asp Tyr Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125


Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
    130                 135                 140
```

```
Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
145                 150                 155                 160


Ser Ala Thr Ser Ser Val Ser Tyr Ile His Trp Tyr Gln Gln Arg Pro
                165                 170                 175


Gly Gln Ser Pro Arg Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala Ser
            180                 185                 190


Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Tyr Thr
        195                 200                 205


Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
    210                 215                 220


Gln Gln Arg Ser Ser Ser Pro Phe Thr Phe Gly Ser Gly Thr Lys Val
225                 230                 235                 240


Glu Ile Lys



<210>  343
<211>  63
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CD8 leader sequence

<400>  343
atggccctgc ccgtgaccgc tttgctgctc cccctggcgc tgctgctgca cgccgccagg       60

cca                                                                     63


<210>  344
<211>  21
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD8 leader sequence

<400>  344

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15


His Ala Ala Arg Pro
            20


<210>  345
<211>  135
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CD8 hinge domain sequence
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```
<400>  345
acgacaaccc cggcccccag accaccaacg ccagccccca ccatcgccag ccaacccctg       60

tctctgagac cagaagcctg taggcctgcc gccggtggag ctgtgcacac aagaggactg      120

gatttcgcct gtgat                                                       135


<210>  346
<211>  45
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD8 hinge domain sequence

<400>  346

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1               5                   10                  15


Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
            20                  25                  30


Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
        35                  40                  45


<210>  347
<211>  66
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CD4 hinge domain sequence

<400>  347
tcgggacagg tcctgctgga atccaacatc aaggttctgc ccacatggtc caccccggtg       60

cagcca                                                                  66


<210>  348
<211>  22
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD4 hinge domain sequence

<400>  348

Ser Gly Gln Val Leu Leu Glu Ser Asn Ile Lys Val Leu Pro Thr Trp
1               5                   10                  15


Ser Thr Pro Val Gln Pro
            20


<210>  349
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
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<223> CD28 hinge domain sequence

<400> 349
aaacaccttt gtccaagtcc cctatttccc ggaccttcta agccc   45

<210> 350
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> CD28 hinge domain sequence

<400> 350

Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro
1   5   10   15

<210> 351

<400> 351
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<210> 352

<400> 352
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<210> 353

<400> 353
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<210> 354

<400> 354
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<210> 355

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<210> 356

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<210> 357

<400> 357
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<210> 358

<400> 358
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<210> 359

<400> 359
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<210> 360

<400> 360
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<210> 361
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> CD3 zeta transmembrane domain sequence

<400> 361
ctctgctacc tgctggatgg aatcctcttc atctatggtg tcattctcac tgccttgttc 60

ctg 63

<210> 362
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3 zeta transmembrane domain sequence

<400> 362

Leu Cys Tyr Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly Val Ile Leu
1 5 10 15

Thr Ala Leu Phe Leu
20

<210> 363
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> CD8 transmembrane domain sequence

<400> 363
atctacattt gggccccgct cgcaggcaca tgtggagtgc tcctcctctc cctggtgatt 60

accctgtact gc 72

<210> 364
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> CD8 transmembrane domain sequence

<400> 364

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
1 5 10 15

Ser Leu Val Ile Thr Leu Tyr Cys
20

<210> 365
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> CD4 transmembrane domain sequence

<400> 365
atggccctga ttgtgctggg gggcgtcgcc ggcctcctgc ttttcattgg gctaggcatc   60

ttcttc   66

<210> 366
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> CD4 transmembrane domain sequence

<400> 366

Met Ala Leu Ile Val Leu Gly Gly Val Ala Gly Leu Leu Leu Phe Ile
1   5   10   15

Gly Leu Gly Ile Phe Phe
            20

<210> 367
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> CD28 transmembrane domain sequence

<400> 367
ttttgggtgc tggtggtggt tggtggagtc ctggcttgct atagcttgct agtaacagtg   60

gcctttatta ttttctgggt g   81

<210> 368
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> CD28 transmembrane domain sequence

<400> 368

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
1   5   10   15

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
            20   25

<210> 369
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> 41BB transmembrane domain sequence

<400> 369

atcatctcct tctttcttgc gctgacgtcg actgcgttgc tcttcctgct gttcttcctc 60

acgctccgtt tctctgttgt t 81

<210> 370
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> 41BB transmembrane domain sequence

<400> 370

Ile Ile Ser Phe Phe Leu Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu
1 5 10 15

Leu Phe Phe Leu Thr Leu Arg Phe Ser Val Val
20 25

<210> 371
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> OX40 transmembrane domain sequence

<400> 371
gttgccgcca tcctgggcct gggcctggtg ctggggctgc tgggccccct ggccatcctg 60

ctggccctgt acctgctc 78

<210> 372
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> OX40 transmembrane domain sequence

<400> 372

Val Ala Ala Ile Leu Gly Leu Gly Leu Val Leu Gly Leu Leu Gly Pro
1 5 10 15

Leu Ala Ile Leu Leu Ala Leu Tyr Leu Leu
20 25

<210> 373
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> CD3 zeta domain sequence

<400> 373
cgcgttaagt tctcccgatc agccgacgcg cctgcttaca agcagggcca gaaccaactg 60

tacaacgagc tgaatctcgg tagacgggaa gagtacgacg tgttggacaa acggagaggc 120

cgcgacccag aaatgggcgg caagcctcgc aggaaaaacc cccaggaggg actgtacaat 180 gagttgcaga aagataagat ggcagaagct tatagcgaga tcggaatgaa gggggaaagg 240

agacgaggga aaggacacga cggcctttat cagggcctgt ccacagcaac aaaagatacg 300

tatgacgccc tccatatgca ggcacttcca ccacgg 336

<210> 374
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3 zeta domain sequence

<400> 374

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly
1   5   10   15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
            20   25   30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
        35   40   45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
    50   55   60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65   70   75   80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
                85   90   95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            100   105   110

<210> 375
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> CD3 zeta domain variant sequence

<400> 375
agagtgaagt tcagcaggag cgcagacgcc cccgcgtacc agcagggcca gaaccagctc 60

tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 120

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 180

gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 240

cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc 300

tacgacgccc ttcacatgca ggccctgccc cctcgc 336

<210> 376

<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3 zeta domain variant sequence

<400> 376

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1   5   10   15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
            20   25   30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
        35   40   45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
    50   55   60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65   70   75   80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
                85   90   95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            100   105   110

<210> 377
<211> 123
<212> DNA
<213> Artificial Sequence

<220>
<223> CD28 domain sequence

<400> 377
agaagcaagc ggtctcggct cctgcattct gattacatga acatgacccc aagaagacca   60

ggccccacca ggaaacatta ccagccctac gctccgccac gcgacttcgc tgcctaccgg   120

tcc   123

<210> 378
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> CD28 domain sequence

<400> 378

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
1   5   10   15

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
            20   25   30

```
Pro Arg Asp Phe Ala Ala Tyr Arg Ser
        35                  40


<210>  379
<211>  126
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  41BB domain sequence

<400>  379
aaaaggggcc gcaaaaaact cctttacatt tttaagcagc cttttatgag gccagtacag       60

acgactcaag aggaagacgg gtgctcatgc cgctttcctg aggaggagga aggagggtgc      120

gaactg                                                                 126


<210>  380
<211>  42
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  41BB domain sequence

<400>  380

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
1               5                   10                  15


Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
            20                  25                  30


Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
        35                  40


<210>  381

<400>  381
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<210>  382

<400>  382
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<210>  383

<400>  383
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<210>  384

<400>  384
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<210>  385

<400>  385
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<210> 386

<400> 386
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<210> 387

<400> 387
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<210> 388

<400> 388
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<210> 389

<400> 389
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<210> 390

<400> 390
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<210> 391
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> HumanizeE6 scFV (VHVL) sequence

<400> 391
gaggtgcagc tggtggagtc tgggggaggc ctggtcaagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt aggtatggca tgagctgggt ccgccaggct 120

ccagggaaga ggctggagtg ggtctcaacc attagtggcg gaggcaccta catatactac 180

ccagactcag tgaagggccg attcaccatc tccagagaca acgccaagaa caccctgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtac cagagataac 300

tatggccgca actatgatta tggcatggat tattggggcc agggcaccct ggtgaccgtg 360

agcagcggcg gtggcggatc cggcggtggc ggatccggcg gtggcggatc cgaaattgtg 420

ttgacacagt ctccagccac cctgtctttg tctccagggg aaagagccac cctcacctgc 480

agcgccacca gcagtgttag ctacatccac tggtaccaac agaggcctgg ccagagcccc 540

aggctcctca tctatagcac ctccaacctg gccagcggca tcccagccag gttcagtggc 600

agtgggtctg ggagcgacta cactctcacc atcagcagcc tagagcctga agattttgca 660

gtttattact gtcagcagcg tagcagctcc cctttcacct ttggcagcgg caccaaagtg 720

gaaattaaa 729

<210> 392
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> HumanizeE6 scFV (VHVL) sequence

<400> 392

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
            20   25   30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Arg Leu Glu Trp Val
        35   40   45

Ser Thr Ile Ser Gly Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Thr Arg Asp Asn Tyr Gly Arg Asn Tyr Asp Tyr Gly Met Asp Tyr Trp
            100   105   110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115   120   125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
    130   135   140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
145   150   155   160

Ser Ala Thr Ser Ser Val Ser Tyr Ile His Trp Tyr Gln Gln Arg Pro
                165   170   175

Gly Gln Ser Pro Arg Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala Ser
            180   185   190

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Tyr Thr
        195   200   205

Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
    210   215   220

Gln Gln Arg Ser Ser Ser Pro Phe Thr Phe Gly Ser Gly Thr Lys Val
225   230   235   240

Glu Ile Lys

<210> 393
<211> 729
<212> DNA

<213> Artificial Sequence

<220>
<223> HumanizeE6 scFV (VLVH) sequence

<400> 393
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc   60

ctcacctgca gcgccaccag cagtgttagc tacatccact ggtaccaaca gaggcctggc   120

cagagcccca ggctcctcat ctatagcacc tccaacctgg ccagcggcat cccagccagg   180

ttcagtggca gtgggtctgg gagcgactac actctcacca tcagcagcct agagcctgaa   240

gattttgcag tttattactg tcagcagcgt agcagctccc ctttcacctt tggcagcggc   300

accaaagtgg aaattaaagg cggtggcgga tccggcggtg gcggatccgg cggtggcgga   360

tccgaggtgc agctggtgga gtctggggga ggcctggtca agcctggggg gtccctgaga   420

ctctcctgtg cagcctctgg attcaccttc agtaggtatg gcatgagctg ggtccgccag   480

gctccaggga agaggctgga gtgggtctca accattagtg gcggaggcac ctacatatac   540

tacccagact cagtgaaggg ccgattcacc atctccagag acaacgccaa gaacaccctg   600

tatctgcaaa tgaacagcct gagagccgag gacacggctg tgtattactg taccagagat   660

aactatggcc gcaactatga ttatggcatg gattattggg gccagggcac cctggtgacc   720

gtgagcagc   729

<210> 394
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> HumanizeE6 scFV (VLVH) sequence

<400> 394

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1   5   10   15

Glu Arg Ala Thr Leu Thr Cys Ser Ala Thr Ser Ser Val Ser Tyr Ile
            20   25   30

His Trp Tyr Gln Gln Arg Pro Gly Gln Ser Pro Arg Leu Leu Ile Tyr
        35   40   45

Ser Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
    50   55   60

Gly Ser Gly Ser Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65   70   75   80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Ser Ser Pro Phe Thr
                85   90   95

Phe Gly Ser Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly
            100   105   110

```
Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
        115                 120                 125


Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
    130                 135                 140


Ala Ser Gly Phe Thr Phe Ser Arg Tyr Gly Met Ser Trp Val Arg Gln
145                 150                 155                 160


Ala Pro Gly Lys Arg Leu Glu Trp Val Ser Thr Ile Ser Gly Gly Gly
                165                 170                 175


Thr Tyr Ile Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
            180                 185                 190


Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
        195                 200                 205


Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Arg Asp Asn Tyr Gly Arg
    210                 215                 220


Asn Tyr Asp Tyr Gly Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
225                 230                 235                 240


Val Ser Ser



<210>  395
<211>  747
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  HumanizeC2 scFV (VHVL) sequence

<400>  395
gaggtgcagc tggtggagtc tgggggaggc ctggtcaagc ctggggggtc cctgagactc       60

tcctgtgcag cctctggatt caccttcagt ggctatgcca tgagctgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtctcaacc attagtagtg gcggaaccta catatactac      180

cccgactcag tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat      240

ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagacttggg      300

ggggataatt actacgaata cttcgatgtc tggggcaaag ggaccacggt caccgtctcc      360

tccggcggtg gcggatccgg cggtggcgga tccggcggtg gcggatccga cattgtgctg      420

acccagtctc cagcctcctt ggccgtgtct ccaggacaga gggccaccat cacctgcaga      480

gccagtaaga gtgtcagtac cagcggatac tcctacatgc actggtatca gcagaaacca      540

ggacaacctc ctaaactcct gatttacctg gcatccaatc tggagagcgg ggtcccagcc      600

aggttcagcg gcagtgggtc tgggaccgat ttcaccctca caattaatcc tgtggaagct      660
```

aatgatactg caaattatta ctgtcagcac agtagggagc tgcctttcac attcggcgga 720

gggaccaagg tggagatcaa acgaact 747

<210> 396
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> HumanizeC2 scFV (VHVL) sequence

<400> 396

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr Phe Asp Val Trp Gly
            100                 105                 110


Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125


Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro
    130                 135                 140


Ala Ser Leu Ala Val Ser Pro Gly Gln Arg Ala Thr Ile Thr Cys Arg
145                 150                 155                 160


Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr Met His Trp Tyr
                165                 170                 175


Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser
            180                 185                 190


Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205


Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asn Asp Thr Ala
    210                 215                 220
```

Asn Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Phe Thr Phe Gly Gly
225   230   235   240

Gly Thr Lys Val Glu Ile Lys Arg Thr
                245

<210> 397
<211> 747
<212> DNA
<213> Artificial Sequence

<220>
<223> HumanizeE6 scFV (VLVH) sequence

<400> 397
gacattgtgc tgacccagtc tccagcctcc ttggccgtgt ctccaggaca gagggccacc   60

atcacctgca gagccagtaa gagtgtcagt accagcggat actcctacat gcactggtat   120

cagcagaaac caggacaacc tcctaaactc ctgatttacc tggcatccaa tctggagagc   180

ggggtcccag ccaggttcag cggcagtggg tctgggaccg atttcaccct cacaattaat   240

cctgtggaag ctaatgatac tgcaaattat tactgtcagc acagtaggga gctgcctttc   300

acattcggcg gagggaccaa ggtggagatc aaacgaactg gcggtggcgg atccggcggt   360

ggcggatccg gcggtggcgg atccgaggtg cagctggtgg agtctggggg aggcctggtc   420

aagcctgggg ggtccctgag actctcctgt gcagcctctg gattcacctt cagtggctat   480

gccatgagct gggtccgcca ggctccaggg aaggggctgg agtgggtctc aaccattagt   540

agtggcggaa cctacatata ctaccccgac tcagtgaagg gccgattcac catctccaga   600

gacaacgcca agaactcact gtatctgcaa atgaacagcc tgagagccga ggacacggcc   660

gtgtattact gtgcgagact tggggggggat aattactacg aatacttcga tgtctggggc   720

aaagggacca cggtcaccgt ctcctcc   747

<210> 398
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> HumanizeE6 scFV (VLVH) sequence

<400> 398

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Pro Gly
1   5   10   15

Gln Arg Ala Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30

Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45

Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala

```
    50                  55                  60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn
65                  70                  75                  80

Pro Val Glu Ala Asn Asp Thr Ala Asn Tyr Tyr Cys Gln His Ser Arg
                85                  90                  95

Glu Leu Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
            100                 105                 110

Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
    130                 135                 140

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
145                 150                 155                 160

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
                165                 170                 175

Ser Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val
            180                 185                 190

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
        195                 200                 205

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
    210                 215                 220

Ala Arg Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr Phe Asp Val Trp Gly
225                 230                 235                 240

Lys Gly Thr Thr Val Thr Val Ser Ser
                245


<210>  399
<211>  15
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  G4S1 linker sequence

<400>  399
ggcggtggcg gatcc                                                        15


<210>  400
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
```

```
<223>  G4S1 linker sequence

<400>  400

Gly Gly Gly Gly Ser
1               5


<210>  401
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  [G4S1]x3 linker sequence

<400>  401
ggcggtggcg gatccggcgg tggcggatcc ggcggtggcg gatcc                        45


<210>  402
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  [G4S1]x3 linker sequence

<400>  402

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1               5                   10                  15


<210>  403
<211>  24
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  8 aa GS linker sequence

<400>  403
ggcggttccg gcggtggatc cgga                                               24


<210>  404
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  8 aa GS linker sequence

<400>  404

Gly Gly Ser Gly Gly Gly Ser Gly
1               5


<210>  405
<211>  39
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  12 aa GS linker sequence

<400>  405
```

ggcggttccg gcggtggatc cggcggtggc ggatccgga 39

<210> 406
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 12 aa GS linker sequence

<400> 406

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
1 5 10

<210> 407
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> 13 aa GS linker sequence

<400> 407
ggcggtggat ccggcggtgg cggatccggc ggtggatcc 39

<210> 408
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 13 aa GS linker sequence

<400> 408

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10

<210> 409
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> 22 aa GS linker sequence

<400> 409
ggcggtggaa gcggcggtgg cggatccggc agcggcggaa gcggcggtgg cggatccggc 60

ggtgga 66

<210> 410
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> 22 aa GS linker sequence

<400> 410

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Ser Gly Gly Ser Gly Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly
20

<210> 411
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> 24 aa GS linker sequence

<400> 411
ggcggttccg gcggtggatc cggcggtggc ggatccggag gcggttccgg cggtggatcc 60

ggcggtggcg gatccgga 78

<210> 412
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> 24 aa GS linker sequence

<400> 412

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly
20

<210> 413
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse C3 Heavy chain variable region sequence

<400> 413
caggtccagc tgcagcagtc tgggcctgag ctggtgaggc ctggggtctc agtgaagatt 60

tcctgcaagg gttccggcta cagattcact gattatgcta tgaactgggt gaagcagagt 120

catgcaaaga gtctagagtg gattggagtt attagtactt tctctggtaa tacaaacttc 180

aaccagaagt ttaagggcaa ggccacaatg actgtagaca aatcctccag cacagcctat 240

atggaacttg ccagattgac atctgaggat tctgccatgt attactgtgc aagatcggat 300

tactacggcc catactttga ctactggggc caaggcacca ctctcacagt ctcctca 357

<210> 414
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse C3 Heavy chain variable region sequence

<400> 414

```
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg Pro Gly Val
1               5                   10                  15


Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Arg Phe Thr Asp Tyr
            20                  25                  30


Ala Met Asn Trp Val Lys Gln Ser His Ala Lys Ser Leu Glu Trp Ile
        35                  40                  45


Gly Val Ile Ser Thr Phe Ser Gly Asn Thr Asn Phe Asn Gln Lys Phe
    50                  55                  60


Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Met Tyr Tyr Cys
                85                  90                  95


Ala Arg Ser Asp Tyr Tyr Gly Pro Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Thr Leu Thr Val Ser Ser
        115


<210>  415
<211>  90
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse C3 heavy chain variable framework region 1 (FWR1) sequence

<400>  415
caggtccagc tgcagcagtc tgggcctgag ctggtgaggc ctggggtctc agtgaagatt       60

tcctgcaagg gttccggcta cagattcact                                        90


<210>  416
<211>  30
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse C3 heavy chain variable framework region 1 (FWR1) sequence

<400>  416

Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg Pro Gly Val
1               5                   10                  15


Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Arg Phe Thr
            20                  25                  30


<210>  417
<211>  15
<212>  DNA
<213>  Artificial Sequence
```

<220>
<223> Mouse C3 heavy chain variable complementarity determining regions
       1 (CDR1) sequence

<400> 417
gattatgcta tgaac   15

<210> 418
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse C3 heavy chain variable complementarity determining regions
       1 (CDR1) sequence

<400> 418

Asp Tyr Ala Met Asn
1   5

<210> 419
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse C3 heavy chain variable framework region 2 (FWR2) sequence

<400> 419
tgggtgaagc agagtcatgc aaagagtcta gagtggattg ga   42

<210> 420
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse C3 heavy chain variable framework region 2 (FWR2) sequence

<400> 420

Trp Val Lys Gln Ser His Ala Lys Ser Leu Glu Trp Ile Gly
1   5   10

<210> 421
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse C3 heavy chain variable complementarity determining regions
       2 (CDR2) sequence

<400> 421
gttattagta ctttctctgg taatacaaac ttcaaccaga agtttaaggg c   51

<210> 422
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> Mouse C3 heavy chain variable complementarity determining regions
       2 (CDR2) sequence

<400> 422

Val Ile Ser Thr Phe Ser Gly Asn Thr Asn Phe Asn Gln Lys Phe Lys
1   5   10   15

Gly

<210> 423
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse C3 heavy chain variable framework region 3 (FWR3) acid
       sequence

<400> 423
aaggccacaa tgactgtaga caaatcctcc agcacagcct atatggaact tgccagattg   60

acatctgagg attctgccat gtattactgt gcaaga   96

<210> 424
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse C3 heavy chain variable framework region 3 (FWR3) acid
       sequence

<400> 424

Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu
1   5   10   15

Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Met Tyr Tyr Cys Ala Arg
            20   25   30

<210> 425
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse C3 heavy chain variable complementarity determining regions
       3 (CDR3) sequence

<400> 425
tcggattact acggcccata ctttgactac   30

<210> 426
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse C3 heavy chain variable complementarity determining regions
       3 (CDR3) sequence

<400> 426

Ser Asp Tyr Tyr Gly Pro Tyr Phe Asp Tyr
1   5   10

<210> 427

<400> 427
000

<210> 428

<400> 428
000

<210> 429

<400> 429
000

<210> 430

<400> 430
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<210> 431

<400> 431
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<210> 432

<400> 432
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<210> 433

<400> 433
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<210> 434

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<210> 435

<400> 435
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<210> 436

<400> 436
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<210> 437

<400> 437
000

<210> 438

<400> 438
000

<210> 439
<211> 357
<212> DNA

<213> Artificial Sequence

<220>
<223> Humanized C3 heavy chain variable region sequence from IGHV118*04

<400> 439
```
caggttcagc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc       60

tcctgcaagg cttctggtta cacctttacc gactacgcca tgaactgggt gcgacaggcc      120

cctggacaag ggcttgagtg gatgggagtg atcagcacct tcagcggtaa cacaaacttc      180

aaccagaagt tcaagggcag agtcaccatg accacagaca catccacgag cacagcctac      240

atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagaagcgac      300

tactacggcc catacttcga ctactggggc cagggcacca ccctgaccgt gtccagc         357
```

<210> 440
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized C3 heavy chain variable region sequence from IGHV118*04

<400> 440

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30


Ala Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Val Ile Ser Thr Phe Ser Gly Asn Thr Asn Phe Asn Gln Lys Phe
    50                  55                  60


Lys Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Ser Asp Tyr Tyr Gly Pro Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Thr Leu Thr Val Ser Ser
        115
```

<210> 441
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized C3 heavy chain variable framework region 1 (FWR1) acid
       sequence

<400> 441
caggttcagc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggtta cacctttacc 90

<210> 442
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized C3 heavy chain variable framework region 1 (FWR1) acid
sequence

<400> 442

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
20 25 30

<210> 443
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized C3 heavy chain variable complementarity determining
regions 1 (CDR1) sequence

<400> 443
gactacgcca tgaac 15

<210> 444
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized C3 heavy chain variable complementarity determining
regions 1 (CDR1) sequence

<400> 444

Asp Tyr Ala Met Asn
1 5

<210> 445
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized C3 heavy chain variable framework region 2 (FWR2) acid
sequence

<400> 445
tgggtgcgac aggcccctgg acaagggctt gagtggatgg ga 42

<210> 446
<211> 14

```
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C3 heavy chain variable framework region 2 (FWR2) acid
       sequence

<400>  446

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1               5                   10


<210>  447
<211>  51
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C3 heavy chain variable complementarity determining
       regions 2 (CDR2) sequence

<400>  447
gtgatcagca ccttcagcgg taacacaaac ttcaaccaga agttcaaggg c                51


<210>  448
<211>  17
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C3 heavy chain variable complementarity determining
       regions 2 (CDR2) sequence

<400>  448

Val Ile Ser Thr Phe Ser Gly Asn Thr Asn Phe Asn Gln Lys Phe Lys
1               5                   10                  15


Gly



<210>  449
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C3 heavy chain variable framework region 3 (FWR3) acid
       sequence

<400>  449
agagtcacca tgaccacaga cacatccacg agcacagcct acatggagct gaggagcctg       60

agatctgacg acacggccgt gtattactgt gcgaga                                 96


<210>  450
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C3 heavy chain variable framework region 3 (FWR3) acid
       sequence
```

<400> 450

Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu
1   5   10   15

Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg
            20   25   30

<210> 451
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized C3 heavy chain variable complementarity determining
       regions 3 (CDR3) sequence

<400> 451
agcgactact acggcccata cttcgactac   30

<210> 452
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized C3 heavy chain variable complementarity determining
       regions 3 (CDR3) sequence

<400> 452

Ser Asp Tyr Tyr Gly Pro Tyr Phe Asp Tyr
1   5   10

<210> 453
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized C3 IgG1 heavy chain sequence

<400> 453
caggttcagc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc   60

tcctgcaagg cttctggtta cacctttacc gactacgcca tgaactgggt gcgacaggcc   120

cctggacaag ggcttgagtg gatgggagtg atcagcacct tcagcggtaa cacaaacttc   180

aaccagaagt tcaagggcag agtcaccatg accacagaca catccacgag cacagcctac   240

atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagaagcgac   300

tactacggcc catacttcga ctactggggc cagggcacca ccctgaccgt gtccagcgct   360

agcaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc   420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg   480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga   540

ctctactccc tcagcagcgt ggtgacagtg ccctccagca gcttgggcac ccagacctac   600

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa   660

```
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct ggggggaccg      720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag      780

gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac      840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc      900

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag      960

tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa     1020

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggaggagatg     1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc     1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg     1200

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag     1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag     1320

aagagcctct ccctgtctcc gggtaaatga taa                                  1353
```

<210> 454
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized C3 IgG1 heavy chain sequence

<400> 454

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30


Ala Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Val Ile Ser Thr Phe Ser Gly Asn Thr Asn Phe Asn Gln Lys Phe
    50                  55                  60


Lys Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Ser Asp Tyr Tyr Gly Pro Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125


Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
```

```
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
```

```
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430


Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445


Lys




<210>  455
<211>  1341
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C3 IgG2 heavy chain sequence

<400>  455
caggttcagc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc       60

tcctgcaagg cttctggtta cacctttacc gactacgcca tgaactgggt gcgacaggcc      120

cctggacaag ggcttgagtg gatgggagtg atcagcacct tcagcggtaa cacaaacttc      180

aaccagaagt tcaagggcag agtcaccatg accacagaca catccacgag cacagcctac      240

atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagaagcgac      300

tactacggcc catacttcga ctactggggc cagggcacca ccctgaccgt gtccagcgcc      360

tccaccaagg gcccatcggt cttccccctg gcgccctgct ccaggagcac ctccgagagc      420

acagccgccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg      480

aactcaggcg ctctgaccag cggcgtgcac accttcccag ctgtcctaca gtcctcagga      540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca acttcggcac ccagacctac      600

acctgcaacg tagatcacaa gcccagcaac accaaggtgg acaagacagt tgagcgcaaa      660

tgttgtgtcg agtgcccacc gtgcccagca ccacctgtgg caggaccgtc agtcttcctc      720

ttccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacgtgcgtg      780

gtggtggacg tgagccacga agaccccgag gtccagttca actggtacgt ggacggcgtg      840

gaggtgcata atgccaagac aaagccacgg gaggagcagt tcaacagcac gttccgtgtg      900

gtcagcgtcc tcaccgttgt gcaccaggac tggctgaacg gcaaggagta caagtgcaag      960

gtctccaaca aaggcctccc agcccccatc gagaaaacca tctccaaaac caaagggcag     1020

ccccgagaac cacaggtgta caccctgccc ccatcccggg aggagatgac caagaaccag     1080

gtcagcctga cctgcctggt caaaggcttc taccccagcg acatcgccgt ggagtgggag     1140

agcaatgggc agccggagaa caactacaag accacacctc ccatgctgga ctccgacggc     1200

tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc     1260

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc     1320

ctgtctccgg gtaaatagta a                                               1341
```

<210> 456
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized C3 IgG2 heavy chain sequence

<400> 456

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20   25   30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Val Ile Ser Thr Phe Ser Gly Asn Thr Asn Phe Asn Gln Lys Phe
    50   55   60

Lys Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Ser Asp Tyr Tyr Gly Pro Tyr Phe Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115   120   125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
    130   135   140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145   150   155   160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165   170   175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180   185   190

Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro
        195   200   205

Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu
    210   215   220

Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu
225   230   235   240

```
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                245                 250                 255


Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln
            260                 265                 270


Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        275                 280                 285


Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu
    290                 295                 300


Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305                 310                 315                 320


Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335


Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            340                 345                 350


Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365


Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380


Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly
385                 390                 395                 400


Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                405                 410                 415


Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            420                 425                 430


His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445


<210>  457

<400>  457
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<210>  458
<211>  336
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse C3 Light Chain variable region sequence

<400>  458
gatgttttga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc       60
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atctcttgca gatctagtca gaccattgta catagtaatg gaaacaccta tttagaatgg   120

tacctgcaga aaccaggcca gtctccaaag ctcctgatct acaaagtttc caaccgattt   180

tctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc   240

aacagagtgg aggctgagga tctgggagtt tattactgct ttcaaggttc acatgttcca   300

ttcacgttcg gctcggggac aaagttggaa ataaaa   336

<210> 459
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse C3 Light Chain variable region sequence

<400> 459

Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1   5   10   15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Thr Ile Val His Ser
            20   25   30

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35   40   45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
    50   55   60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65   70   75   80

Asn Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
                85   90   95

Ser His Val Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 460
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse C3 light chain variable framework region 1 (FWR1) sequence

<400> 460
gatgttttga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc   60

atctcttgc   69

<210> 461
<211> 23
<212> PRT
<213> Artificial Sequence

<220>

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<223>  Mouse C3 light chain variable framework region 1 (FWR1) sequence

<400>  461

Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1               5                   10                  15


Asp Gln Ala Ser Ile Ser Cys
            20


<210>  462
<211>  48
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse C3 light chain variable complementarity determining regions
       1 (CDR1) sequence

<400>  462
agatctagtc agaccattgt acatagtaat ggaaacacct atttagaa                    48


<210>  463
<211>  16
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse C3 light chain variable complementarity determining regions
       1 (CDR1) sequence

<400>  463

Arg Ser Ser Gln Thr Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1               5                   10                  15


<210>  464
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse C3 light chain variable framework region 2 (FWR2) sequence

<400>  464
tggtacctgc agaaaccagg ccagtctcca aagctcctga tctac                       45


<210>  465
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse C3 light chain variable framework region 2 (FWR2) sequence

<400>  465

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr
1               5                   10                  15


<210>  466
<211>  21
<212>  DNA
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<213>  Artificial Sequence

<220>
<223>  Mouse C3 light chain variable complementarity determining regions
       2 (CDR2) sequence

<400>  466
aaagtttcca accgattttc t                                                 21


<210>  467
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse C3 light chain variable complementarity determining regions
       2 (CDR2) sequence

<400>  467

Lys Val Ser Asn Arg Phe Ser
1               5


<210>  468
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse C3 light chain variable framework region 3 (FWR3) sequence

<400>  468
ggggtcccag acaggttcag tggcagtgga tcagggacag atttcacact caagatcaac       60

agagtggagg ctgaggatct gggagtttat tactgc                                 96


<210>  469
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse C3 light chain variable framework region 3 (FWR3) sequence

<400>  469

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1               5                   10                  15


Leu Lys Ile Asn Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
            20                  25                  30


<210>  470
<211>  27
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse C3 light chain variable complementarity determining regions
       3 (CDR3) sequence

<400>  470
tttcaaggtt cacatgttcc attcacg                                           27
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<210>  471
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse C3 light chain variable complementarity determining regions
       3 (CDR3) sequence

<400>  471

Phe Gln Gly Ser His Val Pro Phe Thr
1               5


<210>  472

<400>  472
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<210>  473

<400>  473
000

<210>  474

<400>  474
000

<210>  475

<400>  475
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<210>  476

<400>  476
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<210>  477

<400>  477
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<210>  478

<400>  478
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<210>  479

<400>  479
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<210>  480

<400>  480
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<210>  481

<400>  481
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<210>  482

<400>  482
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<210>  483

<400>  483
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<210>  484

<400>  484
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<210>  485

<400>  485
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<210>  486
<211>  342
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C3 light chain variable region sequence from IGKV229*03

<400>  486
gatattgtga tgacccagac tccactctct ctgtccgtca cccctggaca gccggcctcc       60

atctcctgca ggtctagtca gaccattgtc catagtaatg gaaacaccta tttggagtgg      120

tacctgcaga agccaggcca gtctccacag ctcctgatct ataaggtttc caaccggttc      180

tctggagtgc cagataggtt cagtggcagc gggtcaggga cagatttcac actgaaaatc      240

agccgggtgg aggctgagga tgttggggtt tattactgct tccaaggtag ccacgtgcct      300

ttcaccttcg gcggagggac caaggtggag atcaaacgaa ct                         342


<210>  487
<211>  114
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C3 light chain variable region sequence from IGKV229*03

<400>  487

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1               5                   10                  15


Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Thr Ile Val His Ser
            20                  25                  30


Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35                  40                  45


Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60


Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80
```

```
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln Gly
                85                  90                  95


Ser His Val Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


Arg Thr



<210>  488
<211>  69
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C3 light chain variable framework region 1 (FWR1) acid
       sequence

<400>  488
gatattgtga tgacccagac tccactctct ctgtccgtca cccctggaca gccggcctcc       60

atctcctgc                                                               69


<210>  489
<211>  23
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C3 light chain variable framework region 1 (FWR1) acid
       sequence

<400>  489

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1               5                   10                  15


Gln Pro Ala Ser Ile Ser Cys
            20


<210>  490
<211>  47
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C3 light chain variable complementarity determining
       regions 1 (CDR1) sequence

<400>  490
ggtctagtca gaccattgtc catagtaatg gaaacaccta tttggag                     47


<210>  491
<211>  16
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C3 light chain variable complementarity determining
       regions 1 (CDR1) sequence

<400>  491
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Arg Ser Ser Gln Thr Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1   5   10   15

<210> 492
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized C3 light chain variable framework region 2 (FWR2) acid sequence

<400> 492
tggtacctgc agaagccagg ccagtctcca cagctcctga tctat   45

<210> 493
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized C3 light chain variable framework region 2 (FWR2) acid sequence

<400> 493

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr
1   5   10   15

<210> 494
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized C3 light chain variable complementarity determining regions 2 (CDR2) sequence

<400> 494
aaggtttcca accggttctc t   21

<210> 495
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized C3 light chain variable complementarity determining regions 2 (CDR2) sequence

<400> 495

Lys Val Ser Asn Arg Phe Ser
1   5

<210> 496
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized C3 light chain variable framework region 3 (FWR3) acid sequence

<400> 496
ggagtgccag ataggttcag tggcagcggg tcagggacag atttcacact gaaaatcagc   60

cgggtggagg ctgaggatgt tggggtttat tactgc   96

<210> 497
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized C3 light chain variable framework region 3 (FWR3) acid
       sequence

<400> 497

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1   5   10   15

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys
            20   25   30

<210> 498
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized C3 light chain variable complementarity determining
       regions 3 (CDR3) sequence

<400> 498
ttccaaggta gccacgtgcc tttcacc   27

<210> 499
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized C3 light chain variable complementarity determining
       regions 3 (CDR3) sequence

<400> 499

Phe Gln Gly Ser His Val Pro Phe Thr
1   5

<210> 500
<211> 666
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized C3 lambda light chain sequence

<400> 500
gatattgtga tgacccagac tccactctct ctgtccgtca cccctggaca gccggcctcc   60

atctcctgca ggtctagtca gaccattgtc catagtaatg gaaacaccta tttggagtgg   120

tacctgcaga agccaggcca gtctccacag ctcctgatct ataaggtttc caaccggttc   180

```
tctggagtgc cagataggtt cagtggcagc gggtcaggga cagatttcac actgaaaatc      240

agccgggtgg aggctgagga tgttggggtt tattactgct tccaaggtag ccacgtgcct      300

ttcaccttcg gcggagggac caaggtggag atcaaacgaa ctggtcagcc caaggctgcc      360

ccctcggtca ctctgttccc gccctcctct gaggagcttc aagccaacaa ggccacactg      420

gtgtgtctca taagtgactt ctacccggga gccgtgacag tggcctggaa ggcagatagc      480

agccccgtca aggcgggagt ggagaccacc acaccctcca aacaaagcaa caacaagtac      540

gcggccagca gctatctgag cctgacgcct gagcagtgga agtcccacag aagctacagc      600

tgccaggtca cgcatgaagg gagcaccgtg gagaagacag tggcccctac agaatgttca      660

tagtaa                                                                 666


<210>  501
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C3 lambda light chain sequence

<400>  501

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1               5                   10                  15


Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Thr Ile Val His Ser
            20                  25                  30


Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35                  40                  45


Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60


Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80


Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln Gly
                85                  90                  95


Ser His Val Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


Arg Thr Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro
        115                 120                 125


Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile
    130                 135                 140


Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser
145                 150                 155                 160
```

Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser
165 170 175

Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln
180 185 190

Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser
195 200 205

Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
210 215 220

<210> 502
<211> 666
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized C3 Kappa light chain

<400> 502
gatattgtga tgacccagac tccactctct ctgtccgtca cccctggaca gccggcctcc 60

atctcctgca ggtctagtca gaccattgtc catagtaatg gaaacaccta tttggagtgg 120

tacctgcaga agccaggcca gtctccacag ctcctgatct ataaggtttc caaccggttc 180

tctggagtgc cagataggtt cagtggcagc gggtcaggga cagatttcac actgaaaatc 240

agccgggtgg aggctgagga tgttggggtt tattactgct tccaaggtag ccacgtgcct 300

ttcaccttcg gcggagggac caaggtggag atcaaacgaa ctacggtggc tgcaccatct 360

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 420

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 480

caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540

ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

tagtaa 666

<210> 503
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized C3 Kappa light chain

<400> 503

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Thr Ile Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser

35 40 45

Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

Ser His Val Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 504

<400> 504
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<210> 505
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse C8 heavy chain variable region sequence

<400> 505
gaagtgatgg tcgtggaaag cggcggtggt ctggtaaagc cggggggatc ccttaagctt 60

tcttgcgccg catccgggtt cacgttctcc ggctatgcca tgtcctgggt ccgacagact 120

cccgaaaagc gcttggaatg ggtggccact atctcctccg gggggacgta catctactac 180

cccgacagtg tgaaaggaag atttacaata tctcgcgaca acgcaaaaaa taccttgtat 240

```
cttcaaatga gctccctgcg gtcagaggac actgccatgt actattgcgc ccgcctgggc      300

ggcgacaatt actatgagta t                                                321


<210>  506
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse C8 heavy chain variable region sequence

<400>  506

Glu Val Met Val Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
        35                  40                  45


Ala Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95


Ala Arg Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr
            100                 105


<210>  507
<211>  15
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse C8 heavy chain variable complementarity determining region
       1 (CDR1) sequence

<400>  507
ggctatgcca tgtcc                                                        15


<210>  508
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse C8 heavy chain variable complementarity determining region
       1 (CDR1) sequence

<400>  508

Gly Tyr Ala Met Ser
1               5
```

<210> 509
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse C8 heavy chain variable complementarity determining region 2 (CDR2) sequence

<400> 509
actatctcct ccgggggac gtacatctac taccccgaca gtgtgaaagg a 51

<210> 510
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse C8 heavy chain variable complementarity determining region 2 (CDR2) sequence

<400> 510

Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val Lys
1 5 10 15

Gly

<210> 511
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse C8 heavy chain variable complementarity determining region 3 (CDR3) sequence

<400> 511
ctgggcggcg acaattacta tgagtat 27

<210> 512
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse C8 heavy chain variable complementarity determining region 3 (CDR3) sequence

<400> 512

Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr
1 5

<210> 513

<400> 513
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<210> 514

<400> 514
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<210> 515

<400> 515
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<210> 516

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<210> 524

<400> 524
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<210> 525
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized C8 heavy chain variable region sequence from IGHV321*04

<400> 525
gaggtgcagc tggtggagtc tgggggaggc ctggtcaagc ctgggggtc cctgagactc   60

tcctgtgcag cctctggatt caccttcagt ggctatgcca tgagctgggt ccgccaggct   120

ccagggaagg ggctggagtg ggtctcaacc attagtagtg gcggaaccta catatactac   180

cctgactcag tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat   240 ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagactgggc 300

ggcgataact attatgaata ttggggcaaa gggaccacgg tcaccgtctc ctcc 354

<210> 526
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized C8 heavy chain variable region sequence from IGHV321*04

<400> 526

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr Trp Gly Lys Gly Thr
100 105 110

Thr Val Thr Val Ser Ser
115

<210> 527
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized C8 heavy chain variable framework region 1 (FWR1) sequence

<400> 527
gaggtgcagc tggtggagtc tgggggaggc ctggtcaagc ctggggggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt 90

<210> 528
<211> 30
<212> PRT
<213> Artificial Sequence

<220>

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<223>  Humanized C8 heavy chain variable framework region 1 (FWR1)
       sequence

<400>  528

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            20                  25                  30


<210>  529
<211>  15
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C8 heavy chain variable complementarity determining
       region 1 (CDR1) sequence

<400>  529
ggctatgcca tgagc                                                        15


<210>  530
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C8 heavy chain variable complementarity determining
       region 1 (CDR1) sequence

<400>  530

Gly Tyr Ala Met Ser
1               5


<210>  531
<211>  42
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C8 heavy chain variable framework region 2 (FWR2)
       sequence

<400>  531
tgggtccgcc aggctccagg gaaggggctg gagtgggtct ca                          42


<210>  532
<211>  14
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C8 heavy chain variable framework region 2 (FWR2)
       sequence

<400>  532

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
1               5                   10
```

```
<210>  533
<211>  51
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C8 heavy chain variable complementarity determining
       region 2 (CDR2) sequence

<400>  533
accattagta gtggcggaac ctacatatac taccctgact cagtgaaggg c                51


<210>  534
<211>  17
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C8 heavy chain variable complementarity determining
       region 2 (CDR2) sequence

<400>  534

Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val Lys
1               5                   10                  15


Gly



<210>  535
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C8 heavy chain variable framework region 3 (FWR3)
       sequence

<400>  535
cgattcacca tctccagaga caacgccaag aactcactgt atctgcaaat gaacagcctg       60

agagccgagg acacggccgt gtattactgt gcgaga                                 96


<210>  536
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C8 heavy chain variable framework region 3 (FWR3)
       sequence

<400>  536

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
1               5                   10                  15


Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
            20                  25                  30


<210>  537
<211>  27
<212>  DNA
```

<213> Artificial Sequence

<220>
<223> Humanized C8 heavy chain variable complementarity determining
region 3 (CDR3) sequence

<400> 537
ctgggcggcg ataactatta tgaatat   27

<210> 538
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized C8 heavy chain variable complementarity determining
region 3 (CDR3) sequence

<400> 538

Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr
1   5

<210> 539
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized C8 IgG1 heavy chain sequence

<400> 539
gaggtgcagc tggtggagtc tgggggaggc ctggtcaagc ctgggggggtc cctgagactc   60

tcctgtgcag cctctggatt caccttcagt ggctatgcca tgagctgggt ccgccaggct   120

ccagggaagg ggctggagtg ggtctcaacc attagtagtg gcggaaccta catatactac   180

cctgactcag tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat   240

ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagactgggc   300

ggcgataact attatgaata ttggggcaaa gggaccacgg tcaccgtctc ctccgctagc   360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca   420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac   480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc   540

tactccctca gcagcgtggt gacagtgccc tccagcagct tgggcaccca gacctacatc   600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaatct   660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca   720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc   780

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg   840

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg   900

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac   960

aagtgcaagg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc   1020

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc   1080

```
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg     1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac     1200

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag     1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag     1320

agcctctccc tgtctccggg taaatgataa                                      1350


<210>  540
<211>  448
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C8 IgG1 heavy chain sequence

<400>  540

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr Trp Gly Lys Gly Thr
            100                 105                 110


Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125


Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140


Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160


Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175


Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190
```

```
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205


Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220


His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225                 230                 235                 240


Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255


Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270


Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285


Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300


Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320


Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                325                 330                 335


Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350


Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365


Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380


Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                 390                 395                 400


Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415


Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430


Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445


<210>  541
<211>  1338
<212>  DNA
<213>  Artificial Sequence
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<220>
<223> Humanized C8 IgG2 heavy chain sequence

<400> 541
gaggtgcagc tggtggagtc tgggggaggc ctggtcaagc ctggggggtc cctgagactc   60

tcctgtgcag cctctggatt caccttcagt ggctatgcca tgagctgggt ccgccaggct   120

ccagggaagg ggctggagtg ggtctcaacc attagtagtg gcggaaccta catatactac   180

cctgactcag tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat   240

ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagactgggc   300

ggcgataact attatgaata ttggggcaaa gggaccacgg tcaccgtctc ctccgcctcc   360

accaagggcc catcggtctt ccccctggcg ccctgctcca ggagcacctc cgagagcaca   420

gccgccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac   480

tcaggcgctc tgaccagcgg cgtgcacacc ttcccagctg tcctacagtc ctcaggactc   540

tactccctca gcagcgtggt gaccgtgccc tccagcaact tcggcaccca gacctacacc   600

tgcaacgtag atcacaagcc cagcaacacc aaggtggaca agacagttga gcgcaaatgt   660

tgtgtcgagt gcccaccgtg cccagcacca cctgtggcag gaccgtcagt cttcctcttc   720

cccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac gtgcgtggtg   780

gtggacgtga gccacgaaga ccccgaggtc cagttcaact ggtacgtgga cggcgtggag   840

gtgcataatg ccaagacaaa gccacgggag gagcagttca acagcacgtt ccgtgtggtc   900

agcgtcctca ccgttgtgca ccaggactgg ctgaacggca aggagtacaa gtgcaaggtc   960

tccaacaaag gcctcccagc ccccatcgag aaaaccatct ccaaaaccaa agggcagccc   1020

cgagaaccac aggtgtacac cctgccccca tcccgggagg agatgaccaa gaaccaggtc   1080

agcctgacct gcctggtcaa aggcttctac cccagcgaca tcgccgtgga gtgggagagc   1140

aatgggcagc cggagaacaa ctacaagacc acacctccca tgctggactc cgacggctcc   1200

ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc   1260

tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg   1320

tctccgggta aatagtaa   1338

<210> 542
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized C8 IgG2 heavy chain sequence

<400> 542

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
            20   25   30

```
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr Trp Gly Lys Gly Thr
            100                 105                 110

Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr
    290                 295                 300
```

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305   310   315   320

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
                325   330   335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
            340   345   350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355   360   365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370   375   380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser
385   390   395   400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
                405   410   415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            420   425   430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435   440

<210> 543
<211> 306
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse C8 light chain variable region sequence

<400> 543
gacatcgtca ttacgcagac ccctgccagt cttgccgttt ctctgggcca gagggccact   60

atcagttaca gggcgagtaa gtctgtgagt accagcggct atagttacat gcattggaac   120

cagcagaaac cgggacagcc accacgcctg cttatttatc tggtgtctaa tcttgagtcc   180

ggggtgcccg ccaggttcag cggcagcggc tctgggaccg acttcacact caacattcat   240

ccagtggaag aagaggacgc tgctacatac tactgtcaac acattcggga actgaccagg   300

agtgaa   306

<210> 544
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse C8 light chain variable region sequence

<400> 544

Asp Ile Val Ile Thr Gln Thr Pro Ala Ser Leu Ala Val Ser Leu Gly

```
1               5                   10                  15


Gln Arg Ala Thr Ile Ser Tyr Arg Ala Ser Lys Ser Val Ser Thr Ser
            20                  25                  30


Gly Tyr Ser Tyr Met His Trp Asn Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45


Arg Leu Leu Ile Tyr Leu Val Ser Asn Leu Glu Ser Gly Val Pro Ala
    50                  55                  60


Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80


Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ile Arg
                85                  90                  95


Glu Leu Thr Arg Ser Glu
            100


<210>  545
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse C8 light chain variable complementarity determining region
       1 (CDR1) sequence

<400>  545
agggcgagta agtctgtgag taccagcggc tatagttaca tgcat                       45


<210>  546
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse C8 light chain variable complementarity determining region
       1 (CDR1) sequence

<400>  546

Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr Met His
1               5                   10                  15


<210>  547
<211>  21
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse C8 light chain variable complementarity determining region
       2 (CDR2) sequence

<400>  547
ctggtgtcta atcttgagtc c                                                 21


<210>  548
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```
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse C8 light chain variable complementarity determining region
       2 (CDR2) sequence

<400>  548

Leu Val Ser Asn Leu Glu Ser
1               5


<210>  549
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse C8 light chain variable complementarity determining region
       3 (CDR3) sequence

<400>  549
caacacattc gggaactgac caggagtgaa                                        30


<210>  550
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse C8 light chain variable complementarity determining region
       3 (CDR3) sequence

<400>  550

Gln His Ile Arg Glu Leu Thr Arg Ser Glu
1               5                   10


<210>  551

<400>  551
000

<210>  552

<400>  552
000

<210>  553

<400>  553
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<210>  554

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<210>  556
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<400> 556
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<210> 564

<400> 564
000

<210> 565
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized C8 light chain variable region sequence from NCBI
       germline z00023

<400> 565

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gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc       60

atcaactgca gggccagcaa gagtgttagc accagcggct acagctacat gcactggtac      120

cagcagaaac caggacagcc tcctaagctg ctcatttacc tggtgtctaa cctggaatcc      180

ggggtccctg accgattcag tggcagcggg tctgggacag atttcactct caccatcagc      240

agcctgcagg ctgaagatgt ggcagtttat tactgtcaac acattcggga actgaccagg      300

agtgaattcg gcggagggac caaggtggag atcaaacgaa ct                         342
```

<210> 566
<211> 114
<212> PRT

```
<213>  Artificial Sequence

<220>
<223>  Humanized C8 light chain variable region sequence from NCBI
       germline z00023

<400>  566

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15


Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20                  25                  30


Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45


Lys Leu Leu Ile Tyr Leu Val Ser Asn Leu Glu Ser Gly Val Pro Asp
    50                  55                  60


Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80


Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln His Ile Arg
                85                  90                  95


Glu Leu Thr Arg Ser Glu Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


Arg Thr



<210>  567
<211>  69
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C8 light chain variable framework region 1 (FWR1)
       sequence

<400>  567
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc       60

atcaactgc                                                               69


<210>  568
<211>  23
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C8 light chain variable framework region 1 (FWR1)
       sequence

<400>  568

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15
```

```
Glu Arg Ala Thr Ile Asn Cys
            20


<210>  569
<211>  42
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C8 light chain variable complementarity determining
       region 1 (CDR1) sequence

<400>  569
agggccagca agagtgttag caccagcggc tacagctaca tg                          42


<210>  570
<211>  14
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C8 light chain variable complementarity determining
       region 1 (CDR1) sequence

<400>  570

Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr Met
1               5                   10


<210>  571
<211>  48
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C8 light chain variable framework region 2 (FWR2)
       sequence

<400>  571
cactggtacc agcagaaacc aggacagcct cctaagctgc tcatttac                    48


<210>  572
<211>  16
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C8 light chain variable framework region 2 (FWR2)
       sequence

<400>  572

His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
1               5                   10                  15


<210>  573
<211>  21
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C8 light chain variable complementarity determining
       region 2 (CDR2) sequence
```

```
<400>  573
ctggtgtcta acctggaatc c                                                 21


<210>  574
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C8 light chain variable complementarity determining
       region 2 (CDR2) sequence

<400>  574

Leu Val Ser Asn Leu Glu Ser
1               5


<210>  575
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C8 light chain variable framework region 3 (FWR3)
       sequence

<400>  575
ggggtccctg accgattcag tggcagcggg tctgggacag atttcactct caccatcagc       60

agcctgcagg ctgaagatgt ggcagtttat tactgt                                 96


<210>  576
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C8 light chain variable framework region 3 (FWR3)
       sequence

<400>  576

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1               5                   10                  15


Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
            20                  25                  30


<210>  577
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C8 light chain variable complementarity determining
       region 3 (CDR3) sequence

<400>  577
caacacattc gggaactgac caggagtgaa                                        30


<210>  578
<211>  10
```

```
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C8 light chain variable complementarity determining
       region 3 (CDR3) sequence

<400>  578

Gln His Ile Arg Glu Leu Thr Arg Ser Glu
1               5                   10


<210>  579
<211>  666
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C8 Lambda light chain sequence

<400>  579
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc       60

atcaactgca gggccagcaa gagtgttagc accagcggct acagctacat gcactggtac      120

cagcagaaac caggacagcc tcctaagctg ctcatttacc tggtgtctaa cctggaatcc      180

ggggtccctg accgattcag tggcagcggg tctgggacag atttcactct caccatcagc      240

agcctgcagg ctgaagatgt ggcagtttat tactgtcaac acattcggga actgaccagg      300

agtgaattcg gcggagggac caaggtggag atcaaacgaa ctggtcagcc caaggctgcc      360

ccctcggtca ctctgttccc gccctcctct gaggagcttc aagccaacaa ggccacactg      420

gtgtgtctca taagtgactt ctacccggga gccgtgacag tggcctggaa ggcagatagc      480

agccccgtca aggcgggagt ggagaccacc acaccctcca aacaaagcaa caacaagtac      540

gcggccagca gctatctgag cctgacgcct gagcagtgga agtcccacag aagctacagc      600

tgccaggtca cgcatgaagg gagcaccgtg gagaagacag tggcccctac agaatgttca      660

tagtaa                                                                 666


<210>  580
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C8 Lambda light chain sequence

<400>  580

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15


Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20                  25                  30


Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45
```

Lys Leu Leu Ile Tyr Leu Val Ser Asn Leu Glu Ser Gly Val Pro Asp
    50   55   60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln His Ile Arg
                85   90   95

Glu Leu Thr Arg Ser Glu Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

Arg Thr Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro
        115   120   125

Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile
    130   135   140

Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser
145   150   155   160

Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser
                165   170   175

Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln
            180   185   190

Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser
        195   200   205

Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
    210   215   220

<210> 581
<211> 666
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized C8 Kappa light chain sequence

<400> 581
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc   60

atcaactgca gggccagcaa gagtgttagc accagcggct acagctacat gcactggtac   120

cagcagaaac caggacagcc tcctaagctg ctcatttacc tggtgtctaa cctggaatcc   180

ggggtccctg accgattcag tggcagcggg tctgggacag atttcactct caccatcagc   240

agcctgcagg ctgaagatgt ggcagtttat tactgtcaac acattcggga actgaccagg   300

agtgaattcg gcggagggac caaggtggag atcaaacgaa ctacggtggc tgcaccatct   360

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc   420

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc   480

```
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc      540

ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc      600

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt      660

tagtaa                                                                 666


<210>  582
<211>  220
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized C8 Kappa light chain sequence

<400>  582

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15


Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20                  25                  30


Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45


Lys Leu Leu Ile Tyr Leu Val Ser Asn Leu Glu Ser Gly Val Pro Asp
    50                  55                  60


Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80


Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln His Ile Arg
                85                  90                  95


Glu Leu Thr Arg Ser Glu Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


Arg Thr Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
        115                 120                 125


Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130                 135                 140


Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145                 150                 155                 160


Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165                 170                 175


Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180                 185                 190


Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
        195                 200                 205
```

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210   215   220

<210> 583

<400> 583
000

<210> 584
<211> 942
<212> DNA
<213> Artificial Sequence

<220>
<223> CART E6 CD8 sequence

<400> 584
gaggtccagc tggttgagag tggcggtggg ctggttaagc ctggcggctc cctgcggctg   60

agctgcgccg cgagtggatt tactttcagc cgatatggga tgagttgggt gcggcaagct   120

cccgggaaga ggctggaatg ggtctcaaca atctccgggg ggggcactta catctattac   180

cccgactcag tcaaggggag atttaccatt tcacgagaca acgctaagaa taccctgtat   240

ttgcagatga attctctgag agcagaggac acagctgttt actattgtac ccgcgacaac   300

tatggcagga actacgacta cggtatggac tattggggac aagggacatt ggttacagtg   360

agcagtggcg gcgggggcag cggaggagga ggcagcggtg gggggggcag cgagatagtg   420

ctcacgcagt cacccgcgac tctcagtctc tcacctgggg aacgagctac cctgacgtgc   480

tctgctacct cctcagtgtc atatattcac tggtatcagc aacggcccgg gcagtcccct   540

agattgctca tttatagtac ctctaatctg gcctcaggta tccctgcacg attttctgga   600

tctggttcag gttctgatta caccctcact atctctagcc tggagcctga agactttgcc   660

gtttattact gccagcagag gtctagctcc ccattcacct ttgggagtgg gaccaaggtt   720

gaaattaaaa cgacaacccc ggcccccaga ccaccaacgc cagcccccac catcgccagc   780

caacccctgt ctctgagacc agaagcctgt aggcctgccg ccggtggagc tgtgcacaca   840

agaggactgg atttcgcctg tgatatctac atttgggccc cgctcgcagg cacatgtgga   900

gtgctcctcc tctccctggt gattaccctg tactgctgat aa   942

<210> 585
<211> 312
<212> PRT
<213> Artificial Sequence

<220>
<223> CART E6 CD8 sequence

<400> 585

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
            20   25   30

```
Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Arg Leu Glu Trp Val
        35                  40                  45

Ser Thr Ile Ser Gly Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Thr Arg Asp Asn Tyr Gly Arg Asn Tyr Asp Tyr Gly Met Asp Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
    130                 135                 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
145                 150                 155                 160

Ser Ala Thr Ser Ser Val Ser Tyr Ile His Trp Tyr Gln Gln Arg Pro
                165                 170                 175

Gly Gln Ser Pro Arg Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala Ser
            180                 185                 190

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Tyr Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
    210                 215                 220

Gln Gln Arg Ser Ser Ser Pro Phe Thr Phe Gly Ser Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
                245                 250                 255

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
            260                 265                 270

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
        275                 280                 285

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
    290                 295                 300
```

