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(54) Titre : TRAITEMENT DU CANCER AU MOYEN D'UN RECEPTEUR D'ANTIGENE CHIMERIQUE EN COMBINAISON AVEC UN INHIBITEUR D'UNE MOLECULE DE MACROPHAGE PRO-M2

(54) Title: TREATMENT OF CANCER USING A CHIMERIC ANTIGEN RECEPTOR IN COMBINATION WITH AN INHIBITOR OF A PRO-M2 MACROPHAGE MOLECULE

(57) Abrégé/Abstract:
The invention provides compositions and methods for treating diseases associated with expression of an antigen, e.g., a solid tumor antigen or antigen expressed on a tumor associated with TAMs and/or MDSCs, by administering a recombinant T cell comprising a CAR binding to said antigen, as described herein, in combination with an inhibitor of a pro-M2 macrophage molecule, e.g., described herein. The invention also provides kits and compositions described herein.

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(54) **Title:** TREATMENT OF CANCER USING A CHIMERIC ANTIGEN RECEPTOR IN COMBINATION WITH AN INHIBITOR OF A PRO-M2 MACROPHAGE MOLECULE

(57) **Abstract:** The invention provides compositions and methods for treating diseases associated with expression of an antigen, e.g., a solid tumor antigen or antigen expressed on a tumor associated with TAMs and/or MDSCs, by administering a recombinant T cell comprising a CAR binding to said antigen, as described herein, in combination with an inhibitor of a pro-M2 macrophage molecule, e.g., described herein. The invention also provides kits and compositions described herein.

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JUMBO APPLICATIONS/PATENTS

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RELATED APPLICATIONS

[001] This application claims priority to U.S. Serial No. 62/369589 filed August 1, 2016, the contents of which are incorporated herein by reference in its entirety.

SEQUENCE LISTING

[002] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in their entirety. Said ASCII copy, created on July 31, 2017, is named N2067-7113WO_SL.txt and is 1,549,304 bytes in size.

FIELD OF THE INVENTION

[003] The present invention relates generally to the use of T cells engineered to express a Chimeric Antigen Receptor (CAR), e.g., in combination with another agent such as, e.g., an inhibitor of a pro-M2 macrophage molecule, e.g., an inhibitor of IL-13, IL-13Rα1, IL-4, IL-4Rα, IL-10 or CSF-1, to treat a disease associated with expression of a cancer antigen, e.g., a solid tumor antigen or antigen on a cancer cell associated with tumor associated macrophages.

BACKGROUND OF THE INVENTION

[004] Many patients with malignancies are incurable with standard therapy. In addition, traditional treatment options often have serious side effects. Attempts have been made in cancer immunotherapy, however, several obstacles render this a very difficult goal to achieve clinical effectiveness. Although hundreds of so-called tumor antigens have been identified, these are generally derived from self and thus are poorly immunogenic. Furthermore, tumors use several mechanisms to render themselves hostile to the initiation and propagation of immune attack. Some of these mechanisms involve non-tumor cells that can be associated with the tumor cells, for example tumor-associated macrophages (TAMs), that can have a phenotype that is inhibitory to the immune response, e.g., an M2 phenotype.

[005] Recent developments using chimeric antigen receptor (CAR) modified autologous T cell (CART) therapy, which relies on redirecting T cells to a suitable cell-surface molecule on cancer cells such as B cell malignancies, show promising results in harnessing the power of the immune system to treat B cell malignancies and other cancers (see, e.g., Sadelain et al., Cancer Discovery 3:388-398 (2013)). The clinical results of the murine derived CART19 (i.e., "CTL019") have shown promise in establishing complete remissions in patients suffering with CLL as well as in childhood ALL (see, e.g., Kalos et al., Sci Transl Med 3:95ra73 (2011), Porter et al., NEJM 365:725-733 (2011), Grupp et al., NEJM 368:1509-1518 (2013)). Besides the ability for the chimeric antigen receptor on the genetically modified T cells to recognize and destroy the targeted cells, a successful therapeutic T cell therapy needs to have the ability to proliferate and persist over time, remain effective in an environment that inhibits their function, and to further monitor for malignant cell escapees. The variable quality of T cells, as well as *in vivo* anergy, suppression or exhaustion will have effects on CAR-transformed T cells' performance, over which skilled practitioners have limited control at this time. While certain CAR-transformed T cell products have proven effective, there is a need for CAR-transfromed T cell therapies with enhanced efficacy, e.g., enhanced efficacy against solid tumors and their associated immunoinhibitory tumor microenvironment (TME).

SUMMARY OF THE INVENTION

[006] The disclosure features, at least in part, compositions and methods of treating disorders such as cancer (e.g., solid tumors or tumors associated with tumor-associated macrophages) using immune effector cells (e.g., T cells or NK cells) that express a chimeric antigen receptor (CAR) molecule, e.g., a CAR that binds to a tumor antigen, e.g., an antigen expressed on the surface of a solid tumor or tumor associated with tumor-associated macrophages. The compositions include, and the methods include administering, immune effector cells (e.g., T cells or NK cells) expressing a tumor targeting CAR, in combination with an inhibitor of a pro-M2 macrophage molecule (e.g., an inhibitor of colony stimulating factor-1 (CSF-1), interleukin 10 (IL-10), interleukin 13 (IL-13), interleukin 4 (IL-4) or a receptor present on the surface of macrophage cells for IL-13 or IL-4, e.g., IL-13Rα1 or IL-4Rα). In some embodiments, the combination maintains or has better clinical effectiveness, e.g., against a solid tumor or tumor associated with tumor-associated macrophages, as compared to either