```
Ser Leu Val Ile Thr Leu Tyr Cys
305                 310


<210>  586
<211>  960
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CART C2 CD8 CD8 sequence - NCD8lshuMNC2scFvCD8ecd fragment CD8
       transmembraneC

<400>  586
gaagtgcagc tcgtagagag tggcgggggga ctggtgaagc ccggtggaag cctcagactc       60

agttgcgccg cctcaggttt cactttttca ggttacgcca tgtcctgggt aagacaggca      120

ccggggaaag gactcgagtg ggtgtctact atcagctcag gaggcactta tatatattat      180

cctgactctg taaaaggccg atttacgatt tctcgcgaca atgcaaagaa ctccctctac      240

ctccaaatga acagtcttag ggcagaagac actgctgtat actattgtgc acgcctcggc      300

ggcgacaact actacgagta ctttgacgtg tgggggaaag ggactaccgt gacagtttca      360

agcggaggag gtggctcagg tggaggcggg tcaggggggg gaggaagtga tattgtgctc      420

acacaatccc cagcctccct ggctgtgtct cccggccaac gcgctacaat tacatgtcgg      480

gcctccaaaa gcgtgagcac cagcggctac agctacatgc actggtatca acagaaacca      540

ggacaacccc ccaaactgtt gatttatctc gcttcaaact tggagtccgg cgtgcctgcg      600

cgcttttcag ggagtgggag cggcacagat tttacgctga ctatcaaccc cgtagaagca      660

aacgatacag cgaattatta ttgtcaacat tcccgggaac tcccctttac gttcggcggg      720

ggcacaaagg tcgaaattaa gagaaccacg acaaccccgg cccccagacc accaacgcca      780

gcccccacca tcgccagcca acccctgtct ctgagaccag aagcctgtag gcctgccgcc      840

ggtggagctg tgcacacaag aggactggat ttcgcctgtg atatctacat ttgggccccg      900

ctcgcaggca catgtggagt gctcctcctc tccctggtga ttaccctgta ctgctgataa      960


<210>  587
<211>  318
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CART C2 CD8 CD8 sequence - NCD8lshuMNC2scFvCD8ecd fragment CD8
       transmembraneC

<400>  587

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ser Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr Phe Asp Val Trp Gly
            100                 105                 110

Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro
    130                 135                 140

Ala Ser Leu Ala Val Ser Pro Gly Gln Arg Ala Thr Ile Thr Cys Arg
145                 150                 155                 160

Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr Met His Trp Tyr
                165                 170                 175

Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser
            180                 185                 190

Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asn Asp Thr Ala
    210                 215                 220

Asn Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Phe Thr Phe Gly Gly
225                 230                 235                 240

Gly Thr Lys Val Glu Ile Lys Arg Thr Thr Thr Thr Pro Ala Pro Arg
                245                 250                 255

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
            260                 265                 270

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
        275                 280                 285

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
    290                 295                 300

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
305                 310                 315
```

<210> 588
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> CD8/41BB sequence - N CD8 transmembrane 41BBC

<400> 588
acgacaaccc cggcccccag accaccaacg ccagccccca ccatcgccag ccaacccctg 60

tctctgagac cagaagcctg taggcctgcc gccggtggag ctgtgcacac aagaggactg 120

gatttcgcct gtgatatcta catttgggcc ccgctcgcag gcacatgtgg agtgctcctc 180

ctctccctgg tgattaccct gtactgcaaa aggggccgca aaaaactcct ttacattttt 240

aagcagcctt ttatgaggcc agtacagacg actcaagagg aagacgggtg ctcatgccgc 300

tttcctgagg aggaggaagg agggtgcgaa ctgtgataa 339

<210> 589
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> CD8/41BB sequence - N CD8 transmembrane 41BBC

<400> 589

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1 5 10 15

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
20 25 30

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
35 40 45

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
50 55 60

Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
65 70 75 80

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
85 90 95

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
100 105 110

<210> 590
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> CD8/CD28 sequence - N CD8 transmembrane CD28C

<400> 590
acgacaaccc cggcccccag accaccaacg ccagccccca ccatcgccag ccaacccctg 60

tctctgagac cagaagcctg taggcctgcc gccggtggag ctgtgcacac aagaggactg 120

gatttcgcct gtgatatcta catttgggcc ccgctcgcag gcacatgtgg agtgctcctc 180

ctctccctgg tgattaccct gtactgcaga agcaagcggt ctcggctcct gcattctgat 240

tacatgaaca tgaccccaag aagaccaggc ccccaccagga aacattacca gccctacgct 300

ccgccacgcg acttcgctgc ctaccggtcc tgataa 336

<210> 591
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> CD8/CD28 sequence - N CD8 transmembrane CD28C

<400> 591

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1 5 10 15

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
20 25 30

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
35 40 45

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
50 55 60

Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
65 70 75 80

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
85 90 95

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
100 105 110

<210> 592
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> CD8/CD3z sequence - N CD8 transmembrane CD3zetaC

<400> 592
acgacaaccc cggcccccag accaccaacg ccagccccca ccatcgccag ccaacccctg 60

tctctgagac cagaagcctg taggcctgcc gccggtggag ctgtgcacac aagaggactg 120

gatttcgcct gtgatatcta catttgggcc ccgctcgcag gcacatgtgg agtgctcctc 180

ctctccctgg tgattaccct gtactgccgc gttaagttct cccgatcagc cgacgcgcct 240

```
gcttacaagc agggccagaa ccaactgtac aacgagctga atctcggtag acgggaagag      300

tacgacgtgt tggacaaacg gagaggccgc gacccagaaa tgggcggcaa gcctcgcagg      360

aaaaaccccc aggagggact gtacaatgag ttgcagaaag ataagatggc agaagcttat      420

agcgagatcg gaatgaaggg ggaaaggaga cgagggaaag gacacgacgg cctttatcag      480

ggcctgtcca cagcaacaaa agatacgtat gacgccctcc atatgcaggc acttccacca      540

cggtgataa                                                              549


<210>  593
<211>  181
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD8/CD3z sequence - N CD8 transmembrane CD3zetaC

<400>  593

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1               5                   10                  15


Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
            20                  25                  30


Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
        35                  40                  45


Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
    50                  55                  60


Ile Thr Leu Tyr Cys Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
65                  70                  75                  80


Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
                85                  90                  95


Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
            100                 105                 110


Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
        115                 120                 125


Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
    130                 135                 140


Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
145                 150                 155                 160


Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
                165                 170                 175


Ala Leu Pro Pro Arg
            180
```

<210> 594
<211> 672
<212> DNA
<213> Artificial Sequence

<220>
<223> CD8/CD28/CD3z sequence - N CD8 transmembrane CD28 CD3zetaC

<400> 594

```
acgacaaccc cggcccccag accaccaacg ccagccccca ccatcgccag ccaacccctg       60

tctctgagac cagaagcctg taggcctgcc gccggtggag ctgtgcacac aagaggactg      120

gatttcgcct gtgatatcta catttgggcc ccgctcgcag gcacatgtgg agtgctcctc      180

ctctccctgg tgattaccct gtactgcaga agcaagcggt ctcggctcct gcattctgat      240

tacatgaaca tgaccccaag aagaccaggc ccccaccagga aacattacca gccctacgct      300

ccgccacgcg acttcgctgc ctaccggtcc cgcgttaagt tctcccgatc agccgacgcg      360

cctgcttaca agcagggcca gaaccaactg tacaacgagc tgaatctcgg tagacgggaa      420

gagtacgacg tgttggacaa acggagaggc cgcgacccag aaatgggcgg caagcctcgc      480

aggaaaaacc cccaggaggg actgtacaat gagttgcaga aagataagat ggcagaagct      540

tatagcgaga tcggaatgaa gggggaaagg agacgaggga aaggacacga cggcctttat      600

cagggcctgt ccacagcaac aaaagatacg tatgacgccc tccatatgca ggcacttcca      660

ccacggtgat aa                                                          672
```

<210> 595
<211> 222
<212> PRT
<213> Artificial Sequence

<220>
<223> CD8/CD28/CD3z sequence - N CD8 transmembrane CD28 CD3zetaC

<400> 595

```
Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1               5                   10                  15


Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
            20                  25                  30


Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
        35                  40                  45


Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
    50                  55                  60


Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
65                  70                  75                  80


Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
                85                  90                  95
```

```
Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val
            100                 105                 110

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn
        115                 120                 125

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
    130                 135                 140

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
145                 150                 155                 160

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
                165                 170                 175

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
            180                 185                 190

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
        195                 200                 205

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
    210                 215                 220


<210>  596
<211>  675
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CD8/41BB/CD3z sequence - N CD8 transmembrane 41BB CD3zetaC

<400>  596
acgacaaccc cggcccccag accaccaacg ccagccccca ccatcgccag ccaacccctg       60

tctctgagac cagaagcctg taggcctgcc gccggtggag ctgtgcacac aagaggactg      120

gatttcgcct gtgatatcta catttgggcc ccgctcgcag gcacatgtgg agtgctcctc      180

ctctccctgg tgattaccct gtactgcaaa aggggccgca aaaaactcct ttacattttt      240

aagcagcctt ttatgaggcc agtacagacg actcaagagg aagacgggtg ctcatgccgc      300

tttcctgagg aggaggaagg agggtgcgaa ctgcgcgtta agttctcccg atcagccgac      360

gcgcctgctt acaagcaggg ccagaaccaa ctgtacaacg agctgaatct cggtagacgg      420

gaagagtacg acgtgttgga caaacggaga ggccgcgacc cagaaatggg cggcaagcct      480

cgcaggaaaa acccccagga gggactgtac aatgagttgc agaaagataa gatggcagaa      540

gcttatagcg agatcggaat gaagggggaa aggagacgag ggaaaggaca cgacggcctt      600

tatcagggcc tgtccacagc aacaaaagat acgtatgacg ccctccatat gcaggcactt      660

ccaccacggt gataa                                                       675


<210>  597
<211>  223
```

<212> PRT
<213> Artificial Sequence

<220>
<223> CD8/41BB/CD3z sequence - N CD8 transmembrane 41BB CD3zetaC

<400> 597

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1   5   10   15

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
            20   25   30

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
        35   40   45

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
    50   55   60

Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
65   70   75   80

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
                85   90   95

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg
            100   105   110

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln
        115   120   125

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
    130   135   140

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
145   150   155   160

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
                165   170   175

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
            180   185   190

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
        195   200   205

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
    210   215   220

<210> 598
<211> 798
<212> DNA
<213> Artificial Sequence

<220>
<223> CD8/CD28/41BB/CD3z sequence - N CD8 transmembrane CD28 41BB
       CD3zetaC

<400> 598
acgacaaccc cggcccccag accaccaacg ccagccccca ccatcgccag ccaacccctg   60

tctctgagac cagaagcctg taggcctgcc gccggtggag ctgtgcacac aagaggactg   120

gatttcgcct gtgatatcta catttgggcc ccgctcgcag gcacatgtgg agtgctcctc   180

ctctccctgg tgattaccct gtactgcaga agcaagcggt ctcggctcct gcattctgat   240

tacatgaaca tgaccccaag aagaccaggc cccaccagga aacattacca gccctacgct   300

ccgccacgcg acttcgctgc ctaccggtcc aaaaggggcc gcaaaaaact cctttacatt   360

tttaagcagc cttttatgag gccagtacag acgactcaag aggaagacgg gtgctcatgc   420

cgctttcctg aggaggagga aggagggtgc gaactgcgcg ttaagttctc ccgatcagcc   480

gacgcgcctg cttacaagca gggccagaac caactgtaca acgagctgaa tctcggtaga   540

cgggaagagt acgacgtgtt ggacaaacgg agaggccgcg acccagaaat gggcggcaag   600

cctcgcagga aaaacccccca ggagggactg tacaatgagt tgcagaaaga taagatggca   660

gaagcttata gcgagatcgg aatgaagggg gaaaggagac gagggaaagg acacgacggc   720

ctttatcagg gcctgtccac agcaacaaaa gatacgtatg acgccctcca tatgcaggca   780

cttccaccac ggtgataa   798

<210> 599
<211> 264
<212> PRT
<213> Artificial Sequence

<220>
<223> CD8/CD28/41BB/CD3z sequence - N CD8 transmembrane CD28 41BB
       CD3zetaC

<400> 599

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1   5   10   15

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
            20   25   30

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
        35   40   45

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
    50   55   60

Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
65   70   75   80

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
                85   90   95

```
Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg
            100                 105                 110


Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro
        115                 120                 125


Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu
    130                 135                 140


Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala
145                 150                 155                 160


Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
                165                 170                 175


Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
            180                 185                 190


Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
        195                 200                 205


Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
    210                 215                 220


Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
225                 230                 235                 240


Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
                245                 250                 255


His Met Gln Ala Leu Pro Pro Arg
            260


<210>  600

<400>  600
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<210>  601

<400>  601
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<210> 605

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<210> 607

<400> 607
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<210> 608
<211> 1482
<212> DNA
<213> Artificial Sequence

<220>
<223> CART C2 CD8/CD8/CD28/CD3z sequence - NCD8lshuMNC2scFvCD8ecd
       fragment CD8 transmembrane CD28 CD3zetaC

<400> 608
atggccttgc cagtgacggc cctgctgctg ccattggctc ttctgttgca cgctgccagg   60

cctgaagtgc agctcgtaga gagtggcggg ggactggtga agcccggtgg aagcctcaga   120

ctcagttgcg ccgcctcagg tttcactttt tcaggttacg ccatgtcctg ggtaagacag   180

gcaccgggga aaggactcga gtgggtgtct actatcagct caggaggcac ttatatatat   240

tatcctgact ctgtaaaagg ccgatttacg atttctcgcg acaatgcaaa gaactccctc   300

tacctccaaa tgaacagtct tagggcagaa gacactgctg tatactattg tgcacgcctc   360

ggcggcgaca actactacga gtactttgac gtgtggggga aagggactac cgtgacagtt   420

tcaagcggag gaggtggctc aggtggaggc gggtcagggg ggggaggaag tgatattgtg   480

ctcacacaat ccccagcctc cctggctgtg tctcccggcc aacgcgctac aattacatgt   540

cgggcctcca aaagcgtgag caccagcggc tacagctaca tgcactggta tcaacagaaa   600

ccaggacaac cccccaaact gttgatttat ctcgcttcaa acttggagtc cggcgtgcct   660

gcgcgctttt cagggagtgg gagcggcaca gattttacgc tgactatcaa ccccgtagaa   720

gcaaacgata cagcgaatta ttattgtcaa cattcccggg aactcccctt tacgttcggc   780

gggggcacaa aggtcgaaat taagagaacc acgacaaccc cggcccccag accaccaacg   840

ccagcccccа ccatcgccag ccaacccctg tctctgagac cagaagcctg taggcctgcc   900

gccggtggag ctgtgcacac aagaggactg gatttcgcct gtgatatcta catttgggcc   960

ccgctcgcag gcacatgtgg agtgctcctc ctctccctgg tgattaccct gtactgcaga   1020

agcaagcggt ctcggctcct gcattctgat tacatgaaca tgaccccaag aagaccaggc   1080

cccaccagga aacattacca gccctacgct ccgccacgcg acttcgctgc ctaccggtcc   1140

cgcgttaagt tctcccgatc agccgacgcg cctgcttaca agcagggcca gaaccaactg   1200

tacaacgagc tgaatctcgg tagacgggaa gagtacgacg tgttggacaa acggagaggc   1260

cgcgacccag aaatgggcgg caagcctcgc aggaaaaacc cccaggaggg actgtacaat   1320 gagttgcaga aagataagat ggcagaagct tatagcgaga tcggaatgaa gggggaaagg   1380

agacgaggga aaggacacga cggcctttat cagggcctgt ccacagcaac aaaagatacg   1440

tatgacgccc tccatatgca ggcacttcca ccacggtgat aa   1482

<210> 609
<211> 492
<212> PRT
<213> Artificial Sequence

<220>
<223> CART C2 CD8/CD8/CD28/CD3z sequence - NCD8lshuMNC2scFvCD8ecd
       fragment CD8 transmembrane CD28 CD3zetaC

<400> 609

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1   5   10   15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
            20   25   30

Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
        35   40   45

Thr Phe Ser Gly Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
    50   55   60

Gly Leu Glu Trp Val Ser Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr
65   70   75   80

Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
                85   90   95

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
            100   105   110

Ala Val Tyr Tyr Cys Ala Arg Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr
        115   120   125

Phe Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly
    130   135   140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
145   150   155   160

Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Pro Gly Gln Arg Ala
                165   170   175

Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser
            180   185   190

Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu
        195   200   205

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Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser
    210                 215                 220

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu
225                 230                 235                 240

Ala Asn Asp Thr Ala Asn Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro
                245                 250                 255

Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Thr Thr
            260                 265                 270

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
        275                 280                 285

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
    290                 295                 300

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
305                 310                 315                 320

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
                325                 330                 335

Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
            340                 345                 350

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
        355                 360                 365

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe
    370                 375                 380

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu
385                 390                 395                 400

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
                405                 410                 415

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
            420                 425                 430

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
        435                 440                 445

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
    450                 455                 460

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
465                 470                 475                 480
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Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485                 490


<210>  610
<211>  1485
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CART C2 CD8/CD8/41BB/CD3z sequence #13 - NCD8lshuMNC2scFvCD8ecd
       fragment CD8 transmembrane 41BB CD3zetaC

<400>  610
atggccttgc cagtgacggc cctgctgctg ccattggctc ttctgttgca cgctgccagg       60

cctgaagtgc agctcgtaga gagtggcggg ggactggtga agcccggtgg aagcctcaga      120

ctcagttgcg ccgcctcagg tttcactttt tcaggttacg ccatgtcctg ggtaagacag      180

gcaccgggga aaggactcga gtgggtgtct actatcagct caggaggcac ttatatatat      240

tatcctgact ctgtaaaagg ccgatttacg atttctcgcg acaatgcaaa gaactccctc      300

tacctccaaa tgaacagtct tagggcagaa gacactgctg tatactattg tgcacgcctc      360

ggcggcgaca actactacga gtactttgac gtgtgggggа aagggactac cgtgacagtt      420

tcaagcggag gaggtggctc aggtggaggc gggtcagggg ggggaggaag tgatattgtg      480

ctcacacaat ccccagcctc cctggctgtg tctcccggcc aacgcgctac aattacatgt      540

cgggcctcca aaagcgtgag caccagcggc tacagctaca tgcactggta tcaacagaaa      600

ccaggacaac cccccaaact gttgatttat ctcgcttcaa acttggagtc cggcgtgcct      660

gcgcgctttt cagggagtgg gagcggcaca gattttacgc tgactatcaa ccccgtagaa      720

gcaaacgata cagcgaatta ttattgtcaa cattcccggg aactcccctt tacgttcggc      780

gggggcacaa aggtcgaaat taagagaacc acgacaaccc cggcccccag accaccaacg      840

ccagccccca ccatcgccag ccaacccctg tctctgagac cagaagcctg taggcctgcc      900

gccggtggag ctgtgcacac aagaggactg gatttcgcct gtgatatcta catttgggcc      960

ccgctcgcag gcacatgtgg agtgctcctc ctctccctgg tgattaccct gtactgcaaa     1020

aggggccgca aaaaactcct ttacattttt aagcagcctt ttatgaggcc agtacagacg     1080

actcaagagg aagacgggtg ctcatgccgc tttcctgagg aggaggaagg agggtgcgaa     1140

ctgcgcgtta agttctcccg atcagccgac gcgcctgctt acaagcaggg ccagaaccaa     1200

ctgtacaacg agctgaatct cggtagacgg gaagagtacg acgtgttgga caaacggaga     1260

ggccgcgacc cagaaatggg cggcaagcct cgcaggaaaa acccccagga gggactgtac     1320

aatgagttgc agaaagataa gatggcagaa gcttatagcg agatcggaat gaagggggaa     1380

aggagacgag ggaaaggaca cgacggcctt tatcagggcc tgtccacagc aacaaaagat     1440

acgtatgacg ccctccatat gcaggcactt ccaccacggt gataa                     1485


<210>  611
<211>  493
<212>  PRT
<213>  Artificial Sequence
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<220>
<223>  CART C2 CD8/CD8/41BB/CD3z sequence #13 - NCD8lshuMNC2scFvCD8ecd
       fragment CD8 transmembrane 41BB CD3zetaC

<400>  611

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15


His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
                20                  25                  30


Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
            35                  40                  45


Thr Phe Ser Gly Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
        50                  55                  60


Gly Leu Glu Trp Val Ser Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr
65                  70                  75                  80


Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
                85                  90                  95


Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
                100                 105                 110


Ala Val Tyr Tyr Cys Ala Arg Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr
            115                 120                 125


Phe Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly
        130                 135                 140


Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
145                 150                 155                 160


Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Pro Gly Gln Arg Ala
                165                 170                 175


Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser
                180                 185                 190


Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu
            195                 200                 205


Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser
        210                 215                 220


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu
225                 230                 235                 240


Ala Asn Asp Thr Ala Asn Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro
                245                 250                 255
```

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Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Thr Thr
            260                 265                 270

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
        275                 280                 285

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
    290                 295                 300

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
305                 310                 315                 320

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
                325                 330                 335

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
            340                 345                 350

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
        355                 360                 365

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
    370                 375                 380

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
385                 390                 395                 400

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
                405                 410                 415

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
            420                 425                 430

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
        435                 440                 445

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
    450                 455                 460

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
465                 470                 475                 480

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485                 490
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<210> 612

<400> 612
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<210> 613

<400> 613
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<210> 614

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<210> 616

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<210> 618

<400> 618
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<210> 619

<400> 619
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<210> 620
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> MUC1 truncated extra cellular domain sequence

<400> 620

Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu
1   5   10   15

Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe
            20   25   30

Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr
        35   40

<210> 621
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<223> MUC1 truncated extra cellular domain sequence

<400> 621

Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn
1   5   10   15

```
Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala
            20                  25                  30


Ser Arg Tyr
        35


<210>  622
<211>  24
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  MUC1 truncated extra cellular domain sequence

<400>  622

Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp
1               5                   10                  15


Val Glu Thr Gln Phe Asn Gln Tyr
            20


<210>  623
<211>  24
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  MUC1 truncated extra cellular domain sequence

<400>  623

Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu
1               5                   10                  15


Ala Phe Arg Glu Gly Thr Ile Asn
            20


<210>  624
<211>  28
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer

<400>  624
attctaagct tgggccacca tggaactg                                        28


<210>  625
<211>  41
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer

<400>  625
tctagagttt aaacttacta tttacccgga gacagggaga g                         41


<210>  626
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<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 626
agtatggccc agccggccga ggtgcagctg gtggagtctg g   41

<210> 627
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 627
tagaaggcac agtcgaggct gatcag   26

<210> 628
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 628
attctaagct tgggccacca tggaagc   27

<210> 629
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 629
tctagagttt aaacttacta acactctccc ctgttgaagc   40

<210> 630
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 630
agtatggccc agccggccga aattgtgttg acacagtctc cag   43

<210> 631
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 631
tagaaggcac agtcgaggct gatcag   26

<210> 632
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 632
actgtcatat ggaggtgcag ctggtggagt ctg   33

<210> 633
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 633
actgtctcga gtttaatttc cactttggtg ccgctgc   37

<210> 634
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 634
actgtcatat ggaggtgcag ctggtggagt ctg   33

<210> 635
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 635
actgtaccgg ttttaatttc cactttggtg ccgctgc   37

<210> 636
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 636
cttcttcctc aggagcaagc tcaccgtgg   29

<210> 637
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 637
gagccgtcgg agtccagc   18

<210> 638
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 638
gcacctgaac tcctgggg   18

<210> 639
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 639
tttaatttcc actttggtgc cg   22

<210> 640
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 640
cgcggctagc ttaagcttgg taccgagggc ca   32

<210> 641
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 641
cgcggcggcc gcctgatcag cgggtttaaa cttatc   36

<210> 642
<211> 2151
<212> DNA
<213> Artificial Sequence

<220>
<223> MMP9 sequence

<400> 642
atgagcctct ggcagcccct ggtcctggtg ctcctggtgc tgggctgctg ctttgctgcc   60

cccagacagc gccagtccac ccttgtgctc ttccctggag acctgagaac caatctcacc   120

gacaggcagc tggcagagga atacctgtac cgctatggtt acactcgggt ggcagagatg   180

cgtggagagt cgaaatctct ggggcctgcg ctgctgcttc tccagaagca actgtccctg   240 cccgagaccg gtgagctgga tagcgccacg ctgaaggcca tgcgaacccc acggtgcggg 300

gtcccagacc tgggcagatt ccaaaccttt gagggcgacc tcaagtggca ccaccacaac 360

atcacctatt ggatccaaaa ctactcggaa gacttgccgc gggcggtgat tgacgacgcc 420

tttgcccgcg ccttcgcact gtggagcgcg gtgacgccgc tcaccttcac tcgcgtgtac 480

agccgggacg cagacatcgt catccagttt ggtgtcgcgg agcacggaga cgggtatccc 540

ttcgacggga aggacgggct cctggcacac gcctttcctc ctggccccgg cattcaggga 600

gacgcccatt tcgacgatga cgagttgtgg tccctgggca agggcgtcgt ggttccaact 660

cggtttggaa acgcagatgg cgcggcctgc cacttcccct tcatcttcga gggccgctcc 720

tactctgcct gcaccaccga cggtcgctcc gacggcttgc cctggtgcag taccacggcc 780

aactacgaca ccgacgaccg gtttggcttc tgccccagcg agagactcta cacccaggac 840

ggcaatgctg atgggaaacc ctgccagttt ccattcatct tccaaggcca atcctactcc 900

gcctgcacca cggacggtcg ctccgacggc taccgctggt gcgccaccac cgccaactac 960

gaccgggaca agctcttcgg cttctgcccg acccgagctg actcgacggt gatgggggc 1020

aactcggcgg gggagctgtg cgtcttcccc ttcactttcc tgggtaagga gtactcgacc 1080

tgtaccagcg agggccgcgg agatgggcgc ctctggtgcg ctaccacctc gaactttgac 1140

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cctatgtacc gcttcactga ggggcccccc ttgcataagg acgacgtgaa tggcatccgg 1320

cacctctatg gtcctcgccc tgaacctgag ccacggcctc caaccaccac cacaccgcag 1380

cccacggctc ccccgacggt ctgccccacc ggaccccca ctgtccaccc ctcagagcgc 1440

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ccttctacgg ccactactgt gcctttgagt ccggtggacg atgcctgcaa cgtgaacatc 1560

ttcgacgcca tcgcggagat tgggaaccag ctgtatttgt tcaaggatgg gaagtactgg 1620

cgattctctg agggcagggg gagccggccg cagggcccct tccttatcgc cgacaagtgg 1680

cccgcgctgc cccgcaagct ggactcggtc tttgaggagc ggctctccaa gaagcttttc 1740

ttcttctctg ggcgccaggt gtgggtgtac acaggcgcgt cggtgctggg cccgaggcgt 1800

ctggacaagc tgggcctggg agccgacgtg gcccaggtga ccggggccct ccggagtggc 1860

agggggaaga tgctgctgtt cagcgggcgg cgcctctgga ggttcgacgt gaaggcgcag 1920

atggtggatc cccggagcgc cagcgaggtg gaccggatgt tccccggggt gcctttggac 1980

acgcacgacg tcttccagta ccgagagaaa gcctatttct gccaggaccg cttctactgg 2040

cgcgtgagtt cccggagtga gttgaaccag gtggaccaag tgggctacgt gacctatgac 2100

atcctgcagt gccctgagga cgattacaag gatgacgacg ataagtgata a 2151

<210> 643
<211> 715
<212> PRT

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<213>  Artificial Sequence

<220>
<223>  MMP9 sequence

<400>  643

Met Ser Leu Trp Gln Pro Leu Val Leu Val Leu Leu Val Leu Gly Cys
1               5                   10                  15


Cys Phe Ala Ala Pro Arg Gln Arg Gln Ser Thr Leu Val Leu Phe Pro
            20                  25                  30


Gly Asp Leu Arg Thr Asn Leu Thr Asp Arg Gln Leu Ala Glu Glu Tyr
        35                  40                  45


Leu Tyr Arg Tyr Gly Tyr Thr Arg Val Ala Glu Met Arg Gly Glu Ser
    50                  55                  60


Lys Ser Leu Gly Pro Ala Leu Leu Leu Leu Gln Lys Gln Leu Ser Leu
65                  70                  75                  80


Pro Glu Thr Gly Glu Leu Asp Ser Ala Thr Leu Lys Ala Met Arg Thr
                85                  90                  95


Pro Arg Cys Gly Val Pro Asp Leu Gly Arg Phe Gln Thr Phe Glu Gly
            100                 105                 110


Asp Leu Lys Trp His His His Asn Ile Thr Tyr Trp Ile Gln Asn Tyr
        115                 120                 125


Ser Glu Asp Leu Pro Arg Ala Val Ile Asp Asp Ala Phe Ala Arg Ala
    130                 135                 140


Phe Ala Leu Trp Ser Ala Val Thr Pro Leu Thr Phe Thr Arg Val Tyr
145                 150                 155                 160


Ser Arg Asp Ala Asp Ile Val Ile Gln Phe Gly Val Ala Glu His Gly
                165                 170                 175


Asp Gly Tyr Pro Phe Asp Gly Lys Asp Gly Leu Leu Ala His Ala Phe
            180                 185                 190


Pro Pro Gly Pro Gly Ile Gln Gly Asp Ala His Phe Asp Asp Asp Glu
        195                 200                 205


Leu Trp Ser Leu Gly Lys Gly Val Val Val Pro Thr Arg Phe Gly Asn
    210                 215                 220


Ala Asp Gly Ala Ala Cys His Phe Pro Phe Ile Phe Glu Gly Arg Ser
225                 230                 235                 240


Tyr Ser Ala Cys Thr Thr Asp Gly Arg Ser Asp Gly Leu Pro Trp Cys
                245                 250                 255
```

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Ser Thr Thr Ala Asn Tyr Asp Thr Asp Asp Arg Phe Gly Phe Cys Pro
            260                 265                 270

Ser Glu Arg Leu Tyr Thr Gln Asp Gly Asn Ala Asp Gly Lys Pro Cys
        275                 280                 285

Gln Phe Pro Phe Ile Phe Gln Gly Gln Ser Tyr Ser Ala Cys Thr Thr
    290                 295                 300

Asp Gly Arg Ser Asp Gly Tyr Arg Trp Cys Ala Thr Thr Ala Asn Tyr
305                 310                 315                 320

Asp Arg Asp Lys Leu Phe Gly Phe Cys Pro Thr Arg Ala Asp Ser Thr
                325                 330                 335

Val Met Gly Gly Asn Ser Ala Gly Glu Leu Cys Val Phe Pro Phe Thr
            340                 345                 350

Phe Leu Gly Lys Glu Tyr Ser Thr Cys Thr Ser Glu Gly Arg Gly Asp
        355                 360                 365

Gly Arg Leu Trp Cys Ala Thr Thr Ser Asn Phe Asp Ser Asp Lys Lys
    370                 375                 380

Trp Gly Phe Cys Pro Asp Gln Gly Tyr Ser Leu Phe Leu Val Ala Ala
385                 390                 395                 400

His Glu Phe Gly His Ala Leu Gly Leu Asp His Ser Ser Val Pro Glu
                405                 410                 415

Ala Leu Met Tyr Pro Met Tyr Arg Phe Thr Glu Gly Pro Pro Leu His
            420                 425                 430

Lys Asp Asp Val Asn Gly Ile Arg His Leu Tyr Gly Pro Arg Pro Glu
        435                 440                 445

Pro Glu Pro Arg Pro Pro Thr Thr Thr Thr Pro Gln Pro Thr Ala Pro
    450                 455                 460

Pro Thr Val Cys Pro Thr Gly Pro Pro Thr Val His Pro Ser Glu Arg
465                 470                 475                 480

Pro Thr Ala Gly Pro Thr Gly Pro Pro Ser Ala Gly Pro Thr Gly Pro
                485                 490                 495

Pro Thr Ala Gly Pro Ser Thr Ala Thr Thr Val Pro Leu Ser Pro Val
            500                 505                 510

Asp Asp Ala Cys Asn Val Asn Ile Phe Asp Ala Ile Ala Glu Ile Gly
        515                 520                 525
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Asn Gln Leu Tyr Leu Phe Lys Asp Gly Lys Tyr Trp Arg Phe Ser Glu
    530   535   540

Gly Arg Gly Ser Arg Pro Gln Gly Pro Phe Leu Ile Ala Asp Lys Trp
545   550   555   560

Pro Ala Leu Pro Arg Lys Leu Asp Ser Val Phe Glu Glu Arg Leu Ser
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Lys Lys Leu Phe Phe Phe Ser Gly Arg Gln Val Trp Val Tyr Thr Gly
            580   585   590

Ala Ser Val Leu Gly Pro Arg Arg Leu Asp Lys Leu Gly Leu Gly Ala
        595   600   605

Asp Val Ala Gln Val Thr Gly Ala Leu Arg Ser Gly Arg Gly Lys Met
    610   615   620

Leu Leu Phe Ser Gly Arg Arg Leu Trp Arg Phe Asp Val Lys Ala Gln
625   630   635   640

Met Val Asp Pro Arg Ser Ala Ser Glu Val Asp Arg Met Phe Pro Gly
                645   650   655

Val Pro Leu Asp Thr His Asp Val Phe Gln Tyr Arg Glu Lys Ala Tyr
            660   665   670

Phe Cys Gln Asp Arg Phe Tyr Trp Arg Val Ser Ser Arg Ser Glu Leu
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Asn Gln Val Asp Gln Val Gly Tyr Val Thr Tyr Asp Ile Leu Gln Cys
    690   695   700

Pro Glu Asp Asp Tyr Lys Asp Asp Asp Asp Lys
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<211> 1062
<212> DNA
<213> Artificial Sequence

<220>
<223> MMP9 catalytic domain

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atcgtcatcc agtttggtgt cgcggagcac ggagacgggt atcccttcga cgggaaggac   240

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gatgacgagt tgtggtccct gggcaagggc gtcgtggttc caactcggtt tggaaacgca   360

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ttcggcttct gcccgacccg agctgactcg acggtgatgg ggggcaactc ggcgggggag      720

ctgtgcgtct tccccttcac tttcctgggt aaggagtact cgacctgtac cagcgagggc      780

cgcggagatg ggcgcctctg gtgcgctacc acctcgaact ttgacagcga caagaagtgg      840

ggcttctgcc cggaccaagg atacagtttg ttcctcgtgg cggcgcatga gttcggccac      900

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<212>  PRT
<213>  Artificial Sequence

<220>
<223>  MMP9 catalytic domain

<400>  645

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Thr Tyr Trp Ile Gln Asn Tyr Ser Glu Asp Leu Pro Arg Ala Val Ile
            20                  25                  30


Asp Asp Ala Phe Ala Arg Ala Phe Ala Leu Trp Ser Ala Val Thr Pro
        35                  40                  45


Leu Thr Phe Thr Arg Val Tyr Ser Arg Asp Ala Asp Ile Val Ile Gln
    50                  55                  60


Phe Gly Val Ala Glu His Gly Asp Gly Tyr Pro Phe Asp Gly Lys Asp
65                  70                  75                  80


Gly Leu Leu Ala His Ala Phe Pro Pro Gly Pro Gly Ile Gln Gly Asp
                85                  90                  95


Ala His Phe Asp Asp Asp Glu Leu Trp Ser Leu Gly Lys Gly Val Val
            100                 105                 110


Val Pro Thr Arg Phe Gly Asn Ala Asp Gly Ala Ala Cys His Phe Pro
        115                 120                 125


Phe Ile Phe Glu Gly Arg Ser Tyr Ser Ala Cys Thr Thr Asp Gly Arg
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130 135 140

Ser Asp Gly Leu Pro Trp Cys Ser Thr Thr Ala Asn Tyr Asp Thr Asp
145 150 155 160

Asp Arg Phe Gly Phe Cys Pro Ser Glu Arg Leu Tyr Thr Gln Asp Gly
165 170 175

Asn Ala Asp Gly Lys Pro Cys Gln Phe Pro Phe Ile Phe Gln Gly Gln
180 185 190

Ser Tyr Ser Ala Cys Thr Thr Asp Gly Arg Ser Asp Gly Tyr Arg Trp
195 200 205

Cys Ala Thr Thr Ala Asn Tyr Asp Arg Asp Lys Leu Phe Gly Phe Cys
210 215 220

Pro Thr Arg Ala Asp Ser Thr Val Met Gly Gly Asn Ser Ala Gly Glu
225 230 235 240

Leu Cys Val Phe Pro Phe Thr Phe Leu Gly Lys Glu Tyr Ser Thr Cys
245 250 255

Thr Ser Glu Gly Arg Gly Asp Gly Arg Leu Trp Cys Ala Thr Thr Ser
260 265 270

Asn Phe Asp Ser Asp Lys Lys Trp Gly Phe Cys Pro Asp Gln Gly Tyr
275 280 285

Ser Leu Phe Leu Val Ala Ala His Glu Phe Gly His Ala Leu Gly Leu
290 295 300

Asp His Ser Ser Val Pro Glu Ala Leu Met Tyr Pro Met Tyr Arg Phe
305 310 315 320

Thr Glu Gly Pro Pro Leu His Lys Asp Asp Val Asn Gly Ile Arg His
325 330 335

Leu Tyr Gly Pro Arg Pro Glu Pro Asp Tyr Lys Asp Asp Asp Asp Lys
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<211> 2186
<212> DNA
<213> Artificial Sequence

<220>
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cgcctccgga actccctgcg cctggcgcgc ggccaccgtg gtcccggcaa cggcattaaa 180

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aggacgacgt gaatggcatc cggcacctct atggtcctcg ccctgaacct gattacaagg 3240

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<210> 649
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<400> 649
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ggaggtctat ataagcagag ctggtttagt gaaccgtcag atctctagag ccaccatgag 180

cctctggcag cccctggtcc tggtgctcct ggtgctgggc tgctgctttg ctgcccccag 240

acagcgccag tccacccttg tgctcttccc tggagacctg agaaccaatc tcaccgacag 300

gcagctggca gaggaatacc tgtaccgcta tggttacact cgggtggcag agatgcgtgg 360

agagtcgaaa tctctggggc ctgcgctgct gcttctccag aagcaactgt ccctgcccga 420

gaccggtgag ctggatagcg ccacgctgaa ggccatgcga accccacggt gcggggtccc 480

agacctgggc agattccaaa cctttgaggg cgacctcaag tggcaccacc acaacatcac 540

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ggacgcagac atcgtcatcc agtttggtgt cgcggagcac ggagacgggt atcccttcga 720

cgggaaggac gggctcctgg cacacgcctt tcctcctggc cccggcattc agggagacgc 780

ccatttcgac gatgacgagt tgtggtccct gggcaagggc gtcgtggttc caactcggtt 840

tggaaacgca gatggcgcgg cctgccactt ccccttcatc ttcgagggcc gctcctactc 900

tgcctgcacc accgacggtc gctccgacgg cttgccctgg tgcagtacca cggccaacta 960

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caagctgggc ctgggagccg acgtggccca ggtgaccggg gccctccgga gtggcagggg 2040

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ccaaaccttt gagggcgacc tcaagtggca ccaccacaac atcacctatt ggatccaaaa 240

ctactcggaa gacttgccgc gggcggtgat tgacgacgcc tttgcccgcg ccttcgcact 300

gtggagcgcg gtgacgccgc tcaccttcac tcgcgtgtac agccgggacg cagacatcgt 360

catccagttt ggtgtcgcgg agcacggaga cgggtatccc ttcgacggga aggacgggct 420

cctggcacac gcctttcctc ctggccccgg cattcaggga gacgcccatt tcgacgatga 480

cgagttgtgg tccctgggca agggcgtcgt ggttccaact cggtttggaa acgcagatgg 540

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cgtcttcccc ttcactttcc tgggtaagga gtactcgacc tgtaccagcg agggccgcgg 960

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tgaacctgat tacaaggatg acgacgataa gtgataa 1237

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<223> C2 scFv

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ccagggaagg ggctggagtg ggtctcaacc attagtagtg gcggaaccta catatactac 180

cccgactcag tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagacttggg 300

ggggataatt actacgaata cttcgatgtc tggggcaaag ggaccacggt caccgtctcc 360

tccggcggtg gcggatccgg cggtggcgga tccggcggtg gcggatccga cattgtgctg 420

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aggttcagcg gcagtgggtc tgggaccgat ttcaccctca caattaatcc tgtggaagct 660

aatgatactg caaattatta ctgtcagcac agtagggagc tgcctttcac attcggcgga 720

gggaccaagg tggagatcaa acgaact 747

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<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> C2 scFv

<400> 655

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr Phe Asp Val Trp Gly
100 105 110

Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro
130 135 140

Ala Ser Leu Ala Val Ser Pro Gly Gln Arg Ala Thr Ile Thr Cys Arg
145 150 155 160

Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr Met His Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser
180 185 190

Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly

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        195                 200                 205


Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asn Asp Thr Ala
    210                 215                 220


Asn Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Phe Thr Phe Gly Gly
225                 230                 235                 240


Gly Thr Lys Val Glu Ile Lys Arg Thr
                245


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<211>  72
<212>  DNA
<213>  Artificial Sequence

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<223>  CD8 transmembrane domain

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accctttact gc                                                           72


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<223>  CD8 transmembrane domain

<400>  657

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
1               5                   10                  15


Ser Leu Val Ile Thr Leu Tyr Cys
            20


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<212>  DNA
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<220>
<223>  41BB domain

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gaactg                                                                 126


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<213>  Artificial Sequence

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<223> 41BB domain

<400> 659

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Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
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Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
            20                  25                  30


Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
        35                  40
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<210> 660
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> CD3zeta domain

<400> 660

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tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc      120

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat      180

gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc      240

cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc      300

tacgacgccc ttcacatgca ggccctgccc cctcgc                                336
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<210> 661
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3zeta domain

<400> 661

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Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly
1               5                   10                  15


Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
            20                  25                  30


Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
        35                  40                  45


Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
    50                  55                  60


Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65                  70                  75                  80


Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
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85 90 95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
100 105 110

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       CD8 transmembrane 41BB CD3zetaC

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ccggaggtgc agctggtgga gtctggggga ggcctggtca agcctggggg gtccctgaga   120

ctctcctgtg cagcctctgg attcaccttc agtggctatg ccatgagctg ggtccgccag   180

gctccaggga aggggctgga gtgggtctca accattagta gtggcggaac ctacatatac   240

taccccgact cagtgaaggg ccgattcacc atctccagag acaacgccaa gaactcactg   300

tatctgcaaa tgaacagcct gagagccgag gacacggccg tgtattactg tgcgagactt   360

gggggggata attactacga atacttcgat gtctggggca aagggaccac ggtcaccgtc   420

tcctccggcg gtggcggatc cggcggtggc ggatccggcg gtggcggatc cgacattgtg   480

ctgacccagt ctccagcctc cttggccgtg tctccaggac agagggccac catcacctgc   540

agagccagta agagtgtcag taccagcgga tactcctaca tgcactggta tcagcagaaa   600

ccaggacaac ctcctaaact cctgatttac ctggcatcca atctggagag cggggtccca   660

gccaggttca gcggcagtgg gtctgggacc gatttcaccc tcacaattaa tcctgtggaa   720

gctaatgata ctgcaaatta ttactgtcag cacagtaggg agctgccttt cacattcggc   780

ggagggacca aggtggagat caaacgaact acaacaaccc ctgcccccag acctcctacc   840

ccagccccta caattgccag ccagcctctg agcctgaggc ccgaggcttg tagacctgct   900

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aatgaactgc agaaagataa gatggcggag gcctacagtg agattgggat gaaaggcgag   1380

cgccggaggg gcaaggggca cgatggcctt taccagggtc tcagtacagc caccaaggac   1440 acctacgacg cccttcacat gcaggccctg ccccctcgct gataa   1485

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       CD8 transmembrane 41BB CD3zetaC

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Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
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His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
            20                  25                  30


Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
        35                  40                  45


Thr Phe Ser Gly Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
    50                  55                  60


Gly Leu Glu Trp Val Ser Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr
65                  70                  75                  80


Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
                85                  90                  95


Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
            100                 105                 110


Ala Val Tyr Tyr Cys Ala Arg Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr
        115                 120                 125


Phe Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly
    130                 135                 140


Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
145                 150                 155                 160


Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Pro Gly Gln Arg Ala
                165                 170                 175


Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser
            180                 185                 190


Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu
        195                 200                 205


Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser
    210                 215                 220
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Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu
225                 230                 235                 240

Ala Asn Asp Thr Ala Asn Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro
                245                 250                 255

Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Thr Thr
            260                 265                 270

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
        275                 280                 285

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
    290                 295                 300

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
305                 310                 315                 320

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
                325                 330                 335

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
            340                 345                 350

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
        355                 360                 365

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
    370                 375                 380

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
385                 390                 395                 400

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
                405                 410                 415

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
            420                 425                 430

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
        435                 440                 445

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
    450                 455                 460

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
465                 470                 475                 480

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485                 490
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cgtggactca ggcgtcccgt ctggcccgtt cgcccccgtt tcccccgcca gccccagcgc 1740

ccccctgccc ggcccccgga ttccccgttc ccgcccctac gcccccatcc cctccccgtg 1800

cgcccctccc cgtgcgcccc cctccccgtg cgccccccct ccccgtgcgc ccccctcccc 1860

gtgcgccccc cctccccggg cgccccctc cccgggcgcc ccccctcccc gtgcgccccc 1920

ccctccccgt gcgccccccc tccccgtgcg cgccccgcct cttgcgcccc tgcccccagg 1980

cgagcggctg ccgcggcgcg gggaggggcg ggcgctcggc gactcgtccc cggggccccg 2040

cgcgggcccg ggcagcaggg gcgtgatgtc acggcaggga gggggcgcgg gagccgccgg 2100

gccggcgggg aggcggggga ggtgttttcc agctttaaaa aggcaggagg cagagcgcgg 2160

ccctgcgtca gagcgagact cagaggctcc gaactcgccg gcggagtcgc cgcgccagat 2220

cccagcagca gggcgcgg 2238

<210> 782
<211> 2186
<212> DNA
<213> Artificial Sequence

<220>
<223> NFATc1 Promoter fragment (P2)

<400> 782
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tggccgcaga ggccgggccg gggcgcagag gccgggcgag ctggccgcgc tctgggccgc 120

cgcctccgga actccctgcg cctggcgcgc ggccaccgtg gtcccggcaa cggcattaaa 180

cagagggaaa cagacccggg attccgtcac ccgggcgggg ggataaggac ggctttgaga 240

gcagacagga aaagggagct tttctgcatg gggtgaaaaa attatttatt gaaggaggag 300

gaggcggcag cggaggaagg ggaggggcgg gaggaggagg aagagccggc cgcccccgcc 360

ccggccccgg ctcctcagga gccaagggca gcctcgccag gtcggtcccg ggctcgagga 420

ccgcggctgg ggtcgagggg ctcagtctcc cacgtgaccg gctgggcgcg ccccgccaga 480

cccggcctcg ggattccctc ctcccggcga gtctccgccc gccccgtcct ggaggtgggg 540

agaaggaggg cggggcgggg gggacggaaa ctctccccgc caaatcctgg ccccaggcct 600

ggggacactc gcggcgggaa gatttggagg ggaggggagg gggaggggcg tgggggcgcg 660

gcctcgctgg agtccccctg accccccgac cccgcccac cggcctgggc gtcctcccgc 720

ggcccctcct cccctcccgg cgcccggtgc tctggggcgc gtgccacgcc tggctcggcg 780

ccgtaggggc ccccgcaggt agagacccct ggaaatggcc tcgacgccgc aggagcgagg 840

cggccaccac cccgctaatc cgggcacgtc tctccaggcc gaggcctgcg gtggaaaagc 900 cggggttcca tttgtgctga gtcggggcgg ccgaatggag ccaggcctcg ggacgcggga 960

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cctcctgggc cccgcagcag acacgagttt agcctttggg tttagtttaa atcacataag 1140

ggtgtcgtgc aatcgattta tggtttctac acaccagaca ctttaacctc caaccccccc 1200

catccaagcc aacaagaaaa tgcggtgccg tgttggcagc tgagctgcgc ccgaagagac 1260

gcagggagac gtaagagagg aaagtgtgag tggccggggg gcctcccccc gtcagaagtc 1320

gcgcagtcgc gcccataaaa cgccccctcc gggcggctag ggcaggtgag cgcgtccccg 1380

ggcctcccca cgccggcccc tgccacagag ccgtctaggt cgagcagata tttacagaat 1440

aaaaatgaca ataactcgac gtcccgggac ggccacgcaa tctgttagta atttagcggg 1500

atgggaattt cctttctagg gcctgccagt gaagcgcttt tccaaatttc cacagcgggg 1560

gaagcctgcg attttacata atgacttcag catgccgggc tttctcgaca cccctccccg 1620

gcccccggcc cccgcccccc gccccttttc cagcagggcc gggctccctc cggacacccg 1680

cgtggactca ggcgtcccgt ctggcccgtt cgcccccgtt tcccccgcca gccccagcgc 1740

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ccctccccgt gcgccccccc tccccgtgcg cgccccgcct cttgcgcccc tgcccccagg 1980

cgagcggctg ccgcggcgcg gggaggggcg ggcgctcggc gactcgtccc cggggccccg 2040

cgcgggcccg ggcagcaggg gcgtgatgtc acggcaggga gggggcgcgg gagccgccgg 2100

gccggcgggg aggcggggga ggtgttttcc agctttaaaa aggcaggagg cagagcgcgg 2160

ccctgcgtca gagcgagact cagagg 2186

<210> 783
<211> 1645
<212> DNA
<213> Artificial Sequence

<220>
<223> NFATc1 Promoter fragment (P3)

<400> 783
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gggcgcggcc tcgctggagt ccccctgacc ccccgacccc cgcccaccgg cctgggcgtc 120

ctcccgcggc ccctcctccc ctcccggcgc ccggtgctct ggggcgcgtg ccacgcctgg 180

ctcggcgccg taggggcccc cgcaggtaga gacccctgga aatggcctcg acgccgcagg 240

agcgaggcgg ccaccacccc gctaatccgg gcacgtctct ccaggccgag gcctgcggtg 300

gaaaagccgg ggttccattt gtgctgagtc ggggcggccg aatggagcca ggcctcggga 360

cgcgggacgg acgggctctg gccgcgcacc ttcgcgggct ctgcagcgcc cgaccgcctc 420 ccccggcagg gaggaggcgc ttgtgggggg cacccacggg gcacagtgat ccctgggggt 480

ctgcggacct cctgggcccc gcagcagaca cgagtttagc ctttgggttt agtttaaatc 540

acataagggt gtcgtgcaat cgatttatgg tttctacaca ccagacactt taacctccaa 600

cccccccat ccaaagccaa caagaaaatg cggtgccgtg ttggcagctg agctgcgccc 660

gaagagacgc agggagacgt aagagaggaa agtgtgagtg gccgggggc ctcccccgt 720

cagaagtcgc gcagtcgcgc ccataaaacg ccccctccgg gcggctaggg caggtgagcg 780

cgtccccggg cctccccacg ccggcccctg ccacaggccg tctaggtcga gcagatattt 840

acagaataaa aatgacaata actcgacgtc ccgggacggc cacgcaatct gttagtaatt 900

tagcgggatg ggaatttcct ttctagggcc tgccagtgaa gcgcttttcc aaatttccac 960

agcgggggaa gcctgcgatt ttacataatg acttcagcat gccgggcttt ctcgacaccc 1020

ctccccggcc cccggccccc gccccccgcc ccttttccag cagggccggg ctccctccgg 1080

acacccgcgt ggactcaggc gtcccgtctg gcccgttcgc ccccgtttcc cccgccagcc 1140

ccagcgcccc cctgcccggc ccccggattc cccgttcccg cccctacgcc cccatcccct 1200

ccccgtgcgc ccctccccgt gcgcccccct ccccgtgcgc ccccctccc cgtgcgcccc 1260

cctccccgtg cgcccccct ccccgggcgc ccccctcccc gggcgccccc cctccccgtg 1320

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ccccaggcga gcggctgccg cggcgcgggg aggggcgggc gctcggcgac tcgtccccgg 1440

ggccccgcgc gggcccgggc agcaggggcg tgatgtcacg gcagggaggg ggcgcgggag 1500

ccgccgggcc ggcggggagg cgggggaggt gttttccagc tttaaaaagg caggaggcag 1560

agcgcggccc tgcgtcagag cgagactcag aggctccgaa ctcgccggcg gagtcgccgc 1620

gccagatccc agcagcaggg cgcgg 1645

<210> 784
<211> 927
<212> DNA
<213> Artificial Sequence

<220>
<223> pNFATMMP9cat1 gBLOCK sequence

<400> 784
aagaggaaaa tttgtttcat acagaaggcg ttactagtta ggcgtgtacg gtgggaggcc 60

tatataagca gagctcgttt agtgaaccgt cagatcgcct ggagacgcca tccacgctgt 120

tttgacctcc atagaagaca ccgggaccga tccagcctct cgacattcgt ttctagagcc 180

accatgagcc tctggcagcc cctggtcctg gtgctcctgg tgctgggctg ctgctttgct 240

ttccaaacct ttgagggcga cctcaagtgg caccaccaca acatcaccta ttggatccaa 300

aactactcgg aagacttgcc gcgggcggtg attgacgacg cctttgcccg cgccttcgca 360

ctgtggagcg cggtgacgcc gctcaccttc actcgcgtgt acagccggga cgcagacatc 420

gtcatccagt ttggtgtcgc ggagcacgga gacgggtatc ccttcgacgg gaaggacggg 480

ctcctggcac acgcctttcc tcctggcccc ggcattcagg gagacgccca tttcgacgat 540 gacgagttgt ggtccctggg caagggcgtc gtggttccaa ctcggtttgg aaacgcagat 600

ggcgcggcct gccacttccc cttcatcttc gagggccgct cctactctgc ctgcaccacc 660

gacggtcgct ccgacggctt gccctggtgc agtaccacgg ccaactacga caccgacgac 720

cggtttggct tctgccccag cgagagactc tacacccagg acggcaatgc tgatgggaaa 780

ccctgccagt ttccattcat cttccaaggc caatcctact ccgcctgcac cacggacggt 840

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ggcttctgcc cgacccgagc tgactcg 927

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<210>  804
<211>  13
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NFAT consensus sequence

<400>  804

Ala Thr Gly Gly Ala Ala Ala Ala Asn Ala Thr Cys Asn
1               5                   10


<210>  805
<211>  32
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Current NFAT RE (Form System Biosciences. The sequence is from
       the mouse IL2 promoter.)

<400>  805
aagaggaaaa tttgtttcat acagaaggcg tt                                   32
```

<210> 806
<211> 812
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse IL2 Promoter (highlighted in green the NFAT RE used, highlighted in yellow is the start codon)

<400> 806
aactagagac atataaaata acaccaacat ccttagatac aacccttcct gagaatttat 60

tggacatcat actcttttta aaaagcataa taaacatcaa gacacttaca caaaatatgt 120

taaattaaat ttaaaacaac aacgacaaaa tagtacctca agctcaacaa gcattttagg 180

tgtccttagc ttactatttc tctggctaac tgtatgaagc catctatcac cctgtgtgca 240

attagctcat tgtgtagata agaaggtaaa accatcttga aacaggaaac caatatcctt 300

cctgtctaat caacaaatct aaaagattta ttcttttcat ctatctcctc ttgcgtttgt 360

ccaccacaac aggctgctta caggttcagg atggttttga caaagagaac attttcatga 420

gttacttttg tgtctccacc ccaaagagga aaatttgttt catacagaag gcgttcattg 480

tatgaattaa aactgccacc taagtgtggg ctaacccgac caagagggat ttcacctaaa 540

tccattcagt cagtgtatgg gggtttaaag aaattccaga gagtcatcag aagaggaaaa 600

acaaaaggta atgctttctg ccacacaggt agactctttg aaaatatgtg taatatgtaa 660

aacatcgtga cacccccata ttatttttcc agcattaaca gtataaattg cctcccatgc 720

tgaagagctg cctatcaccc ttgctaatca ctcctcacag tgacctcaag tcctgcaggc 780

atgtacagca tgcagctcgc atcctgtgtc ac 812

<210> 807
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> NFAT RE (Form PRomega. The sequence is from the humane IL2 promoter.)

<400> 807
ggaggaaaaa ctgtttcata cagaaggcgt 30

<210> 808
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Possible NFAT RE from ET1 promoter

<400> 808
tccagggaaa atcggagtag aacaagaggg atg 33

<210> 809
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Possible NFAT RE from ET1 promoter

<400> 809
actgttggaa aacgtaaaca cgttattaaa cggt   34

<210> 810
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Possible NFAT RE from human CD3?

<400> 810
tccttaacgg aaaaacaaaa   20

<210> 811
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Possible NFAT RE from human CD3?

<400> 811
aaaggaaaaa gtatatgttc   20

<210> 812
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Possible NFAT RE from human IL3 promoter

<400> 812
atgccatgga aagggtg   17

<210> 813
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Possible NFAT RE from human GPC6

<400> 813
aaggggaaat gttgagtcta ga   22

<210> 814
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Possible NFAT RE from human growth hormonereleasing hormone

<400> 814
aacttggaaa agcatag   17

<210> 815
<211> 5320

<212> DNA
<213> Artificial Sequence

<220>
<223> NFATc1 promoter large

<400> 815
ttatgccgtc tagaggagac atactttcta ctcaaagcta cacacataga ctacaacgat   60

gggaaaagac gacacaccaa cagcgacttc aggaaagctg gagtggctgc taatgttaga   120

caaaataggc tttttaaaaa aggttttatt aaagaggaat gtttcgtaat gataaaagca   180

ctaatctgtg agaaagatac aacaatgata aacatacgtg cagctaataa gagagctcca   240

aaatctatga agcaaaaact cacagaatga ggggagaagc agttctacaa cagagaatgg   300

ggacttcgat actccacttt caataatgga tacaacaacc aggcagataa caaggcaaca   360

gaaggcctga acaacagtat aaaccaatta gacctaccag atatctatag ctagcacact   420

ccacccaacg acagcagaat acacattctt ctcaagcgca caagtaacat cctccaggat   480

gggccatgtt ctaggccatc aaacaaactc aggtggtttg aggccagagg cctctctttt   540

aaccaccaca ctagggcctt cggaggaggc aagcagagag ttgtcaaaga ggccctcagg   600

actgggtgca gtggctcatg actgtaatcc cagcacttta gaaggctgag gcacaaggat   660

cttttgagct caggagttca agaaatgagc acttatccac tgggcgcggt ggctcacgcc   720

agtaatccag cactttggga ggcttaggcg ggcggatcaa gaggtcagaa gctcaagacc   780

agcctgacca acatggtgaa accccgtctc tactaaaagt acaaaaatta gccgggcgtg   840

gtggcgcaca cctgtaatcc cagctacttg ggaggctgag gcaggagaat cacttgaacc   900

cgggaggtgg aggttgcagt gagtggagat cacaccattg caccccagcc tgggcaacag   960

agcgagactc cgtctcaaaa aaaaaaaaaa aaaaaaagaa agaaagaaaa agaaaaaaaa   1020

agtgagcatg tattttgcca gagtctggag attagaatta aattagcaaa ccagaattat   1080

agaaaaagct atttactttt aagtaaacag ctgagatttt tttttttaag tcagtgtgaa   1140

tgaagctcac agccatggtt ggagctgaga aagaaggatt tccctttagt tatgcacctg   1200

tgtcagcacc ttctgacttt ccttctaaag tctggggtgt tcctgaggat ccgtaagttt   1260

ggggttcagg gtttctacag catgctgtta cttgtgaaac atctctttaa ccatgtccca   1320

gagttgccca ggagtttaag accagcctga gcaacatagc aagacctcat ctcaacaaca   1380

acaaaaatta gaaataaatt agccaggtgt ggtgacatgt gcctgtagtc ccagctactc   1440

agaaggctga ggcatgagga tcacttgggc ccaggaagtt ggggctgcag ggagccctgt   1500

tcatgccgct gcactccagc ctgcaagaca gagcagaaaa aaagaatcag gatcctgggc   1560

agagggagga gaggggaccg gggtccagca agcacttggg gattgactga atggcgttgg   1620

ggagagatga ctccaaagtc ctggagtggg tgagaatgac tgcgagtggc ttttaggtgg   1680

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ctgatccatt ggtgatctga gtttttagac atggtggtag tccatgaggt gggtgttcat   1860 gctaagagtt tagacaggga aacctatgaa gcccttagca accctccagg gaaggggcgt 1920

ggttaaagag atgtttcata agtaacagca tggtatagaa actctgaacc ccaaatgtat 1980

gggtcctcag gaacacccca gactttagaa ggaaagtcag aaggtgctga cacgggtgta 2040

taactaaagg gaaatccttc tttctcagct ccaaccatgg ctgtgaggtt cattcacact 2100

gacttaaaaa aaaaaatctc agtttactta aaagtaaata gctttttcta taattctggt 2160

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agaagggggt ggattctgag ttgagtcaaa acctcaaaga cccctgatgg gaaaagctct 2340

caagtgacca ccgctgtggg ccagaatgca aaactgcagg aacagaacat tcgcaggaac 2400

agaacacagt cgtattaagt gattttcccg agcaggaagt ggcatctggc ctgcggttca 2460

gtagggggag gaaagggtgg gcgcacctgc ccctggctgg cgcacctgcc aggtagcccc 2520

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gaaacagacc cgggattccg tcacccgggc ggggggataa ggacggcttt gagagcagac 3240

aggaaaaggg agcttttctg catggggtga aaaaattatt tattgaagga ggaggaggcg 3300

gcagcggagg aaggggaggg gcgggaggag gaggaagagc cggccgcccc cgccccggcc 3360

ccggctcctc aggagccaag ggcagcctcg ccaggtcggt cccgggctcg aggaccgcgg 3420

ctggggtcga ggggctcagt ctcccacgtg accggctggg cgcgccccgc cagacccggc 3480

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actcgcggcg ggaagatttg gaggggaggg gagggggagg ggcgtggggg cgcggcctcg 3660

ctggagtccc cctgaccccc cgacccccgc ccaccggcct gggcgtcctc ccgcggcccc 3720

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gggcccccgc aggtagagac ccctggaaat ggcctcgacg ccgcaggagc gaggcggcca 3840

ccaccccgct aatccgggca cgtctctcca ggccgaggcc tgcggtggaa aagccggggt 3900

tccatttgtg ctgagtcggg gcggccgaat ggagccaggc ctcgggacgc gggacggacg 3960

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gaggcgcttg tggggggcac ccacggggca cagtgatccc tgggggtctg cggacctcct     4080

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gtgcaatcga tttatggttt ctacacacca gacactttaa cctccaaccc cccccatcca     4200

aagccaacaa gaaaatgcgg tgccgtgttg gcagctgagc tgcgcccgaa gagacgcagg     4260

gagacgtaag agaggaaagt gtgagtggcc ggggggcctc cccccgtcag aagtcgcgca     4320

gtcgcgccca taaaacgccc cctccgggcg gctagggcag gtgagcgcgt ccccgggcct     4380

ccccacgccg gcccctgcca caggccgtct aggtcgagca gatatttaca gaataaaaat     4440

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cccgggcagc aggggcgtga tgtcacggca gggagggggc gcgggagccg ccgggccggc     5100

ggggaggcgg gggaggtgtt ttccagcttt aaaaaggcag gaggcagagc gcggccctgc     5160

gtcagagcga gactcagagg ctccgaactc gccggcggag tcgccgcgcc agatcccagc     5220

agcagggcgc gggcaccggg gcgcgggcag ggctcggagc caccgcgcag gtcctagggc     5280

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<210>  816
<211>  361
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  NFATc3 promoter sequence

<400>  816
gcagccaggc agggtgggcg cgcgtagggg gcggggccgg gcgcgcggca gggcgcgaga       60

gcgcacccgc ggcggcggtg gcggcgactg tgggggggcg gcggggaaca ttggctaagc      120

cgacagtgga ggcttaggca ccggtggcgg gcggctgcgg ttcctggtgc tgctcggcgc      180

gcggccagct ttcggaacgg aacgctcggc gtcgcgggcc ccgcccggaa agtttgccgt      240

ggagtcgcga cctcttggcc cgcgcggccc ggcatgaagc ggcgttgagg agctgctgcc      300

gccgcttgcc gctgccgccg ccgccgcctg aggaggagct gcagcaccct gggccacgcc      360
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g 361

<210> 817
<211> 430
<212> DNA
<213> Artificial Sequence

<220>
<223> NFATc2 promoter sequence 1

<400> 817
cagagagagg ctgcgttcag actggggcac tgccatcccc tccgcatcat ggggtctgtg 60

gaccaaggta actgactctc gatcccttcc agccttttcc gctcgctcct cccggccctt 120

tcctgctgct cccgtcccgg gcagcacttt cagctcccgg cagaggtcgg tgcgggaggc 180

ctggggaccc cgctcgccct cggcgcacag gtagcggggc ccgcggaggg gcgcccgcgc 240

cccggccagg gaagggacac ttgggaaggc gactttggac aactttacgc gggggcaggg 300

aagtgtccca ggccgggatt ccctaggcca gtctgtcggg aggattttcc tctccacggg 360

acaccgggag ggattctcgc tactaaccgc tggctgttta accgtttcag cactcggctt 420

ttgacagcaa 430

<210> 818
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> NFATc2 promoter sequence 2

<400> 818
catcatgggg tctgtggacc aaggtaactg actctcgatc ccttccagcc ttttccgctc 60

gctc 64

<210> 819
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> NFATc1 response element consensus

<400> 819
catttttcc at 12

<210> 820
<211> 8
<212> DNA
<213> Artificial Sequence

<220>
<223> NFATc1 response element consensus

<400> 820
tttttcca 8

<210> 821
<211> 119

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<212>  DNA
<213>  Artificial Sequence

<220>
<223>  NFAT response elements contained within the Foxp3 enhancer region

<400>  821
acttgaaaat gagataaatg ttcacctatg ttggcttcta gtctctttta tggcttcatt       60

ttttccattt actatagagg ttaagagtgt gggtactgga gccagactgt ctgggacaa       119


<210>  822
<211>  65
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N+20

<400>  822

Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu
1               5                   10                  15


Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe
            20                  25                  30


Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser
        35                  40                  45


Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly
    50                  55                  60


Ala
65


<210>  823
<211>  38
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N+20/C27

<400>  823

Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu
1               5                   10                  15


Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe
            20                  25                  30


Asn Gln Tyr Lys Thr Glu
        35


<210>  824
<211>  45
<212>  PRT
<213>  Artificial Sequence
```

<220>
<223> N+9/C9

<400> 824

Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp
1   5   10   15

Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr
            20   25   30

Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro
        35   40   45

<210> 825
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<223> C10

<400> 825

Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys
1   5   10   15

Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val
            20   25   30

Ser Asp Val
        35

<210> 826
<211> 885
<212> DNA
<213> Artificial Sequence

<220>
<223> NME7AB

<400> 826
atggaaaaaa cgctggccct gattaaaccg gatgcaatct ccaaagctgg cgaaattatc   60

gaaattatca acaaagcggg tttcaccatc acgaaactga aaatgatgat gctgagccgt   120

aaagaagccc tggattttca tgtcgaccac cagtctcgcc cgtttttcaa tgaactgatt   180

caattcatca ccacgggtcc gattatcgca atggaaattc tgcgtgatga cgctatctgc   240

gaatggaaac gcctgctggg cccggcaaac tcaggtgttg cgcgtaccga tgccagtgaa   300

tccattcgcg ctctgtttgg caccgatggt atccgtaatg cagcacatgg tccggactca   360

ttcgcatcgg cagctcgtga aatggaactg tttttcccga gctctggcgg ttgcggtccg   420

gcaaacaccg ccaaatttac caattgtacg tgctgtattg tcaaaccgca cgcagtgtca   480

gaaggcctgc tgggtaaaat tctgatggca atccgtgatg ctggctttga aatctcggcc   540

atgcagatgt tcaacatgga ccgcgttaac gtcgaagaat tctacgaagt ttacaaaggc   600

gtggttaccg aatatcacga tatggttacg gaaatgtact ccggtccgtg cgtcgcgatg   660

```
gaaattcagc aaaacaatgc caccaaaacg tttcgtgaat tctgtggtcc ggcagatccg      720

gaaatcgcac gtcatctgcg tccgggtacc ctgcgcgcaa tttttggtaa aacgaaaatc      780

cagaacgctg tgcactgtac cgatctgccg gaagacggtc tgctggaagt tcaatacttt      840

ttcaaaattc tggataatct cgagcaccac caccaccacc actga                      885


<210>  827
<211>  294
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NME7AB

<400>  827

Met Glu Lys Thr Leu Ala Leu Ile Lys Pro Asp Ala Ile Ser Lys Ala
1               5                   10                  15


Gly Glu Ile Ile Glu Ile Ile Asn Lys Ala Gly Phe Thr Ile Thr Lys
            20                  25                  30


Leu Lys Met Met Met Leu Ser Arg Lys Glu Ala Leu Asp Phe His Val
        35                  40                  45


Asp His Gln Ser Arg Pro Phe Phe Asn Glu Leu Ile Gln Phe Ile Thr
    50                  55                  60


Thr Gly Pro Ile Ile Ala Met Glu Ile Leu Arg Asp Asp Ala Ile Cys
65                  70                  75                  80


Glu Trp Lys Arg Leu Leu Gly Pro Ala Asn Ser Gly Val Ala Arg Thr
                85                  90                  95


Asp Ala Ser Glu Ser Ile Arg Ala Leu Phe Gly Thr Asp Gly Ile Arg
            100                 105                 110


Asn Ala Ala His Gly Pro Asp Ser Phe Ala Ser Ala Ala Arg Glu Met
        115                 120                 125


Glu Leu Phe Phe Pro Ser Ser Gly Gly Cys Gly Pro Ala Asn Thr Ala
    130                 135                 140


Lys Phe Thr Asn Cys Thr Cys Cys Ile Val Lys Pro His Ala Val Ser
145                 150                 155                 160


Glu Gly Leu Leu Gly Lys Ile Leu Met Ala Ile Arg Asp Ala Gly Phe
                165                 170                 175


Glu Ile Ser Ala Met Gln Met Phe Asn Met Asp Arg Val Asn Val Glu
            180                 185                 190


Glu Phe Tyr Glu Val Tyr Lys Gly Val Val Thr Glu Tyr His Asp Met
```

195 200 205

Val Thr Glu Met Tyr Ser Gly Pro Cys Val Ala Met Glu Ile Gln Gln
210 215 220

Asn Asn Ala Thr Lys Thr Phe Arg Glu Phe Cys Gly Pro Ala Asp Pro
225 230 235 240

Glu Ile Ala Arg His Leu Arg Pro Gly Thr Leu Arg Ala Ile Phe Gly
245 250 255

Lys Thr Lys Ile Gln Asn Ala Val His Cys Thr Asp Leu Pro Glu Asp
260 265 270

Gly Leu Leu Glu Val Gln Tyr Phe Phe Lys Ile Leu Asp Asn Leu Glu
275 280 285

His His His His His His
290

<210> 828
<211> 783
<212> DNA
<213> Artificial Sequence

<220>
<223> Human NME7 x1

<400> 828
atgatgatgc tttcaaggaa agaagcattg gattttcatg tagatcacca gtcaagaccc 60

tttttcaatg agctgatcca gtttattaca actggtccta ttattgccat ggagatttta 120

agagatgatg ctatatgtga atggaaaaga ctgctgggac ctgcaaactc tggagtggca 180

cgcacagatg cttctgaaag cattagagcc ctctttggaa cagatggcat aagaaatgca 240

gcgcatggcc ctgattcttt tgcttctgcg gccagagaaa tggagttgtt ttttccttca 300

agtggaggtt gtgggccggc aaacactgct aaatttacta attgtacctg ttgcattgtt 360

aaaccccatg ctgtcagtga aggactgttg ggaaagatcc tgatggctat ccgagatgca 420

ggttttgaaa tctcagctat gcagatgttc aatatggatc gggttaatgt tgaggaattc 480

tatgaagttt ataaaggagt agtgaccgaa tatcatgaca tggtgacaga aatgtattct 540

ggcccttgtg tagcaatgga gattcaacag aataatgcta caaagacatt tcgagaattt 600

tgtggacctg ctgatcctga aattgcccgg catttacgcc ctggaactct cagagcaatc 660

tttggtaaaa ctaagatcca gaatgctgtt cactgtactg atctgccaga ggatggccta 720

ttagaggttc aatacttctt caagatcttg gataatctcg agcaccacca ccaccaccac 780

tga 783

<210> 829
<211> 260
<212> PRT
<213> Artificial Sequence

<220>
<223> Human NME7 x1

<400> 829

Met Met Met Leu Ser Arg Lys Glu Ala Leu Asp Phe His Val Asp His
1   5   10   15

Gln Ser Arg Pro Phe Phe Asn Glu Leu Ile Gln Phe Ile Thr Thr Gly
            20   25   30

Pro Ile Ile Ala Met Glu Ile Leu Arg Asp Asp Ala Ile Cys Glu Trp
        35   40   45

Lys Arg Leu Leu Gly Pro Ala Asn Ser Gly Val Ala Arg Thr Asp Ala
    50   55   60

Ser Glu Ser Ile Arg Ala Leu Phe Gly Thr Asp Gly Ile Arg Asn Ala
65   70   75   80

Ala His Gly Pro Asp Ser Phe Ala Ser Ala Ala Arg Glu Met Glu Leu
                85   90   95

Phe Phe Pro Ser Ser Gly Gly Cys Gly Pro Ala Asn Thr Ala Lys Phe
            100   105   110

Thr Asn Cys Thr Cys Cys Ile Val Lys Pro His Ala Val Ser Glu Gly
        115   120   125

Leu Leu Gly Lys Ile Leu Met Ala Ile Arg Asp Ala Gly Phe Glu Ile
    130   135   140

Ser Ala Met Gln Met Phe Asn Met Asp Arg Val Asn Val Glu Glu Phe
145   150   155   160

Tyr Glu Val Tyr Lys Gly Val Val Thr Glu Tyr His Asp Met Val Thr
                165   170   175

Glu Met Tyr Ser Gly Pro Cys Val Ala Met Glu Ile Gln Gln Asn Asn
            180   185   190

Ala Thr Lys Thr Phe Arg Glu Phe Cys Gly Pro Ala Asp Pro Glu Ile
        195   200   205

Ala Arg His Leu Arg Pro Gly Thr Leu Arg Ala Ile Phe Gly Lys Thr
    210   215   220

Lys Ile Gln Asn Ala Val His Cys Thr Asp Leu Pro Glu Asp Gly Leu
225   230   235   240

Leu Glu Val Gln Tyr Phe Phe Lys Ile Leu Asp Asn Leu Glu His His
                245   250   255

```
His His His His
            260


<210>  830
<211>  426
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse Antibody 17H6 Heavy chain: DNA sequence - Signal sequence
       FR1CDR1FR2CDR2FR3CDR3FR4

<400>  830
atgaagttgt ggctgaactg gattttcctt gtaacacttt taaatggtat ccagtgtgag       60

gtgaagctgg tggagtctgg aggaggcttg gtacagcctg ggggttctct gagactctcc      120

tgtgcaactt ctgggttcac cttcactgat tactacatga gctgggtccg ccagcctcca      180

agaaaggcac ttgagtggtt gggttttatt agaaacaaag ctaatggtta cacagcagag      240

tacagtgcgt ctgtgaaggg tcggttcacc atctccagag atgtttccca aaacctcctc      300

tatcttcaaa tgaacatcct gagagctgag gacagtgcca cttattactg tgcaaaagat      360

tactacggta gtaaccctgc ctggtttgct tactggggcc aagggactct ggtcactgtc      420

tctgca                                                                 426


<210>  831
<211>  142
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse Antibody 17H6 Heavy chain: Amino acid sequence - Signal
       peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400>  831

Met Lys Leu Trp Leu Asn Trp Ile Phe Leu Val Thr Leu Leu Asn Gly
1               5                   10                  15


Ile Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln
            20                  25                  30


Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe
        35                  40                  45


Thr Asp Tyr Tyr Met Ser Trp Val Arg Gln Pro Pro Arg Lys Ala Leu
    50                  55                  60


Glu Trp Leu Gly Phe Ile Arg Asn Lys Ala Asn Gly Tyr Thr Ala Glu
65                  70                  75                  80


Tyr Ser Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Val Ser
                85                  90                  95


Gln Asn Leu Leu Tyr Leu Gln Met Asn Ile Leu Arg Ala Glu Asp Ser
            100                 105                 110
```

```
Ala Thr Tyr Tyr Cys Ala Lys Asp Tyr Tyr Gly Ser Asn Pro Ala Trp
        115                 120                 125


Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
    130                 135                 140


<210>  832
<211>  90
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 17H6 heavy chain variable framework 1 (FW1) sequence

<400>  832
gaggtgaagc tggtggagtc tggaggaggc ttggtacagc ctgggggttc tctgagactc       60

tcctgtgcaa cttctgggtt caccttcact                                        90


<210>  833
<211>  30
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 17H6 heavy chain variable framework 1 (FW1) sequence

<400>  833

Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Thr
            20                  25                  30


<210>  834
<211>  15
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 17H6 heavy chain variable complementarity determining
       regions 1 (CDR1) sequence

<400>  834
gattactaca tgagc                                                        15


<210>  835
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 17H6 heavy chain variable complementarity determining
       regions 1 (CDR1) sequence

<400>  835

Asp Tyr Tyr Met Ser
1               5
```

<210> 836
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse 17H6 heavy chain variable framework 2 (FW2) sequence

<400> 836
gaggtgaagc tggtggagtc tggaggaggc ttggtacagc ctgggggttc tctgagactc   60

tcctgtgcaa cttctgggtt caccttcact   90

<210> 837
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse 17H6 heavy chain variable framework 2 (FW2) sequence

<400> 837

Trp Val Arg Gln Pro Pro Arg Lys Ala Leu Glu Trp Leu Gly
1   5   10

<210> 838
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse 17H6 heavy chain variable complementarity determining
       regions 2 (CDR2) sequence

<400> 838
tttattagaa acaaagctaa tggttacaca gcagagtaca gtgcgtctgt gaagggt   57

<210> 839
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse 17H6 heavy chain variable complementarity determining
       regions 2 (CDR2) sequence

<400> 839

Phe Ile Arg Asn Lys Ala Asn Gly Tyr Thr Ala Glu Tyr Ser Ala Ser
1   5   10   15

Val Lys Gly

<210> 840
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse 17H6 heavy chain variable framework 3 (FW3) sequence

<400> 840
cggttcacca tctccagaga tgtttcccaa aacctcctct atcttcaaat gaacatcctg   60

agagctgagg acagtgccac ttattactgt gcaaaa   96

<210> 841
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse 17H6 heavy chain variable framework 3 (FW3) sequence

<400> 841

Arg Phe Thr Ile Ser Arg Asp Val Ser Gln Asn Leu Leu Tyr Leu Gln
1   5   10   15

Met Asn Ile Leu Arg Ala Glu Asp Ser Ala Thr Tyr Tyr Cys Ala Lys
            20   25   30

<210> 842
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse 17H6 heavy chain variable complementarity determining
       regions 3 (CDR3) sequence

<400> 842
gattactacg gtagtaaccc tgcctggttt gcttac   36

<210> 843
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse 17H6 heavy chain variable framework 4 (FW4) sequence

<400> 843
tggggccaag ggactctggt cactgtctct gca   33

<210> 844
<211> 393
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse Antibody 17H6 Light chain: DNA sequence - Signal sequence
       FR1CDR1FR2CDR2FR3CDR3FR4

<400> 844
atgaagttgc ctgtgaggct gttggtgctg atgttctgga ttcctgcttc caacagtgat   60

attttgatga cccagactcc actctccctg cctgtcagtc ttggagatca agcctccatc   120

tcttgcagat ctagtcagag cattgtacat agtagtggaa acaccttttt agaatggtac   180

ctgcagaaac ctggccagtc tccaaagctc ctgatctaca aagtttccaa ccgattttct   240

ggggtcccag acaggttcag tggcagtgga tcagggatag atttcacact caagatcagc   300

```
agagtggagg ctgaggatct gggagtttat tactgctttc aaggttcaca tgttcctttc      360

acgttcggct cggggacaaa gttggaaata aaa                                   393


<210>  845
<211>  131
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse Antibody 17H6 Light chain: Amino acid sequence - Signal
       peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400>  845

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
1               5                   10                  15


Ser Asn Ser Asp Ile Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val
            20                  25                  30


Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile
        35                  40                  45


Val His Ser Ser Gly Asn Thr Phe Leu Glu Trp Tyr Leu Gln Lys Pro
    50                  55                  60


Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
65                  70                  75                  80


Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Ile Asp Phe Thr
                85                  90                  95


Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
            100                 105                 110


Phe Gln Gly Ser His Val Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu
        115                 120                 125


Glu Ile Lys
    130


<210>  846
<211>  69
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 17H6 light chain variable framework 1 (FW1) sequence

<400>  846
gatattttga tgacccagac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc       60

atctcttgc                                                               69


<210>  847
<211>  23
<212>  PRT
```

```
<213>  Artificial Sequence

<220>
<223>  Mouse 17H6 light chain variable framework 1 (FW1) sequence

<400>  847

Asp Ile Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1               5                   10                  15


Asp Gln Ala Ser Ile Ser Cys
            20


<210>  848
<211>  48
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 17H6 light chain variable complementarity determining
       regions 1 (CDR1) sequence

<400>  848
agatctagtc agagcattgt acatagtagt ggaaacacct ttttagaa                    48


<210>  849
<211>  16
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 17H6 light chain variable complementarity determining
       regions 1 (CDR1) sequence

<400>  849

Arg Ser Ser Gln Ser Ile Val His Ser Ser Gly Asn Thr Phe Leu Glu
1               5                   10                  15


<210>  850
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 17H6 light chain variable framework 2 (FW2) sequence

<400>  850
tggtacctgc agaaacctgg ccagtctcca aagctcctga tctac                       45


<210>  851
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 17H6 light chain variable framework 2 (FW2) sequence

<400>  851

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr
1               5                   10                  15
```

```
<210>  852
<211>  21
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 17H6 light chain variable complementarity determining
       regions 2 (CDR2) sequence

<400>  852
aaagtttcca accgattttc t                                                21


<210>  853
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 17H6 light chain variable complementarity determining
       regions 2 (CDR2) sequence

<400>  853

Lys Val Ser Asn Arg Phe Ser
1               5


<210>  854
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 17H6 light chain variable framework 3 (FW3) sequence

<400>  854
ggggtcccag acaggttcag tggcagtgga tcagggatag atttcacact caagatcagc      60

agagtggagg ctgaggatct gggagtttat tactgc                                96


<210>  855
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 17H6 light chain variable framework 3 (FW3) sequence

<400>  855

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Ile Asp Phe Thr
1               5                   10                  15


Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
            20                  25                  30


<210>  856
<211>  27
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 17H6 light chain variable complementarity determining
       regions 3 (CDR3) sequence
```

<400> 856
tttcaaggtt cacatgttcc tttcacg   27

<210> 857
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse 17H6 light chain variable complementarity determining
       regions 3 (CDR3) sequence

<400> 857

Phe Gln Gly Ser His Val Pro Phe Thr
1   5

<210> 858
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse 17H6 light chain variable framework 4 (FW4) sequence

<400> 858
ttcggctcgg ggacaaagtt ggaaataaaa   30

<210> 859
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse 17H6 light chain variable framework 4 (FW4) sequence

<400> 859

Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
1   5   10

<210> 860
<211> 408
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 39H5 Heavy chain: DNA sequence - Signal
       sequenceFR1CDR1FR2CDR2FR3CDR3FR4

<400> 860
atggcttggg tgtggacctt gctattcctg atggcagctg cccaaagtgc ccaagcacag   60

atccagttgg tgcagtctgg acctgagctg aagaagcctg gagagacagt caagatctcc   120

tgcaaggctt ctgggtatac cttcacaaac tatggaatga actgggtgaa gcaggctcca   180

ggaaagggtt taaagtggat gggctggata aacacctaca ctggagagcc aacatatgtt   240

ggtgacttca agggacggtt tgccttctct ttggagacct ctgccagcac tgcctatttg   300

cagatcaaca acctcaaaaa tgaggacacg gctacatatt tttgtgttag aggtatccac   360

ggctacgtgg actactgggg ccaaggcacc actctcacag tctcctca   408

<210> 861
<211> 136
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 39H5 Heavy chain: Amino acid sequence - Signal peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400> 861

```
Met Ala Trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
1               5                   10                  15


Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
            20                  25                  30


Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45


Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60


Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Val
65                  70                  75                  80


Gly Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
                85                  90                  95


Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr
            100                 105                 110


Tyr Phe Cys Val Arg Gly Ile His Gly Tyr Val Asp Tyr Trp Gly Gln
        115                 120                 125


Gly Thr Thr Leu Thr Val Ser Ser
    130                 135
```

<210> 862
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 39H5 heavy chain variable framework 1 (FW1) sequence

<400> 862

```
cagatccagt tggtgcagtc tggacctgag ctgaagaagc ctggagagac agtcaagatc       60

tcctgcaagg cttctgggta taccttcaca                                        90
```

<210> 863
<211> 30
<212> PRT
<213> Artificial Sequence

<220>

```
<223>  Mouse antibody 39H5 heavy chain variable framework 1 (FW1)
       sequence

<400>  863

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1               5                   10                  15


Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
            20                  25                  30


<210>  864
<211>  15
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 39H5 heavy chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  864
aactatggaa tgaac                                                        15


<210>  865
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 39H5 heavy chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  865

Asn Tyr Gly Met Asn
1               5


<210>  866
<211>  42
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 39H5 heavy chain variable framework 2 (FW2)
       sequence

<400>  866
tgggtgaagc aggctccagg aaagggttta aagtggatgg gc                          42


<210>  867
<211>  14
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 39H5 heavy chain variable framework 2 (FW2)
       sequence

<400>  867

Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met Gly
1               5                   10
```

<210> 868
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 39H5 heavy chain variable complementarity
       determining regions 2 (CDR2) sequence

<400> 868
tggataaaca cctacactgg agagccaaca tatgttggtg acttcaaggg a   51

<210> 869
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 39H5 heavy chain variable complementarity
       determining regions 2 (CDR2) sequence

<400> 869

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Val Gly Asp Phe Lys
1   5   10   15

Gly

<210> 870
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 39H5 heavy chain variable framework 3 (FW3)
       sequence

<400> 870
cggtttgcct tctctttgga gacctctgcc agcactgcct atttgcagat caacaacctc   60

aaaaatgagg acacggctac atatttttgt gttaga   96

<210> 871
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 39H5 heavy chain variable framework 3 (FW3)
       sequence

<400> 871

Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu Gln
1   5   10   15

Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys Val Arg
            20   25   30

<210> 872
<211> 24
<212> DNA

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<213>  Artificial Sequence

<220>
<223>  Mouse antibody 39H5 heavy chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  872
ggtatccacg gctacgtgga ctac                                              24


<210>  873
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 39H5 heavy chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  873

Gly Ile His Gly Tyr Val Asp Tyr
1               5


<210>  874
<211>  33
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 39H5 heavy chain variable framework 4 (FW4)
       sequence

<400>  874
tggggccaag gcaccactct cacagtctcc tca                                    33


<210>  875
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 39H5 heavy chain variable framework 4 (FW4)
       sequence

<400>  875

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
1               5                   10


<210>  876
<211>  393
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 39H5 Light chain: DNA sequence - Signal
       sequenceFR1CDR1FR2CDR2FR3CDR3FR4

<400>  876
atgaagttgc ctgttaggct gttggtgctg atgttctgga ttcctgcttc cagcagtgat       60

gttttgatga cccaaactcc actctccctg cctgtcagtc ttggagatca agcctccatc      120

tcttgcagat ctagtcagag cattgtacat agaaatggaa acacctattt agaatggtac      180
```

```
ctgcagaaac caggccagtc tccaaagctc ctgatctaca aagtttccaa ccgattttct      240

ggggtcccag acaggttcag tggcagtgga tcagggacag atttcacact caagatcagc      300

agagtggagg ctgaggatct gggagtttat tactgctttc aaggttcaca tcttccgtgg      360

acgttcggtg gaggcaccaa gctggaaatc aaa                                   393


<210>  877
<211>  131
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 39H5 Light chain: Amino acid sequence - Signal
       peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400>  877

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
1               5                   10                  15


Ser Ser Ser Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val
            20                  25                  30


Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile
        35                  40                  45


Val His Arg Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro
    50                  55                  60


Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
65                  70                  75                  80


Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
                85                  90                  95


Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
            100                 105                 110


Phe Gln Gly Ser His Leu Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
        115                 120                 125


Glu Ile Lys
    130


<210>  878
<211>  69
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 39H5 light chain variable framework 1 (FW1)
       sequence

<400>  878
gatgttttga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc       60

atctcttgc                                                               69
```

```
<210>  879
<211>  23
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 39H5 light chain variable framework 1 (FW1)
       sequence

<400>  879

Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1               5                   10                  15


Asp Gln Ala Ser Ile Ser Cys
            20


<210>  880
<211>  48
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 39H5 light chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  880
agatctagtc agagcattgt acatagaaat ggaaacacct atttagaa                    48


<210>  881
<211>  16
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 39H5 light chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  881

Arg Ser Ser Gln Ser Ile Val His Arg Asn Gly Asn Thr Tyr Leu Glu
1               5                   10                  15


<210>  882
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 39H5 light chain variable framework 2 (FW2)
       sequence

<400>  882
tggtacctgc agaaaccagg ccagtctcca aagctcctga tctac                       45


<210>  883
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 39H5 light chain variable framework 2 (FW2)
```

```
       sequence

<400>  883

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr
1               5                   10                  15


<210>  884
<211>  21
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 39H5 light chain variable complementarity
       determining regions 2 (CDR2) sequence

<400>  884
aaagtttcca accgattttc t                                               21


<210>  885
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 39H5 light chain variable complementarity
       determining regions 2 (CDR2) sequence

<400>  885

Lys Val Ser Asn Arg Phe Ser
1               5


<210>  886
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 39H5 light chain variable framework 3 (FW3)
       sequence

<400>  886
ggggtcccag acaggttcag tggcagtgga tcagggacag atttcacact caagatcagc       60

agagtggagg ctgaggatct gggagtttat tactgc                                 96


<210>  887
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 39H5 light chain variable framework 3 (FW3)
       sequence

<400>  887

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1               5                   10                  15


Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
            20                  25                  30
```

<210> 888
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 39H5 light chain variable complementarity determining regions 3 (CDR3) sequence

<400> 888
tttcaaggtt cacatcttcc gtggacg 27

<210> 889
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 39H5 light chain variable complementarity determining regions 3 (CDR3) sequence

<400> 889

Phe Gln Gly Ser His Leu Pro Trp Thr
1 5

<210> 890
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 39H5 light chain variable framework 4 (FW4) sequence

<400> 890
ttcggtggag gcaccaagct ggaaatcaaa 30

<210> 891
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 39H5 light chain variable framework 4 (FW4) sequence

<400> 891

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> 892
<211> 411
<212> DNA
<213> Artificial Sequence

<220>
<223> Antibody 3C5 Heavy chain: DNA sequence - Signal sequenceFR1CDR1FR2CDR2FR3CDR3FR4

<400> 892
atggcttggg tgtggacctt gctgttcctg atggcagctg cccaaagtgc ccaagcacag 60

```
atccagttgg tgcagtctgg acctgagctg aagaagcctg gagagacagt caagatctcc      120

tgcaaggctt ctgggtatac cttcacaaac tatggaatga actgggtgaa gcaggctcca      180

ggaaagggtt taaagtggat gggctggata aacacctaca ctggaaagcc aacatatgct      240

gatgacttca agggacggtt tgccttctct ttggagacct ctgccagcac tgcctatttg      300

cagatcaaca acctcaaaaa tgaggacacg gctacatatt tctgtgcaag agggggacta      360

gatggttact acggctactg gggccaaggc accactctca cagtctcctc a               411
```

<210> 893
<211> 137
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody 3C5 Heavy chain: Amino acid sequence - Signal peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400> 893

```
Met Ala Trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
1               5                   10                  15


Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
            20                  25                  30


Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45


Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60


Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Lys Pro Thr Tyr Ala
65                  70                  75                  80


Asp Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
                85                  90                  95


Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr
            100                 105                 110


Tyr Phe Cys Ala Arg Gly Gly Leu Asp Gly Tyr Tyr Gly Tyr Trp Gly
        115                 120                 125


Gln Gly Thr Thr Leu Thr Val Ser Ser
    130                 135
```

<210> 894
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 3C5 heavy chain variable framework 1 (FW1) sequence

<400> 894
cagatccagt tggtgcagtc tggacctgag ctgaagaagc ctggagagac agtcaagatc   60

tcctgcaagg cttctgggta taccttcaca   90

<210> 895
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 3C5 heavy chain variable framework 1 (FW1)
       sequence

<400> 895

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1   5   10   15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
            20   25   30

<210> 896
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 3C5 heavy chain variable complementarity
       determining regions 1 (CDR1) sequence

<400> 896
aactatggaa tgaac   15

<210> 897
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 3C5 heavy chain variable complementarity
       determining regions 1 (CDR1) sequence

<400> 897

Asn Tyr Gly Met Asn
1   5

<210> 898
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 3C5 heavy chain variable framework 2 (FW2)
       sequence

<400> 898
tgggtgaagc aggctccagg aaagggttta aagtggatgg gc   42

<210> 899
<211> 14
<212> PRT

<213> Artificial Sequence

<220>
<223> Mouse antibody 3C5 heavy chain variable framework 2 (FW2)
sequence

<400> 899

Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met Gly
1 5 10

<210> 900
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 3C5 heavy chain variable complementarity
determining regions 2 (CDR2) sequence

<400> 900
tggataaaca cctacactgg aaagccaaca tatgctgatg acttcaaggg a 51

<210> 901
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 3C5 heavy chain variable complementarity
determining regions 2 (CDR2) sequence

<400> 901

Trp Ile Asn Thr Tyr Thr Gly Lys Pro Thr Tyr Ala Asp Asp Phe Lys
1 5 10 15

Gly

<210> 902
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 3C5 heavy chain variable framework 3 (FW3)
sequence

<400> 902
cggtttgcct tctctttgga gacctctgcc agcactgcct atttgcagat caacaacctc 60

aaaaatgagg acacggctac atatttctgt gcaaga 96

<210> 903
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 3C5 heavy chain variable framework 3 (FW3)
sequence

<400> 903

```
Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu Gln
1               5                   10                  15


Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg
            20                  25                  30


<210>  904
<211>  27
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 3C5 heavy chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  904
gggggactag atggttacta cggctac                                          27


<210>  905
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 3C5 heavy chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  905

Gly Gly Leu Asp Gly Tyr Tyr Gly Tyr
1               5


<210>  906
<211>  33
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 3C5 heavy chain variable framework 4 (FW4)
       sequence

<400>  906
tggggccaag gcaccactct cacagtctcc tca                                   33


<210>  907
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 3C5 heavy chain variable framework 4 (FW4)
       sequence

<400>  907

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
1               5                   10


<210>  908
<211>  393
<212>  DNA
<213>  Artificial Sequence
```

```
<220>
<223>  Antibody 3C5 Light chain: DNA sequence (393 bp) - Signal
      sequenceFR1CDR1FR2CDR2FR3CDR3FR4

<400>  908
atgagtcctg cccagttcct gtttctgcta gtgctctcga ttcaggaaac caacggtgat       60

gttgtgatgg ctcagacccc actcactttg tcggttacca ttggacaacc agcctccatc      120

tcttgcaaat caagtcagag cctcttacat agtaaaggaa agacatattt gaattggtta      180

ttacagaggc caggccagtc tccaaagctc ctaatctatc tggtgtctaa actggaatct      240

ggagtccctg acaggttcag tggcagtgga tcagggacag atttcacact gaaaatcagc      300

agagtggagg ctgaagattt gggagtttat tactgcttgc aaactacaca ttttccgtgg      360

acgttcggtg gaggcaccaa gctggaaatc aaa                                   393


<210>  909
<211>  131
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Antibody 3C5 Light chain: Amino acid sequence (131 aa) - Signal
      peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400>  909

Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Ser Ile Gln Glu
1               5                   10                  15


Thr Asn Gly Asp Val Val Met Ala Gln Thr Pro Leu Thr Leu Ser Val
            20                  25                  30


Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu
        35                  40                  45


Leu His Ser Lys Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro
    50                  55                  60


Gly Gln Ser Pro Lys Leu Leu Ile Tyr Leu Val Ser Lys Leu Glu Ser
65                  70                  75                  80


Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
                85                  90                  95


Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
            100                 105                 110


Leu Gln Thr Thr His Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
        115                 120                 125


Glu Ile Lys
    130


<210>  910
```

```
<211>  69
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 3C5 light chain variable framework 1 (FW1)
       sequence

<400>  910
gatgttgtga tggctcagac cccactcact ttgtcggtta ccattggaca accagcctcc       60

atctcttgc                                                               69


<210>  911
<211>  23
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 3C5 light chain variable framework 1 (FW1)
       sequence

<400>  911

Asp Val Val Met Ala Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly
1               5                   10                  15


Gln Pro Ala Ser Ile Ser Cys
            20


<210>  912
<211>  48
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 39H5 light chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  912
aaatcaagtc agagcctctt acatagtaaa ggaaagacat atttgaat                    48


<210>  913
<211>  16
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 39H5 light chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  913

Lys Ser Ser Gln Ser Leu Leu His Ser Lys Gly Lys Thr Tyr Leu Asn
1               5                   10                  15


<210>  914
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 3C5 light chain variable framework 2 (FW2)
       sequence
```

<400> 914
tggttattac agaggccagg ccagtctcca aagctcctaa tctat   45

<210> 915
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 3C5 light chain variable framework 2 (FW2)
       sequence

<400> 915

Trp Leu Leu Gln Arg Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr
1   5   10   15

<210> 916
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 3C5 light chain variable complementarity
       determining regions 2 (CDR2) sequence

<400> 916
ctggtgtcta aactggaatc t   21

<210> 917
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 3C5 light chain variable complementarity
       determining regions 2 (CDR2) sequence

<400> 917

Leu Val Ser Lys Leu Glu Ser
1   5

<210> 918
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 3C5 light chain variable framework 3 (FW3)
       sequence

<400> 918
ggagtccctg acaggttcag tggcagtgga tcagggacag atttcacact gaaaatcagc   60

agagtggagg ctgaagattt gggagtttat tactgc   96

<210> 919
<211> 32
<212> PRT
<213> Artificial Sequence

<220>

<223> Mouse antibody 3C5 light chain variable framework 3 (FW3)
sequence

<400> 919

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1   5   10   15

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
            20   25   30

<210> 920
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 3C5 light chain variable complementarity
determining regions 3 (CDR3) sequence

<400> 920
ttgcaaacta cacattttcc gtggacg   27

<210> 921
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 3C5 light chain variable complementarity
determining regions 3 (CDR3) sequence

<400> 921

Leu Gln Thr Thr His Phe Pro Trp Thr
1   5

<210> 922
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 3C5 light chain variable framework 4 (FW4)
sequence

<400> 922
ttcggtggag gcaccaagct ggaaatcaaa   30

<210> 923
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 3C5 light chain variable framework 4 (FW4)
sequence

<400> 923

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
1   5   10

```
<210>  924
<211>  420
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 8A9 Heavy chain: DNA sequence (420 bp) - Signal
       sequenceFR1CDR1FR2CDR2FR3CDR3FR4

<400>  924
atgaagttgt ggctgaactg gattttcctt gtaacacttt taaatggtat ccagtgtgag       60

gtggagctgg tggagtctgg aggaggcttg gtacagcctg ggggttctct gagactctcc      120

tgtgcaactt ctgggttcac cttcactgat cactacatga gctgggtccg ccagcctcca      180

ggaaaggcac ttgagtggtt gggatttatt agaaacaaag ctaatggtta cacaacagag      240

tacagtgcat ctgtgaaggg tcggttcacc atctccagag ataattccca aagcatcctc      300

tatcttcaaa tgaaaaccct gagaactgag gacagtgcca cttattactg tgcaagacct      360

tctgactggg actcctggtt tgcttactgg ggccaaggga ctctggtcac tgtctctgca      420


<210>  925
<211>  140
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 8A9 Heavy chain: Amino acid sequence (140 aa) -
       Signal peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400>  925

Met Lys Leu Trp Leu Asn Trp Ile Phe Leu Val Thr Leu Leu Asn Gly
1               5                   10                  15


Ile Gln Cys Glu Val Glu Leu Val Glu Ser Gly Gly Gly Leu Val Gln
            20                  25                  30


Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe
        35                  40                  45


Thr Asp His Tyr Met Ser Trp Val Arg Gln Pro Pro Gly Lys Ala Leu
    50                  55                  60


Glu Trp Leu Gly Phe Ile Arg Asn Lys Ala Asn Gly Tyr Thr Thr Glu
65                  70                  75                  80


Tyr Ser Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
                85                  90                  95


Gln Ser Ile Leu Tyr Leu Gln Met Lys Thr Leu Arg Thr Glu Asp Ser
            100                 105                 110


Ala Thr Tyr Tyr Cys Ala Arg Pro Ser Asp Trp Asp Ser Trp Phe Ala
        115                 120                 125


Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
```

130   135   140

<210> 926
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 8A9 heavy chain variable framework 1 (FW1)
       sequence

<400> 926
gaggtggagc tggtggagtc tggaggaggc ttggtacagc ctgggggttc tctgagactc   60

tcctgtgcaa cttctgggtt caccttcact   90

<210> 927
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 8A9 heavy chain variable framework 1 (FW1)
       sequence

<400> 927

Glu Val Glu Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Thr
            20   25   30

<210> 928
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 8A9 heavy chain variable complementarity
       determining regions 1 (CDR1) sequence

<400> 928
gatcactaca tgagc   15

<210> 929
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 8A9 heavy chain variable complementarity
       determining regions 1 (CDR1) sequence

<400> 929

Asp His Tyr Met Ser
1   5

<210> 930
<211> 42
<212> DNA
<213> Artificial Sequence

```
<220>
<223>  Mouse antibody 8A9 heavy chain variable framework 2 (FW2)
       sequence

<400>  930
tgggtccgcc agcctccagg aaaggcactt gagtggttgg ga                          42


<210>  931
<211>  14
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 8A9 heavy chain variable framework 2 (FW2)
       sequence

<400>  931

Trp Val Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Gly
1               5                   10


<210>  932
<211>  57
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 8A9 heavy chain variable complementarity
       determining regions 2 (CDR2) sequence

<400>  932
tttattagaa acaaagctaa tggttacaca acagagtaca gtgcatctgt gaagggt          57


<210>  933
<211>  19
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 8A9 heavy chain variable complementarity
       determining regions 2 (CDR2) sequence

<400>  933

Phe Ile Arg Asn Lys Ala Asn Gly Tyr Thr Thr Glu Tyr Ser Ala Ser
1               5                   10                  15


Val Lys Gly



<210>  934
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 8A9 heavy chain variable framework 3 (FW3)
       sequence

<400>  934
cggttcacca tctccagaga taattcccaa agcatcctct atcttcaaat gaaaaccctg       60

agaactgagg acagtgccac ttattactgt gcaaga                                 96
```

```
<210>  935
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 8A9 heavy chain variable framework 3 (FW3)
       sequence

<400>  935

Arg Phe Thr Ile Ser Arg Asp Asn Ser Gln Ser Ile Leu Tyr Leu Gln
1               5                   10                  15


Met Lys Thr Leu Arg Thr Glu Asp Ser Ala Thr Tyr Tyr Cys Ala Arg
            20                  25                  30


<210>  936
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 8A9 heavy chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  936
ccttctgact gggactcctg gtttgcttac                                        30


<210>  937
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 8A9 heavy chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  937

Pro Ser Asp Trp Asp Ser Trp Phe Ala Tyr
1               5                   10


<210>  938
<211>  33
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 8A9 heavy chain variable framework 4 (FW4)
       sequence

<400>  938
tggggccaag ggactctggt cactgtctct gca                                    33


<210>  939
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 8A9 heavy chain variable framework 4 (FW4)
```

```
       sequence

<400>  939

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
1               5                   10


<210>  940
<211>  393
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 8A9 Light chain: DNA sequence (393 bp) - Signal
       sequenceFR1CDR1FR2CDR2FR3CDR3FR4

<400>  940
atgaagttgc ctgttaggct gttggtgctg atgttctgga ttcctgcttc cagcagtgat       60

gttttgatga cccaaactcc actctccctg cctgtcagtc ttggtgatca agcctccatc      120

tcttgcagat ctagtcagag cattgtacat agtaatggca acacctattt agattggtac      180

ttgcagaaac caggccagtc tccaaagctc ctgatctaca gagtttccaa ccgattttct      240

ggggtcccag acaggttcag tggcagtgga tcagggacag atttcacact caagatcagc      300

agagtggagg ctgaggatct gggactttat tactgttttc aaggttcaca tgttccgtgg      360

gcgttcggtg gaggcaccaa gctggaaatc aaa                                   393


<210>  941
<211>  131
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 8A9 Light chain: Amino acid sequence (131 aa) -
       Signal peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400>  941

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
1               5                   10                  15


Ser Ser Ser Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val
            20                  25                  30


Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile
        35                  40                  45


Val His Ser Asn Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro
    50                  55                  60


Gly Gln Ser Pro Lys Leu Leu Ile Tyr Arg Val Ser Asn Arg Phe Ser
65                  70                  75                  80


Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
                85                  90                  95


Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Leu Tyr Tyr Cys
```

```
            100                 105                 110


Phe Gln Gly Ser His Val Pro Trp Ala Phe Gly Gly Gly Thr Lys Leu
        115                 120                 125


Glu Ile Lys
    130


<210>  942
<211>  69
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 8A9 light chain variable framework 1 (FW1)
       sequence

<400>  942
gatgttttga tgacccaaac tccactctcc ctgcctgtca gtcttggtga tcaagcctcc       60

atctcttgc                                                               69


<210>  943
<211>  23
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 8A9 light chain variable framework 1 (FW1)
       sequence

<400>  943

Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1               5                   10                  15


Asp Gln Ala Ser Ile Ser Cys
            20


<210>  944
<211>  48
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 8A9 light chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  944
agatctagtc agagcattgt acatagtaat ggcaacacct atttagat                    48


<210>  945
<211>  16
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 8A9 light chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  945
```

```
Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Asp
1               5                   10                  15


<210>  946
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 8A9 light chain variable framework 2 (FW2)
       sequence

<400>  946
tggtacttgc agaaaccagg ccagtctcca aagctcctga tctac                       45


<210>  947
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 8A9 light chain variable framework 2 (FW2)
       sequence

<400>  947

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr
1               5                   10                  15


<210>  948
<211>  21
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 8A9 light chain variable complementarity
       determining regions 2 (CDR2) sequence

<400>  948
agagtttcca accgattttc t                                                 21


<210>  949
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 8A9 light chain variable complementarity
       determining regions 2 (CDR2) sequence

<400>  949

Arg Val Ser Asn Arg Phe Ser
1               5


<210>  950
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 8A9 light chain variable framework 3 (FW3)
       sequence
```

```
<400>  950
ggggtcccag acaggttcag tggcagtgga tcagggacag atttcacact caagatcagc       60

agagtggagg ctgaggatct gggactttat tactgt                                 96


<210>  951
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 8A9 light chain variable framework 3 (FW3)
       sequence

<400>  951

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1               5                   10                  15


Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Leu Tyr Tyr Cys
            20                  25                  30


<210>  952
<211>  27
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 8A9 light chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  952
tttcaaggtt cacatgttcc gtgggcg                                           27


<210>  953
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 8A9 light chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  953

Phe Gln Gly Ser His Val Pro Trp Ala
1               5


<210>  954
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 8A9 light chain variable framework 4 (FW4)
       sequence

<400>  954
ttcggtggag gcaccaagct ggaaatcaaa                                        30


<210>  955
<211>  10
<212>  PRT
```

<213> Artificial Sequence

<220>
<223> Mouse antibody 8A9 light chain variable framework 4 (FW4)
       sequence

<400> 955

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
1   5   10

<210> 956
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 18G12 Heavy chain: DNA sequence (399 bp) - Signal
       sequenceFR1CDR1FR2CDR2FR3CDR3FR4

<400> 956
atgggatgga gctatatcat cctctttttg gtcgcaacag ctacaggtgt ccactcccag   60

gtccaactgc agcagtctgg ggctgaactg gtgaagcctg gggcttcagt gaagttgtcc   120

tgcaaggctt ctggctacac cttcaccggc tactttttgt actgggtgaa gcagaggcct   180

ggacaaggcc ttgagtggat tggggggatt aatcctgaca atggtggtat tgacttcaat   240

gagaagttca ggaacaaggc cacactgact gtagacaaat cctccagcac agcctacatg   300

caactcagca gcctgacatc tgaggactct gcggtctatt attgtacatt actaataggg   360

aactattggg gccaaggcac cactctcaca gtctcctca   399

<210> 957
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 18G12 Heavy chain: Amino acid sequence (133 aa) -
       Signal peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400> 957

Met Gly Trp Ser Tyr Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1   5   10   15

Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys
            20   25   30

Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35   40   45

Thr Gly Tyr Phe Leu Tyr Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
    50   55   60

Glu Trp Ile Gly Gly Ile Asn Pro Asp Asn Gly Gly Ile Asp Phe Asn
65   70   75   80

Glu Lys Phe Arg Asn Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser

```
                85                  90                  95


Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110


Tyr Tyr Cys Thr Leu Leu Ile Gly Asn Tyr Trp Gly Gln Gly Thr Thr
        115                 120                 125


Leu Thr Val Ser Ser
    130


<210>  958
<211>  90
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18G12 heavy chain variable framework 1 (FW1)
       sequence

<400>  958
caggtccaac tgcagcagtc tggggctgaa ctggtgaagc ctggggcttc agtgaagttg       60

tcctgcaagg cttctggcta caccttcacc                                        90


<210>  959
<211>  30
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18G12 heavy chain variable framework 1 (FW1)
       sequence

<400>  959

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
            20                  25                  30


<210>  960
<211>  15
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 39H5 heavy chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  960
ggctactttt tgtac                                                        15


<210>  961
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 39H5 heavy chain variable complementarity
```

```
       determining regions 1 (CDR1) sequence

<400>  961

Gly Tyr Phe Leu Tyr
1               5


<210>  962
<211>  42
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18G12 heavy chain variable framework 2 (FW2)
       sequence

<400>  962
tgggtgaagc agaggcctgg acaaggcctt gagtggattg gg                          42


<210>  963
<211>  14
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18G12 heavy chain variable framework 2 (FW2)
       sequence

<400>  963

Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
1               5                   10


<210>  964
<211>  51
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18G12 heavy chain variable complementarity
       determining regions 2 (CDR2) sequence

<400>  964
gggattaatc ctgacaatgg tggtattgac ttcaatgaga agttcaggaa c                51


<210>  965
<211>  17
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18G12 heavy chain variable complementarity
       determining regions 2 (CDR2) sequence

<400>  965

Gly Ile Asn Pro Asp Asn Gly Gly Ile Asp Phe Asn Glu Lys Phe Arg
1               5                   10                  15


Asn



<210>  966
```

<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 18G12 heavy chain variable framework 3 (FW3)
       sequence

<400> 966
aaggccacac tgactgtaga caaatcctcc agcacagcct acatgcaact cagcagcctg   60

acatctgagg actctgcggt ctattattgt acatta   96

<210> 967
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 18G12 heavy chain variable framework 3 (FW3)
       sequence

<400> 967

Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln
1   5   10   15

Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Thr Leu
            20   25   30

<210> 968
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 18G12 heavy chain variable complementarity
       determining regions 3 (CDR3) sequence

<400> 968
ctaataggga actat   15

<210> 969
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 18G12 heavy chain variable complementarity
       determining regions 3 (CDR3) sequence

<400> 969

Leu Ile Gly Asn Tyr
1   5

<210> 970
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 18G12 heavy chain variable framework 4 (FW4)
       sequence

<400> 970
tggggccaag gcaccactct cacagtctcc tca   33

<210> 971
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 18G12 heavy chain variable framework 4 (FW4) sequence

<400> 971

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
1   5   10

<210> 972
<211> 393
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 18G12 Light chain: DNA sequence (393 bp) - Signal sequenceFR1CDR1FR2CDR2FR3CDR3FR4

<400> 972
atgagtcctg cccagttcct gtttctgtta gtgctctgga ttcgggaaac caatggtgat   60

gttgtgatga cccagactcc actcactttg tcggtaacca ttggacagcc agcctccatc   120

tcttgcaagt caagtcagag cctcttacat agtgatggaa agacatattt gatttggttg   180

ttacagaggc caggccagtc tccaaagcgc ctaatctatc tggtgtctaa actggactct   240

ggagtccctg acaggttcac tggcagtgga tcagggacag atttcacact gaaaatcagc   300

agagtggagg ctgaggattt gggagtttat ttttgctgtc aaggtacaca ttttccgtgg   360

acgttcggtg gaggcaccat gctggaaatc aaa   393

<210> 973
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 18G12 Light chain: Amino acid sequence (131 aa) - Signal peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400> 973

Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu
1   5   10   15

Thr Asn Gly Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val
            20   25   30

Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu
        35   40   45

Leu His Ser Asp Gly Lys Thr Tyr Leu Ile Trp Leu Leu Gln Arg Pro

    50   55   60

Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser
65   70   75   80

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
                85   90   95

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
            100   105   110

Cys Gln Gly Thr His Phe Pro Trp Thr Phe Gly Gly Gly Thr Met Leu
        115   120   125

Glu Ile Lys
    130

<210> 974
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 18G12 light chain variable framework 1 (FW1)
       sequence

<400> 974
gatgttgtga tgacccagac tccactcact ttgtcggtaa ccattggaca gccagcctcc   60

atctcttgc   69

<210> 975
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 18G12 light chain variable framework 1 (FW1)
       sequence

<400> 975

Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly
1   5   10   15

Gln Pro Ala Ser Ile Ser Cys
            20

<210> 976
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 18G12 light chain variable complementarity
       determining regions 1 (CDR1) sequence

<400> 976
aagtcaagtc agagcctctt acatagtgat ggaaagacat atttgatt   48

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<210>  977
<211>  16
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18G12 light chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  977

Lys Ser Ser Gln Ser Leu Leu His Ser Asp Gly Lys Thr Tyr Leu Ile
1               5                   10                  15


<210>  978
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18G12 light chain variable framework 2 (FW2)
       sequence

<400>  978
tggttgttac agaggccagg ccagtctcca aagcgcctaa tctat                       45


<210>  979
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18G12 light chain variable framework 2 (FW2)
       sequence

<400>  979

Trp Leu Leu Gln Arg Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr
1               5                   10                  15


<210>  980
<211>  21
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18G12 light chain variable complementarity
       determining regions 2 (CDR2) sequence

<400>  980
ctggtgtcta aactggactc t                                                 21


<210>  981
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18G12 light chain variable complementarity
       determining regions 2 (CDR2) sequence

<400>  981

Leu Val Ser Lys Leu Asp Ser
```

1   5

<210> 982
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 18G12 light chain variable framework 3 (FW3)
       sequence

<400> 982
ggagtccctg acaggttcac tggcagtgga tcagggacag atttcacact gaaaatcagc   60

agagtggagg ctgaggattt gggagtttat ttttgc   96

<210> 983
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 18G12 light chain variable framework 3 (FW3)
       sequence

<400> 983

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
1   5   10   15

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
            20   25   30

<210> 984
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 18G12 light chain variable complementarity
       determining regions 3 (CDR3) sequence

<400> 984
tgtcaaggta cacattttcc gtggacg   27

<210> 985
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 18G12 light chain variable complementarity
       determining regions 3 (CDR3) sequence

<400> 985

Cys Gln Gly Thr His Phe Pro Trp Thr
1   5

<210> 986
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 18G12 light chain variable framework 4 (FW4)
       sequence

<400> 986
ttcggtggag gcaccatgct ggaaatcaaa   30

<210> 987
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 18G12 light chain variable framework 4 (FW4)
       sequence

<400> 987

Phe Gly Gly Gly Thr Met Leu Glu Ile Lys
1   5   10

<210> 988
<211> 416
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 20A10 Heavy chain: DNA sequence (417 bp) - Signal
       sequenceFR1CDR1FR2CDR2FR3CDR3FR4

<400> 988
atgaacttcg ggttcagctt gattttcctt gtccttgttt taaaaggtgt ccagtgtgaa   60

gtgatgctgg tggagtctgg gggaggctta gtgaagcctg gagggtccct gaaactctcc   120

tgtcagcctc tggattcact ttcagtacct atgccatgtc ttggattcgc cagactccag   180

agaagaggct ggagtgggtc gcatccattg gtcgtgctgg ttccacctac tattcagaca   240

gtgtgaaggg ccgattcacc atctccagag ataatgtccg gaacatcctg tacctgcaaa   300

tgagcagtct gaggtctgag gacacggcca tgtattactg tgctagaggc ccgatctaca   360

atgattacga cgagtttgct tactggggcc aagggactct ggtcactgtc tctgca   416

<210> 989
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 20A10 Heavy chain: Amino acid sequence (139 aa) -
       Signal peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400> 989

Met Asn Phe Gly Phe Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
1   5   10   15

Val Gln Cys Glu Val Met Leu Val Glu Ser Gly Gly Gly Leu Val Lys
            20   25   30

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe

```
        35                  40                  45

Ser Thr Tyr Ala Met Ser Trp Ile Arg Gln Thr Pro Glu Lys Arg Leu
    50                  55                  60

Glu Trp Val Ala Ser Ile Gly Arg Ala Gly Ser Thr Tyr Tyr Ser Asp
65                  70                  75                  80

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Val Arg Asn Ile
                85                  90                  95

Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr
            100                 105                 110

Tyr Cys Ala Arg Gly Pro Ile Tyr Asn Asp Tyr Asp Glu Phe Ala Tyr
        115                 120                 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
    130                 135


<210>  990
<211>  90
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 20A10 heavy chain variable framework 1 (FW1)
       sequence

<400>  990
gaagtgatgc tggtggagtc tgggggaggc ttagtgaagc ctggagggtc cctgaaactc       60

tcctgtgcag cctctggatt cactttcagt                                        90


<210>  991
<211>  30
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 20A10 heavy chain variable framework 1 (FW1)
       sequence

<400>  991

Glu Val Met Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            20                  25                  30


<210>  992
<211>  15
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 20A10 heavy chain variable complementarity
       determining regions 1 (CDR1) sequence
```

<400> 992
acctatgcca tgtct 15

<210> 993
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 20A10 heavy chain variable complementarity determining regions 1 (CDR1) sequence

<400> 993

Thr Tyr Ala Met Ser
1 5

<210> 994
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 20A10 heavy chain variable framework 2 (FW2) sequence

<400> 994
tggattcgcc agactccaga gaagaggctg gagtgggtcg ca 42

<210> 995
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 20A10 heavy chain variable framework 2 (FW2) sequence

<400> 995

Trp Ile Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val Ala
1 5 10

<210> 996
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 20A10 heavy chain variable complementarity determining regions 2 (CDR2) sequence

<400> 996
tccattggtc gtgctggttc cacctactat tcagacagtg tgaagggc 48

<210> 997
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 20A10 heavy chain variable complementarity determining regions 2 (CDR2) sequence

<400> 997

Ser Ile Gly Arg Ala Gly Ser Thr Tyr Tyr Ser Asp Ser Val Lys Gly
1   5   10   15

<210> 998
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 20A10 heavy chain variable framework 3 (FW3) sequence

<400> 998
cgattcacca tctccagaga taatgtccgg aacatcctgt acctgcaaat gagcagtctg 60

aggtctgagg acacggccat gtattactgt gctaga 96

<210> 999
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 20A10 heavy chain variable framework 3 (FW3) sequence

<400> 999

Arg Phe Thr Ile Ser Arg Asp Asn Val Arg Asn Ile Leu Tyr Leu Gln
1   5   10   15

Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys Ala Arg
            20   25   30

<210> 1000
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 20A10 heavy chain variable complementarity determining regions 3 (CDR3) sequence

<400> 1000
ggcccgatct acaatgatta cgacgagttt gcttac 36

<210> 1001
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 20A10 heavy chain variable complementarity determining regions 3 (CDR3) sequence

<400> 1001

Gly Pro Ile Tyr Asn Asp Tyr Asp Glu Phe Ala Tyr
1   5   10

<210> 1002
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 20A10 heavy chain variable framework 4 (FW4) sequence

<400> 1002
tggggccaag ggactctggt cactgtctct gca 33

<210> 1003
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 20A10 heavy chain variable framework 4 (FW4) sequence

<400> 1003

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
1 5 10

<210> 1004
<211> 396
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 20A10 Light chain: DNA sequence (396 bp) - Signal sequenceFR1CDR1FR2CDR2FR3CDR3FR4

<400> 1004
atggaatcac agactcaggt cttcctctcc ctgctgctct gggtatctgg tacctgtggg 60

aacattatga tgacacagtc gccatcatct ctggctgtgt ctgcaggaga aaaggtcact 120

atgagctgta agtccagtca aagtgtttta tacagttcaa atcagaagaa ctatttggcc 180

tggtaccagc agaaaccagg gcagtctcct aaactgctga tctactgggc atccactagg 240

gaatctggtg tccctgatcg cttcacaggc agtggatctg ggacagattt tactcttacc 300

atcagcagtg tacaagctga agacctggca gtttattact gtcatcaata cctctcctcg 360

ctcacgttcg gtgctgggac caagctggag ctgaaa 396

<210> 1005
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 20A10 Light chain: Amino acid sequence (132 aa) - Signal peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400> 1005

Met Glu Ser Gln Thr Gln Val Phe Leu Ser Leu Leu Leu Trp Val Ser
1 5 10 15

Gly Thr Cys Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala

            20   25   30

Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
        35   40   45

Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
    50   55   60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65   70   75   80

Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
                85   90   95

Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
            100   105   110

Tyr Cys His Gln Tyr Leu Ser Ser Leu Thr Phe Gly Ala Gly Thr Lys
        115   120   125

Leu Glu Leu Lys
    130

<210> 1006
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 20A10 light chain variable framework 1 (FW1)
       sequence

<400> 1006
aacattatga tgacacagtc gccatcatct ctggctgtgt ctgcaggaga aaaggtcact   60

atgagctgt   69

<210> 1007
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 20A10 light chain variable framework 1 (FW1)
       sequence

<400> 1007

Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1   5   10   15

Glu Lys Val Thr Met Ser Cys
            20

<210> 1008
<211> 51
<212> DNA
<213> Artificial Sequence

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<220>
<223>  Mouse antibody 20A10 light chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  1008
aagtccagtc aaagtgtttt atacagttca aatcagaaga actatttggc c                51


<210>  1009
<211>  17
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 20A10 light chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  1009

Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu
1               5                   10                  15


Ala



<210>  1010
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 20A10 light chain variable framework 2 (FW2)
       sequence

<400>  1010
tggtaccagc agaaaccagg gcagtctcct aaactgctga tctac                       45


<210>  1011
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 20A10 light chain variable framework 2 (FW2)
       sequence

<400>  1011

Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr
1               5                   10                  15


<210>  1012
<211>  21
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 20A10 light chain variable complementarity
       determining regions 2 (CDR2) sequence

<400>  1012
tgggcatcca ctagggaatc t                                                 21
```

<210> 1013
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 20A10 light chain variable complementarity
       determining regions 2 (CDR2) sequence

<400> 1013

Trp Ala Ser Thr Arg Glu Ser
1   5

<210> 1014
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 20A10 light chain variable framework 3 (FW3)
       sequence

<400> 1014
ggtgtccctg atcgcttcac aggcagtgga tctgggacag attttactct taccatcagc   60

agtgtacaag ctgaagacct ggcagtttat tactgt   96

<210> 1015
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 20A10 light chain variable framework 3 (FW3)
       sequence

<400> 1015

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
1   5   10   15

Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys
            20   25   30

<210> 1016
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 20A10 light chain variable complementarity
       determining regions 3 (CDR3) sequence

<400> 1016
catcaatacc tctcctcgct cacg   24

<210> 1017
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 20A10 light chain variable complementarity

determining regions 3 (CDR3) sequence

<400> 1017

His Gln Tyr Leu Ser Ser Leu Thr
1   5

<210> 1018
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 20A10 light chain variable framework 4 (FW4) sequence

<400> 1018
ttcggtgctg ggaccaagct ggagctgaaa   30

<210> 1019
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 20A10 light chain variable framework 4 (FW4) sequence

<400> 1019

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
1   5   10

<210> 1020
<211> 413
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 25E6 Heavy chain: DNA sequence (414 bp) - Signal sequenceFR1CDR1FR2CDR2FR3CDR3FR4

<400> 1020
atgaacttcg ggctcagctt gattttcctt gccctcattt taaaaggtgt ccagtgtgag   60

gtgcagctgg tggagtctgg gggagactta gtgaagcctg gagggtccct gaaactctcc   120

tgtgcagcct ctggtttcac tttcagtagt tatggaatgt cttgggttcg ccagactcca   180

gacaagaggc tggagtgggt cgcaaccatt agtaatggtg gtagacacac cttctatcca   240

gacagtgtga aggggcgatt caccatctcc agagacaatg ccaagaacac cctgtatctg   300

caaatgagca gtctgaagtt gaggacacag ccatgtattt atgtgtaaga cagactggga   360

cggagggctg gtttgcttac tggggccaag ggactctggt cactgtctct gca   413

<210> 1021
<211> 138
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 25E6 Heavy chain: Amino acid sequence (138 aa) - Signal peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400> 1021

Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Ala Leu Ile Leu Lys Gly
1   5   10   15

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys
            20   25   30

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
        35   40   45

Ser Ser Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu
    50   55   60

Glu Trp Val Ala Thr Ile Ser Asn Gly Gly Arg His Thr Phe Tyr Pro
65   70   75   80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
                85   90   95

Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met
            100   105   110

Tyr Leu Cys Val Arg Gln Thr Gly Thr Glu Gly Trp Phe Ala Tyr Trp
        115   120   125

Gly Gln Gly Thr Leu Val Thr Val Ser Ala
    130   135

<210> 1022
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 25E6 heavy chain variable framework 1 (FW1) sequence

<400> 1022
gaggtgcagc tggtggagtc tgggggagac ttagtgaagc ctggagggtc cctgaaactc   60

tcctgtgcag cctctggttt cactttcagt   90

<210> 1023
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 25E6 heavy chain variable framework 1 (FW1) sequence

<400> 1023

Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly
1   5   10   15

```
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            20                  25                  30


<210>  1024
<211>  15
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 25E6 heavy chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  1024
agttatggaa tgtct                                                        15


<210>  1025
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 25E6 heavy chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  1025

Ser Tyr Gly Met Ser
1               5


<210>  1026
<211>  42
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 25E6 heavy chain variable framework 2 (FW2)
       sequence

<400>  1026
tgggttcgcc agactccaga caagaggctg gagtgggtcg ca                          42


<210>  1027
<211>  14
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 25E6 heavy chain variable framework 2 (FW2)
       sequence

<400>  1027

Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Trp Val Ala
1               5                   10


<210>  1028
<211>  51
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 25E6 heavy chain variable complementarity
       determining regions 2 (CDR2) sequence
```

<400> 1028
accattagta atggtggtag acacaccttc tatccagaca gtgtgaaggg g   51

<210> 1029
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 25E6 heavy chain variable complementarity
       determining regions 2 (CDR2) sequence

<400> 1029

Thr Ile Ser Asn Gly Gly Arg His Thr Phe Tyr Pro Asp Ser Val Lys
1   5   10   15

Gly

<210> 1030
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 25E6 heavy chain variable framework 3 (FW3)
       sequence

<400> 1030
cgattcacca tctccagaga caatgccaag aacaccctgt atctgcaaat gagcagtctg   60

aagtctgagg acacagccat gtatttatgt gtaaga   96

<210> 1031
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 25E6 heavy chain variable framework 3 (FW3)
       sequence

<400> 1031

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln
1   5   10   15

Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Leu Cys Val Arg
            20   25   30

<210> 1032
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 25E6 heavy chain variable complementarity
       determining regions 3 (CDR3) sequence

<400> 1032
cagactggga cggagggctg gtttgcttac   30

```
<210>  1033
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 25E6 heavy chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  1033

Gln Thr Gly Thr Glu Gly Trp Phe Ala Tyr
1               5                   10


<210>  1034
<211>  33
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 25E6 heavy chain variable framework 4 (FW4)
       sequence

<400>  1034
tggggccaag ggactctggt cactgtctct gca                                    33


<210>  1035
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 25E6 heavy chain variable framework 4 (FW4)
       sequence

<400>  1035

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
1               5                   10


<210>  1036
<211>  392
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 25E6 Light chain: DNA sequence (393 bp) - Signal
       sequenceFR1CDR1FR2CDR2FR3CDR3FR4

<400>  1036
atgagtcctg cccagttcct gtttctgtta gtgctctgga ttcgggaaac caacggtgat       60

gttgtgatga cccagactcc actcactttg tcggttacca ttggacaacc agcctccatc      120

tcttgcaagt caagtcagag cctcttagat agtgatggaa agacatattt gaattggttg      180

ttacagaggc caggccagtc tccaaagcgc ctaatctatc tggtgtctaa actggactct      240

ggagtccctg acaggttcac tggcagtgga tcagggacag atttcacact gaaaatcagc      300

agagggaggc tgaggatttg ggagtttatt attgctggca aggtacacat tttcctcaga      360

cgttcggtgg aggcaccaag ctggaaatca aa                                    392
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<210> 1037
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 25E6 Light chain: Amino acid sequence (131 aa) -
       Signal peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400> 1037

Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu
1   5   10   15

Thr Asn Gly Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val
            20   25   30

Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu
        35   40   45

Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro
    50   55   60

Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser
65   70   75   80

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
                85   90   95

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
            100   105   110

Trp Gln Gly Thr His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Leu
        115   120   125

Glu Ile Lys
    130

<210> 1038
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 25E6 light chain variable framework 1 (FW1)
       sequence

<400> 1038
gatgttgtga tgacccagac tccactcact ttgtcggtta ccattggaca accagcctcc   60

atctcttgc   69

<210> 1039
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 25E6 light chain variable framework 1 (FW1)

sequence

<400> 1039

Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly
1   5   10   15

Gln Pro Ala Ser Ile Ser Cys
            20

<210> 1040
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 25E6 light chain variable complementarity
       determining regions 1 (CDR1) sequence

<400> 1040
aagtcaagtc agagcctctt agatagtgat ggaaagacat atttgaat   48

<210> 1041
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 25E6 light chain variable complementarity
       determining regions 1 (CDR1) sequence

<400> 1041

Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn
1   5   10   15

<210> 1042
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 25E6 light chain variable framework 2 (FW2)
       sequence

<400> 1042
tggttgttac agaggccagg ccagtctcca aagcgcctaa tctat   45

<210> 1043
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 25E6 light chain variable framework 2 (FW2)
       sequence

<400> 1043

Trp Leu Leu Gln Arg Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr
1   5   10   15

<210> 1044

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 25E6 light chain variable complementarity
determining regions 2 (CDR2) sequence

<400> 1044
ctggtgtcta aactggactc t   21

<210> 1045
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 25E6 light chain variable complementarity
determining regions 2 (CDR2) sequence

<400> 1045

Leu Val Ser Lys Leu Asp Ser
1   5

<210> 1046
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 25E6 light chain variable framework 3 (FW3)
sequence

<400> 1046
ggagtccctg acaggttcac tggcagtgga tcagggacag atttcacact gaaaatcagc   60

agagtggagg ctgaggattt gggagtttat tattgc   96

<210> 1047
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 25E6 light chain variable framework 3 (FW3)
sequence

<400> 1047

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
1   5   10   15

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
            20   25   30

<210> 1048
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 25E6 light chain variable complementarity
determining regions 3 (CDR3) sequence

<400> 1048
tggcaaggta cacattttcc tcagacg   27

<210> 1049
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 25E6 light chain variable complementarity
       determining regions 3 (CDR3) sequence

<400> 1049

Trp Gln Gly Thr His Phe Pro Gln Thr
1   5

<210> 1050
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 25E6 light chain variable framework 4 (FW4)
       sequence

<400> 1050
ttcggtggag gcaccaagct ggaaatcaaa   30

<210> 1051
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 25E6 light chain variable framework 4 (FW4)
       sequence

<400> 1051

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
1   5   10

<210> 1052
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 28F9 Heavy chain: DNA sequence (399 bp) - Signal
       sequenceFR1CDR1FR2CDR2FR3CDR3FR4

<400> 1052
atgggatgga gctatatcat cctctttttg gtagcaacag ctacaggtgt ccactcccag   60

gtccaactgc agcagcctgg ggctgaactg gtgcagcctg gggcttcagt gaagttgtcc   120

tgcaaggctt ctggctacac cttcaccggc tactttttgt actgggtgaa gcagaggcct   180

ggacatggcc ttgagtggat tgggggaatt catcctagca atggtgatac tgacttcaat   240

gagaagttca agaacaaggc cacactgact gtagacatat cctccagcac tgcctacatg   300

caactcagca gcctgacatc tgaggactct gcggtctatt attgtacatt actaataggg   360 gtctactggg gccaaggcac cactctcaca gtctcctca 399

<210> 1053
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 28F9 Heavy chain: Amino acid sequence (133 aa) - Signal peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400> 1053

Met Gly Trp Ser Tyr Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Gln
20 25 30

Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Gly Tyr Phe Leu Tyr Trp Val Lys Gln Arg Pro Gly His Gly Leu
50 55 60

Glu Trp Ile Gly Gly Ile His Pro Ser Asn Gly Asp Thr Asp Phe Asn
65 70 75 80

Glu Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Ile Ser Ser Ser
85 90 95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Thr Leu Leu Ile Gly Val Tyr Trp Gly Gln Gly Thr Thr
115 120 125

Leu Thr Val Ser Ser
130

<210> 1054
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 28F9 heavy chain variable framework 1 (FW1) sequence

<400> 1054
caggtccaac tgcagcagcc tggggctgaa ctggtgcagc ctggggcttc agtgaagttg 60

tcctgcaagg cttctggcta caccttcacc 90

<210> 1055
<211> 30
<212> PRT

<213> Artificial Sequence

<220>
<223> Mouse antibody 28F9 heavy chain variable framework 1 (FW1)
       sequence

<400> 1055

Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Gln Pro Gly Ala
1   5   10   15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
            20   25   30

<210> 1056
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 28F9 heavy chain variable complementarity
       determining regions 1 (CDR1) sequence

<400> 1056
ggctactttt tgtac   15

<210> 1057
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 28F9 heavy chain variable complementarity
       determining regions 1 (CDR1) sequence

<400> 1057

Gly Tyr Phe Leu Tyr
1   5

<210> 1058
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 28F9 heavy chain variable framework 2 (FW2)
       sequence

<400> 1058
tgggtgaagc agaggcctgg acatggcctt gagtggattg gg   42

<210> 1059
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 28F9 heavy chain variable framework 2 (FW2)
       sequence

<400> 1059

Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile Gly

1   5   10

<210> 1060
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 28F9 heavy chain variable complementarity determining regions 2 (CDR2) sequence

<400> 1060
ggaattcatc ctagcaatgg tgatactgac ttcaatgaga agttcaagaa c   51

<210> 1061
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 28F9 heavy chain variable complementarity determining regions 2 (CDR2) sequence

<400> 1061

Gly Ile His Pro Ser Asn Gly Asp Thr Asp Phe Asn Glu Lys Phe Lys
1   5   10   15

Asn

<210> 1062
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 28F9 heavy chain variable framework 3 (FW3) sequence

<400> 1062
aaggccacac tgactgtaga catatcctcc agcactgcct acatgcaact cagcagcctg   60

acatctgagg actctgcggt ctattattgt acatta   96

<210> 1063
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 28F9 heavy chain variable framework 3 (FW3) sequence

<400> 1063

Lys Ala Thr Leu Thr Val Asp Ile Ser Ser Ser Thr Ala Tyr Met Gln
1   5   10   15

Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Thr Leu
            20   25   30

```
<210>  1064
<211>  15
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 28F9 heavy chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  1064
ctaatagggg tctac                                                        15


<210>  1065
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 28F9 heavy chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  1065

Leu Ile Gly Val Tyr
1               5


<210>  1066
<211>  33
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 28F9 heavy chain variable framework 4 (FW4)
       sequence

<400>  1066
tggggccaag gcaccactct cacagtctcc tca                                    33


<210>  1067
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 28F9 heavy chain variable framework 4 (FW4)
       sequence

<400>  1067

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
1               5                   10


<210>  1068
<211>  393
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 28F9 Light chain: DNA sequence (393 bp) - Signal
       sequenceFR1CDR1FR2CDR2FR3CDR3FR4

<400>  1068
atgagtcctg cccagttcct gtttctgtta gtgctctgga ttcgggaaac caacggtgat       60

gttgtgatga cccagactcc actcactttg tcggttacca ttggacaacc agcctccatc      120
```

tcttgcaagt caagtcagag cctcttacat agtgatggaa agacatattt gatttggttg   180

ttacagaggc caggccagtc tccaaagcgc ctaatctatc tggtgtctaa actggactct   240

ggagtccctg acaggttcac cggcagtgga tcagggacag atttcacact gaaaatcagc   300

agagtggagg ctgaggattt gggagtttat ttttgctgtc aaggtacaca ttttccgtgg   360

acgttcggtg gaggcaccat gctggaaatc aaa   393

<210> 1069
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 28F9 Light chain: Amino acid sequence (131 aa) - Signal peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400> 1069

Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu
1   5   10   15

Thr Asn Gly Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val
            20   25   30

Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu
        35   40   45

Leu His Ser Asp Gly Lys Thr Tyr Leu Ile Trp Leu Leu Gln Arg Pro
    50   55   60

Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser
65   70   75   80

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
                85   90   95

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
            100   105   110

Cys Gln Gly Thr His Phe Pro Trp Thr Phe Gly Gly Gly Thr Met Leu
        115   120   125

Glu Ile Lys
    130

<210> 1070
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 28F9 light chain variable framework 1 (FW1) sequence

<400> 1070

```
gatgttgtga tgacccagac tccactcact ttgtcggtta ccattggaca accagcctcc       60

atctcttgc                                                               69


<210>  1071
<211>  23
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 28F9 light chain variable framework 1 (FW1)
       sequence

<400>  1071

Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly
1               5                   10                  15


Gln Pro Ala Ser Ile Ser Cys
            20


<210>  1072
<211>  48
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 28F9 light chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  1072
aagtcaagtc agagcctctt acatagtgat ggaaagacat atttgatt                    48


<210>  1073
<211>  16
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 28F9 light chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  1073

Lys Ser Ser Gln Ser Leu Leu His Ser Asp Gly Lys Thr Tyr Leu Ile
1               5                   10                  15


<210>  1074
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 28F9 light chain variable framework 2 (FW2)
       sequence

<400>  1074
tggttgttac agaggccagg ccagtctcca aagcgcctaa tctat                       45


<210>  1075
<211>  15
<212>  PRT
<213>  Artificial Sequence
```

<220>
<223> Mouse antibody 28F9 light chain variable framework 2 (FW2)
       sequence

<400> 1075

```
Trp Leu Leu Gln Arg Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr
1               5                   10                  15
```

<210> 1076
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 28F9 light chain variable complementarity
       determining regions 2 (CDR2) sequence

<400> 1076
```
ctggtgtcta aactggactc t                                                21
```

<210> 1077
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 28F9 light chain variable complementarity
       determining regions 2 (CDR2) sequence

<400> 1077

```
Leu Val Ser Lys Leu Asp Ser
1               5
```

<210> 1078
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 28F9 light chain variable framework 3 (FW3)
       sequence

<400> 1078
```
ggagtccctg acaggttcac cggcagtgga tcagggacag atttcacact gaaaatcagc      60

agagtggagg ctgaggattt gggagtttat ttttgc                                96
```

<210> 1079
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 28F9 light chain variable framework 3 (FW3)
       sequence

<400> 1079

```
Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
1               5                   10                  15
```

```
Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
            20                  25                  30


<210>  1080
<211>  27
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 28F9 light chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  1080
tgtcaaggta cacattttcc gtggacg                                          27


<210>  1081
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 28F9 light chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  1081

Cys Gln Gly Thr His Phe Pro Trp Thr
1               5


<210>  1082
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 28F9 light chain variable framework 4 (FW4)
       sequence

<400>  1082
ttcggtggag gcaccatgct ggaaatcaaa                                       30


<210>  1083
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 28F9 light chain variable framework 4 (FW4)
       sequence

<400>  1083

Phe Gly Gly Gly Thr Met Leu Glu Ile Lys
1               5                   10


<210>  1084
<211>  411
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18B4 Heavy chain: DNA sequence (411 bp) - Signal
       sequenceFR1CDR1FR2CDR2FR3CDR3FR4
```

<400> 1084
atgtacttgg gactgaacta tgtattcata gtttttctct taaatggtgt ccagagtgaa   60

gtgaaacttg aggagtctgg aggaggcttg gtgcaacctg ggggatccat gaaactctct   120

tgtgctgcct ctggattcac ttttaatgac gcctggatgg actgggtccg ccagtctcca   180

gagaaggggc ttgagtgggt tgctgaaatt agaagcacag ctaatattca tacaacatac   240

tatgctgagt ctgtccaagg gaggttcacc atctcaagag atgattccaa aagtagtgtc   300

tacctgcaaa tgaacagctt gagagctgaa gacactggca tttattattg taccccatta   360

ctctacggat ttgcttactg gggccaaggg actctggtca ctgtctctgc a   411

<210> 1085
<211> 137
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 18B4 Heavy chain: Amino acid sequence (137 aa) -
       Signal peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400> 1085

Met Tyr Leu Gly Leu Asn Tyr Val Phe Ile Val Phe Leu Leu Asn Gly
1   5   10   15

Val Gln Ser Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln
            20   25   30

Pro Gly Gly Ser Met Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
        35   40   45

Asn Asp Ala Trp Met Asp Trp Val Arg Gln Ser Pro Glu Lys Gly Leu
    50   55   60

Glu Trp Val Ala Glu Ile Arg Ser Thr Ala Asn Ile His Thr Thr Tyr
65   70   75   80

Tyr Ala Glu Ser Val Gln Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
                85   90   95

Lys Ser Ser Val Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
            100   105   110

Gly Ile Tyr Tyr Cys Thr Pro Leu Leu Tyr Gly Phe Ala Tyr Trp Gly
        115   120   125

Gln Gly Thr Leu Val Thr Val Ser Ala
    130   135

<210> 1086
<211> 90
<212> DNA
<213> Artificial Sequence

<220>

<223> Mouse antibody 18B4 heavy chain variable framework 1 (FW1)
       sequence

<400> 1086
gaagtgaaac ttgaggagtc tggaggaggc ttggtgcaac ctgggggatc catgaaactc   60

tcttgtgctg cctctggatt cacttttaat   90

<210> 1087
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 18B4 heavy chain variable framework 1 (FW1)
       sequence

<400> 1087

Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Met Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
            20   25   30

<210> 1088
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 18B4 heavy chain variable complementarity
       determining regions 1 (CDR1) sequence

<400> 1088
gacgcctgga tggac   15

<210> 1089
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 18B4 heavy chain variable complementarity
       determining regions 1 (CDR1) sequence

<400> 1089

Asp Ala Trp Met Asp
1   5

<210> 1090
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 18B4 heavy chain variable framework 2 (FW2)
       sequence

<400> 1090
tgggtccgcc agtctccaga gaaggggctt gagtgggttg ct   42

```
<210>  1091
<211>  14
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18B4 heavy chain variable framework 2 (FW2)
       sequence

<400>  1091

Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala
1               5                   10


<210>  1092
<211>  57
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18B4 heavy chain variable complementarity
       determining regions 2 (CDR2) sequence

<400>  1092
gaaattagaa gcacagctaa tattcataca acatactatg ctgagtctgt ccaaggg          57


<210>  1093
<211>  19
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18B4 heavy chain variable complementarity
       determining regions 2 (CDR2) sequence

<400>  1093

Glu Ile Arg Ser Thr Ala Asn Ile His Thr Thr Tyr Tyr Ala Glu Ser
1               5                   10                  15


Val Gln Gly



<210>  1094
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18B4 heavy chain variable framework 3 (FW3)
       sequence

<400>  1094
aggttcacca tctcaagaga tgattccaaa agtagtgtct acctgcaaat gaacagcttg       60

agagctgaag acactggcat ttattattgt acccca                                 96


<210>  1095
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18B4 heavy chain variable framework 3 (FW3)
```

```
       sequence

<400>  1095

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ser Val Tyr Leu Gln
1               5                   10                  15


Met Asn Ser Leu Arg Ala Glu Asp Thr Gly Ile Tyr Tyr Cys Thr Pro
            20                  25                  30


<210>  1096
<211>  21
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18B4 heavy chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  1096
ttactctacg gatttgctta c                                                21


<210>  1097
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18B4 heavy chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  1097

Leu Leu Tyr Gly Phe Ala Tyr
1               5


<210>  1098
<211>  33
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18B4 heavy chain variable framework 4 (FW4)
       sequence

<400>  1098
tggggccaag ggactctggt cactgtctct gca                                   33


<210>  1099
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18B4 heavy chain variable framework 4 (FW4)
       sequence

<400>  1099

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
1               5                   10


<210>  1100
```

```
<211>  393
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18B4 Light chain: DNA sequence (393 bp) - Signal
       sequenceFR1CDR1FR2CDR2FR3CDR3FR4

<400>  1100
atgaagttgc ctgttaggct gttggtgctg atgttctgga ttcctgcttc cagcagtgat       60

gttgtgatga cccaaagtcc actctccctg cctgtcagtc ttggagatca agcctccatc      120

tcttgcagaa ctagtcagag ccttgtacac agtaatggaa acacctattt acattggcac      180

ctgcagaagc caggccagtc tccaaaggtc ctgatctaca aagtttccag ccgattttct      240

ggggtcccag acaggttcag tggcagtgga tcggggacag atttcacact caagatcagc      300

agagtggagg ctgaggatct gggagtttat ttctgctctc aaaatacaca tgttccgtac      360

acgttcggag gggggaccaa gctggaaata aaa                                   393


<210>  1101
<211>  131
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18B4 Light chain: Amino acid sequence (131 aa) -
       Signal peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400>  1101

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
1               5                   10                  15


Ser Ser Ser Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val
            20                  25                  30


Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Thr Ser Gln Ser Leu
        35                  40                  45


Val His Ser Asn Gly Asn Thr Tyr Leu His Trp His Leu Gln Lys Pro
    50                  55                  60


Gly Gln Ser Pro Lys Val Leu Ile Tyr Lys Val Ser Ser Arg Phe Ser
65                  70                  75                  80


Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
                85                  90                  95


Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
            100                 105                 110


Ser Gln Asn Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
        115                 120                 125


Glu Ile Lys
    130
```

<210> 1102
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 18B4 light chain variable framework 1 (FW1)
       sequence

<400> 1102
gatgttgtga tgacccaaag tccactctcc ctgcctgtca gtcttggaga tcaagcctcc   60

atctcttgc   69

<210> 1103
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 18B4 light chain variable framework 1 (FW1)
       sequence

<400> 1103

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly
1   5   10   15

Asp Gln Ala Ser Ile Ser Cys
            20

<210> 1104
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 18B4 light chain variable complementarity
       determining regions 1 (CDR1) sequence

<400> 1104
agaactagtc agagccttgt acacagtaat ggaaacacct atttacat   48

<210> 1105
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 18B4 light chain variable complementarity
       determining regions 1 (CDR1) sequence

<400> 1105

Arg Thr Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His
1   5   10   15

<210> 1106
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 18B4 light chain variable framework 2 (FW2)
       sequence

<400> 1106
```
tggcacctgc agaagccagg ccagtctcca aaggtcctga tctac                        45
```

<210> 1107
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 18B4 light chain variable framework 2 (FW2)
       sequence

<400> 1107

```
Trp His Leu Gln Lys Pro Gly Gln Ser Pro Lys Val Leu Ile Tyr
1               5                   10                  15
```

<210> 1108
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 18B4 light chain variable complementarity
       determining regions 2 (CDR2) sequence

<400> 1108
```
aaagtttcca gccgattttc t                                                  21
```

<210> 1109
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 18B4 light chain variable complementarity
       determining regions 2 (CDR2) sequence

<400> 1109

```
Lys Val Ser Ser Arg Phe Ser
1               5
```

<210> 1110
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 18B4 light chain variable framework 3 (FW3)
       sequence

<400> 1110
```
ggggtcccag acaggttcag tggcagtgga tcggggacag atttcacact caagatcagc       60

agagtggagg ctgaggatct gggagtttat ttctgc                                  96
```

<210> 1111
<211> 32
<212> PRT

```
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18B4 light chain variable framework 3 (FW3)
       sequence

<400>  1111

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1               5                   10                  15


Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
            20                  25                  30


<210>  1112
<211>  27
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18B4 light chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  1112
tctcaaaata cacatgttcc gtacacg                                          27


<210>  1113
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18B4 light chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  1113

Ser Gln Asn Thr His Val Pro Tyr Thr
1               5


<210>  1114
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18B4 light chain variable framework 4 (FW4)
       sequence

<400>  1114
ttcggagggg ggaccaagct ggaaataaaa                                       30


<210>  1115
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 18B4 light chain variable framework 4 (FW4)
       sequence

<400>  1115

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
```

```
1               5                   10


<210>  1116
<211>  408
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse Antibody IE4 Heavy chain: DNA sequence (408 bp) - Signal
       sequenceFR1CDR1FR2CDR2FR3CDR3FR4

<400>  1116
atggaatggc cttgtatctt tctcttcctc ctgtcagtaa ctgaaggtgt ccactcccag       60

gttcagctgc agcagtctgg ggctgagctg gtgaggcctg ggtcctcagt gaagatttcc      120

tgtaaggctt ctggctatgc attcagtacc tactggatga actgggtgaa gcagaggcct      180

ggacagggtc ttgagtggat tggacagatt tatcctggag atagtgatac taactacaat      240

ggaaagttca agggtaaagc cacactgact gcagacaagt cctccaacac agcctacatg      300

cagctcagca gcctaacatc tgaggactct gcggtctttt tctgtgcaag aggtaaccac      360

gcctctatgg actactgggg tcaaggaacc tcagtcaccg tctcctca                   408


<210>  1117
<211>  136
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse Antibody IE4 Heavy chain: Amino acid sequence (136 aa) -
       Signal peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400>  1117

Met Glu Trp Pro Cys Ile Phe Leu Phe Leu Leu Ser Val Thr Glu Gly
1               5                   10                  15


Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
            20                  25                  30


Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe
        35                  40                  45


Ser Thr Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
    50                  55                  60


Glu Trp Ile Gly Gln Ile Tyr Pro Gly Asp Ser Asp Thr Asn Tyr Asn
65                  70                  75                  80


Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Asn
                85                  90                  95


Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110


Phe Phe Cys Ala Arg Gly Asn His Ala Ser Met Asp Tyr Trp Gly Gln
        115                 120                 125
```

```
Gly Thr Ser Val Thr Val Ser Ser
    130                 135


<210>  1118
<211>  90
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse Antibody IE4 heavy chain variable framework 1 (FW1)
       sequence

<400>  1118
caggttcagc tgcagcagtc tggggctgag ctggtgaggc ctgggtcctc agtgaagatt       60

tcctgtaagg cttctggcta tgcattcagt                                        90


<210>  1119
<211>  30
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse Antibody IE4 heavy chain variable framework 1 (FW1)
       sequence

<400>  1119

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
1               5                   10                  15


Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser
            20                  25                  30


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<400>  1120
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<210>  1121

<400>  1121
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<210> 1196

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<210> 1197

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<210> 1198

<400> 1198
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<210> 1199

<400> 1199
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<210> 1200
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody IE4 heavy chain variable complementarity determining regions 1 (CDR1) sequence

<400> 1200
acctactgga tgaac   15

<210> 1201
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody IE4 heavy chain variable complementarity determining regions 1 (CDR1) sequence

<400> 1201

Thr Tyr Trp Met Asn
1   5

<210> 1202
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody IE4 heavy chain variable framework 2 (FW2) sequence

<400> 1202
tgggtgaagc agaggcctgg acagggtctt gagtggattg ga   42

<210> 1203
<211> 14

<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody IE4 heavy chain variable framework 2 (FW2)
       sequence

<400> 1203

Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
1   5   10

<210> 1204
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody IE4 heavy chain variable complementarity
       determining regions 2 (CDR2) sequence

<400> 1204
cagatttatc ctggagatag tgatactaac tacaatggaa agttcaaggg t   51

<210> 1205
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody IE4 heavy chain variable complementarity
       determining regions 2 (CDR2) sequence

<400> 1205

Gln Ile Tyr Pro Gly Asp Ser Asp Thr Asn Tyr Asn Gly Lys Phe Lys
1   5   10   15

Gly

<210> 1206
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody IE4 heavy chain variable framework 3 (FW3)
       sequence

<400> 1206
aaagccacac tgactgcaga caagtcctcc aacacagcct acatgcagct cagcagccta   60

acatctgagg actctgcggt ctttttctgt gcaaga   96

<210> 1207
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody IE4 heavy chain variable framework 3 (FW3)
       sequence

<400> 1207

Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Asn Thr Ala Tyr Met Gln
1   5   10   15

Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Phe Phe Cys Ala Arg
            20   25   30

<210> 1208
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody IE4 heavy chain variable complementarity
       determining regions 3 (CDR3) sequence

<400> 1208
ggtaaccacg cctctatgga ctac   24

<210> 1209
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody IE4 heavy chain variable complementarity
       determining regions 3 (CDR3) sequence

<400> 1209

Gly Asn His Ala Ser Met Asp Tyr
1   5

<210> 1210
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody IE4 heavy chain variable framework 4 (FW4)
       sequence

<400> 1210
tggggtcaag gaacctcagt caccgtctcc tca   33

<210> 1211
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody IE4 heavy chain variable framework 4 (FW4)
       sequence

<400> 1211

Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
1   5   10

<210> 1212
<211> 393
<212> DNA

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<213>  Artificial Sequence

<220>
<223>  Mouse Antibody IE4 Light chain: DNA sequence (393 bp) - Signal
       sequenceFR1CDR1FR2CDR2FR3CDR3FR4

<400>  1212
atgaagttgc ctgttaggct gttggtgctg atgttctgga ttcctgcttc cagcagtgat       60

gttgtgatga cccaaactcc actctccctg cctgtcagtc ttggagatca agcctccatc      120

tcttgcagat ctagtcagag ccttgtacac agtaatggaa acacctattt acattggtac      180

ctgcagaagc caggccagtc tccaaagctc ctgatctaca aagtttccaa ccgattttct      240

ggggtcccag acaggttcag tggcagtgga tcagggacag atttcacact caagatcagc      300

agagtggagg ctgaggatct gggagtttat ttctgctctc aaaaaacaca tgttccgtgg      360

acgttcggtg gaggcaccaa gctggaaatc aaa                                   393


<210>  1213
<211>  131
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse Antibody IE4 Light chain: Amino acid sequence (131 aa) -
       Signal peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400>  1213

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
1               5                   10                  15


Ser Ser Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
            20                  25                  30


Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
        35                  40                  45


Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
    50                  55                  60


Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
65                  70                  75                  80


Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
                85                  90                  95


Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
            100                 105                 110


Ser Gln Lys Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
        115                 120                 125


Glu Ile Lys
    130
```

```
<210>  1214
<211>  69
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody IE4 light chain variable framework 1 (FW1)
       sequence

<400>  1214
gatgttgtga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc       60

atctcttgc                                                               69


<210>  1215
<211>  23
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody IE4 light chain variable framework 1 (FW1)
       sequence

<400>  1215

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1               5                   10                  15


Asp Gln Ala Ser Ile Ser Cys
            20


<210>  1216
<211>  48
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody IE4 light chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  1216
agatctagtc agagccttgt acacagtaat ggaaacacct atttacat                    48


<210>  1217
<211>  16
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody IE4 light chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  1217

Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His
1               5                   10                  15


<210>  1218
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody IE4 light chain variable framework 2 (FW2)
```

```
       sequence

<400>  1218
tggtacctgc agaagccagg ccagtctcca aagctcctga tctac                       45


<210>  1219
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody IE4 light chain variable framework 2 (FW2)
       sequence

<400>  1219

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr
1               5                   10                  15


<210>  1220
<211>  21
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody IE4 light chain variable complementarity
       determining regions 2 (CDR2) sequence

<400>  1220
aaagtttcca accgattttc t                                                 21


<210>  1221
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody IE4 light chain variable complementarity
       determining regions 2 (CDR2) sequence

<400>  1221

Lys Val Ser Asn Arg Phe Ser
1               5


<210>  1222
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody IE4 light chain variable framework 3 (FW3)
       sequence

<400>  1222
ggggtcccag acaggttcag tggcagtgga tcagggacag atttcacact caagatcagc       60

agagtggagg ctgaggatct gggagtttat ttctgc                                 96


<210>  1223
<211>  32
<212>  PRT
<213>  Artificial Sequence
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```
<220>
<223>  Mouse antibody IE4 light chain variable framework 3 (FW3)
       sequence

<400>  1223

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1               5                   10                  15


Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
            20                  25                  30


<210>  1224
<211>  27
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody IE4 light chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  1224
tctcaaaaaa cacatgttcc gtggacg                                         27


<210>  1225
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody IE4 light chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  1225

Ser Gln Lys Thr His Val Pro Trp Thr
1               5


<210>  1226
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody IE4 light chain variable framework 4 (FW4)
       sequence

<400>  1226
ttcggtggag gcaccaagct ggaaatcaaa                                      30


<210>  1227
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody IE4 light chain variable framework 4 (FW4)
       sequence

<400>  1227

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
1               5                   10
```

<210> 1228
<211> 411
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 29H1 Heavy chain: DNA sequence (411 bp) - Signal sequenceFR1CDR1FR2CDR2FR3CDR3FR4

<400> 1228
atgtacttgg gactgaacta tgtattcata gtttttctct taaatggtgt ccagagtgaa   60

gtgaagcttg aggagtctgg aggaggcttg gtacaacctg gaggatccat gaaactctct   120

tgtgctgcct ctggattcac ttttagtgac gcctggatgg actgggtccg ccagtctcca   180

gagaaggggc ttgaatgggt tgctgaaatt agaagcaaag ctactaatca tgcaacatac   240

tatgctgagt ctgtgaaagg gaggttcacc atctcaagag atgattccaa aagtagtgtc   300

tacctgcaaa tgaacagctt aagagctgaa gacactggca tttattactg taccccccta   360

ctttacgggt ttgcttactg gggccaaggg actctggtca ctgtctctgc a   411

<210> 1229
<211> 137
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 29H1 Heavy chain: Amino acid sequence (137 aa) - Signal peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400> 1229

Met Tyr Leu Gly Leu Asn Tyr Val Phe Ile Val Phe Leu Leu Asn Gly
1   5   10   15

Val Gln Ser Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln
            20   25   30

Pro Gly Gly Ser Met Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
        35   40   45

Ser Asp Ala Trp Met Asp Trp Val Arg Gln Ser Pro Glu Lys Gly Leu
    50   55   60

Glu Trp Val Ala Glu Ile Arg Ser Lys Ala Thr Asn His Ala Thr Tyr
65   70   75   80

Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
                85   90   95

Lys Ser Ser Val Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
            100   105   110

Gly Ile Tyr Tyr Cys Thr Pro Leu Leu Tyr Gly Phe Ala Tyr Trp Gly
        115   120   125

```
Gln Gly Thr Leu Val Thr Val Ser Ala
    130                 135


<210>  1230
<211>  90
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 29H1 heavy chain variable framework 1 (FW1)
       sequence

<400>  1230
gaagtgaagc ttgaggagtc tggaggaggc ttggtacaac ctggaggatc catgaaactc       60

tcttgtgctg cctctggatt cacttttagt                                        90


<210>  1231
<211>  30
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 29H1 heavy chain variable framework 1 (FW1)
       sequence

<400>  1231

Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Met Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            20                  25                  30


<210>  1232
<211>  15
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 29H1 heavy chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  1232
gacgcctgga tggac                                                        15


<210>  1233
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 29H1 heavy chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  1233

Asp Ala Trp Met Asp
1               5


<210>  1234
<211>  42
<212>  DNA
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<213> Artificial Sequence

<220>
<223> Mouse antibody 29H1 heavy chain variable framework 2 (FW2)
       sequence

<400> 1234
tgggtccgcc agtctccaga gaaggggctt gaatgggttg ct   42

<210> 1235
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 29H1 heavy chain variable framework 2 (FW2)
       sequence

<400> 1235

Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala
1   5   10

<210> 1236
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 29H1 heavy chain variable complementarity
       determining regions 2 (CDR2) sequence

<400> 1236
gaaattagaa gcaaagctac taatcatgca acatactatg ctgagtctgt gaaaggg   57

<210> 1237
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 29H1 heavy chain variable complementarity
       determining regions 2 (CDR2) sequence

<400> 1237

Glu Ile Arg Ser Lys Ala Thr Asn His Ala Thr Tyr Tyr Ala Glu Ser
1   5   10   15

Val Lys Gly

<210> 1238
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 29H1 heavy chain variable framework 3 (FW3)
       sequence

<400> 1238
aggttcacca tctcaagaga tgattccaaa agtagtgtct acctgcaaat gaacagctta   60

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agagctgaag acactggcat ttattactgt accccc                              96


<210>  1239
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 29H1 heavy chain variable framework 3 (FW3)
       sequence

<400>  1239

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ser Val Tyr Leu Gln
1               5                   10                  15


Met Asn Ser Leu Arg Ala Glu Asp Thr Gly Ile Tyr Tyr Cys Thr Pro
            20                  25                  30


<210>  1240
<211>  21
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 29H1 heavy chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  1240
ctactttacg ggtttgctta c                                              21


<210>  1241
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 29H1 heavy chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  1241

Leu Leu Tyr Gly Phe Ala Tyr
1               5


<210>  1242
<211>  33
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 29H1 heavy chain variable framework 4 (FW4)
       sequence

<400>  1242
tggggccaag ggactctggt cactgtctct gca                                 33


<210>  1243
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
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```
<223>  Mouse antibody 29H1 heavy chain variable framework 4 (FW4)
       sequence

<400>  1243

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
1               5                   10


<210>  1244
<211>  393
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 29H1 Light chain: DNA sequence (393 bp) - Signal
       sequenceFR1CDR1FR2CDR2FR3CDR3FR4

<400>  1244
atgaagttgc ctgttaggct gttggtgctg atgttctgga ttcctgcttc cagcagtgat       60

gttgtgatga cccaaactcc actctccctg cctgtcagtc ttggagatca agcctccatc      120

tcttgcagat ctggtcagag ccttgtacac agtaatggac acacctattt acattggtac      180

ctgcagaagc caggccagtc tccaaggctc ctgatctaca aagtttccaa ccgattttct      240

ggggtcccag acaggttcag tggcagtgga tcaagggcag atttcacact caagatcagc      300

agagtggagg ctgaggatct gggagtttat ttctgctctc aaactacaca tgttccgtgg      360

acgttcggtg gaggcaccaa gctggaaatc aaa                                   393


<210>  1245
<211>  131
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 29H1 Light chain: Amino acid sequence (131 aa) -
       Signal peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400>  1245

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
1               5                   10                  15


Ser Ser Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
            20                  25                  30


Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Gly Gln Ser Leu
        35                  40                  45


Val His Ser Asn Gly His Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
    50                  55                  60


Gly Gln Ser Pro Arg Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
65                  70                  75                  80


Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Arg Ala Asp Phe Thr
                85                  90                  95
```

```
Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
            100                 105                 110


Ser Gln Thr Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
        115                 120                 125


Glu Ile Lys
    130


<210>  1246
<211>  69
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 29H1 light chain variable framework 1 (FW1)
       sequence

<400>  1246
gatgttgtga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc       60

atctcttgc                                                               69


<210>  1247
<211>  23
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 29H1 light chain variable framework 1 (FW1)
       sequence

<400>  1247

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1               5                   10                  15


Asp Gln Ala Ser Ile Ser Cys
            20


<210>  1248
<211>  48
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 29H1 light chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  1248
agatctggtc agagccttgt acacagtaat ggacacacct atttacat                    48


<210>  1249
<211>  16
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 29H1 light chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  1249
```

Arg Ser Gly Gln Ser Leu Val His Ser Asn Gly His Thr Tyr Leu His
1   5   10   15

<210> 1250
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 29H1 light chain variable framework 2 (FW2)
       sequence

<400> 1250
tggtacctgc agaagccagg ccagtctcca aggctcctga tctac   45

<210> 1251
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 29H1 light chain variable framework 2 (FW2)
       sequence

<400> 1251

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Arg Leu Leu Ile Tyr
1   5   10   15

<210> 1252
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 29H1 light chain variable complementarity
       determining regions 2 (CDR2) sequence

<400> 1252
aaagtttcca accgattttc t   21

<210> 1253
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 29H1 light chain variable complementarity
       determining regions 2 (CDR2) sequence

<400> 1253

Lys Val Ser Asn Arg Phe Ser
1   5

<210> 1254
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 29H1 light chain variable framework 3 (FW3)
       sequence

```
<400>  1254
ggggtcccag acaggttcag tggcagtgga tcaagggcag atttcacact caagatcagc       60

agagtggagg ctgaggatct gggagtttat ttctgc                                 96


<210>  1255
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 29H1 light chain variable framework 3 (FW3)
       sequence

<400>  1255

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Arg Ala Asp Phe Thr
1               5                   10                  15


Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
            20                  25                  30


<210>  1256
<211>  27
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 29H1 light chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  1256
tctcaaacta cacatgttcc gtggacg                                           27


<210>  1257
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 29H1 light chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  1257

Ser Gln Thr Thr His Val Pro Trp Thr
1               5


<210>  1258
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 29H1 light chain variable framework 4 (FW4)
       sequence

<400>  1258
ttcggtggag gcaccaagct ggaaatcaaa                                        30


<210>  1259
<211>  10
```

<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 29H1 light chain variable framework 4 (FW4)
       sequence

<400> 1259

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
1   5   10

<210> 1260
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 31A1 Heavy chain: DNA sequence (399 bp) - Signal
       sequenceFR1CDR1FR2CDR2FR3CDR3FR4

<400> 1260
atggaaaggc actggatctt tctcttcctg ttttcagtaa ctgcaggtgt ccactcccag   60

gtccagcttc agcagtctgg ggctgaactg gcaaaacctg gggcctcagt gaagatgtcc   120

tgcaaggctt ctggctacac ctttactagc tactggatgc actgggtaaa acagaggcct   180

ggacagggtc tggaatggat tggatacatt aatcctagca ctggttatac tgagtacaat   240

cagaagttca aggacaaggc cacattgact gcagacaaat cctccagcac agcctacatg   300

caactgagca gcctgacatc tgaggactct gcagtctatt actgtgcaag agcctacatt   360

gactactggg gccaaggcac cactctcaca gtctcctca   399

<210> 1261
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 31A1 Heavy chain: Amino acid sequence (133 aa) -
       Signal peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400> 1261

Met Glu Arg His Trp Ile Phe Leu Phe Leu Phe Ser Val Thr Ala Gly
1   5   10   15

Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Lys
            20   25   30

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35   40   45

Thr Ser Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
    50   55   60

Glu Trp Ile Gly Tyr Ile Asn Pro Ser Thr Gly Tyr Thr Glu Tyr Asn
65   70   75   80

```
Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
                85                  90                  95


Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110


Tyr Tyr Cys Ala Arg Ala Tyr Ile Asp Tyr Trp Gly Gln Gly Thr Thr
        115                 120                 125


Leu Thr Val Ser Ser
    130


<210>  1262
<211>  90
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 31A1 heavy chain variable framework 1 (FW1)
       sequence

<400>  1262
caggtccagc ttcagcagtc tggggctgaa ctggcaaaac ctggggcctc agtgaagatg       60

tcctgcaagg cttctggcta cacctttact                                        90


<210>  1263
<211>  30
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 31A1 heavy chain variable framework 1 (FW1)
       sequence

<400>  1263

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
            20                  25                  30


<210>  1264
<211>  15
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 31A1 heavy chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  1264
agctactgga tgcac                                                        15


<210>  1265
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
```

<223> Mouse antibody 31A1 heavy chain variable complementarity
       determining regions 1 (CDR1) sequence

<400> 1265

Ser Tyr Trp Met His
1   5

<210> 1266
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 31A1 heavy chain variable framework 2 (FW2)
       sequence

<400> 1266
tgggtaaaac agaggcctgg acagggtctg gaatggattg ga   42

<210> 1267
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 31A1 heavy chain variable framework 2 (FW2)
       sequence

<400> 1267

Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
1   5   10

<210> 1268
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 31A1 heavy chain variable complementarity
       determining regions 2 (CDR2) sequence

<400> 1268
tacattaatc ctagcactgg ttatactgag tacaatcaga agttcaagga c   51

<210> 1269
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 31A1 heavy chain variable complementarity
       determining regions 2 (CDR2) sequence

<400> 1269

Tyr Ile Asn Pro Ser Thr Gly Tyr Thr Glu Tyr Asn Gln Lys Phe Lys
1   5   10   15

Asp

<210> 1270
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 31A1 heavy chain variable framework 3 (FW3)
sequence

<400> 1270
aaggccacat tgactgcaga caaatcctcc agcacagcct acatgcaact gagcagcctg 60

acatctgagg actctgcagt ctattactgt gcaaga 96

<210> 1271
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 31A1 heavy chain variable framework 3 (FW3)
sequence

<400> 1271

Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln
1 5 10 15

Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 1272
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 31A1 heavy chain variable complementarity
determining regions 3 (CDR3) sequence

<400> 1272
gcctacattg actac 15

<210> 1273
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 31A1 heavy chain variable complementarity
determining regions 3 (CDR3) sequence

<400> 1273

Ala Tyr Ile Asp Tyr
1 5

<210> 1274
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 31A1 heavy chain variable framework 4 (FW4)

sequence

<400> 1274
tggggccaag gcaccactct cacagtctcc tca 33

<210> 1275
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 31A1 heavy chain variable framework 4 (FW4)
sequence

<400> 1275

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
1 5 10

<210> 1276
<211> 393
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 31A1 Light chain: DNA sequence (393 bp) - Signal
sequenceFR1CDR1FR2CDR2FR3CDR3FR4

<400> 1276
atgaagttgc ctgttaggct gttggtgctg atgttctgga ttcctgcttc cagcagtgat 60

gttttgatga cccaaactcc actctccctg cctgtcagtc ttggagatca agcctccttc 120

tcttgcagat ctagtcagag cattgtacat agtaatggaa acacctattt agaatggtac 180

ctgcagaaac caggccagtc tccaaagctc ctgatctaca aagtttccaa ccgattttct 240

ggggtcccag acaggttcag tggcagtgga tcagggacag atttcacact caagatcaac 300

agagtggagg ctgaggatct gggagtttat tactgctttc aagtttcaca ttttccgtgg 360

acgttcggtg gaggcaccaa gctggaaatc aaa 393

<210> 1277
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 31A1 Light chain: Amino acid sequence (131 aa) -
Signal peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400> 1277

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
1 5 10 15

Ser Ser Ser Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val
20 25 30

Ser Leu Gly Asp Gln Ala Ser Phe Ser Cys Arg Ser Ser Gln Ser Ile
35 40 45

```
Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro
    50                  55                  60


Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
65                  70                  75                  80


Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
                85                  90                  95


Leu Lys Ile Asn Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
            100                 105                 110


Phe Gln Val Ser His Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
        115                 120                 125


Glu Ile Lys
    130


<210>  1278
<211>  69
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 31A1 light chain variable framework 1 (FW1)
       sequence

<400>  1278
gatgttttga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc       60

ttctcttgc                                                               69


<210>  1279
<211>  23
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 31A1 light chain variable framework 1 (FW1)
       sequence

<400>  1279

Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1               5                   10                  15


Asp Gln Ala Ser Phe Ser Cys
            20


<210>  1280
<211>  48
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 31A1 light chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  1280
agatctagtc agagcattgt acatagaaat ggaaacacct atttagaa                    48
```

```
<210>  1281
<211>  16
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 31A1 light chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  1281

Arg Ser Ser Gln Ser Ile Val His Arg Asn Gly Asn Thr Tyr Leu Glu
1               5                   10                  15


<210>  1282
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 31A1 light chain variable framework 2 (FW2)
       sequence

<400>  1282
tggtacctgc agaaaccagg ccagtctcca aagctcctga tctac                       45


<210>  1283
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 31A1 light chain variable framework 2 (FW2)
       sequence

<400>  1283

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr
1               5                   10                  15


<210>  1284
<211>  21
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 31A1 light chain variable complementarity
       determining regions 2 (CDR2) sequence

<400>  1284
aaagtttcca accgattttc t                                                 21


<210>  1285
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 31A1 light chain variable complementarity
       determining regions 2 (CDR2) sequence

<400>  1285
```

```
Lys Val Ser Asn Arg Phe Ser
1               5


<210>  1286
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 31A1 light chain variable framework 3 (FW3)
       sequence

<400>  1286
ggggtcccag acaggttcag tggcagtgga tcagggacag atttcacact caagatcaac       60

agagtggagg ctgaggatct gggagtttat tactgc                                 96


<210>  1287
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 31A1 light chain variable framework 3 (FW3)
       sequence

<400>  1287

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1               5                   10                  15


Leu Lys Ile Asn Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
            20                  25                  30


<210>  1288
<211>  27
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 31A1 light chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  1288
tttcaagttt cacattttcc gtggacg                                           27


<210>  1289
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 31A1 light chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  1289

Phe Gln Val Ser His Phe Pro Trp Thr
1               5


<210>  1290
<211>  30
<212>  DNA
```

<213> Artificial Sequence

<220>
<223> Mouse antibody 31A1 light chain variable framework 4 (FW4)
sequence

<400> 1290
ttcggtggag gcaccaagct ggaaatcaaa   30

<210> 1291
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 31A1 light chain variable framework 4 (FW4)
sequence

<400> 1291

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
1   5   10

<210> 1292
<211> 411
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 32C1 Heavy chain: DNA sequence (411 bp) - Signal
sequenceFR1CDR1FR2CDR2FR3CDR3FR4

<400> 1292
atgtacttgg gactgaactg tgtattcata gtttttctct taaaaggtgt ccagagtgaa   60

gtgaagcttg aggagtctgg aggaggcttg gtgcaatctg gaggatccat gaaactctcc   120

tgtgttgcct ctggattcac tttcagtaat tactggatga actgggtccg ccagtctcca   180

gagaaggggc ttgagtgggt tgctgaaatt agattgaaat ctaataatta tgcaatacat   240

tatgcggagt ctgtgaaggg gaggttcacc atctcaagag atgattccaa aagtagtgtc   300

tacctgcaaa tgaacaactt aagagctgaa gacactggca tttattactg taccagggtc   360

ccgggactgg atgcttactg gggccaaggg actctggtca ctgtctctgc a   411

<210> 1293
<211> 137
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 32C1 Heavy chain: Amino acid sequence (137 aa) -
Signal peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400> 1293

Met Tyr Leu Gly Leu Asn Cys Val Phe Ile Val Phe Leu Leu Lys Gly
1   5   10   15

Val Gln Ser Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln
            20   25   30

Ser Gly Gly Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Thr Phe
        35   40   45

Ser Asn Tyr Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu
    50   55   60

Glu Trp Val Ala Glu Ile Arg Leu Lys Ser Asn Asn Tyr Ala Ile His
65   70   75   80

Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
                85   90   95

Lys Ser Ser Val Tyr Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr
            100   105   110

Gly Ile Tyr Tyr Cys Thr Arg Val Pro Gly Leu Asp Ala Tyr Trp Gly
        115   120   125

Gln Gly Thr Leu Val Thr Val Ser Ala
    130   135

<210> 1294
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 32C1 heavy chain variable framework 1 (FW1)
       sequence

<400> 1294
gaagtgaagc ttgaggagtc tggaggaggc ttggtgcaat ctggaggatc catgaaactc   60

tcctgtgttg cctctggatt cactttcagt   90

<210> 1295
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 32C1 heavy chain variable framework 1 (FW1)
       sequence

<400> 1295

Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Gly
1   5   10   15

Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser
            20   25   30

<210> 1296
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 32C1 heavy chain variable complementarity

       determining regions 1 (CDR1) sequence

<400> 1296
aattactgga tgaac   15

<210> 1297
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 32C1 heavy chain variable complementarity
       determining regions 1 (CDR1) sequence

<400> 1297

Asn Tyr Trp Met Asn
1   5

<210> 1298
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 32C1 heavy chain variable framework 2 (FW2)
       sequence

<400> 1298
tgggtccgcc agtctccaga gaaggggctt gagtgggttg ct   42

<210> 1299
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 32C1 heavy chain variable framework 2 (FW2)
       sequence

<400> 1299

Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala
1   5   10

<210> 1300
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 32C1 heavy chain variable complementarity
       determining regions 2 (CDR2) sequence

<400> 1300
gaaattagat tgaaatctaa taattatgca atacattatg cggagtctgt gaagggg   57

<210> 1301
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 32C1 heavy chain variable complementarity

```
       determining regions 2 (CDR2) sequence

<400>  1301

Glu Ile Arg Leu Lys Ser Asn Asn Tyr Ala Ile His Tyr Ala Glu Ser
1               5                   10                  15


Val Lys Gly




<210>  1302
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 32C1 heavy chain variable framework 3 (FW3)
       sequence

<400>  1302
aggttcacca tctcaagaga tgattccaaa agtagtgtct acctgcaaat gaacaactta       60

agagctgaag acactggcat ttattactgt accagg                                 96


<210>  1303
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 32C1 heavy chain variable framework 3 (FW3)
       sequence

<400>  1303

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ser Val Tyr Leu Gln
1               5                   10                  15


Met Asn Asn Leu Arg Ala Glu Asp Thr Gly Ile Tyr Tyr Cys Thr Arg
            20                  25                  30


<210>  1304
<211>  21
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 32C1 heavy chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  1304
gtcccgggac tggatgctta c                                                 21


<210>  1305
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 32C1 heavy chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  1305
```

```
Val Pro Gly Leu Asp Ala Tyr
1               5


<210>  1306
<211>  33
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 32C1 heavy chain variable framework 4 (FW4)
       sequence

<400>  1306
tggggccaag ggactctggt cactgtctct gca                                    33


<210>  1307
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 32C1 heavy chain variable framework 4 (FW4)
       sequence

<400>  1307

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
1               5                   10


<210>  1308
<211>  393
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 32C1 Light chain: DNA sequence (393 bp) - Signal
       sequenceFR1CDR1FR2CDR2FR3CDR3FR4

<400>  1308
atgaagttgc ctgttaggct gttggtgctg atgttctgga ttcctgcttc cagcagtgat       60

gttgtgatga cccaaactcc actctccctg cctgtcagtc ttggagatca agcctccatc      120

tcttgcagat ctagtcagag ccttgtacac agtaatggaa acacctattt acattggtac      180

ctgcagaagc caggccagtc tccaaagctc ctgatctaca aagtttccaa ccgattttct      240

ggggtcccag acaggttcag tggcagtgga tcagggacag atttcacact caagatcagc      300

agtgtggagg ctgaggatct gggagtttat ttctgctctc aaattacaca tgttccgtac      360

acgttcggag gggggaccaa tctggaaata aaa                                   393


<210>  1309
<211>  131
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 32C1 Light chain: Amino acid sequence (131 aa) -
       Signal peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400>  1309
```

```
Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
1               5                   10                  15


Ser Ser Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
            20                  25                  30


Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
        35                  40                  45


Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
    50                  55                  60


Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
65                  70                  75                  80


Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
                85                  90                  95


Leu Lys Ile Ser Ser Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
            100                 105                 110


Ser Gln Ile Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Asn Leu
        115                 120                 125


Glu Ile Lys
    130


<210>  1310
<211>  69
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 32C1 light chain variable framework 1 (FW1)
       sequence

<400>  1310
gatgttgtga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc       60

atctcttgc                                                               69


<210>  1311
<211>  23
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 32C1 light chain variable framework 1 (FW1)
       sequence

<400>  1311

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1               5                   10                  15


Asp Gln Ala Ser Ile Ser Cys
            20
```

<210> 1312
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 32C1 light chain variable complementarity determining regions 1 (CDR1) sequence

<400> 1312
agatctagtc agagccttgt acacagtaat ggaaacacct atttacat 48

<210> 1313
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 32C1 light chain variable complementarity determining regions 1 (CDR1) sequence

<400> 1313

```
Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His
1               5                   10                  15
```

<210> 1314
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 32C1 light chain variable framework 2 (FW2) sequence

<400> 1314
tggtacctgc agaagccagg ccagtctcca aagctcctga tctac 45

<210> 1315
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 32C1 light chain variable framework 2 (FW2) sequence

<400> 1315

```
Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr
1               5                   10                  15
```

<210> 1316
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 32C1 light chain variable complementarity determining regions 2 (CDR2) sequence

<400> 1316
aaagtttcca accgattttc t 21

```
<210>  1317
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 32C1 light chain variable complementarity
       determining regions 2 (CDR2) sequence

<400>  1317

Lys Val Ser Asn Arg Phe Ser
1               5


<210>  1318
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 32C1 light chain variable framework 3 (FW3)
       sequence

<400>  1318
ggggtcccag acaggttcag tggcagtgga tcagggacag atttcacact caagatcagc       60

agtgtggagg ctgaggatct gggagtttat ttctgc                                  96


<210>  1319
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 32C1 light chain variable framework 3 (FW3)
       sequence

<400>  1319

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1               5                   10                  15


Leu Lys Ile Ser Ser Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
            20                  25                  30


<210>  1320
<211>  27
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 32C1 light chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  1320
tctcaaatta cacatgttcc gtacacg                                           27


<210>  1321
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
```

<223> Mouse antibody 32C1 light chain variable complementarity
       determining regions 3 (CDR3) sequence

<400> 1321

Ser Gln Ile Thr His Val Pro Tyr Thr
1   5

<210> 1322
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 32C1 light chain variable framework 4 (FW4)
       sequence

<400> 1322
ttcggagggg ggaccaatct ggaaataaaa   30

<210> 1323
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 32C1 light chain variable framework 4 (FW4)
       sequence

<400> 1323

Phe Gly Gly Gly Thr Asn Leu Glu Ile Lys
1   5   10

<210> 1324
<211> 423
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 45C11 Heavy chain: DNA sequence (423 bp) - Signal
       sequenceFR1CDR1FR2CDR2FR3CDR3FR4

<400> 1324
atgaaatgca gctgggttat cttcttcctg atggcagtgg ttacaggggt caattcagag   60

gttcagctgc agcagtctgg ggcagacctt gtgaagccag gggcctcagt caagttgtcc   120

tgcacagctt ctggcttcaa cattaaagac acctttatgc actgggtgaa gcagaggcct   180

gaacagggcc tggagtggat tggaaggatt gatcctgcga atggtaatac taaatatgac   240

ccgaaattcc agggcaaggc cactataaca gcagacacat cctccaacac agcctacctg   300

cagctcagca gcctgacatc tgaggacact gccgtctatt actgtgctaa accgtatggt   360

aactacggct attactatgc tttggactac tggggtcaag gaacctcagt caccgtctcc   420

tca   423

<210> 1325
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 45C11 Heavy chain: Amino acid sequence (141 aa) -
      Signal peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400> 1325

Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
1   5   10   15

Val Asn Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Asp Leu Val Lys
            20   25   30

Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile
        35   40   45

Lys Asp Thr Phe Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu
    50   55   60

Glu Trp Ile Gly Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Tyr Asp
65   70   75   80

Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn
                85   90   95

Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
            100   105   110

Tyr Tyr Cys Ala Lys Pro Tyr Gly Asn Tyr Gly Tyr Tyr Tyr Ala Leu
        115   120   125

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
    130   135   140

<210> 1326
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 45C11 heavy chain variable framework 1 (FW1)
      sequence

<400> 1326
gaggttcagc tgcagcagtc tggggcagac cttgtgaagc caggggcctc agtcaagttg   60

tcctgcacag cttctggctt caacattaaa   90

<210> 1327
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 45C11 heavy chain variable framework 1 (FW1)
      sequence

<400> 1327

Glu Val Gln Leu Gln Gln Ser Gly Ala Asp Leu Val Lys Pro Gly Ala

```
1               5                   10                  15


Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys
            20                  25                  30


<210>  1328
<211>  15
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 45C11 heavy chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  1328
gacaccttta tgcac                                                          15


<210>  1329
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 45C11 heavy chain variable complementarity
       determining regions 1 (CDR1) sequence

<400>  1329

Asp Thr Phe Met His
1               5


<210>  1330
<211>  42
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 45C11 heavy chain variable framework 2 (FW2)
       sequence

<400>  1330
tgggtgaagc agaggcctga acagggcctg gagtggattg ga                             42


<210>  1331
<211>  14
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 45C11 heavy chain variable framework 2 (FW2)
       sequence

<400>  1331

Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
1               5                   10


<210>  1332
<211>  51
<212>  DNA
<213>  Artificial Sequence

<220>
```

```
<223>  Mouse antibody 45C11 heavy chain variable complementarity
       determining regions 2 (CDR2) sequence

<400>  1332
aggattgatc ctgcgaatgg taatactaaa tatgacccga aattccaggg c                51


<210>  1333
<211>  17
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 45C11 heavy chain variable complementarity
       determining regions 2 (CDR2) sequence

<400>  1333

Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Tyr Asp Pro Lys Phe Gln
1               5                   10                  15


Gly




<210>  1334
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 45C11 heavy chain variable framework 3 (FW3)
       sequence

<400>  1334
aaggccacta taacagcaga cacatcctcc aacacagcct acctgcagct cagcagcctg       60

acatctgagg acactgccgt ctattactgt gctaaa                                 96


<210>  1335
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 45C11 heavy chain variable framework 3 (FW3)
       sequence

<400>  1335

Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr Leu Gln
1               5                   10                  15


Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys
            20                  25                  30


<210>  1336
<211>  39
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 45C11 heavy chain variable complementarity
       determining regions 3 (CDR3) sequence
```

<400> 1336
ccgtatggta actacggcta ttactatgct ttggactac   39

<210> 1337
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 45C11 heavy chain variable complementarity
       determining regions 3 (CDR3) sequence

<400> 1337

Pro Tyr Gly Asn Tyr Gly Tyr Tyr Tyr Ala Leu Asp Tyr
1   5   10

<210> 1338
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 45C11 heavy chain variable framework 4 (FW4)
       sequence

<400> 1338
tggggtcaag gaacctcagt caccgtctcc tca   33

<210> 1339
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 45C11 heavy chain variable framework 4 (FW4)
       sequence

<400> 1339

Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
1   5   10

<210> 1340
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 45C11 Light chain: DNA sequence (381 bp) - Signal
       sequenceFR1CDR1FR2CDR2FR3CDR3FR4

<400> 1340
atgaggttcc aggttcaggt tctggggctc cttctgctct ggatatcagg tgcccagtgt   60

gatgtccaga taacccagtc tccatcttat cttgctgcat ctcctggaga aaccattact   120

attaattgca gggcaagtaa gagcattagc aaatatttag cctggtatca agagaaacct   180

gggaaaacta ataagcttct tatctactct ggatccactt tgcaatctgg aattccatca   240

aggttcagtg gcagtggatc tggtacagat ttcactctca ccatcagtag cctggagcct   300

gaagattttg caatgtatta ctgtcaacag cataatgaat tcccgtggac gttcggtgga   360 ggcaccaagc tggaaatcaa a   381

<210> 1341
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 45C11 Light chain: Amino acid sequence (127 aa) - Signal peptideFR1CDR1FR2CDR2FR3CDR3FR4

<400> 1341

```
Met Arg Phe Gln Val Gln Val Leu Gly Leu Leu Leu Leu Trp Ile Ser
1               5                   10                  15


Gly Ala Gln Cys Asp Val Gln Ile Thr Gln Ser Pro Ser Tyr Leu Ala
            20                  25                  30


Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala Ser Lys Ser
        35                  40                  45


Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Thr Asn
    50                  55                  60


Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly Ile Pro Ser
65                  70                  75                  80


Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
                85                  90                  95


Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln Gln His Asn
            100                 105                 110


Glu Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
        115                 120                 125
```

<210> 1342
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 45C11 light chain variable framework 1 (FW1) sequence

<400> 1342

```
gatgtccaga taacccagtc tccatcttat cttgctgcat ctcctggaga aaccattact       60

attaattgc                                                               69
```

<210> 1343
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 45C11 light chain variable framework 1 (FW1) sequence

<400> 1343

Asp Val Gln Ile Thr Gln Ser Pro Ser Tyr Leu Ala Ala Ser Pro Gly
1   5   10   15

Glu Thr Ile Thr Ile Asn Cys
            20

<210> 1344
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 45C11 light chain variable complementarity
       determining regions 1 (CDR1) sequence

<400> 1344
agggcaagta agagcattag caaatattta gcc   33

<210> 1345
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 45C11 light chain variable complementarity
       determining regions 1 (CDR1) sequence

<400> 1345

Arg Ala Ser Lys Ser Ile Ser Lys Tyr Leu Ala
1   5   10

<210> 1346
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse antibody 45C11 light chain variable framework 2 (FW2)
       sequence

<400> 1346
tggtatcaag agaaacctgg gaaaactaat aagcttctta tctac   45

<210> 1347
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse antibody 45C11 light chain variable framework 2 (FW2)
       sequence

<400> 1347

Trp Tyr Gln Glu Lys Pro Gly Lys Thr Asn Lys Leu Leu Ile Tyr
1   5   10   15

<210> 1348
<211> 21

```
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 45C11 light chain variable complementarity
       determining regions 2 (CDR2) sequence

<400>  1348
tctggatcca ctttgcaatc t                                                 21


<210>  1349
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 45C11 light chain variable complementarity
       determining regions 2 (CDR2) sequence

<400>  1349

Ser Gly Ser Thr Leu Gln Ser
1               5


<210>  1350
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 45C11 light chain variable framework 3 (FW3)
       sequence

<400>  1350
ggaattccat caaggttcag tggcagtgga tctggtacag atttcactct caccatcagt       60

agcctggagc ctgaagattt tgcaatgtat tactgt                                 96


<210>  1351
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 45C11 light chain variable framework 3 (FW3)
       sequence

<400>  1351

Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1               5                   10                  15


Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys
            20                  25                  30


<210>  1352
<211>  27
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 45C11 light chain variable complementarity
       determining regions 3 (CDR3) sequence
```

```
<400>  1352
caacagcata atgaattccc gtggacg                                          27


<210>  1353
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 45C11 light chain variable complementarity
       determining regions 3 (CDR3) sequence

<400>  1353

Gln Gln His Asn Glu Phe Pro Trp Thr
1               5


<210>  1354
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 45C11 light chain variable framework 4 (FW4)
       sequence

<400>  1354
ttcggtggag gcaccaagct ggaaatcaaa                                       30


<210>  1355
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse antibody 45C11 light chain variable framework 4 (FW4)
       sequence

<400>  1355

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
1               5                   10


<210>  1356
<211>  90
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 5C6F3 heavy chain variable framework 1 (FW1) sequence

<400>  1356
gaagtgatgc tggtggagtc tgggggaggc ttagtgaagc ctggagggtc cctgaaactc      60

tcctgtgcag cctctggatt cactttcagt                                       90


<210>  1357
<211>  30
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 5C6F3 heavy chain variable framework 1 (FW1) sequence
```

```
<400>  1357

Glu Val Met Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            20                  25                  30


<210>  1358
<211>  15
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 5C6F3 heavy chain variable complementarity determining
       regions 1 (CDR1) sequence

<400>  1358
acctatgcca tgtct                                                        15


<210>  1359
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 5C6F3 heavy chain variable complementarity determining
       regions 1 (CDR1) sequence

<400>  1359

Thr Tyr Ala Met Ser
1               5


<210>  1360
<211>  42
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 5C6F3 heavy chain variable framework 2 (FW2) sequence

<400>  1360
tgggttcgcc agactccgga gaagaggctg gagtgggtcg ca                          42


<210>  1361
<211>  14
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 5C6F3 heavy chain variable framework 2 (FW2) sequence

<400>  1361

Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val Ala
1               5                   10


<210>  1362
<211>  51
<212>  DNA
<213>  Artificial Sequence
```

```
<220>
<223>  Mouse 5C6F3 heavy chain variable complementarity determining
       regions 2 (CDR2) sequence

<400>  1362
gccattagta atggtggtgg ttacacctac tatccagaca gtctgaaggg g                51


<210>  1363
<211>  17
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 5C6F3 heavy chain variable complementarity determining
       regions 2 (CDR2) sequence

<400>  1363

Ala Ile Ser Asn Gly Gly Gly Tyr Thr Tyr Tyr Pro Asp Ser Leu Lys
1               5                   10                  15


Gly



<210>  1364
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 5C6F3 heavy chain variable framework 3 (FW3) sequence

<400>  1364
cgattcacca tctccagaga caatgccaag aacaccctgt acctgcaaat gagcagtctg       60

aggtctgagg acacggccac gtattactgt gcaaga                                 96


<210>  1365
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 5C6F3 heavy chain variable framework 3 (FW3) sequence

<400>  1365

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln
1               5                   10                  15


Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg
            20                  25                  30


<210>  1366
<211>  27
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 5C6F3 heavy chain variable complementarity determining
       regions 3 (CDR3) sequence

<400>  1366
```

```
cgttactatg atcactactt tgactac                                           27


<210>  1367
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 5C6F3 heavy chain variable complementarity determining
       regions 3 (CDR3) sequence

<400>  1367

Arg Tyr Tyr Asp His Tyr Phe Asp Tyr
1               5


<210>  1368
<211>  33
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 5C6F3 heavy chain variable framework 4 (FW4) sequence

<400>  1368
tggggccaag gcaccgctct cacggtctcc tca                                    33


<210>  1369
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 5C6F3 heavy chain variable framework 4 (FW4) sequence

<400>  1369

Trp Gly Gln Gly Thr Ala Leu Thr Val Ser Ser
1               5                   10


<210>  1370
<211>  69
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 5C6F3 light chain variable framework 1 (FR1) sequence

<400>  1370
gatgttttga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc       60

atctcttgc                                                               69


<210>  1371
<211>  23
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 5C6F3 light chain variable framework 1 (FR1) sequence

<400>  1371

Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
```

```
1               5                   10                  15


Asp Gln Ala Ser Ile Ser Cys
            20


<210>  1372
<211>  48
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 5C6F3 light chain variable complementarity determining
       regions 1 (CDR1) sequence

<400>  1372
agatctagtc agaccattgt acatagtaat ggaaacacct atttagaa                    48


<210>  1373
<211>  16
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 5C6F3 light chain variable complementarity determining
       regions 1 (CDR1) sequence

<400>  1373

Arg Ser Ser Gln Thr Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1               5                   10                  15


<210>  1374
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 5C6F3 light chain variable framework 2 (FR2) sequence

<400>  1374
tggtacctgc agaaaccagg ccagtctcca aagctcctga tctac                       45


<210>  1375
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 5C6F3 light chain variable framework 2 (FR2) sequence

<400>  1375

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr
1               5                   10                  15


<210>  1376
<211>  21
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 5C6F3 light chain variable complementarity determining
       regions 2 (CDR2) sequence
```

```
<400>  1376
aaagtttcca accgattttc t                                                 21


<210>  1377
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 5C6F3 light chain variable complementarity determining
       regions 2 (CDR2) sequence

<400>  1377

Lys Val Ser Asn Arg Phe Ser
1               5


<210>  1378
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 5C6F3 light chain variable framework 3 (FR3) sequence

<400>  1378
ggggtcccag acaggttcag tggcagtgga tcagggacag atttcacact caagatcagc       60

agggtggagg ctgaggatct gggagtttat tactgc                                 96


<210>  1379
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 5C6F3 light chain variable framework 3 (FR3) sequence

<400>  1379

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1               5                   10                  15


Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
            20                  25                  30


<210>  1380
<211>  27
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 5C6F3 light chain variable complementarity determining
       regions 3 (CDR3) sequence

<400>  1380
tttcaagatt cacatgttcc tctcacg                                           27


<210>  1381
<211>  9
<212>  PRT
<213>  Artificial Sequence
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<220>
<223> Mouse 5C6F3 light chain variable complementarity determining
       regions 3 (CDR3) sequence

<400> 1381

Phe Gln Asp Ser His Val Pro Leu Thr
1   5

<210> 1382
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse 5C6F3 light chain variable framework 4 (FR4) sequence

<400> 1382
ttcggtgctg ggaccaagct ggagctgaaa   30

<210> 1383
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse 5C6F3 light chain variable framework 4 (FR4) sequence

<400> 1383

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
1   5   10

<210> 1384
<211> 735
<212> DNA
<213> Artificial Sequence

<220>
<223> mu5C6F3 scFv sequence

<400> 1384
gaagtgatgc tggtggagtc tgggggaggc ttagtgaagc ctggagggtc cctgaaactc   60

tcctgtgcag cctctggatt cactttcagt acctatgcca tgtcttgggt tcgccagact   120

ccggagaaga ggctggagtg ggtcgcagcc attagtaatg gtggtggtta cacctactat   180

ccagacagtc tgaaggggcg attcaccatc tccagagaca atgccaagaa caccctgtac   240

ctgcaaatga gcagtctgag gtctgaggac acggccacgt attactgtgc aagacgttac   300

tatgatcact actttgacta ctggggccaa ggcaccgctc tcacggtctc ctcaggtggc   360

ggaggatctg gcggaggtgg aagcggcgga ggcggatccg atgttttgat gacccaaact   420

ccactctccc tgcctgtcag tcttggagat caagcctcca tctcttgcag atctagtcag   480

accattgtac atagtaatgg aaacacctat ttagaatggt acctgcagaa accaggccag   540

tctccaaagc tcctgatcta caaagtttcc aaccgatttt ctggggtccc agacaggttc   600

agtggcagtg gatcagggac agatttcaca ctcaagatca gcagggtgga ggctgaggat   660

ctgggagttt attactgctt tcaagattca catgttcctc tcacgttcgg tgctgggacc   720 aagctggagc tgaaa 735

<210> 1385
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> mu5C6F3 scFv sequence

<400> 1385

```
Glu Val Met Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
        35                  40                  45


Ala Ala Ile Ser Asn Gly Gly Gly Tyr Thr Tyr Tyr Pro Asp Ser Leu
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
                85                  90                  95


Ala Arg Arg Tyr Tyr Asp His Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Ala Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125


Gly Gly Gly Gly Ser Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu
    130                 135                 140


Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
145                 150                 155                 160


Thr Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln
                165                 170                 175


Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
            180                 185                 190


Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        195                 200                 205


Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
    210                 215                 220
```

Tyr Cys Phe Gln Asp Ser His Val Pro Leu Thr Phe Gly Ala Gly Thr
225   230   235   240

Lys Leu Glu Leu Lys
                245

<210> 1386
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse 3C2B1 heavy chain variable framework 1 (CDR1) sequence

<400> 1386
gaagtgatgc tggtggagtc tgggggaggc ttagtgaagc ctggagggtc cctgaaactc   60

tcctgtgcag cctctggaat cactttcagt   90

<210> 1387
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse 3C2B1 heavy chain variable framework 1 (CDR1) sequence

<400> 1387

Glu Val Met Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1   5   10   15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Ile Thr Phe Ser
            20   25   30

<210> 1388
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse 3C2B1 heavy chain variable complementarity determining
       regions 1 (CDR1) sequence

<400> 1388
acctatacca tgtcg   15

<210> 1389
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse 3C2B1 heavy chain variable complementarity determining
       regions 1 (CDR1) sequence

<400> 1389

Thr Tyr Thr Met Ser
1   5

<210> 1390
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse 3C2B1 heavy chain variable framework 2 (CDR2) sequence

<400> 1390
tgggttcgcc agactccgga gaagaggctg gagtgggtcg ca   42

<210> 1391
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse 3C2B1 heavy chain variable framework 2 (CDR2) sequence

<400> 1391

Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val Ala
1   5   10

<210> 1392
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse 3C2B1 heavy chain variable complementarity determining
       regions 2 (CDR2) sequence

<400> 1392
accattagta ctggtggtga taaaacctac tattcagaca gtgtgaaggg t   51

<210> 1393
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse 3C2B1 heavy chain variable complementarity determining
       regions 2 (CDR2) sequence

<400> 1393

Thr Ile Ser Thr Gly Gly Asp Lys Thr Tyr Tyr Ser Asp Ser Val Lys
1   5   10   15

Gly

<210> 1394
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse 3C2B1 heavy chain variable framework 3 (CDR3) sequence

<400> 1394
cgattcacca tctccagaga caatgccaag aacaacctgt acctccaaat gagcagtctg   60

```
aggtctgagg acacggcctt gtattactgt gcaagg                              96


<210>  1395
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 3C2B1 heavy chain variable framework 3 (CDR3) sequence

<400>  1395

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Asn Leu Tyr Leu Gln
1               5                   10                  15


Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Arg
            20                  25                  30


<210>  1396
<211>  36
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 3C2B1 heavy chain variable complementarity determining
       regions 3 (CDR3) sequence

<400>  1396
ggaaccacgg ctatgtatta ctatgctatg gactac                              36


<210>  1397
<211>  12
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 3C2B1 heavy chain variable complementarity determining
       regions 3 (CDR3) sequence

<400>  1397

Gly Thr Thr Ala Met Tyr Tyr Tyr Ala Met Asp Tyr
1               5                   10


<210>  1398
<211>  33
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 3C2B1 heavy chain variable framework 4 (CDR4) sequence

<400>  1398
tggggtcaag gaacctcagt caccgtctcc tca                                 33


<210>  1399
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 3C2B1 heavy chain variable framework 4 (CDR4) sequence
```

```
<400>  1399

Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
1               5                   10


<210>  1400
<211>  69
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 3C2B1 light chain variable framework 1 (FW1) sequence

<400>  1400
gacattgtgc tgacacagtc tcctgcttcc ttagctgtat ctctggggca gagggccacc       60

atctcatgc                                                               69


<210>  1401
<211>  23
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 3C2B1 light chain variable framework 1 (FW1) sequence

<400>  1401

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15


Gln Arg Ala Thr Ile Ser Cys
            20


<210>  1402
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 3C2B1 light chain variable complementarity determining
       regions 1 (CDR1) sequence

<400>  1402
agggccagca aaagtatcag tacatctgac tataattata ttcac                       45


<210>  1403
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 3C2B1 light chain variable complementarity determining
       regions 1 (CDR1) sequence

<400>  1403

Arg Ala Ser Lys Ser Ile Ser Thr Ser Asp Tyr Asn Tyr Ile His
1               5                   10                  15


<210>  1404
<211>  45
<212>  DNA
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```
<213>  Artificial Sequence

<220>
<223>  Mouse 3C2B1 light chain variable framework 2 (FW2) sequence

<400>  1404
tggtaccaac agaaaccagg acagccaccc aaactcctca tctat                       45


<210>  1405
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 3C2B1 light chain variable framework 2 (FW2) sequence

<400>  1405

Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
1               5                   10                  15


<210>  1406
<211>  21
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 3C2B1 light chain variable complementarity determining
       regions 2 (CDR2) sequence

<400>  1406
cttgcatcca acctagaatc t                                                 21


<210>  1407
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 3C2B1 light chain variable complementarity determining
       regions 2 (CDR2) sequence

<400>  1407

Leu Ala Ser Asn Leu Glu Ser
1               5


<210>  1408
<211>  95
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 3C2B1 light chain variable framework 3 (FW3) sequence

<400>  1408
gggtccctgc caggttcagt ggcagtgggt ctgggacaga cttcaccctc aacatccatc      60

ctgtggagga agaagatgct gcaacctatt actgt                                  95


<210>  1409
<211>  32
<212>  PRT
<213>  Artificial Sequence
```

<220>
<223> Mouse 3C2B1 light chain variable framework 3 (FW3) sequence

<400> 1409

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1   5   10   15

Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys
            20   25   30

<210> 1410
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse 3C2B1 light chain variable complementarity determining
       regions 3 (CDR3) sequence

<400> 1410
cagcacagta gggagcttcc tctcacg   27

<210> 1411
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse 3C2B1 light chain variable complementarity determining
       regions 3 (CDR3) sequence

<400> 1411

Gln His Ser Arg Glu Leu Pro Leu Thr
1   5

<210> 1412
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse 3C2B1 light chain variable framework 4 (FW4) sequence

<400> 1412
ttcggtgctg ggaccaagct ggagctgaaa   30

<210> 1413
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse 3C2B1 light chain variable framework 4 (FW4) sequence

<400> 1413

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
1   5   10

<210> 1414

<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse B12 heavy chain variable framework 1 (FW1) sequence

<400> 1414
caggcgcagc tgaaggagtc aggacctggc ctggtggcgc cctcacagag cctgtccatc   60

acttgcactg tctctgggtt ttcattaacc   90

<210> 1415
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse B12 heavy chain variable framework 1 (FW1) sequence

<400> 1415

Gln Ala Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
1   5   10   15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr
            20   25   30

<210> 1416
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse B12 heavy chain variable complementarity determining
       regions 1 (CDR1) sequence

<400> 1416
agctatggtg tacac   15

<210> 1417
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse B12 heavy chain variable complementarity determining
       regions 1 (CDR1) sequence

<400> 1417

Ser Tyr Gly Val His
1   5

<210> 1418
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse B12 heavy chain variable framework 2 (FW2) sequence

<400> 1418
tgggttcgcc agcctccagg aaagggtctg gagtggctgg ga   42

<210> 1419
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse B12 heavy chain variable framework 2 (FW2) sequence

<400> 1419

```
Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly
1               5                   10
```

<210> 1420
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse B12 heavy chain variable complementarity determining regions 2 (CDR2) sequence

<400> 1420

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gtaatatggc ctggtggaag cacaaattat aattcgactc tcatgtccag aatg             54
```

<210> 1421
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse B12 heavy chain variable complementarity determining regions 2 (CDR2) sequence

<400> 1421

```
Val Ile Trp Pro Gly Gly Ser Thr Asn Tyr Asn Ser Thr Leu Met Ser
1               5                   10                  15


Arg Met
```

<210> 1422
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse B12 heavy chain variable framework 3 (FW3) sequence

<400> 1422

```
cggatcatca aagacaactc caagagccaa gttttcttaa aaatgaacag tctgcaaatt       60

gatgacacag ccatgtacta ctgtgccaga                                        90
```

<210> 1423
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse B12 heavy chain variable framework 3 (FW3) sequence

<400> 1423

Arg Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
1   5   10   15

Ser Leu Gln Ile Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg
            20   25   30

<210> 1424
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse B12 heavy chain variable complementarity determining
       regions 3 (CDR3) sequence

<400> 1424
gatcggacac ctcgggtggg ggcctggttt gcttac   36

<210> 1425
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse B12 heavy chain variable complementarity determining
       regions 3 (CDR3) sequence

<400> 1425

Asp Arg Thr Pro Arg Val Gly Ala Trp Phe Ala Tyr
1   5   10

<210> 1426
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse B12 heavy chain variable framework 4 (FW4) sequence

<400> 1426
tggggccaag ggactctggt cactgtctct gcag   34

<210> 1427
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse B12 heavy chain variable framework 4 (FW4) sequence

<400> 1427

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
1   5   10

<210> 1428
<211> 69
<212> DNA
<213> Artificial Sequence

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<220>
<223>  Mouse B12 light chain variable framework 1 (FR1) sequence

<400>  1428
atcattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc       60

atatcctgc                                                               69


<210>  1429
<211>  23
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B12 light chain variable framework 1 (FR1) sequence

<400>  1429

Ile Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15


Gln Arg Ala Thr Ile Ser Cys
            20


<210>  1430
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B12 light chain variable complementarity determining
       regions 1 (CDR1) sequence

<400>  1430
agagccagtg agagtgttgc tacttatggc aataatttta tgcag                       45


<210>  1431
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B12 light chain variable complementarity determining
       regions 1 (CDR1) sequence

<400>  1431

Arg Ala Ser Glu Ser Val Ala Thr Tyr Gly Asn Asn Phe Met Gln
1               5                   10                  15


<210>  1432
<211>  90
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B2 heavy chain variable framework 1 (FW1) sequence

<400>  1432
gaagtggtgc tggtggagtc tgggggaggc ttagtggagc ctggagggtc cctgaaactc       60

tcctgtgtag cctctggatt cgctttcagt                                        90
```

<210> 1433
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse B2 heavy chain variable framework 1 (FW1) sequence

<400> 1433

```
Glu Val Val Leu Val Glu Ser Gly Gly Gly Leu Val Glu Pro Gly Gly
1               5                   10                  15


Ser Leu Lys Leu Ser Cys Val Ala Ser Gly Phe Ala Phe Ser
            20                  25                  30
```

<210> 1434
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse B2 heavy chain variable complementarity determining regions
       1 (CDR1) sequence

<400> 1434

```
acctttgcca tgtct                                                        15
```

<210> 1435
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse B2 heavy chain variable complementarity determining regions
       1 (CDR1) sequence

<400> 1435

```
Thr Phe Ala Met Ser
1               5
```

<210> 1436
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse B2 heavy chain variable framework 2 (FW2) sequence

<400> 1436

```
tggattcgcc agactccgga gaagaggctg gagtgggtcg ca                          42
```

<210> 1437
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse B2 heavy chain variable framework 2 (FW2) sequence

<400> 1437

```
Trp Ile Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val Ala
1               5                   10


<210>  1438
<211>  51
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B2 heavy chain variable complementarity determining regions
       2 (CDR2) sequence

<400>  1438
gccattagta atggtggtgg ttacacctac tatccagaca ctctgaaggg g                51


<210>  1439
<211>  17
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B2 heavy chain variable complementarity determining regions
       2 (CDR2) sequence

<400>  1439

Ala Ile Ser Asn Gly Gly Gly Tyr Thr Tyr Tyr Pro Asp Thr Leu Lys
1               5                   10                  15


Gly



<210>  1440
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B2 heavy chain variable framework 3 (FW3) sequence

<400>  1440
cgattctcca tctccagaga caatgccaag aataccctgt acctgcaaat gagtagtctg       60

aggtctgagg acacggccgt gtattactgt gcaaga                                 96


<210>  1441
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B2 heavy chain variable framework 3 (FW3) sequence

<400>  1441

Arg Phe Ser Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln
1               5                   10                  15


Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
            20                  25                  30


<210>  1442
```

```
<211>  27
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B2 heavy chain variable complementarity determining regions
       3 (CDR3) sequence

<400>  1442
cgctactatg atctctactt tgactta                                          27


<210>  1443
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B2 heavy chain variable complementarity determining regions
       3 (CDR3) sequence

<400>  1443

Arg Tyr Tyr Asp Leu Tyr Phe Asp Leu
1               5


<210>  1444
<211>  33
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B2 heavy chain variable framework 4 (FW4) sequence

<400>  1444
tggggccgag gcacctctct catagtctcc tca                                   33


<210>  1445
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B2 heavy chain variable framework 4 (FW4) sequence

<400>  1445

Trp Gly Arg Gly Thr Ser Leu Ile Val Ser Ser
1               5                   10


<210>  1446
<211>  69
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B2 light chain variable framework 1 (FR1) sequence

<400>  1446
gatattctga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc      60

atttcttgc                                                              69


<210>  1447
<211>  23
```

```
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B2 light chain variable framework 1 (FR1) sequence

<400>  1447

Asp Ile Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1               5                   10                  15


Asp Gln Ala Ser Ile Ser Cys
            20


<210>  1448
<211>  48
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B2 light chain variable complementarity determining regions
       1 (CDR1) sequence

<400>  1448
agatctagtc agaacattgt acatagtaat ggaaacacct atttagaa                    48


<210>  1449
<211>  16
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B2 light chain variable complementarity determining regions
       1 (CDR1) sequence

<400>  1449

Arg Ser Ser Gln Asn Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1               5                   10                  15


<210>  1450
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B2 light chain variable framework 2 (FR2) sequence

<400>  1450
tggtacctgc agaaaccagg ccagtctcca aagctcctga tctac                       45


<210>  1451
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B2 light chain variable framework 2 (FR2) sequence

<400>  1451

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr
1               5                   10                  15
```

```
<210>  1452
<211>  21
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B2 light chain variable complementarity determining regions
       2 (CDR2) sequence

<400>  1452
aaagtttcca accgattttc t                                                21


<210>  1453
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B2 light chain variable complementarity determining regions
       2 (CDR2) sequence

<400>  1453

Lys Val Ser Asn Arg Phe Ser
1               5


<210>  1454
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B2 light chain variable framework 3 (FR3) sequence

<400>  1454
ggggtccccg acaggttcag tggtagtggg tcagggacag atttcacact caagatcagc       60

agagtggagg ctgaggatct gggagtttat tactgc                                96


<210>  1455
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B2 light chain variable framework 3 (FR3) sequence

<400>  1455

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1               5                   10                  15


Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
            20                  25                  30


<210>  1456
<211>  27
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B2 light chain variable complementarity determining regions
       3 (CDR3) sequence
```

<400> 1456
tttcaagatt cacatgttcc tctcacg   27

<210> 1457
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse B2 light chain variable complementarity determining regions 3 (CDR3) sequence

<400> 1457

Phe Gln Asp Ser His Val Pro Leu Thr
1   5

<210> 1458
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse B2 light chain variable framework 4 (FR4) sequence

<400> 1458
ttcggtgctg ggaccaggct ggagctgaaa   30

<210> 1459
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse B2 light chain variable framework 4 (FR4) sequence

<400> 1459

Phe Gly Ala Gly Thr Arg Leu Glu Leu Lys
1   5   10

<210> 1460
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse B7 heavy chain variable framework 1 (FW1) sequence

<400> 1460
gaggtgcagg tggtggagtc tgggggagac ttagtgaagc ctggagggtc cctgaaactc   60

tcctgtgcag cctctggatt cactttcagt   90

<210> 1461
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse B7 heavy chain variable framework 1 (FW1) sequence

<400> 1461

Glu Val Gln Val Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly
1   5   10   15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            20   25   30

<210> 1462
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse B7 heavy chain variable complementarity determining regions
       1 (CDR1) sequence

<400> 1462
agatatggca tgtct   15

<210> 1463
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse B7 heavy chain variable complementarity determining regions
       1 (CDR1) sequence

<400> 1463

Arg Tyr Gly Met Ser
1   5

<210> 1464
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse B7 heavy chain variable framework 2 (FW2) sequence

<400> 1464
tgggttcgcc agactccaga caagaggctg gagtgggtcg ca   42

<210> 1465
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse B7 heavy chain variable framework 2 (FW2) sequence

<400> 1465

Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Trp Val Ala
1   5   10

<210> 1466
<211> 51
<212> DNA
<213> Artificial Sequence

<220>

<223> Mouse B7 heavy chain variable complementarity determining regions 2 (CDR2) sequence

<400> 1466
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accattagta gtggtggtac ttacatctac tatccagaca gtgtgaaggg g                51
```

<210> 1467
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse B7 heavy chain variable complementarity determining regions 2 (CDR2) sequence

<400> 1467

```
Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val Lys
1               5                   10                  15


Gly
```

<210> 1468
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse B7 heavy chain variable framework 3 (FW3) sequence

<400> 1468
```
cgattcacca tctccagaga caatgccaag aacaccctgt acctgcaaat gagcagtctg       60

aagtctgagg acacagccat gtattactgt gcaagg                                 96
```

<210> 1469
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse B7 heavy chain variable framework 3 (FW3) sequence

<400> 1469

```
Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln
1               5                   10                  15


Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys Ala Arg
            20                  25                  30
```

<210> 1470
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse B7 heavy chain variable complementarity determining regions 3 (CDR3) sequence

<400> 1470
```
gataactacg gtagtagcta cgactatgct atggactac                              39
```

<210> 1471
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse B7 heavy chain variable complementarity determining regions 3 (CDR3) sequence

<400> 1471

Asp Asn Tyr Gly Ser Ser Tyr Asp Tyr Ala Met Asp Tyr
1   5   10

<210> 1472
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse B7 heavy chain variable framework 4 (FW4) sequence

<400> 1472
tggggtcaag gaacctcagt caccgtctcc tca   33

<210> 1473
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse B7 heavy chain variable framework 4 (FW4) sequence

<400> 1473

Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
1   5   10

<210> 1474
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse B7 light chain variable framework 1 (FR1) sequence

<400> 1474
gatgttttga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc   60

atctcttgc   69

<210> 1475
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse B7 light chain variable framework 1 (FR1) sequence

<400> 1475

Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1   5   10   15

```
Asp Gln Ala Ser Ile Ser Cys
            20


<210>  1476
<211>  48
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B7 light chain variable complementarity determining regions
       1 (CDR1) sequence

<400>  1476
agatctagtc agaccattgt acatagtaat ggaaacacct atttagaa                    48


<210>  1477
<211>  16
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B7 light chain variable complementarity determining regions
       1 (CDR1) sequence

<400>  1477

Arg Ser Ser Gln Thr Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1               5                   10                  15


<210>  1478
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B7 light chain variable framework 2 (FR2) sequence

<400>  1478
tggtacctgc aaaaaccagg ccagtctcca aagctcctga tctac                       45


<210>  1479
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B7 light chain variable framework 2 (FR2) sequence

<400>  1479

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr
1               5                   10                  15


<210>  1480
<211>  21
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B7 light chain variable complementarity determining regions
       2 (CDR2) sequence
```

```
<400>  1480
aaagtttcca accgattttc t                                                 21


<210>  1481
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B7 light chain variable complementarity determining regions
       2 (CDR2) sequence

<400>  1481

Lys Val Ser Asn Arg Phe Ser
1               5


<210>  1482
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B7 light chain variable framework 3 (FR3) sequence

<400>  1482
ggggtcccag acaggttcag tggcagtgga tcagggacag atttcacact caagatcagc       60

agggtggagg ctgaggatct gggagtttat tactgc                                 96


<210>  1483
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B7 light chain variable framework 3 (FR3) sequence

<400>  1483

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1               5                   10                  15


Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
            20                  25                  30


<210>  1484
<211>  27
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B7 light chain variable complementarity determining regions
       3 (CDR3) sequence

<400>  1484
tttcaagatt cacatgttcc tctcacg                                           27


<210>  1485
<211>  9
<212>  PRT
<213>  Artificial Sequence
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<220>
<223> Mouse B7 light chain variable complementarity determining regions
       3 (CDR3) sequence

<400> 1485

Phe Gln Asp Ser His Val Pro Leu Thr
1   5

<210> 1486
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse B7 light chain variable framework 4 (FR4) sequence

<400> 1486
ttcggtgctg ggaccaagct ggagctgaaa   30

<210> 1487
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse B7 light chain variable framework 4 (FR4) sequence

<400> 1487

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
1   5   10

<210> 1488
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse 8C7F3 heavy chain variable framework 1 (FW1) sequence

<400> 1488
gaagtgatgc tggtggagtc tgggggaggc ttagtgaagc ctggagggtc cctgaaactc   60

tcctgtgcag cctctggatt cactttcagt   90

<210> 1489
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse 8C7F3 heavy chain variable framework 1 (FW1) sequence

<400> 1489

Glu Val Met Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1   5   10   15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            20   25   30

<210> 1490

<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse 8C7F3 heavy chain variable complementarity determining regions 1 (CDR1) sequence

<400> 1490
acctatgcca tgtct   15

<210> 1491
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse 8C7F3 heavy chain variable complementarity determining regions 1 (CDR1) sequence

<400> 1491

Thr Tyr Ala Met Ser
1   5

<210> 1492
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse 8C7F3 heavy chain variable framework 2 (FW2) sequence

<400> 1492
tgggttcgcc agactccgga gaagaggctg gagtgggtcg ca   42

<210> 1493
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse 8C7F3 heavy chain variable framework 2 (FW2) sequence

<400> 1493

Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val Ala
1   5   10

<210> 1494
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse 8C7F3 heavy chain variable complementarity determining regions 2 (CDR2) sequence

<400> 1494
gccattagta atggtggtgg ttacacctac tatccagaca gtctgaaggg g   51

<210> 1495
<211> 17
<212> PRT

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<213>  Artificial Sequence

<220>
<223>  Mouse 8C7F3 heavy chain variable complementarity determining
       regions 2 (CDR2) sequence

<400>  1495

Ala Ile Ser Asn Gly Gly Gly Tyr Thr Tyr Tyr Pro Asp Ser Leu Lys
1               5                   10                  15


Gly




<210>  1496
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 8C7F3 heavy chain variable framework 3 (FW3) sequence

<400>  1496
cgattcacca tctccagaga caatgccaag aacaccctgt acctgcaaat gagcagtctg       60

aggtctgagg acacggccac gtattactgt gcaaga                                 96


<210>  1497
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 8C7F3 heavy chain variable framework 3 (FW3) sequence

<400>  1497

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln
1               5                   10                  15


Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg
            20                  25                  30


<210>  1498
<211>  27
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 8C7F3 heavy chain variable complementarity determining
       regions 3 (CDR3) sequence

<400>  1498
cgttactatg atcactactt tgactac                                           27


<210>  1499
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 8C7F3 heavy chain variable complementarity determining
       regions 3 (CDR3) sequence
```

<400> 1499

Arg Tyr Tyr Asp His Tyr Phe Asp Tyr
1   5

<210> 1500
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse 8C7F3 heavy chain variable framework 4 (FW4) sequence

<400> 1500
tggggccaag gcaccgctct cacggtctcc tca   33

<210> 1501
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse 8C7F3 heavy chain variable framework 4 (FW4) sequence

<400> 1501

Trp Gly Gln Gly Thr Ala Leu Thr Val Ser Ser
1   5   10

<210> 1502
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse 8C7F3 light chain variable framework 1 (FR1) sequence

<400> 1502
atcattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc   60

atatcctgc   69

<210> 1503
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse 8C7F3 light chain variable framework 1 (FR1) sequence

<400> 1503

Ile Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1   5   10   15

Gln Arg Ala Thr Ile Ser Cys
            20

<210> 1504
<211> 45
<212> DNA
<213> Artificial Sequence

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<220>
<223>  Mouse 8C7F3 light chain variable complementarity determining
       regions 1 (CDR1) sequence

<400>  1504
agagccagtg agagtgttgc tacttatggc aataatttta tgcag                       45


<210>  1505
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 8C7F3 light chain variable complementarity determining
       regions 1 (CDR1) sequence

<400>  1505

Arg Ala Ser Glu Ser Val Ala Thr Tyr Gly Asn Asn Phe Met Gln
1               5                   10                  15


<210>  1506
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 8C7F3 light chain variable framework 2 (FR2) sequence

<400>  1506
tggtatcagc agaaaccagg acagccaccc aaactcctca tctat                       45


<210>  1507
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 8C7F3 light chain variable framework 2 (FR2) sequence

<400>  1507

Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
1               5                   10                  15


<210>  1508
<211>  21
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 8C7F3 light chain variable complementarity determining
       regions 2 (CDR2) sequence

<400>  1508
cttgcatcca ccctagattc t                                                 21


<210>  1509
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
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```
<223>  Mouse 8C7F3 light chain variable complementarity determining
       regions 2 (CDR2) sequence

<400>  1509

Leu Ala Ser Thr Leu Asp Ser
1               5


<210>  1510
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 8C7F3 light chain variable framework 3 (FR3) sequence

<400>  1510
ggggtccctg ccaggttcag tggcagtggg tctaggacag acttcaccct caccattgat       60

cctgtggagg ctgatgatgc tgcaacctat tactgt                                 96


<210>  1511
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 8C7F3 light chain variable framework 3 (FR3) sequence

<400>  1511

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr
1               5                   10                  15


Leu Thr Ile Asp Pro Val Glu Ala Asp Asp Ala Ala Thr Tyr Tyr Cys
            20                  25                  30


<210>  1512
<211>  27
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 8C7F3 light chain variable complementarity determining
       regions 3 (CDR3) sequence

<400>  1512
cagcaaaata atgaggatcc tccgacg                                           27


<210>  1513
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 8C7F3 light chain variable complementarity determining
       regions 3 (CDR3) sequence

<400>  1513

Gln Gln Asn Asn Glu Asp Pro Pro Thr
1               5
```

```
<210>  1514
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse 8C7F3 light chain variable framework 4 (FR4) sequence

<400>  1514
ttcggtggag gcaccaagct ggaaatcaag                                        30


<210>  1515
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 8C7F3 light chain variable framework 4 (FR4) sequence

<400>  1515

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
1               5                   10


<210>  1516
<211>  90
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse H11 heavy chain variable framework 1 (FW1) sequence

<400>  1516
gaagtggtgc tggtggagtc tgggggaggc ttagtggagc ctggagggtc cctgaaactc       60

tcctgtgtag cctctggatt cgcttttagt                                        90


<210>  1517
<211>  30
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse H11 heavy chain variable framework 1 (FW1) sequence

<400>  1517

Glu Val Val Leu Val Glu Ser Gly Gly Gly Leu Val Glu Pro Gly Gly
1               5                   10                  15


Ser Leu Lys Leu Ser Cys Val Ala Ser Gly Phe Ala Phe Ser
            20                  25                  30


<210>  1518
<211>  15
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse H11 heavy chain variable complementarity determining
       regions 1 (CDR1) sequence

<400>  1518
acctttgcca tgtct                                                        15
```

<210> 1519
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse H11 heavy chain variable complementarity determining regions 1 (CDR1) sequence

<400> 1519

Thr Phe Ala Met Ser
1   5

<210> 1520
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse H11 heavy chain variable framework 2 (FW2) sequence

<400> 1520
tggattcgcc agactccgga gaagaggctg gagtgggtcg ca   42

<210> 1521
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse H11 heavy chain variable framework 2 (FW2) sequence

<400> 1521

Trp Ile Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val Ala
1   5   10

<210> 1522
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse H11 heavy chain variable complementarity determining regions 2 (CDR2) sequence

<400> 1522
gccattagta atggtggtgg ttacacttac tatccagaca ctctgaaggg g   51

<210> 1523
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse H11 heavy chain variable complementarity determining regions 2 (CDR2) sequence

<400> 1523

Ala Ile Ser Asn Gly Gly Gly Tyr Thr Tyr Tyr Pro Asp Thr Leu Lys
1   5   10   15

Gly

<210> 1524
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse H11 heavy chain variable framework 3 (FW3) sequence

<400> 1524
cgattcacca tctccagaga caatgccaag aataccctgt acctgcaaat gagtagtctg 60

aggtctgagg acacggccgt gtattactgt gcaaga 96

<210> 1525
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse H11 heavy chain variable framework 3 (FW3) sequence

<400> 1525

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 1526
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse H11 heavy chain variable complementarity determining
regions 3 (CDR3) sequence

<400> 1526
cgctactatg atctctactt tgactta 27

<210> 1527
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse H11 heavy chain variable complementarity determining
regions 3 (CDR3) sequence

<400> 1527

Arg Tyr Tyr Asp Leu Tyr Phe Asp Leu
1 5

<210> 1528
<211> 33
<212> DNA

<213> Artificial Sequence

<220>
<223> Mouse H11 heavy chain variable framework 4 (FW4) sequence

<400> 1528
tggggccaag gcacctctct catagtctcc tca   33

<210> 1529
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse H11 heavy chain variable framework 4 (FW4) sequence

<400> 1529

Trp Gly Gln Gly Thr Ser Leu Ile Val Ser Ser
1   5   10

<210> 1530
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse H11 light chain variable framework 1 (FR1) sequence

<400> 1530
gatattctga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc   60

atttcttgc   69

<210> 1531
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse H11 light chain variable framework 1 (FR1) sequence

<400> 1531

Asp Ile Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1   5   10   15

Asp Gln Ala Ser Ile Ser Cys
            20

<210> 1532
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse H11 light chain variable complementarity determining
       regions 1 (CDR1) sequence

<400> 1532
agatctagtc agaacattgt acatagtaat ggaaacacct atttagaa   48

<210> 1533

<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse H11 light chain variable complementarity determining
       regions 1 (CDR1) sequence

<400> 1533

Arg Ser Ser Gln Asn Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1   5   10   15

<210> 1534
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse H11 light chain variable framework 2 (FR2) sequence

<400> 1534
tggtacctgc agaaaccagg ccagtctcca aagctcctga tctac   45

<210> 1535
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse H11 light chain variable framework 2 (FR2) sequence

<400> 1535

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr
1   5   10   15

<210> 1536
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse H11 light chain variable complementarity determining
       regions 2 (CDR2) sequence

<400> 1536
aaagtttcca accgattttc t   21

<210> 1537
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse H11 light chain variable complementarity determining
       regions 2 (CDR2) sequence

<400> 1537

Lys Val Ser Asn Arg Phe Ser
1   5

<210> 1538

```
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse H11 light chain variable framework 3 (FR3) sequence

<400>  1538
ggggtccccg acaggttcag tggtagtggg tcagggacag atttcacact caagatcagc       60

agagtggagg ctgaggatct gggagtttat tactgc                                 96


<210>  1539
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse H11 light chain variable framework 3 (FR3) sequence

<400>  1539

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1               5                   10                  15


Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
            20                  25                  30


<210>  1540
<211>  27
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse H11 light chain variable complementarity determining
       regions 3 (CDR3) sequence

<400>  1540
tttcaagatt cacatgttcc tctcacg                                           27


<210>  1541
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse H11 light chain variable complementarity determining
       regions 3 (CDR3) sequence

<400>  1541

Phe Gln Asp Ser His Val Pro Leu Thr
1               5


<210>  1542
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse H11 light chain variable framework 4 (FR4) sequence

<400>  1542
ttcggtgctg ggaccaggct ggagctgaaa                                        30
```

```
<210>  1543
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse H11 light chain variable framework 4 (FR4) sequence

<400>  1543

Phe Gly Ala Gly Thr Arg Leu Glu Leu Lys
1               5                   10


<210>  1544
<211>  90
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B9 heavy chain variable framework 1 (FW1) sequence

<400>  1544
gaggtgcagg tggtggagtc tgggggagac ttagtgaagc ctggagggtc cctgaaactc       60

tcctgtgcag cctctggatt cactttcagt                                        90


<210>  1545
<211>  30
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B9 heavy chain variable framework 1 (FW1) sequence

<400>  1545

Glu Val Gln Val Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            20                  25                  30


<210>  1546
<211>  15
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B9 heavy chain variable complementarity determining regions
       1 (CDR1) sequence

<400>  1546
agatatggca tgtct                                                        15


<210>  1547
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B9 heavy chain variable complementarity determining regions
       1 (CDR1) sequence
```

```
<400>  1547

Arg Tyr Gly Met Ser
1               5


<210>  1548
<211>  42
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B9 heavy chain variable framework 2 (FW2) sequence

<400>  1548
tgggttcgcc agactccaga caagaggctg gagtgggtcg ca                          42


<210>  1549
<211>  14
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B9 heavy chain variable framework 2 (FW2) sequence

<400>  1549

Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Trp Val Ala
1               5                   10


<210>  1550
<211>  51
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B9 heavy chain variable complementarity determining regions
       2 (CDR2) sequence

<400>  1550
accattagta gtggtggtac ttacatctac tatccagaca gtgtgaaggg g                51


<210>  1551
<211>  17
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B9 heavy chain variable complementarity determining regions
       2 (CDR2) sequence

<400>  1551

Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr Tyr Pro Asp Ser Val Lys
1               5                   10                  15


Gly



<210>  1552
<211>  93
<212>  DNA
<213>  Artificial Sequence
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```
<220>
<223>  Mouse B9 heavy chain variable framework 3 (FW3) sequence

<400>  1552
cgattcacca tctccagaga caatgccaag aacaccctgt acctgcaaat gagcagtctg       60

aagtctgagg acacagccat gtattactgt gca                                    93


<210>  1553
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B9 heavy chain variable framework 3 (FW3) sequence

<400>  1553

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln
1               5                   10                  15


Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys Ala Arg
            20                  25                  30


<210>  1554
<211>  42
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B9 heavy chain variable complementarity determining regions
       3 (CDR3) sequence

<400>  1554
agggataact acggtagtag ctacgactat gctatggact ac                          42


<210>  1555
<211>  13
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B9 heavy chain variable complementarity determining regions
       3 (CDR3) sequence

<400>  1555

Asp Asn Tyr Gly Ser Ser Tyr Asp Tyr Ala Met Asp Tyr
1               5                   10


<210>  1556
<211>  33
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B9 heavy chain variable framework 4 (FW4) sequence

<400>  1556
tggggtcaag gaacctcagt caccgtctcc tct                                    33


<210>  1557
```

```
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B9 heavy chain variable framework 4 (FW4) sequence

<400>  1557

Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
1               5                   10


<210>  1558
<211>  69
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B9 light chain variable framework 1 (FR1) sequence

<400>  1558
caaattgttc tcacccagtc tccagcaatc atgtctgcat ctccagggga ggaggtcacc       60

ctaacctgc                                                               69


<210>  1559
<211>  23
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B9 light chain variable framework 1 (FR1) sequence

<400>  1559

Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
1               5                   10                  15


Glu Glu Val Thr Leu Thr Cys
            20


<210>  1560
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B9 light chain variable complementarity determining regions
       1 (CDR1) sequence

<400>  1560
agtgccagct caagtgtaag ttacatgcac                                        30


<210>  1561
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B9 light chain variable complementarity determining regions
       1 (CDR1) sequence

<400>  1561
```

```
Ser Ala Ser Ser Ser Val Ser Tyr Met His
1               5                   10


<210>  1562
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B9 light chain variable framework 2 (FR2) sequence

<400>  1562
tggttccagc agaggccagg cacttctccc aaactctgga tttat                       45


<210>  1563
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B9 light chain variable framework 2 (FR2) sequence

<400>  1563

Trp Phe Gln Gln Arg Pro Gly Thr Ser Pro Lys Leu Trp Ile Tyr
1               5                   10                  15


<210>  1564
<211>  21
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B9 light chain variable complementarity determining regions
       2 (CDR2) sequence

<400>  1564
accacatcca acctggcttc t                                                 21


<210>  1565
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B9 light chain variable complementarity determining regions
       2 (CDR2) sequence

<400>  1565

Thr Thr Ser Asn Leu Ala Ser
1               5


<210>  1566
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B9 light chain variable framework 3 (FR3) sequence

<400>  1566
ggagtccctg ctcgcttcag tggcagtgga tctgggacct cttactctct cacaatcagc       60
```

```
cgaatggagg ctgaagatgc tgccacttat tactgc                            96


<210>  1567
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B9 light chain variable framework 3 (FR3) sequence

<400>  1567

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser
1               5                   10                  15


Leu Thr Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
            20                  25                  30


<210>  1568
<211>  24
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B9 light chain variable complementarity determining regions
       3 (CDR3) sequence

<400>  1568
cagcaaagga gtagttaccc attc                                         24


<210>  1569
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B9 light chain variable complementarity determining regions
       3 (CDR3) sequence

<400>  1569

Gln Gln Arg Ser Ser Tyr Pro Phe
1               5


<210>  1570
<211>  33
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B9 light chain variable framework 4 (FR4) sequence

<400>  1570
acgttcggct cggggacaaa gttggaaata aaa                               33


<210>  1571
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B9 light chain variable framework 4 (FR4) sequence
```

<400> 1571

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> 1572
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> mu3C2B1 scFv sequence

<400> 1572
gaagtgatgc tggtggagtc tgggggaggc ttagtgaagc ctggagggtc cctgaaactc 60

tcctgtgcag cctctggaat cactttcagt acctatacca tgtcgtgggt tcgccagact 120

ccggagaaga ggctggagtg ggtcgcaacc attagtactg gtggtgataa aacctactat 180

tcagacagtg tgaagggtcg attcaccatc tccagagaca atgccaagaa caacctgtac 240

ctccaaatga gcagtctgag gtctgaggac acggccttgt attactgtgc aaggggaacc 300

acggctatgt attactatgc tatggactac tggggtcaag gaacctcagt caccgtctcc 360

tcaggtggcg gaggatctgg cggaggtgga agcggcggag gcggatccga cattgtgctg 420

acacagtctc ctgcttcctt agctgtatct ctggggcaga gggccaccat ctcatgcagg 480

gccagcaaaa gtatcagtac atctgactat aattatattc actggtacca acagaaacca 540

ggacagccac ccaaactcct catctatctt gcatccaacc tagaatctgg ggtccctgcc 600

aggttcagtg gcagtgggtc tgggacagac ttcaccctca acatccatcc tgtggaggaa 660

gaagatgctg caacctatta ctgtcagcac agtagggagc ttcctctcac gttcggtgct 720

gggaccaagc tggagctgaa a 741

<210> 1573
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> mu3C2B1 scFv sequence

<400> 1573

Glu Val Met Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Ile Thr Phe Ser Thr Tyr
20 25 30

Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Thr Gly Gly Asp Lys Thr Tyr Tyr Ser Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Asn Leu Tyr

```
65                  70                  75                  80

Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Thr Thr Ala Met Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro
    130                 135                 140

Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg
145                 150                 155                 160

Ala Ser Lys Ser Ile Ser Thr Ser Asp Tyr Asn Tyr Ile His Trp Tyr
                165                 170                 175

Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser
            180                 185                 190

Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala
    210                 215                 220

Thr Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Leu Thr Phe Gly Ala
225                 230                 235                 240

Gly Thr Lys Leu Glu Leu Lys
                245


<210>  1574
<211>  741
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  mu20A10 scFv full sequence

<400>  1574
gaagtgatgc tggtggaatc tggcggcgga ctggttaagc ctggcggatc tctgaagctg       60

agctgtgccg ccagcggctt cacctttagc acatacgcca tgagctggat ccggcagacc      120

cctgagaaga gactggaatg ggttgccagc atcggcagag ccggcagcac ctactacagc      180

gattctgtga agggcagatt caccatcagc cgggacaacg tgcggaacat cctgtacctg      240

cagatgagca gcctgcggag cgaggatacc gccatgtact actgtgccag aggacccatc      300

tacaacgact acgacgagtt cgcctattgg ggccagggca cactggttac agtttctgct      360

ggtggcggag gatctggcgg aggtggaagc ggcggaggcg gatccaatat catgatgaca      420
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cagagcccca gcagcctggc tgtgtctgct ggcgagaaag tgaccatgtc ctgcaagagc   480

agccagagcg tgctgtactc cagcaaccag aagaactacc tggcctggta tcagcagaag   540

cccggccagt ctcctaagct gctgatctac tgggccagca ccagagaaag cggcgtgccc   600

gatagattca caggcagcgg cagcggaacc gacttcaccc tgacaatcag ctctgtgcag   660

gccgaagatc tggccgtgta ctattgccac cagtacctgt ccagcctgac ctttggcgcc   720

ggaacaaagc tggaactgaa g   741

<210> 1575
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> mu20A10 scFv full sequence

<400> 1575

Glu Val Met Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1   5   10   15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
            20   25   30

Ala Met Ser Trp Ile Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
        35   40   45

Ala Ser Ile Gly Arg Ala Gly Ser Thr Tyr Tyr Ser Asp Ser Val Lys
    50   55   60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Val Arg Asn Ile Leu Tyr Leu
65   70   75   80

Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys Ala
                85   90   95

Arg Gly Pro Ile Tyr Asn Asp Tyr Asp Glu Phe Ala Tyr Trp Gly Gln
            100   105   110

Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly
        115   120   125

Gly Ser Gly Gly Gly Gly Ser Asn Ile Met Met Thr Gln Ser Pro Ser
    130   135   140

Ser Leu Ala Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
145   150   155   160

Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp
                165   170   175

Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala

            180   185   190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
        195   200   205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
    210   215   220

Ala Val Tyr Tyr Cys His Gln Tyr Leu Ser Ser Leu Thr Phe Gly Ala
225   230   235   240

Gly Thr Lys Leu Glu Leu Lys
                245

<210> 1576
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> hu20A10M scFV

<400> 1576
gaggtgcagc tggttgaatc tggcggcgga cttgtgaagc ctggcggatc tctgagactg 60

agctgtgccg ccagcggctt cacctttagc acatacgcca tgagctgggt ccgacaggcc 120

cctggaaaag gccttgaatg ggttgcctct atcggcagag ccggcagcac ctactacagc 180

gattctgtga agggcagatt caccatcagc cgggacaacg ccaagaacag cctgtacctg 240

cagatgaact ccctgagagc cgaggacacc gccgtgtact attgtgccag aggacccatc 300

tacaacgact acgacgagtt cgcctattgg ggccagggca cactggtcac agtcagctct 360

ggcggtggcg gaagcggagg cggtggctcc ggtggcggag gcagcgacat cgtgatgaca 420

cagagccctt ctagcctggc cgtgtctctg ggagagagag ccacaatcag ctgcaagagc 480

agccagagcg tgctgtactc cagcaaccag aagaactacc tggcctggta tcagcagaag 540

cccggacagt ctcccaagct gctgatctac tgggccagca ccagagaaag cggcgtgccc 600

gatagattca caggctctgg cagcggcacc gacttcaccc tgacaattag cagtctgcag 660

gccgaggacg tggccgtgta ctactgtcac cagtacctga gcagcctgac ctttggcggc 720

ggaacaaagg tggaaatcaa g 741

<210> 1577
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> hu20A10M scFV

<400> 1577

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1   5   10   15

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Ser Ile Gly Arg Ala Gly Ser Thr Tyr Tyr Ser Asp Ser Val Lys
    50                  55                  60


Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65                  70                  75                  80


Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Gly Pro Ile Tyr Asn Asp Tyr Asp Glu Phe Ala Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125


Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Ser
    130                 135                 140


Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser
145                 150                 155                 160


Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp
                165                 170                 175


Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala
            180                 185                 190


Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
        195                 200                 205


Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val
    210                 215                 220


Ala Val Tyr Tyr Cys His Gln Tyr Leu Ser Ser Leu Thr Phe Gly Gly
225                 230                 235                 240


Gly Thr Lys Val Glu Ile Lys
                245


<210>  1578
<211>  744
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  hu20A10C2 scFV

<400>  1578
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gaggtgcagc tggttgaatc tggcggcgga cttgtgaagc ctggcggatc tctgagactg 60

agctgtgccg ccagcggctt cacctttagc acatacgcca tgagctgggt ccgacaggcc 120

cctggaaaag gccttgaatg ggttgcctct atcggcagag ccggcagcac ctactacagc 180

gattctgtga agggcagatt caccatcagc cgggacaacg ccaagaacag cctgtacctg 240

cagatgaact ccctgagagc cgaggacacc gccgtgtact attgtgccag aggacccatc 300

tacaacgact acgacgagtt cgcctattgg ggccagggca cactggtcac agtcagctct 360

ggcggtggcg gaagcggagg cggtggctcc ggtggcggag gcagcgacat tgtgctgacc 420

cagtctccag cctccttggc cgtgtctcca ggacagaggg ccaccatcac ctgcaagagc 480

agccagagcg tgctgtactc cagcaaccag aagaactacc tggcctggta tcagcagaaa 540

ccaggacaac ctcctaaact cctgatttac tgggccagca ccagagaaag cggggtccca 600

gccaggttca gcggcagtgg gtctgggacc gatttcaccc tcacaattaa tcctgtggaa 660

gctaatgata ctgcaaatta ttactgtcac cagtacctga gcagcctgac cttcggcgga 720

gggaccaagg tggagatcaa acga 744

<210> 1579
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> hu20A10C2 scFV

<400> 1579

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Ser Ile Gly Arg Ala Gly Ser Thr Tyr Tyr Ser Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gly Pro Ile Tyr Asn Asp Tyr Asp Glu Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

```
Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Ala
    130                 135                 140

Ser Leu Ala Val Ser Pro Gly Gln Arg Ala Thr Ile Thr Cys Lys Ser
145                 150                 155                 160

Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp
                165                 170                 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
            180                 185                 190

Ser Thr Arg Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
        195                 200                 205

Gly Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asn Asp Thr
    210                 215                 220

Ala Asn Tyr Tyr Cys His Gln Tyr Leu Ser Ser Leu Thr Phe Gly Gly
225                 230                 235                 240

Gly Thr Lys Val Glu Ile Lys Arg
                245


<210>  1580
<211>  744
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  hu20A10N scFV

<400>  1580
caggtgcagc tggttgaatc tggcggcgga cttgtgaagc ctggcggatc tctgagactg       60

agctgtgccg ccagcggctt cacctttagc acatacgcca tgagctggat cagacaggcc      120

cctggcaaag gcctggaatg ggtggcgtct attggcagag ccggcagcac ctactacagc      180

gactctgtga agggcagatt caccatcagc cgggacaacg ccaagaacag cctgtacctg      240

cagatgaact ccctgagagc cgaggacacc gccgtgtact attgtgccag aggacccatc      300

tacaacgact acgacgagtt cgcctattgg ggccagggca cactggtcac agtttctagc      360

ggcggtggcg gaagcggagg cggtggctcc ggtggcggag gcagcgaaat tgtgctgaca      420

cagagccccg ccacactgtc actttctcca ggcgaaagag ccacactgag ctgcaagagc      480

agccagagcg tgctgtactc cagcaaccag aagaactacc tggcctggta tcagcagaag      540

cccggccaag ctcctcggct gctgatctat tgggccagca caagagagag cggcatccct      600

gccagatttt ctggcagcgg ctctggcacc gatttcaccc tgaccataag cagcctggaa      660

cctgaggact tcgccgtgta ttactgccac cagtacctga gcagcctgac ctttggcgga      720

ggcaccaagg tggaaatcaa gcgg                                             744


<210>  1581
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<211>  248
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  hu20A10N scFV

<400>  1581

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
            20                  25                  30


Ala Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Ser Ile Gly Arg Ala Gly Ser Thr Tyr Tyr Ser Asp Ser Val Lys
    50                  55                  60


Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65                  70                  75                  80


Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Gly Pro Ile Tyr Asn Asp Tyr Asp Glu Phe Ala Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125


Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala
    130                 135                 140


Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Lys Ser
145                 150                 155                 160


Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp
                165                 170                 175


Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Trp Ala
            180                 185                 190


Ser Thr Arg Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
        195                 200                 205


Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
    210                 215                 220


Ala Val Tyr Tyr Cys His Gln Tyr Leu Ser Ser Leu Thr Phe Gly Gly
225                 230                 235                 240
```

Gly Thr Lys Val Glu Ile Lys Arg
                245

<210> 1582
<211> 1479
<212> DNA
<213> Artificial Sequence

<220>
<223> mu20A10CAR T841BB3z

<400> 1582

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atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg       60

ccggaagtga tgctggtgga atctggcggc ggactggtta agcctggcgg atctctgaag      120

ctgagctgtg ccgccagcgg cttcaccttt agcacatacg ccatgagctg gatccggcag      180

acccctgaga agagactgga atgggttgcc agcatcggca gagccggcag cacctactac      240

agcgattctg tgaagggcag attcaccatc agccgggaca acgtgcggaa catcctgtac      300

ctgcagatga gcagcctgcg gagcgaggat accgccatgt actactgtgc cagaggaccc      360

atctacaacg actacgacga gttcgcctat tggggccagg gcacactggt tacagtttct      420

gctggtggcg gaggatctgg cggaggtgga agcggcggag gcggatccaa tatcatgatg      480

acacagagcc cgagcagcct ggctgtgtct gctggcgaga aagtgaccat gtcctgcaag      540

agcagccaga gcgtgctgta ctccagcaac cagaagaact acctggcctg gtatcagcag      600

aagcccggcc agtctcctaa gctgctgatc tactgggcca gcaccagaga aagcggcgtg      660

cccgatagat tcacaggcag cggcagcgga accgacttca ccctgacaat cagctctgtg      720

caggccgaag atctggccgt gtactattgc caccagtacc tgtccagcct gacctttggc      780

gccggaacaa agctggaact gaagacaaca acccctgccc ccagacctcc taccccagcc      840

cctacaattg ccagccagcc tctgagcctg aggcccgagg cttgtagacc tgctgctggc      900

ggagccgtgc acaccagagg actggatttc gcctgcgaca tctacatctg ggcgcccttg      960

gccgggactt gtggggtcct tctcctgtca ctggttatca ccctttactg caaacggggc     1020

agaaagaaac tcctgtatat attcaaacaa ccatttatga gaccagtaca aactactcaa     1080

gaggaagatg gctgtagctg ccgatttcca gaagaagaag aaggaggatg tgaactgaga     1140

gtgaagttca gcaggagcgc agacgccccc gcgtacaagc agggccagaa ccagctctat     1200

aacgagctca atctaggacg aagagaggag tacgatgttt tggacaagag acgtggccgg     1260

gaccctgaga tggggggaaa gccgagaagg aagaaccctc aggaaggcct gtacaatgaa     1320

ctgcagaaag ataagatggc ggaggcctac agtgagattg ggatgaaagg cgagcgccgg     1380

aggggcaagg ggcacgatgg cctttaccag ggtctcagta cagccaccaa ggacacctac     1440

gacgcccttc acatgcaggc cctgcccct cgctgataa                               1479
```

<210> 1583
<211> 491
<212> PRT
<213> Artificial Sequence

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<220>
<223>  mu20A10CAR T841BB3z

<400>  1583

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15


His Ala Ala Arg Pro Glu Val Met Leu Val Glu Ser Gly Gly Gly Leu
            20                  25                  30


Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
        35                  40                  45


Thr Phe Ser Thr Tyr Ala Met Ser Trp Ile Arg Gln Thr Pro Glu Lys
    50                  55                  60


Arg Leu Glu Trp Val Ala Ser Ile Gly Arg Ala Gly Ser Thr Tyr Tyr
65                  70                  75                  80


Ser Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Val Arg
                85                  90                  95


Asn Ile Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala
            100                 105                 110


Met Tyr Tyr Cys Ala Arg Gly Pro Ile Tyr Asn Asp Tyr Asp Glu Phe
        115                 120                 125


Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly
    130                 135                 140


Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn Ile Met Met
145                 150                 155                 160


Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly Glu Lys Val Thr
                165                 170                 175


Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys
            180                 185                 190


Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu
        195                 200                 205


Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe
    210                 215                 220


Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val
225                 230                 235                 240


Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys His Gln Tyr Leu Ser Ser
                245                 250                 255
```

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Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Thr Thr Thr Pro
            260                 265                 270


Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
        275                 280                 285


Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
    290                 295                 300


Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
305                 310                 315                 320


Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
                325                 330                 335


Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
            340                 345                 350


Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
        355                 360                 365


Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
    370                 375                 380


Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr
385                 390                 395                 400


Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
                405                 410                 415


Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
            420                 425                 430


Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
        435                 440                 445


Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
    450                 455                 460


His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
465                 470                 475                 480


Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485                 490


<210>  1584
<211>  1482
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  hu20A10CAR T841BB3z

<400>  1584
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ccggaggtgc agctggttga atctggcggc ggacttgtga agcctggcgg atctctgaga 120

ctgagctgtg ccgccagcgg cttcaccttt agcacatacg ccatgagctg ggtccgacag 180

gcccctggaa aaggccttga atgggttgcc tctatcggca gagccggcag cacctactac 240

agcgattctg tgaagggcag attcaccatc agccgggaca acgccaagaa cagcctgtac 300

ctgcagatga actccctgag agccgaggac accgccgtgt actattgtgc cagaggaccc 360

atctacaacg actacgacga gttcgcctat tggggccagg gcacactggt cacagtcagc 420

tctggcggtg gcggaagcgg aggcggtggc tccggtggcg gaggcagcga cattgtgctg 480

acccagtctc cagcctcctt ggccgtgtct ccaggacaga gggccaccat cacctgcaag 540

agcagccaga gcgtgctgta ctccagcaac cagaagaact acctggcctg gtatcagcag 600

aaaccaggac aacctcctaa actcctgatt tactgggcca gcaccagaga aagcggggtc 660

ccagccaggt tcagcggcag tgggtctggg accgatttca ccctcacaat taatcctgtg 720

gaagctaatg atactgcaaa ttattactgt caccagtacc tgagcagcct gaccttcggc 780

ggagggacca aggtggagat caaacgaaca acaacccctg cccccagacc tcctacccca 840

gcccctacaa ttgccagcca gcctctgagc ctgaggcccg aggcttgtag acctgctgct 900

ggcggagccg tgcacaccag aggactggat ttcgcctgcg acatctacat ctgggcgccc 960

ttggccggga cttgtggggt ccttctcctg tcactggtta tcacccttta ctgcaaacgg 1020

ggcagaaaga aactcctgta tatattcaaa caaccattta tgagaccagt acaaactact 1080

caagaggaag atggctgtag ctgccgattt ccagaagaag aagaaggagg atgtgaactg 1140

agagtgaagt tcagcaggag cgcagacgcc cccgcgtaca agcagggcca gaaccagctc 1200

tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 1260

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 1320

gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 1380

cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc 1440

tacgacgccc ttcacatgca ggccctgccc cctcgctgat aa 1482

<210> 1585
<211> 492
<212> PRT
<213> Artificial Sequence

<220>
<223> hu20A10CAR T841BB3z

<400> 1585

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

```
Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
        35                  40                  45

Thr Phe Ser Thr Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
    50                  55                  60

Gly Leu Glu Trp Val Ala Ser Ile Gly Arg Ala Gly Ser Thr Tyr Tyr
65                  70                  75                  80

Ser Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
                85                  90                  95

Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
            100                 105                 110

Val Tyr Tyr Cys Ala Arg Gly Pro Ile Tyr Asn Asp Tyr Asp Glu Phe
        115                 120                 125

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
    130                 135                 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu
145                 150                 155                 160

Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Pro Gly Gln Arg Ala Thr
                165                 170                 175

Ile Thr Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys
            180                 185                 190

Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu
        195                 200                 205

Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Ala Arg Phe
    210                 215                 220

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Pro Val
225                 230                 235                 240

Glu Ala Asn Asp Thr Ala Asn Tyr Tyr Cys His Gln Tyr Leu Ser Ser
                245                 250                 255

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Thr Thr
            260                 265                 270

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
        275                 280                 285

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
    290                 295                 300

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
```

305   310   315   320

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
                325   330   335

Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
            340   345   350

Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
        355   360   365

Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
    370   375   380

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu
385   390   395   400

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
                405   410   415

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
            420   425   430

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
        435   440   445

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
    450   455   460

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
465   470   475   480

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485   490

<210> 1586
<211> 1476
<212> DNA
<213> Artificial Sequence

<220>
<223> mu20A10CAR T8283z

<400> 1586
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ccggaagtga tgctggtgga atctggcggc ggactggtta agcctggcgg atctctgaag   120

ctgagctgtg ccgccagcgg cttcaccttt agcacatacg ccatgagctg gatccggcag   180

acccctgaga agagactgga atgggttgcc agcatcggca gagccggcag cacctactac   240

agcgattctg tgaagggcag attcaccatc agccgggaca acgtgcggaa catcctgtac   300

ctgcagatga gcagcctgcg gagcgaggat accgccatgt actactgtgc cagaggaccc   360

atctacaacg actacgacga gttcgcctat tggggccagg gcacactggt tacagtttct   420

```
gctggtggcg gaggatctgg cggaggtgga agcggcggag gcggatccaa tatcatgatg      480

acacagagcc cgagcagcct ggctgtgtct gctggcgaga aagtgaccat gtcctgcaag      540

agcagccaga gcgtgctgta ctccagcaac cagaagaact acctggcctg gtatcagcag      600

aagcccggcc agtctcctaa gctgctgatc tactgggcca gcaccagaga aagcggcgtg      660

cccgatagat tcacaggcag cggcagcgga accgacttca ccctgacaat cagctctgtg      720

caggccgaag atctggccgt gtactattgc caccagtacc tgtccagcct gacctttggc      780

gccggaacaa agctggaact gaagacaaca acccctgccc ccagacctcc taccccagcc      840

cctacaattg ccagccagcc tctgagcctg aggcccgagg cttgtagacc tgctgctggc      900

ggagccgtgc acaccagagg actggatttc gcctgcgaca tctacatctg ggcgcccttg      960

gccgggactt gtggggtcct tctcctgtca ctggttatca ccctttactg caggagtaag     1020

aggagcaggc tcctgcacag tgactacatg aacatgactc ctagaagacc tgggcctacc     1080

agaaagcatt accagcccta tgccccacca cgcgacttcg cagcctatcg ctccagagtg     1140

aagttcagca ggagcgcaga cgcccccgcg tacaagcagg gccagaacca gctctataac     1200

gagctcaatc taggacgaag agaggagtac gatgttttgg acaagagacg tggccgggac     1260

cctgagatgg ggggaaagcc gagaaggaag aaccctcagg aaggcctgta caatgaactg     1320

cagaaagata agatggcgga ggcctacagt gagattggga tgaaaggcga gcgccggagg     1380

ggcaaggggc acgatggcct ttaccagggt ctcagtacag ccaccaagga cacctacgac     1440

gcccttcaca tgcaggccct gccccctcgc tgataa                                1476


<210>  1587
<211>  490
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  mu20A10CAR T8283z

<400>  1587

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15


His Ala Ala Arg Pro Glu Val Met Leu Val Glu Ser Gly Gly Gly Leu
            20                  25                  30


Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
        35                  40                  45


Thr Phe Ser Thr Tyr Ala Met Ser Trp Ile Arg Gln Thr Pro Glu Lys
    50                  55                  60


Arg Leu Glu Trp Val Ala Ser Ile Gly Arg Ala Gly Ser Thr Tyr Tyr
65                  70                  75                  80


Ser Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Val Arg
```

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                85                  90                  95

Asn Ile Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala
            100                 105                 110

Met Tyr Tyr Cys Ala Arg Gly Pro Ile Tyr Asn Asp Tyr Asp Glu Phe
        115                 120                 125

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly
    130                 135                 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn Ile Met Met
145                 150                 155                 160

Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly Glu Lys Val Thr
                165                 170                 175

Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys
            180                 185                 190

Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu
        195                 200                 205

Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe
    210                 215                 220

Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val
225                 230                 235                 240

Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys His Gln Tyr Leu Ser Ser
                245                 250                 255

Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Thr Thr Thr Pro
            260                 265                 270

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
        275                 280                 285

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
    290                 295                 300

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
305                 310                 315                 320

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
                325                 330                 335

Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
            340                 345                 350

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
        355                 360                 365
```

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg
    370   375   380

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
385   390   395   400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
                405   410   415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
            420   425   430

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
        435   440   445

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
    450   455   460

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
465   470   475   480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485   490

<210> 1588
<211> 1479
<212> DNA
<213> Artificial Sequence

<220>
<223> hu20A10CAR T8283z

<400> 1588
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ccggaggtgc agctggttga atctggcggc ggacttgtga agcctggcgg atctctgaga   120

ctgagctgtg ccgccagcgg cttcaccttt agcacatacg ccatgagctg ggtccgacag   180

gcccctggaa aaggccttga atgggttgcc tctatcggca gagccggcag cacctactac   240

agcgattctg tgaagggcag attcaccatc agccgggaca acgccaagaa cagcctgtac   300

ctgcagatga actccctgag agccgaggac accgccgtgt actattgtgc cagaggaccc   360

atctacaacg actacgacga gttcgcctat tggggccagg gcacactggt cacagtcagc   420

tctggcggtg gcggaagcgg aggcggtggc tccggtggcg gaggcagcga cattgtgctg   480

acccagtctc cagcctcctt ggccgtgtct ccaggacaga gggccaccat cacctgcaag   540

agcagccaga gcgtgctgta ctccagcaac cagaagaact acctggcctg gtatcagcag   600

aaaccaggac aacctcctaa actcctgatt tactgggcca gcaccagaga aagcggggtc   660

ccagccaggt tcagcggcag tgggtctggg accgatttca ccctcacaat taatcctgtg   720

gaagctaatg atactgcaaa ttattactgt caccagtacc tgagcagcct gaccttcggc   780 ggagggacca aggtggagat caaacgaaca acaacccctg cccccagacc tcctacccca   840

gcccctacaa ttgccagcca gcctctgagc ctgaggcccg aggcttgtag acctgctgct   900

ggcggagccg tgcacaccag aggactggat ttcgcctgcg acatctacat ctgggcgccc   960

ttggccggga cttgtggggt ccttctcctg tcactggtta tcacccttta ctgcaggagt   1020

aagaggagca ggctcctgca cagtgactac atgaacatga ctcctagaag acctgggcct   1080

accagaaagc attaccagcc ctatgcccca ccacgcgact tcgcagccta tcgctccaga   1140

gtgaagttca gcaggagcgc agacgccccc gcgtacaagc agggccagaa ccagctctat   1200

aacgagctca atctaggacg aagagaggag tacgatgttt tggacaagag acgtggccgg   1260

gaccctgaga tgggggggaaa gccgagaagg aagaaccctc aggaaggcct gtacaatgaa   1320

ctgcagaaag ataagatggc ggaggcctac agtgagattg ggatgaaagg cgagcgccgg   1380

aggggcaagg ggcacgatgg cctttaccag ggtctcagta cagccaccaa ggacacctac   1440

gacgcccttc acatgcaggc cctgcccccct cgctgataa   1479

<210> 1589
<211> 491
<212> PRT
<213> Artificial Sequence

<220>
<223> hu20A10CAR T8283z

<400> 1589

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1   5   10   15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
            20   25   30

Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
        35   40   45

Thr Phe Ser Thr Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
    50   55   60

Gly Leu Glu Trp Val Ala Ser Ile Gly Arg Ala Gly Ser Thr Tyr Tyr
65   70   75   80

Ser Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
                85   90   95

Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
            100   105   110

Val Tyr Tyr Cys Ala Arg Gly Pro Ile Tyr Asn Asp Tyr Asp Glu Phe
        115   120   125

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
    130   135   140

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Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu
145                 150                 155                 160

Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Pro Gly Gln Arg Ala Thr
                165                 170                 175

Ile Thr Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys
            180                 185                 190

Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu
        195                 200                 205

Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Ala Arg Phe
    210                 215                 220

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Pro Val
225                 230                 235                 240

Glu Ala Asn Asp Thr Ala Asn Tyr Tyr Cys His Gln Tyr Leu Ser Ser
                245                 250                 255

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Thr Thr
            260                 265                 270

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
        275                 280                 285

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
    290                 295                 300

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
305                 310                 315                 320

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
                325                 330                 335

Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn
            340                 345                 350

Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr
        355                 360                 365

Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser
    370                 375                 380

Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr
385                 390                 395                 400

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
                405                 410                 415
```

```
Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
            420                 425                 430


Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
        435                 440                 445


Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
    450                 455                 460


His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
465                 470                 475                 480


Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485                 490


<210>  1590
<211>  1479
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  mu20A10CAR T841BB3z1XX

<400>  1590
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ccggaagtga tgctggtgga atctggcggc ggactggtta agcctggcgg atctctgaag      120

ctgagctgtg ccgccagcgg cttcaccttt agcacatacg ccatgagctg gatccggcag      180

acccctgaga agagactgga atgggttgcc agcatcggca gagccggcag cacctactac      240

agcgattctg tgaagggcag attcaccatc agccgggaca acgtgcggaa catcctgtac      300

ctgcagatga gcagcctgcg gagcgaggat accgccatgt actactgtgc cagaggaccc      360

atctacaacg actacgacga gttcgcctat tggggccagg gcacactggt tacagtttct      420

gctggtggcg gaggatctgg cggaggtgga agcggcggag gcggatccaa tatcatgatg      480

acacagagcc cgagcagcct ggctgtgtct gctggcgaga aagtgaccat gtcctgcaag      540

agcagccaga gcgtgctgta ctccagcaac cagaagaact acctggcctg gtatcagcag      600

aagcccggcc agtctcctaa gctgctgatc tactgggcca gcaccagaga aagcggcgtg      660

cccgatagat tcacaggcag cggcagcgga accgacttca ccctgacaat cagctctgtg      720

caggccgaag atctggccgt gtactattgc caccagtacc tgtccagcct gacctttggc      780

gccggaacaa agctggaact gaagacaaca acccctgccc ccagacctcc taccccagcc      840

cctacaattg ccagccagcc tctgagcctg aggcccgagg cttgtagacc tgctgctggc      900

ggagccgtgc acaccagagg actggatttc gcctgcgaca tctacatctg ggcgcccttg      960

gccgggactt gtggggtcct tctcctgtca ctggttatca ccctttactg caaacggggc     1020

agaaagaaac tcctgtatat attcaaacaa ccatttatga gaccagtaca aactactcaa     1080

gaggaagatg gctgtagctg ccgatttcca gaagaagaag aaggaggatg tgaactgaga     1140

gtgaagttca gcaggagcgc agacgccccc gcgtacaagc agggccagaa ccagctctat     1200
```

aacgagctca atctaggacg aagagaggag tacgatgttt tggacaagag acgtggccgg 1260

gaccctgaga tggggggaaa gccgagaagg aagaaccctc aggaaggcct gttcaatgaa 1320

ctgcagaaag ataagatggc ggaggccttc agtgagattg ggatgaaagg cgagcgccgg 1380

aggggcaagg ggcacgatgg cctttttccag ggtctcagta cagccaccaa ggacaccttc 1440

gacgcccttc acatgcaggc cctgcccccct cgctgataa 1479

<210> 1591
<211> 491
<212> PRT
<213> Artificial Sequence

<220>
<223> mu20A10CAR T841BB3z1XX

<400> 1591

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Val Met Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Ser Thr Tyr Ala Met Ser Trp Ile Arg Gln Thr Pro Glu Lys
50 55 60

Arg Leu Glu Trp Val Ala Ser Ile Gly Arg Ala Gly Ser Thr Tyr Tyr
65 70 75 80

Ser Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Val Arg
85 90 95

Asn Ile Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala
100 105 110

Met Tyr Tyr Cys Ala Arg Gly Pro Ile Tyr Asn Asp Tyr Asp Glu Phe
115 120 125

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn Ile Met Met
145 150 155 160

Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly Glu Lys Val Thr
165 170 175

Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys
180 185 190

```
Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu
        195                 200                 205

Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe
    210                 215                 220

Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val
225                 230                 235                 240

Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys His Gln Tyr Leu Ser Ser
                245                 250                 255

Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Thr Thr Thr Pro
            260                 265                 270

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
        275                 280                 285

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
    290                 295                 300

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
305                 310                 315                 320

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
                325                 330                 335

Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
            340                 345                 350

Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
        355                 360                 365

Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
    370                 375                 380

Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr
385                 390                 395                 400

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
                405                 410                 415

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
            420                 425                 430

Pro Gln Glu Gly Leu Phe Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
        435                 440                 445

Ala Phe Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
    450                 455                 460
```

His Asp Gly Leu Phe Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Phe
465 470 475 480

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 1592
<211> 1482
<212> DNA
<213> Artificial Sequence

<220>
<223> hu20A10CAR T841BB3z1XX

<400> 1592
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ccggaggtgc agctggttga atctggcggc ggacttgtga agcctggcgg atctctgaga 120

ctgagctgtg ccgccagcgg cttcaccttt agcacatacg ccatgagctg ggtccgacag 180

gcccctggaa aaggccttga atgggttgcc tctatcggca gagccggcag cacctactac 240

agcgattctg tgaagggcag attcaccatc agccgggaca acgccaagaa cagcctgtac 300

ctgcagatga actccctgag agccgaggac accgccgtgt actattgtgc cagaggaccc 360

atctacaacg actacgacga gttcgcctat tggggccagg gcacactggt cacagtcagc 420

tctggcggtg gcggaagcgg aggcggtggc tccggtggcg gaggcagcga cattgtgctg 480

acccagtctc cagcctcctt ggccgtgtct ccaggacaga gggccaccat cacctgcaag 540

agcagccaga gcgtgctgta ctccagcaac cagaagaact acctggcctg gtatcagcag 600

aaaccaggac aacctcctaa actcctgatt tactgggcca gcaccagaga aagcggggtc 660

ccagccaggt tcagcggcag tgggtctggg accgatttca ccctcacaat taatcctgtg 720

gaagctaatg atactgcaaa ttattactgt caccagtacc tgagcagcct gaccttcggc 780

ggagggacca aggtggagat caaacgaaca acaacccctg cccccagacc tcctacccca 840

gcccctacaa ttgccagcca gcctctgagc ctgaggcccg aggcttgtag acctgctgct 900

ggcggagccg tgcacaccag aggactggat ttcgcctgcg acatctacat ctgggcgccc 960

ttggccggga cttgtggggt ccttctcctg tcactggtta tcacccttta ctgcaaacgg 1020

ggcagaaaga aactcctgta tatattcaaa caaccattta tgagaccagt acaaactact 1080

caagaggaag atggctgtag ctgccgattt ccagaagaag aagaaggagg atgtgaactg 1140

agagtgaagt tcagcaggag cgcagacgcc cccgcgtaca agcagggcca gaaccagctc 1200

tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 1260

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgttcaat 1320

gaactgcaga aagataagat ggcggaggcc ttcagtgaga ttgggatgaa aggcgagcgc 1380

cggaggggca aggggcacga tggcctttttc cagggtctca gtacagccac caaggacacc 1440

ttcgacgccc ttcacatgca ggccctgccc cctcgctgat aa 1482

<210> 1593

<211> 492
<212> PRT
<213> Artificial Sequence

<220>
<223> hu20A10CAR T841BB3z1XX

<400> 1593

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1   5   10   15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
            20   25   30

Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
        35   40   45

Thr Phe Ser Thr Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
    50   55   60

Gly Leu Glu Trp Val Ala Ser Ile Gly Arg Ala Gly Ser Thr Tyr Tyr
65   70   75   80

Ser Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
                85   90   95

Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
            100   105   110

Val Tyr Tyr Cys Ala Arg Gly Pro Ile Tyr Asn Asp Tyr Asp Glu Phe
        115   120   125

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
    130   135   140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu
145   150   155   160

Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Pro Gly Gln Arg Ala Thr
                165   170   175

Ile Thr Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys
            180   185   190

Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu
        195   200   205

Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Ala Arg Phe
    210   215   220

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Pro Val
225   230   235   240

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Glu Ala Asn Asp Thr Ala Asn Tyr Tyr Cys His Gln Tyr Leu Ser Ser
                245                 250                 255


Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Thr Thr
            260                 265                 270


Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
        275                 280                 285


Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
    290                 295                 300


His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
305                 310                 315                 320


Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
                325                 330                 335


Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
            340                 345                 350


Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
        355                 360                 365


Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
    370                 375                 380


Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu
385                 390                 395                 400


Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
                405                 410                 415


Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
            420                 425                 430


Asn Pro Gln Glu Gly Leu Phe Asn Glu Leu Gln Lys Asp Lys Met Ala
        435                 440                 445


Glu Ala Phe Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
    450                 455                 460


Gly His Asp Gly Leu Phe Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
465                 470                 475                 480


Phe Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485                 490


<210>  1594
<211>  1476
<212>  DNA
<213>  Artificial Sequence
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<220>
<223> mu20A10CAR T8283z1XX

<400> 1594
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ccggaagtga tgctggtgga atctggcggc ggactggtta agcctggcgg atctctgaag      120

ctgagctgtg ccgccagcgg cttcaccttt agcacatacg ccatgagctg gatccggcag      180

acccctgaga agagactgga atgggttgcc agcatcggca gagccggcag cacctactac      240

agcgattctg tgaagggcag attcaccatc agccgggaca acgtgcggaa catcctgtac      300

ctgcagatga gcagcctgcg gagcgaggat accgccatgt actactgtgc cagaggaccc      360

atctacaacg actacgacga gttcgcctat tggggccagg gcacactggt tacagtttct      420

gctggtggcg gaggatctgg cggaggtgga agcggcggag gcggatccaa tatcatgatg      480

acacagagcc cgagcagcct ggctgtgtct gctggcgaga aagtgaccat gtcctgcaag      540

agcagccaga gcgtgctgta ctccagcaac cagaagaact acctggcctg gtatcagcag      600

aagcccggcc agtctcctaa gctgctgatc tactgggcca gcaccagaga aagcggcgtg      660

cccgatagat tcacaggcag cggcagcgga accgacttca ccctgacaat cagctctgtg      720

caggccgaag atctggccgt gtactattgc caccagtacc tgtccagcct gacctttggc      780

gccggaacaa agctggaact gaagacaaca acccctgccc ccagacctcc taccccagcc      840

cctacaattg ccagccagcc tctgagcctg aggcccgagg cttgtagacc tgctgctggc      900

ggagccgtgc acaccagagg actggatttc gcctgcgaca tctacatctg ggcgcccttg      960

gccgggactt gtggggtcct tctcctgtca ctggttatca ccctttactg caggagtaag     1020

aggagcaggc tcctgcacag tgactacatg aacatgactc ctagaagacc tgggcctacc     1080

agaaagcatt accagcccta tgccccacca cgcgacttcg cagcctatcg ctccagagtg     1140

aagttcagca ggagcgcaga cgcccccgcg tacaagcagg gccagaacca gctctataac     1200

gagctcaatc taggacgaag agaggagtac gatgttttgg acaagagacg tggccgggac     1260

cctgagatgg ggggaaagcc gagaaggaag aaccctcagg aaggcctgtt caatgaactg     1320

cagaaagata agatggcgga ggccttcagt gagattggga tgaaaggcga gcgccggagg     1380

ggcaaggggc acgatggcct ttttccagggt ctcagtacag ccaccaagga caccttcgac     1440

gcccttcaca tgcaggccct gccccctcgc tgataa                               1476
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<210> 1595
<211> 490
<212> PRT
<213> Artificial Sequence

<220>
<223> mu20A10CAR T8283z1XX

<400> 1595

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Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15
```

```
His Ala Ala Arg Pro Glu Val Met Leu Val Glu Ser Gly Gly Gly Leu
            20                  25                  30

Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
        35                  40                  45

Thr Phe Ser Thr Tyr Ala Met Ser Trp Ile Arg Gln Thr Pro Glu Lys
    50                  55                  60

Arg Leu Glu Trp Val Ala Ser Ile Gly Arg Ala Gly Ser Thr Tyr Tyr
65                  70                  75                  80

Ser Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Val Arg
                85                  90                  95

Asn Ile Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala
            100                 105                 110

Met Tyr Tyr Cys Ala Arg Gly Pro Ile Tyr Asn Asp Tyr Asp Glu Phe
        115                 120                 125

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly
    130                 135                 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn Ile Met Met
145                 150                 155                 160

Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly Glu Lys Val Thr
                165                 170                 175

Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys
            180                 185                 190

Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu
        195                 200                 205

Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe
    210                 215                 220

Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val
225                 230                 235                 240

Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys His Gln Tyr Leu Ser Ser
                245                 250                 255

Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Thr Thr Thr Pro
            260                 265                 270

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
        275                 280                 285

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
```

290 295 300

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
305 310 315 320

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
325 330 335

Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
340 345 350

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
355 360 365

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg
370 375 380

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
385 390 395 400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
405 410 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
420 425 430

Gln Glu Gly Leu Phe Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
435 440 445

Phe Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
450 455 460

Asp Gly Leu Phe Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Phe Asp
465 470 475 480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 1596
<211> 1479
<212> DNA
<213> Artificial Sequence

<220>
<223> hu20A10CAR T8283z1XX

<400> 1596
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ccggaggtgc agctggttga atctggcggc ggacttgtga agcctggcgg atctctgaga 120

ctgagctgtg ccgccagcgg cttcaccttt agcacatacg ccatgagctg ggtccgacag 180

gcccctggaa aaggccttga atgggttgcc tctatcggca gagccggcag cacctactac 240

agcgattctg tgaagggcag attcaccatc agccgggaca acgccaagaa cagcctgtac 300 ctgcagatga actccctgag agccgaggac accgccgtgt actattgtgc cagaggaccc 360

atctacaacg actacgacga gttcgcctat tggggccagg gcacactggt cacagtcagc 420

tctggcggtg gcggaagcgg aggcggtggc tccggtggcg gaggcagcga cattgtgctg 480

acccagtctc cagcctcctt ggccgtgtct ccaggacaga gggccaccat cacctgcaag 540

agcagccaga gcgtgctgta ctccagcaac cagaagaact acctggcctg gtatcagcag 600

aaaccaggac aacctcctaa actcctgatt tactgggcca gcaccagaga aagcggggtc 660

ccagccaggt tcagcggcag tgggtctggg accgatttca ccctcacaat taatcctgtg 720

gaagctaatg atactgcaaa ttattactgt caccagtacc tgagcagcct gaccttcggc 780

ggagggacca aggtggagat caaacgaaca acaacccctg cccccagacc tcctacccca 840

gcccctacaa ttgccagcca gcctctgagc ctgaggcccg aggcttgtag acctgctgct 900

ggcggagccg tgcacaccag aggactggat ttcgcctgcg acatctacat ctgggcgccc 960

ttggccggga cttgtggggt ccttctcctg tcactggtta tcaccctttа ctgcaggagt 1020

aagaggagca ggctcctgca cagtgactac atgaacatga ctcctagaag acctgggcct 1080

accagaaagc attaccagcc ctatgcccca ccacgcgact tcgcagccta tcgctccaga 1140

gtgaagttca gcaggagcgc agacgccccc gcgtacaagc agggccagaa ccagctctat 1200

aacgagctca atctaggacg aagagaggag tacgatgttt tggacaagag acgtggccgg 1260

gaccctgaga tgggggggaaa gccgagaagg aagaaccctc aggaaggcct gttcaatgaa 1320

ctgcagaaag ataagatggc ggaggccttc agtgagattg ggatgaaagg cgagcgccgg 1380

aggggcaagg ggcacgatgg cctttttccag ggtctcagta cagccaccaa ggacaccttc 1440

gacgcccttc acatgcaggc cctgcccccct cgctgataa 1479

<210> 1597
<211> 491
<212> PRT
<213> Artificial Sequence

<220>
<223> hu20A10CAR T8283z1XX

<400> 1597

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Ser Thr Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ala Ser Ile Gly Arg Ala Gly Ser Thr Tyr Tyr

```
65                  70                  75                  80


Ser Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
                85                  90                  95


Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
            100                 105                 110


Val Tyr Tyr Cys Ala Arg Gly Pro Ile Tyr Asn Asp Tyr Asp Glu Phe
        115                 120                 125


Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
    130                 135                 140


Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu
145                 150                 155                 160


Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Pro Gly Gln Arg Ala Thr
                165                 170                 175


Ile Thr Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys
            180                 185                 190


Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu
        195                 200                 205


Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Ala Arg Phe
    210                 215                 220


Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Pro Val
225                 230                 235                 240


Glu Ala Asn Asp Thr Ala Asn Tyr Tyr Cys His Gln Tyr Leu Ser Ser
                245                 250                 255


Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Thr Thr
            260                 265                 270


Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
        275                 280                 285


Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
    290                 295                 300


His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
305                 310                 315                 320


Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
                325                 330                 335


Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn
            340                 345                 350
```

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Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr
        355                 360                 365


Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser
    370                 375                 380


Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr
385                 390                 395                 400


Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
                405                 410                 415


Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
            420                 425                 430


Pro Gln Glu Gly Leu Phe Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
        435                 440                 445


Ala Phe Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
    450                 455                 460


His Asp Gly Leu Phe Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Phe
465                 470                 475                 480


Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485                 490


<210>  1598
<211>  738
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  mu25E6 scFv full sequence

<400>  1598
gaggtgcagc tggtggagtc tgggggagac ttagtgaagc ctggagggtc cctgaaactc       60

tcctgtgcag cctctggttt cactttcagt agttatggaa tgtcttgggt tcgccagact      120

ccagacaaga ggctggagtg ggtcgcaacc attagtaatg gtggtagaca caccttctat      180

ccagacagtg tgaaggggcg attcaccatc tccagagaca atgccaagaa caccctgtat      240

ctgcaaatga gcagtctgaa gtctgaggac acagccatgt atttatgtgt aagacagact      300

gggacggagg gctggtttgc ttactggggc caagggactc tggtcactgt ctctgcaggt      360

ggcggaggat ctggcggagg tggaagcggc ggaggcggat ccgatgttgt gatgacccag      420

actccactca ctttgtcggt taccattgga caaccagcct ccatctcttg caagtcaagt      480

cagagcctct tagatagtga tggaaagaca tatttgaatt ggttgttaca gaggccaggc      540

cagtctccaa agcgcctaat ctatctggtg tctaaactgg actctggagt ccctgacagg      600

ttcactggca gtggatcagg gacagatttc acactgaaaa tcagcagagt ggaggctgag      660
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gatttgggag tttattattg ctggcaaggt acacattttc ctcagacgtt cggtggaggc   720

accaagctgg aaatcaaa   738

<210> 1599
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> mu25E6 scFv full sequence

<400> 1599

Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly
1   5   10   15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30

Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Trp Val
        35   40   45

Ala Thr Ile Ser Asn Gly Gly Arg His Thr Phe Tyr Pro Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Leu Cys
                85   90   95

Val Arg Gln Thr Gly Thr Glu Gly Trp Phe Ala Tyr Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115   120   125

Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Thr
    130   135   140

Leu Ser Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser
145   150   155   160

Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu
                165   170   175

Gln Arg Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys
            180   185   190

Leu Asp Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr
        195   200   205

Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val
    210   215   220

Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gln Thr Phe Gly Gly Gly
225   230   235   240

Thr Lys Leu Glu Ile Lys
                245

<210> 1600
<211> 738
<212> DNA
<213> Artificial Sequence

<220>
<223> hu25E6 full sequence

<400> 1600
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agctgcgccg ccagcggctt cacattcagc agctacggca tgagctgggt gcggcaggcc   120

cctggcaagg gcctggaatg ggtcagcacc atcagcaacg gcggaagaca caccttctac   180

cccgacagcg tgaagggcag attcaccatc tcaagagata acgccaagaa cagcctgtac   240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc cagacagacc   300

ggcacagagg gctggttcgc ctactggggc cagggcaccc tggtgaccgt gtccagcggc   360

ggtggcggaa gcggaggcgg tggctccggt ggcggaggca gcgacatcgt gatgacccag   420

acccctctgt ctctgagcgt gacccctggc cagcctgcca gcatctcttg taaaagcagc   480

cagagcctgc tggacagcga cggcaagacc tacctgaact ggtacctgca gaagcccggc   540

caaagccctc agctgctgat ctacctggtg tccaagctgg atagcggtgt tcctgataga   600

ttcagcggat ctggcagcgg caccgacttc accctgaaga tcagcagagt ggaagccgag   660

gacgtgggcg tgtactactg ctggcagggc acacacttcc cccagacatt cggccagggc   720

accaaggtgg aaatcaag   738

<210> 1601
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> hu25E6 full sequence

<400> 1601

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Thr Ile Ser Asn Gly Gly Arg His Thr Phe Tyr Pro Asp Ser Val

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    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gln Thr Gly Thr Glu Gly Trp Phe Ala Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Thr Pro Leu Ser
    130                 135                 140

Leu Ser Val Thr Pro Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser
145                 150                 155                 160

Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Tyr Leu
                165                 170                 175

Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Val Ser Lys
            180                 185                 190

Leu Asp Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val
    210                 215                 220

Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gln Thr Phe Gly Gln Gly
225                 230                 235                 240

Thr Lys Val Glu Ile Lys
                245


<210>  1602
<211>  1476
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  mu25E6CAR T841BB3z

<400>  1602
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ccggaggtgc agctggtgga gtctgggggа gacttagtga agcctggagg gtccctgaaa      120

ctctcctgtg cagcctctgg tttcactttc agtagttatg gaatgtcttg ggttcgccag      180

actccagaca agaggctgga gtgggtcgca accattagta atggtggtag acacaccttc      240

tatccagaca gtgtgaaggg gcgattcacc atctccagag acaatgccaa gaacaccctg      300
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tatctgcaaa tgagcagtct gaagtctgag gacacagcca tgtatttatg tgtaagacag 360

actgggacgg agggctggtt tgcttactgg ggccaaggga ctctggtcac tgtctctgca 420

ggtggcggag gatctggcgg aggtggaagc ggcggaggcg gatccgatgt tgtgatgacc 480

cagactccac tcactttgtc ggttaccatt ggacaaccag cctccatctc ttgcaagtca 540

agtcagagcc tcttagatag tgatggaaag acatatttga attggttgtt acagaggcca 600

ggccagtctc caaagcgcct aatctatctg gtgtctaaac tggactctgg agtccctgac 660

aggttcactg gcagtggatc agggacagat ttcacactga aaatcagcag agtggaggct 720

gaggatttgg gagtttatta ttgctggcaa ggtacacatt ttcctcagac gttcggtgga 780

ggcaccaagc tggaaatcaa aacaacaacc cctgccccca gacctcctac cccagcccct 840

acaattgcca gccagcctct gagcctgagg cccgaggctt gtagacctgc tgctggcgga 900

gccgtgcaca ccagaggact ggatttcgcc tgcgacatct acatctgggc gcccttggcc 960

gggacttgtg gggtccttct cctgtcactg gttatcaccc tttactgcaa acggggcaga 1020

aagaaactcc tgtatatatt caaacaacca tttatgagac cagtacaaac tactcaagag 1080

gaagatggct gtagctgccg atttccagaa gaagaagaag gaggatgtga actgagagtg 1140

aagttcagca ggagcgcaga cgcccccgcg tacaagcagg gccagaacca gctctataac 1200

gagctcaatc taggacgaag agaggagtac gatgttttgg acaagagacg tggccgggac 1260

cctgagatgg ggggaaagcc gagaaggaag aaccctcagg aaggcctgta caatgaactg 1320

cagaaagata agatggcgga ggcctacagt gagattggga tgaaaggcga gcgccggagg 1380

ggcaaggggc acgatggcct ttaccagggt ctcagtacag ccaccaagga cacctacgac 1440

gcccttcaca tgcaggccct gccccctcgc tgataa 1476

<210> 1603
<211> 490
<212> PRT
<213> Artificial Sequence

<220>
<223> mu25E6CAR T841BB3z

<400> 1603

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1   5   10   15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu
            20   25   30

Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
        35   40   45

Thr Phe Ser Ser Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys
    50   55   60

Arg Leu Glu Trp Val Ala Thr Ile Ser Asn Gly Gly Arg His Thr Phe

65   70   75   80

Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
                85   90   95

Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr
            100   105   110

Ala Met Tyr Leu Cys Val Arg Gln Thr Gly Thr Glu Gly Trp Phe Ala
        115   120   125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly
    130   135   140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr
145   150   155   160

Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly Gln Pro Ala Ser Ile
                165   170   175

Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr
            180   185   190

Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser Pro Lys Arg Leu Ile
        195   200   205

Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro Asp Arg Phe Thr Gly
    210   215   220

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
225   230   235   240

Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gln
                245   250   255

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala
            260   265   270

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
        275   280   285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
    290   295   300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305   310   315   320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
                325   330   335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
            340   345   350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
        355   360   365

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
    370   375   380

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
385   390   395   400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
                405   410   415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
            420   425   430

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
        435   440   445

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
    450   455   460

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
465   470   475   480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485   490

<210> 1604
<211> 1476
<212> DNA
<213> Artificial Sequence

<220>
<223> hu25E6CAR T841BB3z

<400> 1604
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ccggaggtgc agctggtgga atctggcgga ggactggtca agcctggagg cagcctgaga 120

ctgagctgcg ccgccagcgg cttcacattc agcagctacg gcatgagctg ggtgcggcag 180

gcccctggca agggcctgga atgggtcagc accatcagca acggcggaag acacaccttc 240

taccccgaca gcgtgaaggg cagattcacc atctcaagag ataacgccaa gaacagcctg 300

tacctgcaga tgaacagcct gcgggccgag gacaccgccg tgtactactg cgccagacag 360

accggcacag agggctggtt cgcctactgg ggccagggca ccctggtgac cgtgtccagc 420

ggcggtggcg gaagcggagg cggtggctcc ggtggcggag gcagcgacat cgtgatgacc 480

cagacccctc tgtctctgag cgtgacccct ggccagcctg ccagcatctc ttgtaaaagc 540

agccagagcc tgctggacag cgacggcaag acctacctga actggtacct gcagaagccc 600

ggccaaagcc ctcagctgct gatctacctg gtgtccaagc tggatagcgg tgttcctgat 660 agattcagcg gatctggcag cggcaccgac ttcaccctga agatcagcag agtggaagcc 720

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acaattgcca gccagcctct gagcctgagg cccgaggctt gtagacctgc tgctggcgga 900

gccgtgcaca ccagaggact ggatttcgcc tgcgacatct acatctgggc gcccttggcc 960

gggacttgtg gggtccttct cctgtcactg gttatcaccc tttactgcaa acggggcaga 1020

aagaaactcc tgtatatatt caaacaacca tttatgagac cagtacaaac tactcaagag 1080

gaagatggct gtagctgccg atttccagaa gaagaagaag gaggatgtga actgagagtg 1140

aagttcagca ggagcgcaga cgcccccgcg tacaagcagg gccagaacca gctctataac 1200

gagctcaatc taggacgaag agaggagtac gatgttttgg acaagagacg tggccgggac 1260

cctgagatgg ggggaaagcc gagaaggaag aaccctcagg aaggcctgta caatgaactg 1320

cagaaagata agatggcgga ggcctacagt gagattggga tgaaaggcga gcgccggagg 1380

ggcaaggggc acgatggcct ttaccagggt ctcagtacag ccaccaagga cacctacgac 1440

gcccttcaca tgcaggccct gccccctcgc tgataa 1476

<210> 1605
<211> 490
<212> PRT
<213> Artificial Sequence

<220>
<223> hu25E6CAR T841BB3z

<400> 1605

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Ser Ser Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ser Thr Ile Ser Asn Gly Gly Arg His Thr Phe
65 70 75 80

Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Arg Gln Thr Gly Thr Glu Gly Trp Phe Ala
115 120 125

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Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr
145                 150                 155                 160

Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly Gln Pro Ala Ser Ile
                165                 170                 175

Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr
            180                 185                 190

Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
        195                 200                 205

Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro Asp Arg Phe Ser Gly
    210                 215                 220

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
225                 230                 235                 240

Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gln
                245                 250                 255

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala
            260                 265                 270

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
        275                 280                 285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
    290                 295                 300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305                 310                 315                 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
                325                 330                 335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
            340                 345                 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
        355                 360                 365

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
    370                 375                 380

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
385                 390                 395                 400
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Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
                405                 410                 415


Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
            420                 425                 430


Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
        435                 440                 445


Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
    450                 455                 460


Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
465                 470                 475                 480


Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485                 490


<210>  1606
<211>  1473
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  mu25E6CAR T8283z

<400>  1606
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ctctcctgtg cagcctctgg tttcactttc agtagttatg gaatgtcttg ggttcgccag      180

actccagaca agaggctgga gtgggtcgca accattagta atggtggtag acacaccttc      240

tatccagaca gtgtgaaggg gcgattcacc atctccagag acaatgccaa gaacaccctg      300

tatctgcaaa tgagcagtct gaagtctgag gacacagcca tgtatttatg tgtaagacag      360

actgggacgg agggctggtt tgcttactgg ggccaaggga ctctggtcac tgtctctgca      420

ggtggcggag gatctggcgg aggtggaagc ggcggaggcg gatccgatgt tgtgatgacc      480

cagactccac tcactttgtc ggttaccatt ggacaaccag cctccatctc ttgcaagtca      540

agtcagagcc tcttagatag tgatggaaag acatatttga attggttgtt acagaggcca      600

ggccagtctc caaagcgcct aatctatctg gtgtctaaac tggactctgg agtccctgac      660

aggttcactg gcagtggatc agggacagat ttcacactga aaatcagcag agtggaggct      720

gaggatttgg gagtttatta ttgctggcaa ggtacacatt ttcctcagac gttcggtgga      780

ggcaccaagc tggaaatcaa aacaacaacc cctgccccca gacctcctac cccagcccct      840

acaattgcca gccagcctct gagcctgagg cccgaggctt gtagacctgc tgctggcgga      900

gccgtgcaca ccagaggact ggatttcgcc tgcgacatct acatctgggc gcccttggcc      960

gggacttgtg gggtccttct cctgtcactg gttatcaccc tttactgcag gagtaagagg     1020

agcaggctcc tgcacagtga ctacatgaac atgactccta gaagacctgg gcctaccaga     1080
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aagcattacc agccctatgc cccaccacgc gacttcgcag cctatcgctc cagagtgaag 1140

ttcagcagga gcgcagacgc ccccgcgtac aagcagggcc agaaccagct ctataacgag 1200

ctcaatctag gacgaagaga ggagtacgat gttttggaca agagacgtgg ccgggaccct 1260

gagatggggg gaaagccgag aaggaagaac cctcaggaag gcctgtacaa tgaactgcag 1320

aaagataaga tggcggaggc ctacagtgag attgggatga aaggcgagcg ccggaggggc 1380

aaggggcacg atggccttta ccagggtctc agtacagcca ccaaggacac ctacgacgcc 1440

cttcacatgc aggccctgcc ccctcgctga taa 1473

<210> 1607
<211> 489
<212> PRT
<213> Artificial Sequence

<220>
<223> mu25E6CAR T8283z

<400> 1607

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Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15


His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu
            20                  25                  30


Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
        35                  40                  45


Thr Phe Ser Ser Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys
    50                  55                  60


Arg Leu Glu Trp Val Ala Thr Ile Ser Asn Gly Gly Arg His Thr Phe
65                  70                  75                  80


Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
                85                  90                  95


Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr
            100                 105                 110


Ala Met Tyr Leu Cys Val Arg Gln Thr Gly Thr Glu Gly Trp Phe Ala
        115                 120                 125


Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly
    130                 135                 140


Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr
145                 150                 155                 160


Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly Gln Pro Ala Ser Ile
                165                 170                 175
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Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr
            180                 185                 190

Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser Pro Lys Arg Leu Ile
        195                 200                 205

Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro Asp Arg Phe Thr Gly
    210                 215                 220

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
225                 230                 235                 240

Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gln
                245                 250                 255

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala
            260                 265                 270

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
        275                 280                 285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
    290                 295                 300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305                 310                 315                 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
                325                 330                 335

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
            340                 345                 350

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
        355                 360                 365

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
    370                 375                 380

Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu
385                 390                 395                 400

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
                405                 410                 415

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
            420                 425                 430

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
        435                 440                 445
```

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
450 455 460

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
465 470 475 480

Leu His Met Gln Ala Leu Pro Pro Arg
485

<210> 1608
<211> 1473
<212> DNA
<213> Artificial Sequence

<220>
<223> hu25E6CAR T8283z

<400> 1608
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ccggaggtgc agctggtgga atctggcgga ggactggtca agcctggagg cagcctgaga 120

ctgagctgcg ccgccagcgg cttcacattc agcagctacg gcatgagctg ggtgcggcag 180

gcccctggca agggcctgga atgggtcagc accatcagca acggcggaag acacaccttc 240

taccccgaca gcgtgaaggg cagattcacc atctcaagag ataacgccaa gaacagcctg 300

tacctgcaga tgaacagcct gcgggccgag gacaccgccg tgtactactg cgccagacag 360

accggcacag agggctggtt cgcctactgg ggccagggca ccctggtgac cgtgtccagc 420

ggcggtggcg gaagcggagg cggtggctcc ggtggcggag gcagcgacat cgtgatgacc 480

cagacccctc tgtctctgag cgtgacccct ggccagcctg ccagcatctc ttgtaaaagc 540

agccagagcc tgctggacag cgacggcaag acctacctga actggtacct gcagaagccc 600

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agattcagcg gatctggcag cggcaccgac ttcaccctga agatcagcag agtggaagcc 720

gaggacgtgg gcgtgtacta ctgctggcag ggcacacact tcccccagac attcggccag 780

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aagcattacc agccctatgc cccaccacgc gacttcgcag cctatcgctc cagagtgaag 1140

ttcagcagga gcgcagacgc ccccgcgtac aagcagggcc agaaccagct ctataacgag 1200

ctcaatctag gacgaagaga ggagtacgat gttttggaca agagacgtgg ccgggaccct 1260

gagatggggg gaaagccgag aaggaagaac cctcaggaag gcctgtacaa tgaactgcag 1320

aaagataaga tggcggaggc ctacagtgag attgggatga aaggcgagcg ccggaggggc 1380

aaggggcacg atggccttta ccagggtctc agtacagcca ccaaggacac ctacgacgcc 1440

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<210>  1609
<211>  489
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  hu25E6CAR T8283z

<400>  1609

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15


His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
            20                  25                  30


Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
        35                  40                  45


Thr Phe Ser Ser Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys
    50                  55                  60


Gly Leu Glu Trp Val Ser Thr Ile Ser Asn Gly Gly Arg His Thr Phe
65                  70                  75                  80


Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
                85                  90                  95


Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
            100                 105                 110


Ala Val Tyr Tyr Cys Ala Arg Gln Thr Gly Thr Glu Gly Trp Phe Ala
        115                 120                 125


Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140


Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr
145                 150                 155                 160


Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly Gln Pro Ala Ser Ile
                165                 170                 175


Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr
            180                 185                 190


Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
        195                 200                 205


Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro Asp Arg Phe Ser Gly
    210                 215                 220
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Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
225   230   235   240

Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gln
                245   250   255

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala
            260   265   270

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
        275   280   285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
    290   295   300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305   310   315   320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
                325   330   335

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
            340   345   350

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
        355   360   365

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
    370   375   380

Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu
385   390   395   400

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
                405   410   415

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
            420   425   430

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
        435   440   445

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
    450   455   460

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
465   470   475   480

Leu His Met Gln Ala Leu Pro Pro Arg
                485

<210> 1610

<211> 1476
<212> DNA
<213> Artificial Sequence

<220>
<223> mu25E6CAR T841BB3z1XX

<400> 1610
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actccagaca agaggctgga gtgggtcgca accattagta atggtggtag acacaccttc   240

tatccagaca gtgtgaaggg gcgattcacc atctccagag acaatgccaa gaacaccctg   300

tatctgcaaa tgagcagtct gaagtctgag gacacagcca tgtatttatg tgtaagacag   360

actgggacgg agggctggtt tgcttactgg ggccaaggga ctctggtcac tgtctctgca   420

ggtggcggag gatctggcgg aggtggaagc ggcggaggcg gatccgatgt tgtgatgacc   480

cagactccac tcactttgtc ggttaccatt ggacaaccag cctccatctc ttgcaagtca   540

agtcagagcc tcttagatag tgatggaaag acatatttga attggttgtt acagaggcca   600

ggccagtctc caaagcgcct aatctatctg gtgtctaaac tggactctgg agtccctgac   660

aggttcactg gcagtggatc agggacagat ttcacactga aaatcagcag agtggaggct   720

gaggatttgg gagtttatta ttgctggcaa ggtacacatt ttcctcagac gttcggtgga   780

ggcaccaagc tggaaatcaa aacaacaacc cctgccccca gacctcctac cccagcccct   840

acaattgcca gccagcctct gagcctgagg cccgaggctt gtagacctgc tgctggcgga   900

gccgtgcaca ccagaggact ggatttcgcc tgcgacatct acatctgggc gcccttggcc   960

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aagaaactcc tgtatatatt caaacaacca tttatgagac cagtacaaac tactcaagag   1080

gaagatggct gtagctgccg atttccagaa gaagaagaag gaggatgtga actgagagtg   1140

aagttcagca ggagcgcaga cgcccccgcg tacaagcagg gccagaacca gctctataac   1200

gagctcaatc taggacgaag agaggagtac gatgttttgg acaagagacg tggccgggac   1260

cctgagatgg ggggaaagcc gagaaggaag aaccctcagg aaggcctgtt caatgaactg   1320

cagaaagata agatggcgga ggccttcagt gagattggga tgaaaggcga gcgccggagg   1380

ggcaaggggc acgatggcct ttttccagggt ctcagtacag ccaccaagga caccttcgac   1440

gcccttcaca tgcaggccct gccccctcgc tgataa   1476

<210> 1611
<211> 490
<212> PRT
<213> Artificial Sequence

<220>
<223> mu25E6CAR T841BB3z1XX

<400> 1611

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Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu
            20                  25                  30

Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
        35                  40                  45

Thr Phe Ser Ser Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys
    50                  55                  60

Arg Leu Glu Trp Val Ala Thr Ile Ser Asn Gly Gly Arg His Thr Phe
65                  70                  75                  80

Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
                85                  90                  95

Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr
            100                 105                 110

Ala Met Tyr Leu Cys Val Arg Gln Thr Gly Thr Glu Gly Trp Phe Ala
        115                 120                 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr
145                 150                 155                 160

Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly Gln Pro Ala Ser Ile
                165                 170                 175

Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr
            180                 185                 190

Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser Pro Lys Arg Leu Ile
        195                 200                 205

Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro Asp Arg Phe Thr Gly
    210                 215                 220

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
225                 230                 235                 240

Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gln
                245                 250                 255

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala
            260                 265                 270

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
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        275                 280                 285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
    290                 295                 300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305                 310                 315                 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
                325                 330                 335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
            340                 345                 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
        355                 360                 365

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
    370                 375                 380

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
385                 390                 395                 400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
                405                 410                 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
            420                 425                 430

Gln Glu Gly Leu Phe Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
        435                 440                 445

Phe Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
    450                 455                 460

Asp Gly Leu Phe Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Phe Asp
465                 470                 475                 480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485                 490


<210>  1612
<211>  1476
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  hu25E6CAR T841BB3z1XX

<400>  1612
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ctgagctgcg ccgccagcgg cttcacattc agcagctacg gcatgagctg ggtgcggcag      180
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taccccgaca gcgtgaaggg cagattcacc atctcaagag ataacgccaa gaacagcctg 300

tacctgcaga tgaacagcct gcgggccgag gacaccgccg tgtactactg cgccagacag 360

accggcacag agggctggtt cgcctactgg ggccagggca ccctggtgac cgtgtccagc 420

ggcggtggcg gaagcggagg cggtggctcc ggtggcggag gcagcgacat cgtgatgacc 480

cagacccctc tgtctctgag cgtgacccct ggccagcctg ccagcatctc ttgtaaaagc 540

agccagagcc tgctggacag cgacggcaag acctacctga actggtacct gcagaagccc 600

ggccaaagcc ctcagctgct gatctacctg gtgtccaagc tggatagcgg tgttcctgat 660

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gaggacgtgg gcgtgtacta ctgctggcag ggcacacact tcccccagac attcggccag 780

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gagctcaatc taggacgaag agaggagtac gatgttttgg acaagagacg tggccgggac 1260

cctgagatgg ggggaaagcc gagaaggaag aaccctcagg aaggcctgtt caatgaactg 1320

cagaaagata agatggcgga ggccttcagt gagattggga tgaaaggcga gcgccggagg 1380

ggcaaggggc acgatggcct ttttcagggt ctcagtacag ccaccaagga caccttcgac 1440

gcccttcaca tgcaggccct gccccctcgc tgataa 1476

<210> 1613
<211> 490
<212> PRT
<213> Artificial Sequence

<220>
<223> hu25E6CAR T841BB3z1XX

<400> 1613

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
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His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Ser Ser Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys

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    50                  55                  60

Gly Leu Glu Trp Val Ser Thr Ile Ser Asn Gly Gly Arg His Thr Phe
65                  70                  75                  80

Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
                85                  90                  95

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
            100                 105                 110

Ala Val Tyr Tyr Cys Ala Arg Gln Thr Gly Thr Glu Gly Trp Phe Ala
        115                 120                 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr
145                 150                 155                 160

Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly Gln Pro Ala Ser Ile
                165                 170                 175

Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr
            180                 185                 190

Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
        195                 200                 205

Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro Asp Arg Phe Ser Gly
    210                 215                 220

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
225                 230                 235                 240

Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gln
                245                 250                 255

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala
            260                 265                 270

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
        275                 280                 285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
    290                 295                 300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305                 310                 315                 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
                325                 330                 335
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Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
340 345 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
355 360 365

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
370 375 380

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
385 390 395 400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
405 410 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
420 425 430

Gln Glu Gly Leu Phe Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
435 440 445

Phe Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
450 455 460

Asp Gly Leu Phe Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Phe Asp
465 470 475 480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 1614
<211> 1473
<212> DNA
<213> Artificial Sequence

<220>
<223> mu25E6CAR T8283z1XX

<400> 1614
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actccagaca agaggctgga gtgggtcgca accattagta atggtggtag acacaccttc 240

tatccagaca gtgtgaaggg gcgattcacc atctccagag acaatgccaa gaacaccctg 300

tatctgcaaa tgagcagtct gaagtctgag gacacagcca tgtatttatg tgtaagacag 360

actgggacgg agggctggtt tgcttactgg ggccaaggga ctctggtcac tgtctctgca 420

ggtggcggag gatctggcgg aggtggaagc ggcggaggcg gatccgatgt tgtgatgacc 480

cagactccac tcactttgtc ggttaccatt ggacaaccag cctccatctc ttgcaagtca 540 agtcagagcc tcttagatag tgatggaaag acatatttga attggttgtt acagaggcca   600

ggccagtctc caaagcgcct aatctatctg gtgtctaaac tggactctgg agtccctgac   660

aggttcactg gcagtggatc agggacagat ttcacactga aaatcagcag agtggaggct   720

gaggatttgg gagtttatta ttgctggcaa ggtacacatt ttcctcagac gttcggtgga   780

ggcaccaagc tggaaatcaa aacaacaacc cctgccccca gacctcctac cccagcccct   840

acaattgcca gccagcctct gagcctgagg cccgaggctt gtagacctgc tgctggcgga   900

gccgtgcaca ccagaggact ggatttcgcc tgcgacatct acatctgggc gcccttggcc   960

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agcaggctcc tgcacagtga ctacatgaac atgactccta gaagacctgg gcctaccaga   1080

aagcattacc agccctatgc cccaccacgc gacttcgcag cctatcgctc cagagtgaag   1140

ttcagcagga gcgcagacgc ccccgcgtac aagcagggcc agaaccagct ctataacgag   1200

ctcaatctag gacgaagaga ggagtacgat gttttggaca agagacgtgg ccgggaccct   1260

gagatggggg gaaagccgag aaggaagaac cctcaggaag gcctgttcaa tgaactgcag   1320

aaagataaga tggcggaggc cttcagtgag attgggatga aaggcgagcg ccggaggggc   1380

aaggggcacg atggcctttt ccagggtctc agtacagcca ccaaggacac cttcgacgcc   1440

cttcacatgc aggccctgcc ccctcgctga taa   1473

<210> 1615
<211> 489
<212> PRT
<213> Artificial Sequence

<220>
<223> mu25E6CAR T8283z1XX

<400> 1615

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1   5   10   15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu
            20   25   30

Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
        35   40   45

Thr Phe Ser Ser Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys
    50   55   60

Arg Leu Glu Trp Val Ala Thr Ile Ser Asn Gly Gly Arg His Thr Phe
65   70   75   80

Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
                85   90   95

Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr
            100   105   110

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Ala Met Tyr Leu Cys Val Arg Gln Thr Gly Thr Glu Gly Trp Phe Ala
        115                 120                 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr
145                 150                 155                 160

Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly Gln Pro Ala Ser Ile
                165                 170                 175

Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr
            180                 185                 190

Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser Pro Lys Arg Leu Ile
        195                 200                 205

Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro Asp Arg Phe Thr Gly
    210                 215                 220

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
225                 230                 235                 240

Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gln
                245                 250                 255

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala
            260                 265                 270

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
        275                 280                 285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
    290                 295                 300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305                 310                 315                 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
                325                 330                 335

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
            340                 345                 350

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
        355                 360                 365

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
    370                 375                 380
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Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu
385                 390                 395                 400


Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
                405                 410                 415


Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
            420                 425                 430


Glu Gly Leu Phe Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Phe
        435                 440                 445


Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
    450                 455                 460


Gly Leu Phe Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Phe Asp Ala
465                 470                 475                 480


Leu His Met Gln Ala Leu Pro Pro Arg
                485


<210>  1616
<211>  1473
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  hu25E6CAR T8283z1XX

<400>  1616
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gcccctggca agggcctgga atgggtcagc accatcagca acggcggaag acacaccttc      240

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tacctgcaga tgaacagcct gcgggccgag gacaccgccg tgtactactg cgccagacag      360

accggcacag agggctggtt cgcctactgg ggccagggca ccctggtgac cgtgtccagc      420

ggcggtggcg gaagcggagg cggtggctcc ggtggcggag gcagcgacat cgtgatgacc      480

cagacccctc tgtctctgag cgtgacccct ggccagcctg ccagcatctc ttgtaaaagc      540

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ggccaaagcc ctcagctgct gatctacctg gtgtccaagc tggatagcgg tgttcctgat      660

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gccgtgcaca ccagaggact ggatttcgcc tgcgacatct acatctgggc gcccttggcc      960
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gggacttgtg gggtccttct cctgtcactg gttatcaccc tttactgcag gagtaagagg   1020

agcaggctcc tgcacagtga ctacatgaac atgactccta gaagacctgg gcctaccaga   1080

aagcattacc agccctatgc cccaccacgc gacttcgcag cctatcgctc cagagtgaag   1140

ttcagcagga gcgcagacgc cccgcgtac aagcagggcc agaaccagct ctataacgag   1200

ctcaatctag gacgaagaga ggagtacgat gttttggaca agagacgtgg ccgggaccct   1260

gagatggggg gaaagccgag aaggaagaac cctcaggaag gcctgttcaa tgaactgcag   1320

aaagataaga tggcggaggc cttcagtgag attgggatga aaggcgagcg ccggaggggc   1380

aaggggcacg atggcctttt ccagggtctc agtacagcca ccaaggacac cttcgacgcc   1440

cttcacatgc aggccctgcc ccctcgctga taa   1473

<210> 1617
<211> 489
<212> PRT
<213> Artificial Sequence

<220>
<223> hu25E6CAR T8283z1XX

<400> 1617

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1   5   10   15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
            20   25   30

Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
        35   40   45

Thr Phe Ser Ser Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys
    50   55   60

Gly Leu Glu Trp Val Ser Thr Ile Ser Asn Gly Gly Arg His Thr Phe
65   70   75   80

Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
                85   90   95

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
            100   105   110

Ala Val Tyr Tyr Cys Ala Arg Gln Thr Gly Thr Glu Gly Trp Phe Ala
        115   120   125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    130   135   140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr
145   150   155   160

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Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly Gln Pro Ala Ser Ile
                165                 170                 175

Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr
            180                 185                 190

Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
        195                 200                 205

Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro Asp Arg Phe Ser Gly
    210                 215                 220

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
225                 230                 235                 240

Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gln
                245                 250                 255

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala
            260                 265                 270

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
        275                 280                 285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
    290                 295                 300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305                 310                 315                 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
                325                 330                 335

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
            340                 345                 350

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
        355                 360                 365

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
    370                 375                 380

Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu
385                 390                 395                 400

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
                405                 410                 415

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
            420                 425                 430
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Glu Gly Leu Phe Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Phe
        435                 440                 445


Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
    450                 455                 460


Gly Leu Phe Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Phe Asp Ala
465                 470                 475                 480


Leu His Met Gln Ala Leu Pro Pro Arg
                485


<210>  1618
<211>  1533
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  MNC21XX - muMNC2CAR T841BB3z1XX

<400>  1618
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ccggaggtcc agctggagga gtcaggggga ggcttagtga agcctggagg gtccctgaaa      120

ctctcctgtg cagcctctgg attcactttc agtggctatg ccatgtcttg ggttcgccag      180

actccggaga agaggctgga gtgggtcgca accattagta gtggtggtac ttatatctac      240

tatccagaca gtgtgaaggg gcgattcacc atctccagag acaatgccaa gaacaccctg      300

tacctgcaaa tgagcagtct gaggtctgag gacacggcca tgtattactg tgcaagactt      360

ggggggggata attactacga atacttcgat gtctggggcg cagggaccac ggtcaccgtc      420

tcctccgcca aaacgacacc cccatctgtc tatggcggtg gcggatccgg cggtggcgga      480

tccggcggtg gcggatccga cattgtgatc acacagtcta cagcttcctt aggtgtatct      540

ctggggcaga gggccaccat ctcatgcagg gccagcaaaa gtgtcagtac atctggctat      600

agttatatgc actggtacca acagagacca ggacagccac ccaaactcct catctatctt      660

gcatccaacc tagaatctgg ggtccctgcc aggttcagtg gcagtgggtc tgggacagac      720

ttcaccctca acatccatcc tgtggaggag gaggatgctg caacctatta ctgtcagcac      780

agtagggagc ttccgttcac gttcggaggg gggaccaagc tggagataaa acgggctgat      840

gctgcaccaa ctgtatccac aacaacccct gcccccagac ctcctacccc agcccctaca      900

attgccagcc agcctctgag cctgaggccc gaggcttgta gacctgctgc tggcggagcc      960

gtgcacacca gaggactgga tttcgcctgc gacatctaca tctgggcgcc cttggccggg     1020

acttgtgggg tccttctcct gtcactggtt atcacccttt actgcaaacg gggcagaaag     1080

aaactcctgt atatattcaa acaaccattt atgagaccag tacaaactac tcaagaggaa     1140

gatggctgta gctgccgatt tccagaagaa gaagaaggag gatgtgaact gagagtgaag     1200

ttcagcagga gcgcagacgc ccccgcgtac aagcagggcc agaaccagct ctataacgag     1260

ctcaatctag gacgaagaga ggagtacgat gttttggaca agagacgtgg ccgggaccct     1320
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gagatggggg gaaagccgag aaggaagaac cctcaggaag gcctgttcaa tgaactgcag     1380

aaagataaga tggcggaggc cttcagtgag attgggatga aaggcgagcg ccggaggggc     1440

aaggggcacg atggcctttt ccagggtctc agtacagcca ccaaggacac cttcgacgcc     1500

cttcacatgc aggccctgcc ccctcgctga taa                                  1533


<210>  1619
<211>  509
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  MNC21XX - muMNC2CAR T841BB3z1XX

<400>  1619

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15


His Ala Ala Arg Pro Glu Val Gln Leu Glu Glu Ser Gly Gly Gly Leu
            20                  25                  30


Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
        35                  40                  45


Thr Phe Ser Gly Tyr Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys
    50                  55                  60


Arg Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr
65                  70                  75                  80


Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
                85                  90                  95


Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr
            100                 105                 110


Ala Met Tyr Tyr Cys Ala Arg Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr
        115                 120                 125


Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Lys
    130                 135                 140


Thr Thr Pro Pro Ser Val Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly
145                 150                 155                 160


Ser Gly Gly Gly Gly Ser Asp Ile Val Ile Thr Gln Ser Thr Ala Ser
                165                 170                 175


Leu Gly Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser
            180                 185                 190


Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln
        195                 200                 205
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Arg Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu
    210                 215                 220

Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
225                 230                 235                 240

Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr
                245                 250                 255

Tyr Cys Gln His Ser Arg Glu Leu Pro Phe Thr Phe Gly Gly Gly Thr
            260                 265                 270

Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Thr Thr
        275                 280                 285

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
    290                 295                 300

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
305                 310                 315                 320

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
                325                 330                 335

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
            340                 345                 350

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
        355                 360                 365

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
    370                 375                 380

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
385                 390                 395                 400

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
                405                 410                 415

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
            420                 425                 430

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
        435                 440                 445

Lys Asn Pro Gln Glu Gly Leu Phe Asn Glu Leu Gln Lys Asp Lys Met
    450                 455                 460

Ala Glu Ala Phe Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
465                 470                 475                 480
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Lys Gly His Asp Gly Leu Phe Gln Gly Leu Ser Thr Ala Thr Lys Asp
485 490 495

Thr Phe Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
500 505

<210> 1620
<211> 1485
<212> DNA
<213> Artificial Sequence

<220>
<223> huMNC2CAR T841BB3z1XX

<400> 1620
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ctctcctgtg cagcctctgg attcaccttc agtggctatg ccatgagctg ggtccgccag 180

gctccaggga aggggctgga gtgggtctca accattagta gtggcggaac ctacatatac 240

taccccgact cagtgaaggg ccgattcacc atctccagag acaacgccaa gaactcactg 300

tatctgcaaa tgaacagcct gagagccgag gacacggccg tgtattactg tgcgagactt 360

gggggggata attactacga atacttcgat gtctggggca aagggaccac ggtcaccgtc 420

tcctccggcg gtggcggatc cggcggtggc ggatccggcg gtggcggatc cgacattgtg 480

ctgacccagt ctccagcctc cttggccgtg tctccaggac agagggccac catcacctgc 540

agagccagta agagtgtcag taccagcgga tactcctaca tgcactggta tcagcagaaa 600

ccaggacaac ctcctaaact cctgatttac ctggcatcca atctggagag cggggtccca 660

gccaggttca gcggcagtgg gtctgggacc gatttcaccc tcacaattaa tcctgtggaa 720

gctaatgata ctgcaaatta ttactgtcag cacagtaggg agctgccttt cacattcggc 780

ggagggacca aggtggagat caaacgaact acaacaaccc ctgcccccag acctcctacc 840

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gctggcggag ccgtgcacac cagaggactg gatttcgcct gcgacatcta catctgggcg 960

cccttggccg ggacttgtgg ggtccttctc ctgtcactgg ttatcaccct ttactgcaaa 1020

cggggcagaa agaaactcct gtatatattc aaacaaccat ttatgagacc agtacaaact 1080

actcaagagg aagatggctg tagctgccga tttccagaag aagaagaagg aggatgtgaa 1140

ctgagagtga agttcagcag gagcgcagac gcccccgcgt acaagcaggg ccagaaccag 1200

ctctataacg agctcaatct aggacgaaga gaggagtacg atgttttgga caagagacgt 1260

ggccgggacc ctgagatggg gggaaagccg agaaggaaga accctcagga aggcctgttc 1320

aatgaactgc agaaagataa gatggcggag gccttcagtg agattgggat gaaaggcgag 1380

cgccggaggg gcaaggggca cgatggcctt ttccagggtc tcagtacagc caccaaggac 1440

accttcgacg cccttcacat gcaggccctg ccccctcgct gataa 1485

<210> 1621
<211> 493
<212> PRT
<213> Artificial Sequence

<220>
<223> huMNC2CAR T841BB3z1XX

<400> 1621

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Ser Gly Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ser Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr
65 70 75 80

Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Arg Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr
115 120 125

Phe Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
145 150 155 160

Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Pro Gly Gln Arg Ala
165 170 175

Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser
180 185 190

Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu
195 200 205

Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser
210 215 220

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu
225 230 235 240

Ala Asn Asp Thr Ala Asn Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro
                245   250   255

Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Thr Thr
            260   265   270

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
        275   280   285

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
    290   295   300

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
305   310   315   320

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
                325   330   335

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
            340   345   350

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
        355   360   365

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
    370   375   380

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
385   390   395   400

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
                405   410   415

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
            420   425   430

Lys Asn Pro Gln Glu Gly Leu Phe Asn Glu Leu Gln Lys Asp Lys Met
        435   440   445

Ala Glu Ala Phe Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
    450   455   460

Lys Gly His Asp Gly Leu Phe Gln Gly Leu Ser Thr Ala Thr Lys Asp
465   470   475   480

Thr Phe Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485   490

<210> 1622
<211> 1530
<212> DNA
<213> Artificial Sequence

<220>
<223> muMNC2CAR T8283z1XX

<400> 1622
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ccggaggtcc agctggagga gtcaggggga ggcttagtga agcctggagg gtccctgaaa 120

ctctcctgtg cagcctctgg attcactttc agtggctatg ccatgtcttg ggttcgccag 180

actccggaga agaggctgga gtgggtcgca accattagta gtggtggtac ttatatctac 240

tatccagaca gtgtgaaggg gcgattcacc atctccagag acaatgccaa gaacaccctg 300

tacctgcaaa tgagcagtct gaggtctgag gacacggcca tgtattactg tgcaagactt 360

gggggggata attactacga atacttcgat gtctggggcg cagggaccac ggtcaccgtc 420

tcctccgcca aaacgacacc cccatctgtc tatggcggtg gcggatccgg cggtggcgga 480

tccggcggtg gcggatccga cattgtgatc acacagtcta cagcttcctt aggtgtatct 540

ctggggcaga gggccaccat ctcatgcagg gccagcaaaa gtgtcagtac atctggctat 600

agttatatgc actggtacca acagagacca ggacagccac ccaaactcct catctatctt 660

gcatccaacc tagaatctgg ggtccctgcc aggttcagtg gcagtgggtc tgggacagac 720

ttcaccctca acatccatcc tgtggaggag gaggatgctg caacctatta ctgtcagcac 780

agtagggagc ttccgttcac gttcggaggg gggaccaagc tggagataaa acgggctgat 840

gctgcaccaa ctgtatccac aacaacccct gcccccagac ctcctacccc agcccctaca 900

attgccagcc agcctctgag cctgaggccc gaggcttgta gacctgctgc tggcggagcc 960

gtgcacacca gaggactgga tttcgcctgc gacatctaca tctgggcgcc cttggccggg 1020

acttgtgggg tccttctcct gtcactggtt atcacccttt actgcaggag taagaggagc 1080

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cattaccagc cctatgcccc accacgcgac ttcgcagcct atcgctccag agtgaagttc 1200

agcaggagcg cagacgcccc cgcgtacaag cagggccaga accagctcta taacgagctc 1260

aatctaggac gaagagagga gtacgatgtt ttggacaaga gacgtggccg ggaccctgag 1320

atggggggaa agccgagaag gaagaaccct caggaaggcc tgttcaatga actgcagaaa 1380

gataagatgg cggaggcctt cagtgagatt gggatgaaag gcgagcgccg gaggggcaag 1440

gggcacgatg gcctttttcca gggtctcagt acagccacca aggacacctt cgacgccctt 1500

cacatgcagg ccctgccccc tcgctgataa 1530

<210> 1623
<211> 508
<212> PRT
<213> Artificial Sequence

<220>
<223> muMNC2CAR T8283z1XX

<400> 1623

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu

```
1               5                   10                  15

His Ala Ala Arg Pro Glu Val Gln Leu Glu Glu Ser Gly Gly Gly Leu
            20                  25                  30

Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
        35                  40                  45

Thr Phe Ser Gly Tyr Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys
    50                  55                  60

Arg Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr
65                  70                  75                  80

Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
                85                  90                  95

Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr
            100                 105                 110

Ala Met Tyr Tyr Cys Ala Arg Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr
        115                 120                 125

Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Lys
    130                 135                 140

Thr Thr Pro Pro Ser Val Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly
145                 150                 155                 160

Ser Gly Gly Gly Gly Ser Asp Ile Val Ile Thr Gln Ser Thr Ala Ser
                165                 170                 175

Leu Gly Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser
            180                 185                 190

Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln
        195                 200                 205

Arg Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu
    210                 215                 220

Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
225                 230                 235                 240

Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr
                245                 250                 255

Tyr Cys Gln His Ser Arg Glu Leu Pro Phe Thr Phe Gly Gly Gly Thr
            260                 265                 270

Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Thr Thr
        275                 280                 285
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Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
    290                 295                 300

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
305                 310                 315                 320

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
                325                 330                 335

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
            340                 345                 350

Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
        355                 360                 365

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
    370                 375                 380

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe
385                 390                 395                 400

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu
                405                 410                 415

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
            420                 425                 430

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
        435                 440                 445

Asn Pro Gln Glu Gly Leu Phe Asn Glu Leu Gln Lys Asp Lys Met Ala
    450                 455                 460

Glu Ala Phe Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
465                 470                 475                 480

Gly His Asp Gly Leu Phe Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
                485                 490                 495

Phe Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505
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<210> 1624
<211> 1482
<212> DNA
<213> Artificial Sequence

<220>
<223> huMNC2CAR T8283z1XX

<400> 1624

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ccggaggtgc agctggtgga gtctggggga ggcctggtca agcctggggg gtccctgaga      120

ctctcctgtg cagcctctgg attcaccttc agtggctatg ccatgagctg ggtccgccag      180

gctccaggga aggggctgga gtgggtctca accattagta gtggcggaac ctacatatac      240

taccccgact cagtgaaggg ccgattcacc atctccagag acaacgccaa gaactcactg      300

tatctgcaaa tgaacagcct gagagccgag gacacggccg tgtattactg tgcgagactt      360

gggggggata attactacga atacttcgat gtctggggca aagggaccac ggtcaccgtc      420

tcctccggcg gtggcggatc cggcggtggc ggatccggcg gtggcggatc cgacattgtg      480

ctgacccagt ctccagcctc cttggccgtg tctccaggac agagggccac catcacctgc      540

agagccagta agagtgtcag taccagcgga tactcctaca tgcactggta tcagcagaaa      600

ccaggacaac ctcctaaact cctgatttac ctggcatcca atctggagag cggggtccca      660

gccaggttca gcggcagtgg gtctgggacc gatttcaccc tcacaattaa tcctgtggaa      720

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ggagggacca aggtggagat caaacgaact acaacaaccc ctgcccccag acctcctacc      840

ccagccccta caattgccag ccagcctctg agcctgaggc ccgaggcttg tagacctgct      900

gctggcggag ccgtgcacac cagaggactg gatttcgcct gcgacatcta catctgggcg      960

cccttggccg ggacttgtgg ggtccttctc ctgtcactgg ttatcaccct ttactgcagg     1020

agtaagagga gcaggctcct gcacagtgac tacatgaaca tgactcctag aagacctggg     1080

cctaccagaa agcattacca gccctatgcc ccaccacgcg acttcgcagc ctatcgctcc     1140

agagtgaagt tcagcaggag cgcagacgcc cccgcgtaca agcagggcca gaaccagctc     1200

tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc     1260

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgttcaat     1320

gaactgcaga aagataagat ggcggaggcc ttcagtgaga ttgggatgaa aggcgagcgc     1380

cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc     1440

ttcgacgccc ttcacatgca ggccctgccc cctcgctgat aa                        1482
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<210>  1625
<211>  492
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  huMNC2CAR T8283z1XX

<400>  1625

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15


His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
            20                  25                  30


Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
        35                  40                  45
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Thr Phe Ser Gly Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
    50                  55                  60

Gly Leu Glu Trp Val Ser Thr Ile Ser Ser Gly Gly Thr Tyr Ile Tyr
65                  70                  75                  80

Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
                85                  90                  95

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
            100                 105                 110

Ala Val Tyr Tyr Cys Ala Arg Leu Gly Gly Asp Asn Tyr Tyr Glu Tyr
        115                 120                 125

Phe Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly
    130                 135                 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
145                 150                 155                 160

Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Pro Gly Gln Arg Ala
                165                 170                 175

Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser
            180                 185                 190

Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu
        195                 200                 205

Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser
    210                 215                 220

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu
225                 230                 235                 240

Ala Asn Asp Thr Ala Asn Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro
                245                 250                 255

Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Thr Thr
            260                 265                 270

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
        275                 280                 285

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
    290                 295                 300

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
305                 310                 315                 320
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Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
325 330 335

Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
340 345 350

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
355 360 365

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe
370 375 380

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu
385 390 395 400

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
405 410 415

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
420 425 430

Asn Pro Gln Glu Gly Leu Phe Asn Glu Leu Gln Lys Asp Lys Met Ala
435 440 445

Glu Ala Phe Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
450 455 460

Gly His Asp Gly Leu Phe Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
465 470 475 480

Phe Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 1626
<211> 1467
<212> DNA
<213> Artificial Sequence

<220>
<223> MNE61XX - muMNE6CAR T841BB3z1XX

<400> 1626
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggaggtga aggtggtgga gtctggggga gacttagtga agcctggagg gtccctgaaa 120

ctctcctgtg tagtctctgg attcactttc agtagatatg gcatgtcttg ggttcgccag 180

actccaggca agaggctgga gtgggtcgca accattagtg gtggcggtac ttacatctac 240

tatccagaca gtgtgaaggg gcgattcacc atctccagag acaatgccaa gaacaccctg 300

tacctgcaaa tgagcagtct gaagtctgag gacacagcca tgtatcactg tacaagggat 360

aactacggta ggaactacga ctacggtatg gactactggg gtcaaggaac ctcagtcacc 420

gtctcctcag gcggtggcgg atccggcggt ggcggatccg gcggtggcgg atcccaaatt 480 gttctcaccc agtctccagc aatcatgtct gcatctccag gggaggaggt caccctaacc 540

tgcagtgcca cctcaagtgt aagttacata cactggttcc agcagaggcc aggcacttct 600

cccaaactct ggatttatag cacatccaac ctggcttctg gagtccctgt tcgcttcagt 660

ggcagtggat atgggacctc ttactctctc acaatcagcc gaatggaggc tgaagatgct 720

gccacttatt actgccagca aaggagtagt tccccattca cgttcggctc ggggacaaag 780

ttggaaataa aaacaacaac ccctgccccc agacctccta ccccagcccc tacaattgcc 840

agccagcctc tgagcctgag gcccgaggct tgtagacctg ctgctggcgg agccgtgcac 900

accagaggac tggatttcgc ctgcgacatc tacatctggg cgcccttggc cgggacttgt 960

ggggtccttc tcctgtcact ggttatcacc ctttactgca aacggggcag aaagaaactc 1020

ctgtatatat tcaaacaacc atttatgaga ccagtacaaa ctactcaaga ggaagatggc 1080

tgtagctgcc gatttccaga agaagaagaa ggaggatgtg aactgagagt gaagttcagc 1140

aggagcgcag acgcccccgc gtacaagcag ggccagaacc agctctataa cgagctcaat 1200

ctaggacgaa gagaggagta cgatgttttg gacaagagac gtggccggga ccctgagatg 1260

gggggaaagc cgagaaggaa gaaccctcag gaaggcctgt tcaatgaact gcagaaagat 1320

aagatggcgg aggccttcag tgagattggg atgaaaggcg agcgccggag gggcaagggg 1380

cacgatggcc ttttccaggg tctcagtaca gccaccaagg acaccttcga cgcccttcac 1440

atgcaggccc tgccccctcg ctgataa 1467

<210> 1627
<211> 487
<212> PRT
<213> Artificial Sequence

<220>
<223> MNE61XX - muMNE6CAR T841BB3z1XX

<400> 1627

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1   5   10   15

His Ala Ala Arg Pro Glu Val Lys Val Val Glu Ser Gly Gly Asp Leu
            20   25   30

Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Val Val Ser Gly Phe
        35   40   45

Thr Phe Ser Arg Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Gly Lys
    50   55   60

Arg Leu Glu Trp Val Ala Thr Ile Ser Gly Gly Gly Thr Tyr Ile Tyr
65   70   75   80

Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
                85   90   95

Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr
100 105 110

Ala Met Tyr His Cys Thr Arg Asp Asn Tyr Gly Arg Asn Tyr Asp Tyr
115 120 125

Gly Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ile
145 150 155 160

Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Glu
165 170 175

Val Thr Leu Thr Cys Ser Ala Thr Ser Ser Val Ser Tyr Ile His Trp
180 185 190

Phe Gln Gln Arg Pro Gly Thr Ser Pro Lys Leu Trp Ile Tyr Ser Thr
195 200 205

Ser Asn Leu Ala Ser Gly Val Pro Val Arg Phe Ser Gly Ser Gly Tyr
210 215 220

Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu Asp Ala
225 230 235 240

Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Ser Pro Phe Thr Phe Gly
245 250 255

Ser Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
260 265 270

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
275 280 285

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
290 295 300

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
305 310 315 320

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly
325 330 335

Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
340 345 350

Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
355 360 365

Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
370 375 380

Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
385 390 395 400

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
405 410 415

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
420 425 430

Leu Phe Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Phe Ser Glu
435 440 445

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
450 455 460

Phe Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Phe Asp Ala Leu His
465 470 475 480

Met Gln Ala Leu Pro Pro Arg
485

<210> 1628
<211> 1467
<212> DNA
<213> Artificial Sequence

<220>
<223> huMNE6CAR T841BB3z1XX

<400> 1628
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggaggtgc agctggtgga gtctggggga ggcctggtca agcctggggg gtccctgaga 120

ctctcctgtg cagcctctgg attcaccttc agtaggtatg gcatgagctg ggtccgccag 180

gctccaggga agaggctgga gtgggtctca accattagtg gcggaggcac ctacatatac 240

tacccagact cagtgaaggg ccgattcacc atctccagag acaacgccaa gaacaccctg 300

tatctgcaaa tgaacagcct gagagccgag gacacggctg tgtattactg taccagagat 360

aactatggcc gcaactatga ttatggcatg gattattggg gccagggcac cctggtgacc 420

gtgagcagcg gcggtggcgg atccggcggt ggcggatccg gcggtggcgg atccgaaatt 480

gtgttgacac agtctccagc caccctgtct ttgtctccag gggaaagagc caccctcacc 540

tgcagcgcca ccagcagtgt tagctacatc cactggtacc aacagaggcc tggccagagc 600

cccaggctcc tcatctatag cacctccaac ctggccagcg gcatcccagc caggttcagt 660

ggcagtgggt ctgggagcga ctacactctc accatcagca gcctagagcc tgaagatttt 720

gcagtttatt actgtcagca gcgtagcagc tccccttca cctttggcag cggcaccaaa 780

gtggaaatta aaacaacaac ccctgccccc agacctccta ccccagcccc tacaattgcc 840 agccagcctc tgagcctgag gcccgaggct tgtagacctg ctgctggcgg agccgtgcac 900

accagaggac tggatttcgc ctgcgacatc tacatctggg cgcccttggc cgggacttgt 960

ggggtccttc tcctgtcact ggttatcacc ctttactgca aacggggcag aaagaaactc 1020

ctgtatatat tcaaacaacc atttatgaga ccagtacaaa ctactcaaga ggaagatggc 1080

tgtagctgcc gatttccaga agaagaagaa ggaggatgtg aactgagagt gaagttcagc 1140

aggagcgcag acgcccccgc gtacaagcag ggccagaacc agctctataa cgagctcaat 1200

ctaggacgaa gagaggagta cgatgttttg gacaagagac gtggccggga ccctgagatg 1260

gggggaaagc cgagaaggaa gaaccctcag gaaggcctgt tcaatgaact gcagaaagat 1320

aagatggcgg aggccttcag tgagattggg atgaaaggcg agcgccggag gggcaagggg 1380

cacgatggcc ttttccaggg tctcagtaca gccaccaagg acaccttcga cgcccttcac 1440

atgcaggccc tgccccctcg ctgataa 1467

<210> 1629
<211> 487
<212> PRT
<213> Artificial Sequence

<220>
<223> huMNE6CAR T841BB3z1XX

<400> 1629

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Ser Arg Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Arg Leu Glu Trp Val Ser Thr Ile Ser Gly Gly Gly Thr Tyr Ile Tyr
65 70 75 80

Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Thr Arg Asp Asn Tyr Gly Arg Asn Tyr Asp Tyr
115 120 125

Gly Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
130 135 140

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Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile
145                 150                 155                 160


Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
                165                 170                 175


Ala Thr Leu Thr Cys Ser Ala Thr Ser Ser Val Ser Tyr Ile His Trp
            180                 185                 190


Tyr Gln Gln Arg Pro Gly Gln Ser Pro Arg Leu Leu Ile Tyr Ser Thr
        195                 200                 205


Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
    210                 215                 220


Gly Ser Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
225                 230                 235                 240


Ala Val Tyr Tyr Cys Gln Gln Arg Ser Ser Ser Pro Phe Thr Phe Gly
                245                 250                 255


Ser Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
            260                 265                 270


Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
        275                 280                 285


Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
    290                 295                 300


Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
305                 310                 315                 320


Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly
                325                 330                 335


Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
            340                 345                 350


Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
        355                 360                 365


Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
    370                 375                 380


Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
385                 390                 395                 400


Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
                405                 410                 415


Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
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420 425 430

Leu Phe Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Phe Ser Glu
435 440 445

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
450 455 460

Phe Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Phe Asp Ala Leu His
465 470 475 480

Met Gln Ala Leu Pro Pro Arg
485

<210> 1630
<211> 1464
<212> DNA
<213> Artificial Sequence

<220>
<223> muMNE6CAR T84283z1XX

<400> 1630
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggaggtga aggtggtgga gtctgggggga gacttagtga agcctggagg gtccctgaaa 120

ctctcctgtg tagtctctgg attcactttc agtagatatg gcatgtcttg ggttcgccag 180

actccaggca agaggctgga gtgggtcgca accattagtg gtggcggtac ttacatctac 240

tatccagaca gtgtgaaggg gcgattcacc atctccagag acaatgccaa gaacaccctg 300

tacctgcaaa tgagcagtct gaagtctgag gacacagcca tgtatcactg tacaagggat 360

aactacggta ggaactacga ctacggtatg gactactggg gtcaaggaac ctcagtcacc 420

gtctcctcag gcggtggcgg atccggcggt ggcggatccg gcggtggcgg atcccaaatt 480

gttctcaccc agtctccagc aatcatgtct gcatctccag gggaggaggt caccctaacc 540

tgcagtgcca cctcaagtgt aagttacata cactggttcc agcagaggcc aggcacttct 600

cccaaactct ggatttatag cacatccaac ctggcttctg gagtccctgt tcgcttcagt 660

ggcagtggat atgggacctc ttactctctc acaatcagcc gaatggaggc tgaagatgct 720

gccacttatt actgccagca aaggagtagt tccccattca cgttcggctc ggggacaaag 780

ttggaaataa aaacaacaac ccctgccccc agacctccta ccccagcccc tacaattgcc 840

agccagcctc tgagcctgag gcccgaggct tgtagacctg ctgctggcgg agccgtgcac 900

accagaggac tggatttcgc ctgcgacatc tacatctggg cgcccttggc cgggacttgt 960

ggggtccttc tcctgtcact ggttatcacc ctttactgca ggagtaagag gagcaggctc 1020

ctgcacagtg actacatgaa catgactcct agaagacctg ggcctaccag aaagcattac 1080

cagccctatg ccccaccacg cgacttcgca gcctatcgct ccagagtgaa gttcagcagg 1140

agcgcagacg cccccgcgta caagcagggc cagaaccagc tctataacga gctcaatcta 1200

ggacgaagag aggagtacga tgttttggac aagagacgtg gccgggaccc tgagatgggg 1260 ggaaagccga gaaggaagaa ccctcaggaa ggcctgttca atgaactgca gaaagataag 1320

atggcggagg ccttcagtga gattgggatg aaaggcgagc gccggagggg caaggggcac 1380

gatggccttt tccagggtct cagtacagcc accaaggaca ccttcgacgc ccttcacatg 1440

caggccctgc cccctcgctg ataa 1464

<210> 1631
<211> 486
<212> PRT
<213> Artificial Sequence

<220>
<223> muMNE6CAR T84283z1XX

<400> 1631

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Val Lys Val Val Glu Ser Gly Gly Asp Leu
20 25 30

Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Val Val Ser Gly Phe
35 40 45

Thr Phe Ser Arg Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Gly Lys
50 55 60

Arg Leu Glu Trp Val Ala Thr Ile Ser Gly Gly Gly Thr Tyr Ile Tyr
65 70 75 80

Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95

Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr
100 105 110

Ala Met Tyr His Cys Thr Arg Asp Asn Tyr Gly Arg Asn Tyr Asp Tyr
115 120 125

Gly Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ile
145 150 155 160

Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Glu
165 170 175

Val Thr Leu Thr Cys Ser Ala Thr Ser Ser Val Ser Tyr Ile His Trp
180 185 190

Phe Gln Gln Arg Pro Gly Thr Ser Pro Lys Leu Trp Ile Tyr Ser Thr

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        195                 200                 205

Ser Asn Leu Ala Ser Gly Val Pro Val Arg Phe Ser Gly Ser Gly Tyr
    210                 215                 220

Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu Asp Ala
225                 230                 235                 240

Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Ser Pro Phe Thr Phe Gly
                245                 250                 255

Ser Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
            260                 265                 270

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
        275                 280                 285

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
    290                 295                 300

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
305                 310                 315                 320

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys
                325                 330                 335

Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
            340                 345                 350

Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp
        355                 360                 365

Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
    370                 375                 380

Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
385                 390                 395                 400

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
                405                 410                 415

Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
            420                 425                 430

Phe Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Phe Ser Glu Ile
        435                 440                 445

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Phe
    450                 455                 460

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Phe Asp Ala Leu His Met
465                 470                 475                 480
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Gln Ala Leu Pro Pro Arg
485

<210> 1632
<211> 1464
<212> DNA
<213> Artificial Sequence

<220>
<223> huMNE6CAR T84283z1XX

<400> 1632
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggaggtgc agctggtgga gtctggggga ggcctggtca agcctggggg gtccctgaga 120

ctctcctgtg cagcctctgg attcaccttc agtaggtatg gcatgagctg ggtccgccag 180

gctccaggga agaggctgga gtgggtctca accattagtg gcggaggcac ctacatatac 240

tacccagact cagtgaaggg ccgattcacc atctccagag acaacgccaa gaacaccctg 300

tatctgcaaa tgaacagcct gagagccgag gacacggctg tgtattactg taccagagat 360

aactatggcc gcaactatga ttatggcatg gattattggg gccagggcac cctggtgacc 420

gtgagcagcg gcggtggcgg atccggcggt ggcggatccg gcggtggcgg atccgaaatt 480

gtgttgacac agtctccagc caccctgtct ttgtctccag gggaaagagc caccctcacc 540

tgcagcgcca ccagcagtgt tagctacatc cactggtacc aacagaggcc tggccagagc 600

cccaggctcc tcatctatag cacctccaac ctggccagcg gcatcccagc caggttcagt 660

ggcagtgggt ctgggagcga ctacactctc accatcagca gcctagagcc tgaagatttt 720

gcagtttatt actgtcagca gcgtagcagc tcccctttca cctttggcag cggcaccaaa 780

gtggaaatta aaacaacaac ccctgccccc agacctccta ccccagcccc tacaattgcc 840

agccagcctc tgagcctgag gcccgaggct tgtagacctg ctgctggcgg agccgtgcac 900

accagaggac tggatttcgc ctgcgacatc tacatctggg cgcccttggc cgggacttgt 960

ggggtccttc tcctgtcact ggttatcacc ctttactgca ggagtaagag gagcaggctc 1020

ctgcacagtg actacatgaa catgactcct agaagacctg ggcctaccag aaagcattac 1080

cagccctatg ccccaccacg cgacttcgca gcctatcgct ccagagtgaa gttcagcagg 1140

agcgcagacg cccccgcgta caagcagggc cagaaccagc tctataacga gctcaatcta 1200

ggacgaagag aggagtacga tgttttggac aagagacgtg gccgggaccc tgagatgggg 1260

ggaaagccga gaaggaagaa ccctcaggaa ggcctgttca atgaactgca gaaagataag 1320

atggcggagg ccttcagtga gattgggatg aaaggcgagc gccggagggg caaggggcac 1380

gatggccttt tccagggtct cagtacagcc accaaggaca ccttcgacgc ccttcacatg 1440

caggccctgc cccctcgctg ataa 1464

<210> 1633
<211> 486
<212> PRT

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<213>  Artificial Sequence

<220>
<223>  huMNE6CAR T84283z1XX

<400>  1633

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15


His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
            20                  25                  30


Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
        35                  40                  45


Thr Phe Ser Arg Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys
    50                  55                  60


Arg Leu Glu Trp Val Ser Thr Ile Ser Gly Gly Gly Thr Tyr Ile Tyr
65                  70                  75                  80


Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
                85                  90                  95


Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
            100                 105                 110


Ala Val Tyr Tyr Cys Thr Arg Asp Asn Tyr Gly Arg Asn Tyr Asp Tyr
        115                 120                 125


Gly Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
    130                 135                 140


Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile
145                 150                 155                 160


Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
                165                 170                 175


Ala Thr Leu Thr Cys Ser Ala Thr Ser Ser Val Ser Tyr Ile His Trp
            180                 185                 190


Tyr Gln Gln Arg Pro Gly Gln Ser Pro Arg Leu Leu Ile Tyr Ser Thr
        195                 200                 205


Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
    210                 215                 220


Gly Ser Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
225                 230                 235                 240


Ala Val Tyr Tyr Cys Gln Gln Arg Ser Ser Ser Pro Phe Thr Phe Gly
                245                 250                 255
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Ser Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
            260                 265                 270

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
        275                 280                 285

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
    290                 295                 300

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
305                 310                 315                 320

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys
                325                 330                 335

Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
            340                 345                 350

Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp
        355                 360                 365

Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
    370                 375                 380

Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
385                 390                 395                 400

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
                405                 410                 415

Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
            420                 425                 430

Phe Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Phe Ser Glu Ile
        435                 440                 445

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Phe
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Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Phe Asp Ala Leu His Met
465                 470                 475                 480

Gln Ala Leu Pro Pro Arg
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<220>
<223>  Minimal CMV promoter (mCMV)
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ctggagacgc catccacgct gttttgacct ccatagaaga caccgggacc gatccag   117

<210> 1635
<211> 114
<212> DNA
<213> Artificial Sequence

<220>
<223> Minimal IL2 promoter (mIL2P)

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aagagttccc tatcactctc tttaatcact actcacagta acctcaactc ctgc   114

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<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Minimal promoter, miniP

<400> 1636
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<210> 1637
<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> IL18 activated

<400> 1637
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ccgtacttcg gcaagctgga aagcaagctg agcgtgatcc ggaacctgaa cgaccaggtg   120

ctgttcatcg atcagggcaa cagacccctg ttcgaggaca tgaccgacag cgactgcaga   180

gacaacgccc ctcggaccat cttcatcatc agcatgtaca aggacagcca gcctagaggc   240

atggccgtga ccatctctgt gaagtgcgag aagatcagca ccctgagctg cgagaacaag   300

atcatcagct tcaaagagat gaacccgccg gacaacatca aggacaccaa gagcgacatc   360

atattcttcc agcggagcgt gcccggccac gacaacaaga tgcagtttga gagcagcagc   420

tacgagggct acttcctggc ctgcgagaaa gagcgggacc tgttcaagct gatcctgaag   480

aaagaggacg aactgggcga ccgcagcatc atgttcaccg tgcagaacga ggactgataa   540

<210> 1638
<211> 178
<212> PRT
<213> Artificial Sequence

<220>
<223> IL18 activated

<400> 1638

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Ile Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg
        35   40   45

Pro Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro
    50   55   60

Arg Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly
65   70   75   80

Met Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser
                85   90   95

Cys Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn
            100   105   110

Ile Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro
        115   120   125

Gly His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr
    130   135   140

Phe Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys
145   150   155   160

Lys Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn
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Glu Asp

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agctcgttta gtgaaccgtc agatcgcctg gagacgccat ccacgctgtt ttgacctcca   180

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<223> Foxp3NFATc1X6IL18

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ccatttactg cagaggcttc atttttcca tttactgcag aactagttag gcgtgtacgg 180

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<210> 1641
<211> 779
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<223> IL2NFATc1X3IL18

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acgagggcta cttcctggcc tgcgagaaag agcgggacct gttcaagctg atcctgaaga 720

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<212> DNA
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<210> 1643
<211> 2347
<212> DNA
<213> Artificial Sequence

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gaggcctata taagcagagc tcgtttagtg aaccgtcaga tcgcctggag acgccatcca 1680

cgctgttttg acctccatag aagacaccgg gaccgatcca gcctcgagag acccaatgct 1740

agccaccatg gccttaccag tgaccgcctt gctcctgccg ctggccttgc tgctccacgc 1800

cgccaggccg tacttcggca agctggaaag caagctgagc gtgatccgga acctgaacga 1860

ccaggtgctg ttcatcgatc agggcaacag acccctgttc gaggacatga ccgacagcga 1920

ctgcagagac aacgcccctc ggaccatctt catcatcagc atgtacaagg acagccagcc 1980

tagaggcatg gccgtgacca tctctgtgaa gtgcgagaag atcagcaccc tgagctgcga 2040

gaacaagatc atcagcttca aagagatgaa cccgccggac aacatcaagg acaccaagag 2100

cgacatcata ttcttccagc ggagcgtgcc cggccacgac aacaagatgc agtttgagag 2160

cagcagctac gagggctact tcctggcctg cgagaaagag cgggacctgt tcaagctgat 2220

cctgaagaaa gaggacgaac tgggcgaccg cagcatcatg ttcaccgtgc agaacgagga 2280

ctgataa 2287

<210> 1675
<211> 1482
<212> DNA
<213> Artificial Sequence

<220>
<223> pCDH MSCV h20A10-O CAR 41BB

<400> 1675
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ccggaggtgc agctggttga atctggcggc ggacttgtga agcctggcgg atctctgaga 120

ctgagctgtg ccgccagcgg cttcaccttt agcacatacg ccatgagctg ggtccgacag 180

gcccctggaa aaggccttga atgggttgcc tctatcggca gagccggcag cacctactac 240 agcgattctg tgaagggcag attcaccatc agccgggaca acgccaagaa cagcctgtac 300

ctgcagatga actccctgag agccgaggac accgccgtgt actattgtgc cagaggaccc 360

atctacaacg actacgacga gttcgcctat tggggccagg gcacactggt cacagtcagc 420

tctggcggtg gcggaagcgg aggcggtggc tccggtggcg gaggcagcga catcgtgatg 480

acacagagcc ctgatagcct ggccgtgtct ctgggagaga gagccaccat caactgcaag 540

agcagccaga gcgtgctgta ctccagcaac cagaagaact acctggcctg gtatcagcag 600

aagcccggcc agcctcctaa gctgctgatc tactgggcca gcaccagaga aagcggcgtg 660

cccgatagat tttctggcag cggctctggc accgacttca ccctgacaat tagctccctg 720

caggccgagg atgtggccgt gtactactgt caccagtacc tgagcagcct gacctttggc 780

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ttggccggga cttgtggggt ccttctcctg tcactggtta tcacccttta ctgcaaacgg 1020

ggcagaaaga aactcctgta tatattcaaa caaccattta tgagaccagt acaaactact 1080

caagaggaag atggctgtag ctgccgattt ccagaagaag aagaaggagg atgtgaactg 1140

agagtgaagt tcagcaggag cgcagacgcc cccgcgtaca agcagggcca gaaccagctc 1200

tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 1260

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 1320

gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 1380

cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc 1440

tacgacgccc ttcacatgca ggccctgccc cctcgctgat aa 1482

<210> 1676
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> CD8 leader sequence

<400> 1676
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccg 63

<210> 1677
<211> 744
<212> DNA
<213> Artificial Sequence

<220>
<223> h20A10O scFV

<400> 1677
gaggtgcagc tggttgaatc tggcggcgga cttgtgaagc ctggcggatc tctgagactg 60

agctgtgccg ccagcggctt cacctttagc acatacgcca tgagctgggt ccgacaggcc 120 cctggaaaag gccttgaatg ggttgcctct atcggcagag ccggcagcac ctactacagc 180

gattctgtga agggcagatt caccatcagc cgggacaacg ccaagaacag cctgtacctg 240

cagatgaact ccctgagagc cgaggacacc gccgtgtact attgtgccag aggacccatc 300

tacaacgact acgacgagtt cgcctattgg ggccagggca cactggtcac agtcagctct 360

ggcggtggcg gaagcggagg cggtggctcc ggtggcggag gcagcgacat cgtgatgaca 420

cagagccctg atagcctggc cgtgtctctg ggagagagag ccaccatcaa ctgcaagagc 480

agccagagcg tgctgtactc cagcaaccag aagaactacc tggcctggta tcagcagaag 540

cccggccagc ctcctaagct gctgatctac tgggccagca ccagagaaag cggcgtgccc 600

gatagatttt ctggcagcgg ctctggcacc gacttcaccc tgacaattag ctccctgcag 660

gccgaggatg tggccgtgta ctactgtcac cagtacctga gcagcctgac ctttggcggc 720

ggaacaaagg tggaaatcaa gcga 744

<210> 1678
<211> 135
<212> DNA
<213> Artificial Sequence

<220>
<223> CD8 hinge region

<400> 1678
acaacaaccc ctgcccccag acctcctacc ccagccccta caattgccag ccagcctctg 60

agcctgaggc ccgaggcttg tagacctgct gctggcggag ccgtgcacac cagaggactg 120

gatttcgcct gcgac 135

<210> 1679
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> CD8 leader sequence

<400> 1679
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccg 63

<210> 1680
<211> 744
<212> DNA
<213> Artificial Sequence

<220>
<223> h20A10N scFV

<400> 1680
caggtgcagc tggttgaatc tggcggcgga cttgtgaagc ctggcggatc tctgagactg 60

agctgtgccg ccagcggctt cacctttagc acatacgcca tgagctggat cagacaggcc 120

cctggcaaag gcctggaatg ggtggcgtct attggcagag ccggcagcac ctactacagc 180 gactctgtga agggcagatt caccatcagc cgggacaacg ccaagaacag cctgtacctg 240

cagatgaact ccctgagagc cgaggacacc gccgtgtact attgtgccag aggacccatc 300

tacaacgact acgacgagtt cgcctattgg ggccagggca cactggtcac agtttctagc 360

ggcggtggcg gaagcggagg cggtggctcc ggtggcggag gcagcgaaat tgtgctgaca 420

cagagccccg ccacactgtc actttctcca ggcgaaagag ccacactgag ctgcaagagc 480

agccagagcg tgctgtactc cagcaaccag aagaactacc tggcctggta tcagcagaag 540

cccggccaag ctcctcggct gctgatctat tgggccagca caagagagag cggcatccct 600

gccagatttt ctggcagcgg ctctggcacc gatttcaccc tgaccataag cagcctggaa 660

cctgaggact tcgccgtgta ttactgccac cagtacctga gcagcctgac ctttggcgga 720

ggcaccaagg tggaaatcaa gcgg 744

<210> 1681
<211> 135
<212> DNA
<213> Artificial Sequence

<220>
<223> CD8 hinge region

<400> 1681
acaacaaccc ctgcccccag acctcctacc ccagccccta caattgccag ccagcctctg 60

agcctgaggc ccgaggcttg tagacctgct gctggcggag ccgtgcacac cagaggactg 120

gatttcgcct gcgac 135

<210> 1682
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> CD8 transmembrane domain

<400> 1682
atctacatct gggcgccctt ggccgggact tgtggggtcc ttctcctgtc actggttatc 60

accctttact gc 72

<210> 1683
<211> 126
<212> DNA
<213> Artificial Sequence

<220>
<223> 41BB

<400> 1683
aaacggggca gaaagaaact cctgtatata ttcaaacaac catttatgag accagtacaa 60

actactcaag aggaagatgg ctgtagctgc cgatttccag aagaagaaga aggaggatgt 120

gaactg 126

<210> 1684
<211> 342

<212> DNA
<213> Artificial Sequence

<220>
<223> CD3

<400> 1684
agagtgaagt tcagcaggag cgcagacgcc cccgcgtaca agcagggcca gaaccagctc   60

tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc   120

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat   180

gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc   240

cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc   300

tacgacgccc ttcacatgca ggccctgccc cctcgctgat aa   342

<210> 1685
<211> 1482
<212> DNA
<213> Artificial Sequence

<220>
<223> pCDH MSCV h20A10-C2 CAR 41BB

<400> 1685
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg   60

ccggaggtgc agctggttga atctggcggc ggacttgtga agcctggcgg atctctgaga   120

ctgagctgtg ccgccagcgg cttcaccttt agcacatacg ccatgagctg ggtccgacag   180

gcccctggaa aaggccttga atgggttgcc tctatcggca gagccggcag cacctactac   240

agcgattctg tgaagggcag attcaccatc agccgggaca acgccaagaa cagcctgtac   300

ctgcagatga actccctgag agccgaggac accgccgtgt actattgtgc cagaggaccc   360

atctacaacg actacgacga gttcgcctat tggggccagg gcacactggt cacagtcagc   420

tctggcggtg gcggaagcgg aggcggtggc tccggtggcg gaggcagcga cattgtgctg   480

acccagtctc cagcctcctt ggccgtgtct ccaggacaga gggccaccat cacctgcaag   540

agcagccaga gcgtgctgta ctccagcaac cagaagaact acctggcctg gtatcagcag   600

aaaccaggac aacctcctaa actcctgatt tactgggcca gcaccagaga aagcggggtc   660

ccagccaggt tcagcggcag tgggtctggg accgatttca ccctcacaat taatcctgtg   720

gaagctaatg atactgcaaa ttattactgt caccagtacc tgagcagcct gaccttcggc   780

ggagggacca aggtggagat caaacgaaca acaacccctg cccccagacc tcctacccca   840

gcccctacaa ttgccagcca gcctctgagc ctgaggcccg aggcttgtag acctgctgct   900

ggcggagccg tgcacaccag aggactggat ttcgcctgcg acatctacat ctgggcgccc   960

ttggccggga cttgtggggt ccttctcctg tcactggtta tcacccttta ctgcaaacgg   1020

ggcagaaaga aactcctgta tatattcaaa caaccattta tgagaccagt acaaactact   1080

caagaggaag atggctgtag ctgccgattt ccagaagaag aagaaggagg atgtgaactg   1140

agagtgaagt tcagcaggag cgcagacgcc cccgcgtaca agcagggcca gaaccagctc   1200 tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 1260

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 1320

gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 1380

cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc 1440

tacgacgccc ttcacatgca ggccctgccc cctcgctgat aa 1482

<210> 1686
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> CD8 leader sequence

<400> 1686
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccg 63

<210> 1687
<211> 744
<212> DNA
<213> Artificial Sequence

<220>
<223> h20A10C2 scFV

<400> 1687
gaggtgcagc tggttgaatc tggcggcgga cttgtgaagc ctggcggatc tctgagactg 60

agctgtgccg ccagcggctt cacctttagc acatacgcca tgagctgggt ccgacaggcc 120

cctggaaaag gccttgaatg ggttgcctct atcggcagag ccggcagcac ctactacagc 180

gattctgtga agggcagatt caccatcagc cgggacaacg ccaagaacag cctgtacctg 240

cagatgaact ccctgagagc cgaggacacc gccgtgtact attgtgccag aggacccatc 300

tacaacgact acgacgagtt cgcctattgg ggccagggca cactggtcac agtcagctct 360

ggcggtggcg gaagcggagg cggtggctcc ggtggcggag gcagcgacat tgtgctgacc 420

cagtctccag cctccttggc cgtgtctcca ggacagaggg ccaccatcac ctgcaagagc 480

agccagagcg tgctgtactc cagcaaccag aagaactacc tggcctggta tcagcagaaa 540

ccaggacaac ctcctaaact cctgatttac tgggccagca ccagagaaag cggggtccca 600

gccaggttca gcggcagtgg gtctgggacc gatttcaccc tcacaattaa tcctgtggaa 660

gctaatgata ctgcaaatta ttactgtcac cagtacctga gcagcctgac cttcggcgga 720

gggaccaagg tggagatcaa acga 744

<210> 1688
<211> 135
<212> DNA
<213> Artificial Sequence

<220>
<223> CD8 hinge region

<400> 1688
acaacaaccc ctgcccccag acctcctacc ccagccccta caattgccag ccagcctctg   60

agcctgaggc ccgaggcttg tagacctgct gctggcggag ccgtgcacac cagaggactg   120

gatttcgcct gcgac   135

<210> 1689
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> CD8 transmembrane region

<400> 1689
atctacatct gggcgccctt ggccgggact tgtggggtcc ttctcctgtc actggttatc   60

accctttact gc   72

<210> 1690
<211> 126
<212> DNA
<213> Artificial Sequence

<220>
<223> 41BB

<400> 1690
aaacggggca gaaagaaact cctgtatata ttcaaacaac catttatgag accagtacaa   60

actactcaag aggaagatgg ctgtagctgc cgatttccag aagaagaaga aggaggatgt   120

gaactg   126

<210> 1691
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<223> CD3

<400> 1691
agagtgaagt tcagcaggag cgcagacgcc cccgcgtaca agcagggcca gaaccagctc   60

tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc   120

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat   180

gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc   240

cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc   300

tacgacgccc ttcacatgca ggccctgccc cctcgctgat aa   342

<210> 1692
<211> 1479
<212> DNA
<213> Artificial Sequence

<220>
<223> pCDH MSCV h20A10-O CAR CD28 1XX

<400> 1692

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atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg       60

ccggaggtgc agctggttga atctggcggc ggacttgtga agcctggcgg atctctgaga      120

ctgagctgtg ccgccagcgg cttcaccttt agcacatacg ccatgagctg ggtccgacag      180

gcccctggaa aaggccttga atgggttgcc tctatcggca gagccggcag cacctactac      240

agcgattctg tgaagggcag attcaccatc agccgggaca acgccaagaa cagcctgtac      300

ctgcagatga actccctgag agccgaggac accgccgtgt actattgtgc cagaggaccc      360

atctacaacg actacgacga gttcgcctat tggggccagg gcacactggt cacagtcagc      420

tctggcggtg gcggaagcgg aggcggtggc tccggtggcg gaggcagcga catcgtgatg      480

acacagagcc ctgatagcct ggccgtgtct ctgggagaga gagccaccat caactgcaag      540

agcagccaga gcgtgctgta ctccagcaac cagaagaact acctggcctg gtatcagcag      600

aagcccggcc agcctcctaa gctgctgatc tactgggcca gcaccagaga aagcggcgtg      660

cccgatagat tttctggcag cggctctggc accgacttca ccctgacaat tagctccctg      720

caggccgagg atgtggccgt gtactactgt caccagtacc tgagcagcct gacctttggc      780

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ttggccggga cttgtggggt ccttctcctg tcactggtta tcacccttta ctgcaggagt     1020

aagaggagca ggctcctgca cagtgactac atgaacatga ctcctagaag acctgggcct     1080

accagaaagc attaccagcc ctatgcccca ccacgcgact tcgcagccta tcgctccaga     1140

gtgaagttca gcaggagcgc agacgccccc gcgtacaagc agggccagaa ccagctctat     1200

aacgagctca atctaggacg aagagaggag tacgatgttt tggacaagag acgtggccgg     1260

gaccctgaga tggggggaaa gccgagaagg aagaaccctc aggaaggcct gttcaatgaa     1320

ctgcagaaag ataagatggc ggaggccttc agtgagattg ggatgaaagg cgagcgccgg     1380

aggggcaagg ggcacgatgg cctttttccag ggtctcagta cagccaccaa ggacaccttc     1440

gacgcccttc acatgcaggc cctgcccccct cgctgataa                            1479


<210>  1693
<211>  63
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CD8 leader sequence

<400>  1693
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg       60

ccg                                                                    63


<210>  1694
<211>  744
<212>  DNA
<213>  Artificial Sequence
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<220>
<223> h20A10O scFV

<400> 1694
gaggtgcagc tggttgaatc tggcggcgga cttgtgaagc ctggcggatc tctgagactg   60

agctgtgccg ccagcggctt cacctttagc acatacgcca tgagctgggt ccgacaggcc   120

cctggaaaag gccttgaatg ggttgcctct atcggcagag ccggcagcac ctactacagc   180

gattctgtga agggcagatt caccatcagc cgggacaacg ccaagaacag cctgtacctg   240

cagatgaact ccctgagagc cgaggacacc gccgtgtact attgtgccag aggacccatc   300

tacaacgact acgacgagtt cgcctattgg ggccagggca cactggtcac agtcagctct   360

ggcggtggcg gaagcggagg cggtggctcc ggtggcggag gcagcgacat cgtgatgaca   420

cagagccctg atagcctggc cgtgtctctg ggagagagag ccaccatcaa ctgcaagagc   480

agccagagcg tgctgtactc cagcaaccag aagaactacc tggcctggta tcagcagaag   540

cccggccagc ctcctaagct gctgatctac tgggccagca ccagagaaag cggcgtgccc   600

gatagatttt ctggcagcgg ctctggcacc gacttcaccc tgacaattag ctccctgcag   660

gccgaggatg tggccgtgta ctactgtcac cagtacctga gcagcctgac ctttggcggc   720

ggaacaaagg tggaaatcaa gcga   744

<210> 1695
<211> 135
<212> DNA
<213> Artificial Sequence

<220>
<223> CD8 hinge region

<400> 1695
acaacaaccc ctgcccccag acctcctacc ccagccccta caattgccag ccagcctctg   60

agcctgaggc ccgaggcttg tagacctgct gctggcggag ccgtgcacac cagaggactg   120

gatttcgcct gcgac   135

<210> 1696
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> CD8 transmembrane region

<400> 1696
atctacatct gggcgccctt ggccgggact tgtggggtcc ttctcctgtc actggttatc   60

accctttact gc   72

<210> 1697
<211> 123
<212> DNA
<213> Artificial Sequence

<220>
<223> CD28

<400> 1697
aggagtaaga ggagcaggct cctgcacagt gactacatga acatgactcc tagaagacct 60

gggcctacca gaaagcatta ccagccctat gccccaccac gcgacttcgc agcctatcgc 120

tcc 123

<210> 1698
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<223> CD3 1XX

<400> 1698
agagtgaagt tcagcaggag cgcagacgcc cccgcgtaca agcagggcca gaaccagctc 60

tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 120

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgttcaat 180

gaactgcaga aagataagat ggcggaggcc ttcagtgaga ttgggatgaa aggcgagcgc 240

cggaggggca aggggcacga tggcctttttc cagggtctca gtacagccac caaggacacc 300

ttcgacgccc ttcacatgca ggccctgccc cctcgctgat aa 342

<210> 1699
<211> 1479
<212> DNA
<213> Artificial Sequence

<220>
<223> pCDH MSCV h20A10-N CAR CD28 1XX

<400> 1699
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ccgcaggtgc agctggttga atctggcggc ggacttgtga agcctggcgg atctctgaga 120

ctgagctgtg ccgccagcgg cttcaccttt agcacatacg ccatgagctg gatcagacag 180

gcccctggca aaggcctgga atgggtggcg tctattggca gagccggcag cacctactac 240

agcgactctg tgaagggcag attcaccatc agccgggaca acgccaagaa cagcctgtac 300

ctgcagatga actccctgag agccgaggac accgccgtgt actattgtgc cagaggaccc 360

atctacaacg actacgacga gttcgcctat tggggccagg gcacactggt cacagtttct 420

agcggcggtg gcggaagcgg aggcggtggc tccggtggcg gaggcagcga aattgtgctg 480

acacagagcc ccgccacact gtcactttct ccaggcgaaa gagccacact gagctgcaag 540

agcagccaga gcgtgctgta ctccagcaac cagaagaact acctggcctg gtatcagcag 600

aagcccggcc aagctcctcg gctgctgatc tattgggcca gcacaagaga gagcggcatc 660

cctgccagat tttctggcag cggctctggc accgatttca ccctgaccat aagcagcctg 720

gaacctgagg acttcgccgt gtattactgc caccagtacc tgagcagcct gacctttggc 780

ggaggcacca aggtggaaat caagcggaca acaacccctg cccccagacc tcctacccca 840

gcccctacaa ttgccagcca gcctctgagc ctgaggcccg aggcttgtag acctgctgct 900

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ggcggagccg tgcacaccag aggactggat ttcgcctgcg acatctacat ctgggcgccc      960

ttggccggga cttgtggggt ccttctcctg tcactggtta tcaccctttа ctgcaggagt     1020

aagaggagca ggctcctgca cagtgactac atgaacatga ctcctagaag acctgggcct     1080

accagaaagc attaccagcc ctatgcccca ccacgcgact tcgcagccta tcgctccaga     1140

gtgaagttca gcaggagcgc agacgccccc gcgtacaagc agggccagaa ccagctctat     1200

aacgagctca atctaggacg aagagaggag tacgatgttt tggacaagag acgtggccgg     1260

gaccctgaga tggggggaaa gccgagaagg aagaaccctc aggaaggcct gttcaatgaa     1320

ctgcagaaag ataagatggc ggaggccttc agtgagattg ggatgaaagg cgagcgccgg     1380

aggggcaagg ggcacgatgg cctttttccag ggtctcagta cagccaccaa ggacaccttc     1440

gacgcccttc acatgcaggc cctgcccccct cgctgataa                            1479


<210>  1700
<211>  63
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CD8 leader sequence

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ccg                                                                     63


<210>  1701
<211>  744
<212>  DNA
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<220>
<223>  h20A10N scFV

<400>  1701
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gactctgtga agggcagatt caccatcagc cgggacaacg ccaagaacag cctgtacctg      240

cagatgaact ccctgagagc cgaggacacc gccgtgtact attgtgccag aggacccatc      300

tacaacgact acgacgagtt cgcctattgg ggccagggca cactggtcac agtttctagc      360

ggcggtggcg gaagcggagg cggtggctcc ggtggcggag gcagcgaaat tgtgctgaca      420

cagagccccg ccacactgtc actttctcca ggcgaaagag ccacactgag ctgcaagagc      480

agccagagcg tgctgtactc cagcaaccag aagaactacc tggcctggta tcagcagaag      540

cccggccaag ctcctcggct gctgatctat tgggccagca caagagagag cggcatccct      600

gccagatttt ctggcagcgg ctctggcacc gatttcaccc tgaccataag cagcctggaa      660

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ggcaccaagg tggaaatcaa gcgg 744

<210> 1702
<211> 135
<212> DNA
<213> Artificial Sequence

<220>
<223> CD8 hinge region

<400> 1702
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agcctgaggc ccgaggcttg tagacctgct gctggcggag ccgtgcacac cagaggactg 120

gatttcgcct gcgac 135

<210> 1703
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> CD8 transmembrane domain

<400> 1703
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accctttact gc 72

<210> 1704
<211> 123
<212> DNA
<213> Artificial Sequence

<220>
<223> CD28

<400> 1704
aggagtaaga ggagcaggct cctgcacagt gactacatga acatgactcc tagaagacct 60

gggcctacca gaaagcatta ccagccctat gccccaccac gcgacttcgc agcctatcgc 120

tcc 123

<210> 1705
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<223> CD3 1XX

<400> 1705
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tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 120

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgttcaat 180

gaactgcaga aagataagat ggcggaggcc ttcagtgaga ttgggatgaa aggcgagcgc 240

cggaggggca aggggcacga tggcctttttc cagggtctca gtacagccac caaggacacc 300

ttcgacgccc ttcacatgca ggccctgccc cctcgctgat aa 342

<210> 1706
<211> 1479
<212> DNA
<213> Artificial Sequence

<220>
<223> pCDH MSCV h20A10-C2 CAR CD28 1XX

<400> 1706
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ctgagctgtg ccgccagcgg cttcaccttt agcacatacg ccatgagctg ggtccgacag 180

gcccctggaa aaggccttga atgggttgcc tctatcggca gagccggcag cacctactac 240

agcgattctg tgaagggcag attcaccatc agccgggaca acgccaagaa cagcctgtac 300

ctgcagatga actccctgag agccgaggac accgccgtgt actattgtgc cagaggaccc 360

atctacaacg actacgacga gttcgcctat tggggccagg gcacactggt cacagtcagc 420

tctggcggtg gcggaagcgg aggcggtggc tccggtggcg gaggcagcga cattgtgctg 480

acccagtctc cagcctcctt ggccgtgtct ccaggacaga gggccaccat cacctgcaag 540

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aaaccaggac aacctcctaa actcctgatt tactgggcca gcaccagaga aagcggggtc 660

ccagccaggt tcagcggcag tgggtctggg accgatttca ccctcacaat taatcctgtg 720

gaagctaatg atactgcaaa ttattactgt caccagtacc tgagcagcct gaccttcggc 780

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ctgcagaaag ataagatggc ggaggccttc agtgagattg ggatgaaagg cgagcgccgg 1380

aggggcaagg ggcacgatgg cctttttccag ggtctcagta cagccaccaa ggacaccttc 1440

gacgcccttc acatgcaggc cctgcccccct cgctgataa 1479

<210> 1707
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> CD8 leader sequence

<400> 1707
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ccg   63

<210> 1708
<211> 744
<212> DNA
<213> Artificial Sequence

<220>
<223> h20A10C2 scFV

<400> 1708
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cctggaaaag gccttgaatg ggttgcctct atcggcagag ccggcagcac ctactacagc   180

gattctgtga agggcagatt caccatcagc cgggacaacg ccaagaacag cctgtacctg   240

cagatgaact ccctgagagc cgaggacacc gccgtgtact attgtgccag aggacccatc   300

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cagtctccag cctccttggc cgtgtctcca ggacagaggg ccaccatcac ctgcaagagc   480

agccagagcg tgctgtactc cagcaaccag aagaactacc tggcctggta tcagcagaaa   540

ccaggacaac ctcctaaact cctgatttac tgggccagca ccagagaaag cggggtccca   600

gccaggttca gcggcagtgg gtctgggacc gatttcaccc tcacaattaa tcctgtggaa   660

gctaatgata ctgcaaatta ttactgtcac cagtacctga gcagcctgac cttcggcgga   720

gggaccaagg tggagatcaa acga   744

<210> 1709
<211> 135
<212> DNA
<213> Artificial Sequence

<220>
<223> CD8 hinge region

<400> 1709
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agcctgaggc ccgaggcttg tagacctgct gctggcggag ccgtgcacac cagaggactg   120

gatttcgcct gcgac   135

<210> 1710
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> CD8 transmembrane region

<400> 1710
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accctttact gc 72

<210> 1711
<211> 123
<212> DNA
<213> Artificial Sequence

<220>
<223> CD28

<400> 1711
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gggcctacca gaaagcatta ccagccctat gccccaccac gcgacttcgc agcctatcgc 120

tcc 123

<210> 1712
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<223> CD3 1XX

<400> 1712
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tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 120

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgttcaat 180

gaactgcaga aagataagat ggcggaggcc ttcagtgaga ttgggatgaa aggcgagcgc 240

cggaggggca aggggcacga tggcctttttc cagggtctca gtacagccac caaggacacc 300

ttcgacgccc ttcacatgca ggccctgccc cctcgctgat aa 342

<210> 1713
<211> 2380
<212> DNA
<213> Artificial Sequence

<220>
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ctctcctgtg cagcctctgg attcaccttc agtggctatg ccatgagctg ggtccgccag 180

gctccaggga aggggctgga gtgggtctca accattagta gtggcggaac ctacatatac 240

taccccgact cagtgaaggg ccgattcacc atctccagag acaacgccaa gaactcactg 300

tatctgcaaa tgaacagcct gagagccgag gacacggccg tgtattactg tgcgagactt 360

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tcctccggcg gtggcggatc cggcggtggc ggatccggcg gtggcggatc cgacattgtg 480

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gaacccgccg gacaacatca aggacaccaa gagcgacatc atattcttcc agcggagcgt 2220

gcccggccac gacaacaaga tgcagtttga gagcagcagc tacgagggct acttcctggc 2280

ctgcgagaaa gagcgggacc tgttcaagct gatcctgaag aaagaggacg aactgggcga 2340

ccgcagcatc atgttcaccg tgcagaacga ggactgataa 2380

<210> 1714
<211> 63
<212> DNA
<213> Artificial Sequence

<220>

<223> CD8 leader sequence

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ccg 63

<210> 1715
<211> 747
<212> DNA
<213> Artificial Sequence

<220>
<223> C2 scFV

<400> 1715
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aggttcagcg gcagtgggtc tgggaccgat ttcaccctca caattaatcc tgtggaagct 660

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gggaccaagg tggagatcaa acgaact 747

<210> 1716
<211> 135
<212> DNA
<213> Artificial Sequence

<220>
<223> CD8 hinge region

<400> 1716
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agcctgaggc ccgaggcttg tagacctgct gctggcggag ccgtgcacac cagaggactg 120

gatttcgcct gcgac 135

<210> 1717
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> CD8 transmembrane region

<400> 1717

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accctttact gc                                                           72


<210>  1718
<211>  126
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  41BB

<400>  1718
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actactcaag aggaagatgg ctgtagctgc cgatttccag aagaagaaga aggaggatgt      120

gaactg                                                                 126


<210>  1719
<211>  336
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CD3

<400>  1719
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tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc      120

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat      180

gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc      240

cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc      300

tacgacgccc ttcacatgca ggccctgccc cctcgc                                336


<210>  1720
<211>  50
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  plasmid

<400>  1720
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<210>  1721
<211>  168
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  6xNFAT FoxP3

<400>  1721
ggcttcattt tttccattta ctgcagaggc ttcatttttt ccatttactg cagaggcttc       60

atttttttcca tttactgcag aggcttcatt ttttccattt actgcagagg cttcattttt      120

tccatttact gcagaggctt catttttttcc atttactgca gaactagt                  168
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<210> 1722
<211> 118
<212> DNA
<213> Artificial Sequence

<220>
<223> mCMV

<400> 1722
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ctggagacgc catccacgct gttttgacct ccatagaaga caccgggacc gatccagc   118

<210> 1723
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> plasmid

<400> 1723
ctcgagagac ccaatgctag ccacc   25

<210> 1724
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> CD8 leader sequence

<400> 1724
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg   60

ccg   63

<210> 1725
<211> 477
<212> DNA
<213> Artificial Sequence

<220>
<223> IL18

<400> 1725
tacttcggca agctggaaag caagctgagc gtgatccgga acctgaacga ccaggtgctg   60

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aacgcccctc ggaccatctt catcatcagc atgtacaagg acagccagcc tagaggcatg   180

gccgtgacca tctctgtgaa gtgcgagaag atcagcaccc tgagctgcga gaacaagatc   240

atcagcttca aagagatgaa cccgccggac aacatcaagg acaccaagag cgacatcata   300

ttcttccagc ggagcgtgcc cggccacgac aacaagatgc agtttgagag cagcagctac   360

gagggctact tcctggcctg cgagaaagag cgggacctgt tcaagctgat cctgaagaaa   420

gaggacgaac tgggcgaccg cagcatcatg ttcaccgtgc agaacgagga ctgataa   477

<210> 1726

<211> 1482
<212> DNA
<213> Artificial Sequence

<220>
<223> pCDH MSCV hC2 CAR CD28 1XX

<400> 1726
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tatctgcaaa tgaacagcct gagagccgag gacacggccg tgtattactg tgcgagactt 360

gggggggata attactacga atacttcgat gtctggggca aagggaccac ggtcaccgtc 420

tcctccggcg gtggcggatc cggcggtggc ggatccggcg gtggcggatc cgacattgtg 480

ctgacccagt ctccagcctc cttggccgtg tctccaggac agagggccac catcacctgc 540

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gctaatgata ctgcaaatta ttactgtcag cacagtaggg agctgccttt cacattcggc 780

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cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgttcaat 1320

gaactgcaga aagataagat ggcggaggcc ttcagtgaga ttgggatgaa aggcgagcgc 1380

cggaggggca aggggcacga tggccttttc cagggtctca gtacagccac caaggacacc 1440

ttcgacgccc ttcacatgca ggccctgccc cctcgctgat aa 1482

<210> 1727
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> CD8 leader sequence

<400> 1727
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

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ccg                                                                 63


<210>  1728
<211>  747
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  C2 scFV

<400>  1728
gaggtgcagc tggtggagtc tgggggaggc ctggtcaagc ctggggggtc cctgagactc       60

tcctgtgcag cctctggatt caccttcagt ggctatgcca tgagctgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtctcaacc attagtagtg gcggaaccta catatactac      180

cccgactcag tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat      240

ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagacttggg      300

ggggataatt actacgaata cttcgatgtc tggggcaaag ggaccacggt caccgtctcc      360

tccggcggtg gcggatccgg cggtggcgga tccggcggtg gcggatccga cattgtgctg      420

acccagtctc cagcctcctt ggccgtgtct ccaggacaga gggccaccat cacctgcaga      480

gccagtaaga gtgtcagtac cagcggatac tcctacatgc actggtatca gcagaaacca      540

ggacaacctc ctaaactcct gatttacctg gcatccaatc tggagagcgg ggtcccagcc      600

aggttcagcg gcagtgggtc tgggaccgat ttcaccctca caattaatcc tgtggaagct      660

aatgatactg caaattatta ctgtcagcac agtagggagc tgcctttcac attcggcgga      720

gggaccaagg tggagatcaa acgaact                                          747


<210>  1729
<211>  135
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CD8 hinge region

<400>  1729
acaacaaccc ctgcccccag acctcctacc ccagccccta caattgccag ccagcctctg       60

agcctgaggc ccgaggcttg tagacctgct gctggcggag ccgtgcacac cagaggactg      120

gatttcgcct gcgac                                                       135


<210>  1730
<211>  72
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CD8 transmembrane region

<400>  1730
atctacatct gggcgccctt ggccgggact tgtggggtcc ttctcctgtc actggttatc       60

accctttact gc                                                           72
```

<210> 1731
<211> 123
<212> DNA
<213> Artificial Sequence

<220>
<223> CD28

<400> 1731
aggagtaaga ggagcaggct cctgcacagt gactacatga acatgactcc tagaagacct 60

gggcctacca gaaagcatta ccagccctat gccccaccac gcgacttcgc agcctatcgc 120

tcc 123

<210> 1732
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<223> CD3 1XX

<400> 1732
agagtgaagt tcagcaggag cgcagacgcc cccgcgtaca agcagggcca gaaccagctc 60

tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 120

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgttcaat 180

gaactgcaga aagataagat ggcggaggcc ttcagtgaga ttgggatgaa aggcgagcgc 240

cggaggggca aggggcacga tggcctttttc cagggtctca gtacagccac caaggacacc 300

ttcgacgccc ttcacatgca ggccctgccc cctcgctgat aa 342

<210> 1733
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse B12 light chain variable framework 2 (FR2) sequence

<400> 1733
tggtatcagc agaaaccagg acagccaccc aaactcctca tctat 45

<210> 1734
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse B12 light chain variable framework 2 (FR2) sequence

<400> 1734

Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
1 5 10 15

<210> 1735
<211> 21
<212> DNA
<213> Artificial Sequence

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<220>
<223>  Mouse B12 light chain variable complementarity determining
       regions 2 (CDR2) sequence

<400>  1735
cttgcatcca ccctagattc t                                                 21


<210>  1736
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B12 light chain variable complementarity determining
       regions 2 (CDR2) sequence

<400>  1736

Leu Ala Ser Thr Leu Asp Ser
1               5


<210>  1737
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B12 light chain variable framework 3 (FR3) sequence

<400>  1737
ggggtccctg ccaggttcag tggcagtggg tctaggacag acttcaccct caccattgat       60

cctgtggagg ctgatgatgc tgcaacctat tactgt                                 96


<210>  1738
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B12 light chain variable framework 3 (FR3) sequence

<400>  1738

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr
1               5                   10                  15


Leu Thr Ile Asp Pro Val Glu Ala Asp Asp Ala Ala Thr Tyr Tyr Cys
            20                  25                  30


<210>  1739
<211>  27
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B12 light chain variable complementarity determining
       regions 3 (CDR3) sequence

<400>  1739
cagcaaaata atgaggatcc tccgacg                                           27
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```
<210>  1740
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B12 light chain variable complementarity determining
       regions 3 (CDR3) sequence

<400>  1740

Gln Gln Asn Asn Glu Asp Pro Pro Thr
1               5


<210>  1741
<211>  31
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Mouse B12 light chain variable framework 4 (FR4) sequence

<400>  1741
ttcggtggag gcaccaagct ggaaatcaag g                                      31


<210>  1742
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse B12 light chain variable framework 4 (FR4) sequence

<400>  1742

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
1               5                   10


<210>  1743
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  epitope to which NME1 and NME7AB bind part of the 10 membrane
       proximal PRT

<400>  1743

Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala
1               5                   10


<210>  1744
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  epitope to which NME1 and NME7AB bind part of the 10 membrane
       proximal PRT

<400>  1744

Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val
1               5                   10
```

```
<210>  1745
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  epitope to which NME1 and NME7AB bind part of the 10 membrane
       proximal PRT

<400>  1745

Ala Ser Arg Tyr Asn Leu Thr
1               5


<210>  1746
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Fragment of PSMGFR

<400>  1746

Gly Thr Ile Asn Val His Asp Val Glu Thr
1               5                   10


<210>  1747
<211>  4
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Fragment of PSMGFR

<400>  1747

Phe Pro Phe Ser
1


<210>  1748
<211>  20
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Fragment of PSMGFR

<400>  1748

Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu
1               5                   10                  15


Ala Phe Arg Glu
            20


<210>  1749
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
```

<223> Fragment of PSMGFR

<400> 1749

Gln Phe Asn Gln Tyr Lys Thr Glu Ala
1   5

<210> 1750
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Fragment of PSMGFR

<400> 1750

Val Gln Leu Thr Leu Ala Phe Arg Glu
1   5

<210> 1751
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Fragment of PSMGFR

<400> 1751

Ser Val Ser Asp Val
1   5

<210> 1752
<211> 627
<212> DNA
<213> Artificial Sequence

<220>
<223> IL18 sequence

<400> 1752
atagaagaca ccgggaccga tccagcctcg agagacccaa tgctagccac catggcctta   60

ccagtgaccg ccttgctcct gccgctggcc ttgctgctcc acgccgccag gccgtacttc   120

ggcaagctgg aaagcaagct gagcgtgatc cggaacctga acgaccaggt gctgttcatc   180

gatcagggca acagacccct gttcgaggac atgaccgaca gcgactgcag agacaacgcc   240

cctcggacca tcttcatcat cagcatgtac aaggacagcc agcctagagg catggccgtg   300

accatctctg tgaagtgcga gaagatcagc accctgagct gcgagaacaa gatcatcagc   360

ttcaaagaga tgaacccgcc ggacaacatc aaggacacca agagcgacat catattcttc   420

cagcggagcg tgcccggcca cgacaacaag atgcagtttg agagcagcag ctacgagggc   480

tacttcctgg cctgcgagaa agagcgggac ctgttcaagc tgatcctgaa gaaagaggac   540

gaactgggcg accgcagcat catgttcacc gtgcagaacg aggactgata aaagcttggc   600

aatccggtac tgttggtaaa gccacca   627

<210> 1753

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<211>  207
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  IL18 sequence

<400>  1753

Ile Glu Asp Thr Gly Thr Asp Pro Ala Ser Arg Asp Pro Met Leu Ala
1               5                   10                  15


Thr Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu
            20                  25                  30


Leu His Ala Ala Arg Pro Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser
        35                  40                  45


Val Ile Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn
    50                  55                  60


Arg Pro Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala
65                  70                  75                  80


Pro Arg Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg
                85                  90                  95


Gly Met Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Thr Leu
            100                 105                 110


Ser Cys Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp
        115                 120                 125


Asn Ile Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val
    130                 135                 140


Pro Gly His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly
145                 150                 155                 160


Tyr Phe Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu
                165                 170                 175


Lys Lys Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln
            180                 185                 190


Asn Glu Asp Lys Leu Gly Asn Pro Val Leu Leu Val Lys Pro Pro
        195                 200                 205


<210>  1754
<211>  56
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer
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<400> 1754
agggagaccc aagctggcta gttaagcttg gatggcctta ccagtgaccg ccttgc   56

<210> 1755
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 1755
taggccagag aaatgttctg gcattatcag cgagggggca gggcctgc   48

<210> 1756
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 1756
tgccagaaca tttctctgg   19

<210> 1757
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 1757
acagtcgagg ctgatcagcg ggtttaaact tatcagtcct cgttctgcac gg   52

<210> 1758
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 1758
atgcaggccc tgccccctcg ctgataagtt taaactgcca gaacatttct ctggcctaac   60

<210> 1759
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 1759
accggagcga tcgcagatcc ttcgcggccg cttatcagtc ctcgttctgc acggtgaac   59

<210> 1760
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 1760
attgcactag ttgaaagacc ccacctgtag g   31

<210> 1761
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 1761
aatgctctag aatacgggta tccagg   26

<210> 1762
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 1762
atagcgaatt cgtaccgagg gccaccatgg   30

<210> 1763
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 1763
taggcctccc accgtacacg cctaggtacc acgccttctg tatg   44

<210> 1764
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 1764
taggcctccc accgtacacg cctaggtacc tctgcagtaa atgg   44

<210> 1765
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 1765
taaggccatg gtggctagc   19

<210> 1766
<211> 32

<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 1766
aataagttta aactgccaga acatttctct gg   32

<210> 1767
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 1767
atatagcggc cgcttatcag tcctcgttct gcacgg   36

<210> 1768
<211> 347
<212> DNA
<213> Artificial Sequence

<220>
<223> 6x FoxP3NFAT mCMV

<400> 1768
agaacatttc tctggcctaa ctggccggta ccggcttcat tttttccatt tactgcagag   60

gcttcatttt ttccatttac tgcagaggct tcattttttc catttactgc agaggcttca   120

ttttttccat ttactgcaga ggcttcattt tttccattta ctgcagaggc ttcatttttt   180

ccatttactg cagaactagt taggcgtgta cggtgggagg cctatataag cagagctcgt   240

ttagtgaacc gtcagatcgc ctggagacgc catccacgct gttttgacct ccatagaaga   300

caccgggacc gatccagcct cgagagaccc aatgctagcc accatgg   347

<210> 1769
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> 6x FoxP3NFAT mCMV

<400> 1769

Arg Thr Phe Leu Trp Pro Asn Trp Pro Val Pro Ala Ser Phe Phe Pro
1   5   10   15

Phe Thr Ala Glu Ala Ser Phe Phe Pro Phe Thr Ala Glu Ala Ser Phe
            20   25   30

Phe Pro Phe Thr Ala Glu Ala Ser Phe Phe Pro Phe Thr Ala Glu Ala
        35   40   45

Ser Phe Phe Pro Phe Thr Ala Glu Ala Ser Phe Phe Pro Phe Thr Ala
    50   55   60

```
Glu Leu Val Arg Arg Val Arg Trp Glu Ala Tyr Ile Ser Arg Ala Arg
65                  70                  75                  80


Leu Val Asn Arg Gln Ile Ala Trp Arg Arg His Pro Arg Cys Phe Asp
                85                  90                  95


Leu His Arg Arg His Arg Asp Arg Ser Ser Leu Glu Arg Pro Asn Ala
            100                 105                 110


Ser His His Gly
        115


<210>  1770
<211>  343
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  6x FoxP3NFAT mIL2P

<400>  1770
agaacatttc tctggcctaa ctggccggta ccggcttcat tttttccatt tactgcagag       60

gcttcatttt ttccatttac tgcagaggct tcattttttc catttactgc agaggcttca      120

tttttttccat ttactgcaga ggcttcattt tttccattta ctgcagaggc ttcatttttt      180

ccatttactg cagaactagt cattttgaca cccccataat atttttccag aattaacagt      240

ataaattgca tctcttgttc aagagttccc tatcactctc tttaatcact actcacagta      300

acctcaactc ctgcctcgag agacccaatg ctagccacca tgg                        343


<210>  1771
<211>  113
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  6x FoxP3NFAT mIL2P


<220>
<221>  misc_feature
<222>  (113)..(113)
<223>  Xaa can be any naturally occurring amino acid

<400>  1771

Arg Thr Phe Leu Trp Pro Asn Trp Pro Val Pro Ala Ser Phe Phe Pro
1               5                   10                  15


Phe Thr Ala Glu Ala Ser Phe Phe Pro Phe Thr Ala Glu Ala Ser Phe
            20                  25                  30


Phe Pro Phe Thr Ala Glu Ala Ser Phe Phe Pro Phe Thr Ala Glu Ala
        35                  40                  45


Ser Phe Phe Pro Phe Thr Ala Glu Ala Ser Phe Phe Pro Phe Thr Ala
    50                  55                  60
```

Glu Leu Val Ile Leu Thr Pro Pro Tyr Phe Ser Arg Ile Asn Ser Ile
65   70   75   80

Asn Cys Ile Ser Cys Ser Arg Val Pro Tyr His Ser Leu Ser Leu Leu
                85   90   95

Thr Val Thr Ser Thr Pro Ala Ser Arg Asp Pro Met Leu Ala Thr Met
            100   105   110

Xaa

<210> 1772
<211> 260
<212> DNA
<213> Artificial Sequence

<220>
<223> 6x FoxP3NFAT miniP

<400> 1772
agaacatttc tctggcctaa ctggccggta ccggcttcat tttttccatt tactgcagag   60

gcttcatttt ttccatttac tgcagaggct tcattttttc catttactgc agaggcttca   120

ttttttccat ttactgcaga ggcttcattt tttccattta ctgcagaggc ttcatttttt   180

ccatttactg cagaactagt agagggtata taatggaagc tcgacttcca gctcgagaga   240

cccaatgcta gccaccatgg   260

<210> 1773
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<223> 6x FoxP3NFAT miniP

<400> 1773

Arg Thr Phe Leu Trp Pro Asn Trp Pro Val Pro Ala Ser Phe Phe Pro
1   5   10   15

Phe Thr Ala Glu Ala Ser Phe Phe Pro Phe Thr Ala Glu Ala Ser Phe
            20   25   30

Phe Pro Phe Thr Ala Glu Ala Ser Phe Phe Pro Phe Thr Ala Glu Ala
        35   40   45

Ser Phe Phe Pro Phe Thr Ala Glu Ala Ser Phe Phe Pro Phe Thr Ala
    50   55   60

Glu Leu Val Glu Gly Ile Trp Lys Leu Asp Phe Gln Leu Glu Arg Pro
65   70   75   80

Asn Ala Ser His His Gly

```
                85


<210>  1774
<211>  365
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  6x IL2NFAT mCMV

<400>  1774
agaacatttc tctggcctaa ctggccggta ccggaggaaa aactgtttca tacagaaggc       60

gtggaggaaa aactgtttca tacagaaggc gtggaggaaa aactgtttca tacagaaggc      120

gtggaggaaa aactgtttca tacagaaggc gtggaggaaa aactgtttca tacagaaggc      180

gtggaggaaa aactgtttca tacagaaggc gtactagtta ggcgtgtacg gtgggaggcc      240

tatataagca gagctcgttt agtgaaccgt cagatcgcct ggagacgcca tccacgctgt      300

tttgacctcc atagaagaca ccgggaccga tccagcctcg agagacccaa tgctagccac      360

catgg                                                                  365


<210>  1775
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  6x IL2NFAT mCMV

<400>  1775

Arg Thr Phe Leu Trp Pro Asn Trp Pro Val Pro Glu Glu Lys Leu Phe
1               5                   10                  15


His Thr Glu Gly Val Glu Glu Lys Leu Phe His Thr Glu Gly Val Glu
            20                  25                  30


Glu Lys Leu Phe His Thr Glu Gly Val Glu Glu Lys Leu Phe His Thr
        35                  40                  45


Glu Gly Val Glu Glu Lys Leu Phe His Thr Glu Gly Val Glu Glu Lys
    50                  55                  60


Leu Phe His Thr Glu Gly Val Leu Val Arg Arg Val Arg Trp Glu Ala
65                  70                  75                  80


Tyr Ile Ser Arg Ala Arg Leu Val Asn Arg Gln Ile Ala Trp Arg Arg
                85                  90                  95


His Pro Arg Cys Phe Asp Leu His Arg Arg His Arg Asp Arg Ser Ser
            100                 105                 110


Leu Glu Arg Pro Asn Ala Ser His His Gly
        115                 120
```

<210> 1776
<211> 361
<212> DNA
<213> Artificial Sequence

<220>
<223> 6x IL2NFAT mIL2P

<400> 1776
agaacatttc tctggcctaa ctggccggta ccggaggaaa aactgtttca tacagaaggc   60

gtggaggaaa aactgtttca tacagaaggc gtggaggaaa aactgtttca tacagaaggc   120

gtggaggaaa aactgtttca tacagaaggc gtggaggaaa aactgtttca tacagaaggc   180

gtggaggaaa aactgtttca tacagaaggc gtactagtca ttttgacacc cccataatat   240

ttttccagaa ttaacagtat aaattgcatc tcttgttcaa gagttcccta tcactctctt   300

taatcactac tcacagtaac ctcaactcct gcctcgagag acccaatgct agccaccatg   360

g   361

<210> 1777
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 6x IL2NFAT mIL2P

<220>
<221> misc_feature
<222> (119)..(119)
<223> Xaa can be any naturally occurring amino acid

<400> 1777

Arg Thr Phe Leu Trp Pro Asn Trp Pro Val Pro Glu Glu Lys Leu Phe
1   5   10   15

His Thr Glu Gly Val Glu Glu Lys Leu Phe His Thr Glu Gly Val Glu
            20   25   30

Glu Lys Leu Phe His Thr Glu Gly Val Glu Glu Lys Leu Phe His Thr
        35   40   45

Glu Gly Val Glu Glu Lys Leu Phe His Thr Glu Gly Val Glu Glu Lys
    50   55   60

Leu Phe His Thr Glu Gly Val Leu Val Ile Leu Thr Pro Pro Tyr Phe
65   70   75   80

Ser Arg Ile Asn Ser Ile Asn Cys Ile Ser Cys Ser Arg Val Pro Tyr
                85   90   95

His Ser Leu Ser Leu Leu Thr Val Thr Ser Thr Pro Ala Ser Arg Asp
            100   105   110

Pro Met Leu Ala Thr Met Xaa

```
        115


<210>  1778
<211>  278
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  6x IL2NFAT miniP

<400>  1778
agaacatttc tctggcctaa ctggccggta ccggaggaaa aactgtttca tacagaaggc       60

gtggaggaaa aactgtttca tacagaaggc gtggaggaaa aactgtttca tacagaaggc      120

gtggaggaaa aactgtttca tacagaaggc gtggaggaaa aactgtttca tacagaaggc      180

gtggaggaaa aactgtttca tacagaaggc gtactagtag agggtatata atggaagctc      240

gacttccagc tcgagagacc caatgctagc caccatgg                              278


<210>  1779
<211>  92
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  6x IL2NFAT miniP

<400>  1779

Arg Thr Phe Leu Trp Pro Asn Trp Pro Val Pro Glu Glu Lys Leu Phe
1               5                   10                  15


His Thr Glu Gly Val Glu Glu Lys Leu Phe His Thr Glu Gly Val Glu
            20                  25                  30


Glu Lys Leu Phe His Thr Glu Gly Val Glu Glu Lys Leu Phe His Thr
        35                  40                  45


Glu Gly Val Glu Glu Lys Leu Phe His Thr Glu Gly Val Glu Glu Lys
    50                  55                  60


Leu Phe His Thr Glu Gly Val Leu Val Glu Gly Ile Trp Lys Leu Asp
65                  70                  75                  80


Phe Gln Leu Glu Arg Pro Asn Ala Ser His His Gly
                85                  90


<210>  1780
<211>  459
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Human NME1

<400>  1780
atggccaact gtgagcgtac cttcattgcg atcaaaccag atggggtcca gcggggtctt       60

gtgggagaga ttatcaagcg ttttgagcag aaaggattcc gccttgttgg tctgaaattc      120
```

atgcaagctt ccgaagatct tctcaaggaa cactacgttg acctgaagga ccgtccattc 180

tttgccggcc tggtgaaata catgcactca gggccggtag ttgccatggt ctgggagggg 240

ctgaatgtgg tgaagacggg ccgagtcatg ctcggggaga ccaaccctgc agactccaag 300

cctgggacca tccgtggaga cttctgcata caagttggca ggaacattat acatggcagt 360

gattctgtgg agagtgcaga gaaggagatc ggcttgtggt ttcaccctga ggaactggta 420

gattacacga gctgtgctca gaactggatc tatgaatga 459

<210> 1781
<211> 152
<212> PRT
<213> Artificial Sequence

<220>
<223> Human NME1

<400> 1781

Met Ala Asn Cys Glu Arg Thr Phe Ile Ala Ile Lys Pro Asp Gly Val
1 5 10 15

Gln Arg Gly Leu Val Gly Glu Ile Ile Lys Arg Phe Glu Gln Lys Gly
20 25 30

Phe Arg Leu Val Gly Leu Lys Phe Met Gln Ala Ser Glu Asp Leu Leu
35 40 45

Lys Glu His Tyr Val Asp Leu Lys Asp Arg Pro Phe Phe Ala Gly Leu
50 55 60

Val Lys Tyr Met His Ser Gly Pro Val Val Ala Met Val Trp Glu Gly
65 70 75 80

Leu Asn Val Val Lys Thr Gly Arg Val Met Leu Gly Glu Thr Asn Pro
85 90 95

Ala Asp Ser Lys Pro Gly Thr Ile Arg Gly Asp Phe Cys Ile Gln Val
100 105 110

Gly Arg Asn Ile Ile His Gly Ser Asp Ser Val Glu Ser Ala Glu Lys
115 120 125

Glu Ile Gly Leu Trp Phe His Pro Glu Glu Leu Val Asp Tyr Thr Ser
130 135 140

Cys Ala Gln Asn Trp Ile Tyr Glu
145 150

<210> 1782
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Human NME7

<400> 1782
atgaatcata gtgaaagatt cgttttcatt gcagagtggt atgatccaaa tgcttcactt 60

cttcgacgtt atgagctttt attttaccca ggggatggat ctgttgaaat gcatgatgta 120

aagaatcatc gcaccttttt aaagcggacc aaatatgata acctgcactt ggaagattta 180

tttataggca acaaagtgaa tgtcttttct cgacaactgg tattaattga ctatggggat 240

caatatacag ctcgccagct gggcagtagg aaagaaaaaa cgctagccct aattaaacca 300

gatgcaatat caaaggctgg agaaataatt gaaataataa acaaagctgg atttactata 360

accaaactca aaatgatgat gctttcaagg aaagaagcat tggattttca tgtagatcac 420

cagtcaagac cctttttcaa tgagctgatc cagtttatta caactggtcc tattattgcc 480

atggagattt taagagatga tgctatatgt gaatggaaaa gactgctggg acctgcaaac 540

tctggagtgg cacgcacaga tgcttctgaa agcattagag ccctctttgg aacagatggc 600

ataagaaatg cagcgcatgg ccctgattct tttgcttctg cggccagaga aatggagttg 660

ttttttcctt caagtggagg ttgtgggccg gcaaacactg ctaaatttac taattgtacc 720

tgttgcattg ttaaacccca tgctgtcagt gaaggactgt tgggaaagat cctgatggct 780

atccgagatg caggttttga aatctcagct atgcagatgt tcaatatgga tcgggttaat 840

gttgaggaat tctatgaagt ttataaagga gtagtgaccg aatatcatga catggtgaca 900

gaaatgtatt ctggcccttg tgtagcaatg gagattcaac agaataatgc tacaaagaca 960

tttcgagaat tttgtggacc tgctgatcct gaaattgccc ggcatttacg ccctggaact 1020

ctcagagcaa tctttggtaa aactaagatc cagaatgctg ttcactgtac tgatctgcca 1080

gaggatggcc tattagaggt tcaatacttc ttcaagatct tggataatta g 1131

<210> 1783
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Human NME7

<400> 1783

Met Asn His Ser Glu Arg Phe Val Phe Ile Ala Glu Trp Tyr Asp Pro
1 5 10 15

Asn Ala Ser Leu Leu Arg Arg Tyr Glu Leu Leu Phe Tyr Pro Gly Asp
20 25 30

Gly Ser Val Glu Met His Asp Val Lys Asn His Arg Thr Phe Leu Lys
35 40 45

Arg Thr Lys Tyr Asp Asn Leu His Leu Glu Asp Leu Phe Ile Gly Asn
50 55 60

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Lys Val Asn Val Phe Ser Arg Gln Leu Val Leu Ile Asp Tyr Gly Asp
65                  70                  75                  80

Gln Tyr Thr Ala Arg Gln Leu Gly Ser Arg Lys Glu Lys Thr Leu Ala
                85                  90                  95

Leu Ile Lys Pro Asp Ala Ile Ser Lys Ala Gly Glu Ile Ile Glu Ile
            100                 105                 110

Ile Asn Lys Ala Gly Phe Thr Ile Thr Lys Leu Lys Met Met Met Leu
        115                 120                 125

Ser Arg Lys Glu Ala Leu Asp Phe His Val Asp His Gln Ser Arg Pro
    130                 135                 140

Phe Phe Asn Glu Leu Ile Gln Phe Ile Thr Thr Gly Pro Ile Ile Ala
145                 150                 155                 160

Met Glu Ile Leu Arg Asp Asp Ala Ile Cys Glu Trp Lys Arg Leu Leu
                165                 170                 175

Gly Pro Ala Asn Ser Gly Val Ala Arg Thr Asp Ala Ser Glu Ser Ile
            180                 185                 190

Arg Ala Leu Phe Gly Thr Asp Gly Ile Arg Asn Ala Ala His Gly Pro
        195                 200                 205

Asp Ser Phe Ala Ser Ala Ala Arg Glu Met Glu Leu Phe Phe Pro Ser
    210                 215                 220

Ser Gly Gly Cys Gly Pro Ala Asn Thr Ala Lys Phe Thr Asn Cys Thr
225                 230                 235                 240

Cys Cys Ile Val Lys Pro His Ala Val Ser Glu Gly Leu Leu Gly Lys
                245                 250                 255

Ile Leu Met Ala Ile Arg Asp Ala Gly Phe Glu Ile Ser Ala Met Gln
            260                 265                 270

Met Phe Asn Met Asp Arg Val Asn Val Glu Glu Phe Tyr Glu Val Tyr
        275                 280                 285

Lys Gly Val Val Thr Glu Tyr His Asp Met Val Thr Glu Met Tyr Ser
    290                 295                 300

Gly Pro Cys Val Ala Met Glu Ile Gln Gln Asn Asn Ala Thr Lys Thr
305                 310                 315                 320

Phe Arg Glu Phe Cys Gly Pro Ala Asp Pro Glu Ile Ala Arg His Leu
                325                 330                 335

Arg Pro Gly Thr Leu Arg Ala Ile Phe Gly Lys Thr Lys Ile Gln Asn
```

```
            340                 345                 350

Ala Val His Cys Thr Asp Leu Pro Glu Asp Gly Leu Leu Glu Val Gln
        355                 360                 365

Tyr Phe Phe Lys Ile Leu Asp Asn
    370                 375
```

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<210>  1784
<211>  1359
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized C2 IgG1 heavy chain sequence

<400>  1784
gaggtgcagc tggtggagtc tgggggaggc ctggtcaagc ctggggggtc cctgagactc       60

tcctgtgcag cctctggatt caccttcagt ggctatgcca tgagctgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtctcaacc attagtagtg gcggaaccta catatactac      180

cccgactcag tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat      240

ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagacttggg      300

ggggataatt actacgaata cttcgatgtc tggggcaaag ggaccacggt caccgtctcc      360

tccgctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct      420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg      480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc      540

tcaggactct actccctcag cagcgtggtg acagtgccct ccagcagctt gggcacccag      600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag      660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg      720

ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc      780

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac      840

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac      900

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc      960

aaggagtaca agtgcaaggt ctccaacaaa gccctcccag cccccatcga gaaaaccatc     1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggag     1080

gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac     1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc     1200

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg     1260

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac     1320

acgcagaaga gcctctccct gtctccgggt aaatgataa                            1359


<210>  1785
<211>  12
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<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 17H6 heavy chain variable complementarity determining
       regions 3 (CDR3) sequence

<400>  1785

Asp Tyr Tyr Gly Ser Asn Pro Ala Trp Phe Ala Tyr
1               5                   10


<210>  1786
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse 17H6 heavy chain variable framework 4 (FW4) sequence

<400>  1786

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
1               5                   10


<210>  1787
<211>  72
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CD8 transmembrane domain

<400>  1787
atctacatct gggcgccctt ggccgggact tgtggggtcc ttctcctgtc actggttatc        60

accctttact gc                                                            72


<210>  1788
<211>  126
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  41BB

<400>  1788
aaacggggca gaaagaaact cctgtatata ttcaaacaac catttatgag accagtacaa        60

actactcaag aggaagatgg ctgtagctgc cgatttccag aagaagaaga aggaggatgt       120

gaactg                                                                  126


<210>  1789
<211>  342
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CD3

<400>  1789
agagtgaagt tcagcaggag cgcagacgcc cccgcgtaca agcagggcca gaaccagctc        60

tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc       120
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cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 180

gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 240

cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc 300

tacgacgccc ttcacatgca ggccctgccc cctcgctgat aa 342

<210> 1790
<211> 1482
<212> DNA
<213> Artificial Sequence

<220>
<223> pCDH MSCV h20A10-N CAR 41BB

<400> 1790
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgcaggtgc agctggttga atctggcggc ggacttgtga agcctggcgg atctctgaga 120

ctgagctgtg ccgccagcgg cttcaccttt agcacatacg ccatgagctg gatcagacag 180

gcccctggca aaggcctgga atgggtggcg tctattggca gagccggcag cacctactac 240

agcgactctg tgaagggcag attcaccatc agccgggaca acgccaagaa cagcctgtac 300

ctgcagatga actccctgag agccgaggac accgccgtgt actattgtgc cagaggaccc 360

atctacaacg actacgacga gttcgcctat tggggccagg gcacactggt cacagtttct 420

agcggcggtg gcggaagcgg aggcggtggc tccggtggcg gaggcagcga aattgtgctg 480

acacagagcc ccgccacact gtcactttct ccaggcgaaa gagccacact gagctgcaag 540

agcagccaga gcgtgctgta ctccagcaac cagaagaact acctggcctg gtatcagcag 600

aagcccggcc aagctcctcg gctgctgatc tattgggcca gcacaagaga gagcggcatc 660

cctgccagat ttctggcag cggctctggc accgatttca ccctgaccat aagcagcctg 720

gaacctgagg acttcgccgt gtattactgc caccagtacc tgagcagcct gacctttggc 780

ggaggcacca aggtggaaat caagcggaca acaacccctg cccccagacc tcctacccca 840

gcccctacaa ttgccagcca gcctctgagc ctgaggcccg aggcttgtag acctgctgct 900

ggcggagccg tgcacaccag aggactggat ttcgcctgcg acatctacat ctgggcgccc 960

ttggccggga cttgtggggt ccttctcctg tcactggtta tcacccttta ctgcaaacgg 1020

ggcagaaaga aactcctgta tatattcaaa caaccattta tgagaccagt acaaactact 1080

caagaggaag atggctgtag ctgccgattt ccagaagaag aagaaggagg atgtgaactg 1140

agagtgaagt tcagcaggag cgcagacgcc cccgcgtaca agcagggcca gaaccagctc 1200

tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 1260

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 1320

gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 1380

cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc 1440

tacgacgccc ttcacatgca ggccctgccc cctcgctgat aa 1482