therapy alone. Without being bound by theory, it is shown herein that use of an inhibitor of a pro-M2 macrophage molecule (e.g., as described herein) inhibits polarization of macrophages, e.g., tumor-associated macrophages (TAMs) to the M2 phenotype, or reverses the phenotype of M2 macrophages, e.g., tumor-associated macrophages (TAMs), thereby removing a source of inhibition of a function of CAR-expressing cells, e.g., CAR-expressing T cells, e.g., an anti-tumor or proliferative activity of the CAR-expressing cells. The invention further pertains to the use of engineered cells, e.g., immune effector cells (e.g., T cells or NK cells), that express a CAR molecule that binds to a tumor antigen, e.g., a solid tumor antigen or antigen on a tumor cell associated with tumor-associated macrophages, in combination with an inhibitor of a pro-M2 macrophage molecule (e.g., an inhibitor of a pro-M2 macrophage molecule described herein) to treat a disorder associated with expression of a tumor antigen, e.g., a solid tumor antigen or antigen on a tumor associated with tumor-associated macrophages (e.g., a cancer).

[007] In a first aspect, the invention provides a method of treating a subject having a disease associated with expression of a tumor antigen (e.g., a subject having a cancer (e.g., a solid tumor or a tumor associated with tumor-associated macrophages)), including administering to the subject: (i) a CAR therapy including a cell, e.g., a population of immune effector cells, including, e.g., expressing, a chimeric antigen receptor (CAR) (e.g., as described herein). The CAR includes a tumor antigen binding domain (e.g., the tumor antigen binding domain of the CAR binds to CD19 or CD123), a transmembrane domain, and an intracellular signaling domain; and (ii) an inhibitor of a pro-M2 macrophage molecule (e.g., as described herein).

[008] In another aspect, the invention provides a CAR therapy including a cell, e.g., a population of immune effector cells, including (e.g., expressing) a chimeric antigen receptor (CAR) for use in combination with an inhibitor of a pro-M2 macrophage molecule in treating a subject having a disease associated with expression of a tumor antigen (e.g., a subject having a cancer (e.g., a solid tumor or a tumor associated with tumor-associated macrophages)). The CAR includes a tumor antigen binding domain (e.g., the tumor antigen binding domain of the CAR binds to CD19 or CD123), a transmembrane domain, and an intracellular signaling domain.

[009] In embodiments, the CAR therapy and the inhibitor of a pro-M2 macrophage molecule are administered sequentially.

[0010] In embodiments, including in any of the aforementioned aspects and embodiments, the inhibitor of a pro-M2 macrophage molecule is administered prior to the CAR therapy. In embodiments, including in any of the aforementioned aspects and embodiments, the inhibitor of a pro-M2 macrophage molecule and the CAR therapy are administered simultaneously or concurrently.

[0011] In embodiments, including in any of the aforementioned aspects and embodiments, the CAR therapy is administered as (a) single infusion or (b) multiple infusions (e.g., a single dose split into multiple infusions), and the inhibitor of a pro-M2 macrophage molecule is administered as (a) a single dose, or (b) multiple doses (e.g., a first and second, and optionally one or more subsequent doses).

[0012] In embodiments, including in any of the aforementioned aspects and embodiments, a dose of the CAR therapy is administered after (e.g., at least 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 1 week, 2 weeks, 3 weeks, 4 weeks, 5 weeks, or more, after) administration of a first dose of the inhibitor of a pro-M2 macrophage molecule, e.g., and before administration of the second dose of the inhibitor.

[0013] In embodiments, including in any of the aforementioned aspects and embodiments, a dose of the CAR therapy is administered concurrently with (e.g., within 2 days (e.g., within 2 days, 1 day, 24 hours, 12 hours, 6 hours, 4 hours, 2 hours, or less) of), the administration of a first dose of the inhibitor of a pro-M2 macrophage molecule.

[0014] In embodiments, including in any of the aforementioned aspects and embodiments, one or more subsequent doses of the inhibitor of a pro-M2 macrophage molecule are administered after a second dose of the inhibitor of a pro-M2 macrophage molecule.

[0015] In embodiments, including in any of the aforementioned aspects and embodiments, the inhibitor of a pro-M2 macrophage moleculeis administered in more than one dose, and the doses are administered twice a day (BID), once a day, once a week, once every 14 days, or once every month.

[0016] In embodiments, including in any of the aforementioned aspects and embodiments, the administering of the inhibitor of a pro-M2 macrophage molecule includes multiple doses including a duration of at least 7 days, e.g., at least 7 days, 8 days, 9 days, 10 days, 1 week, 2 weeks, 3 weeks, 4 weeks, 5 weeks, 6 weeks, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, or more.

[0017] In embodiments, including in any of the aforementioned aspects and embodiments, the CAR therapy is administered at a dose comprising at least about 5×10^6, 1×10^7, 1.5×10^7, 2×10^7, 2.5×10^7, 3×10^7, 3.5×10^7, 4×10^7, 5×10^7, 1×10^8, 1.5×10^8, 2×10^8, 2.5×10^8, 3×10^8, 3.5×10^8, 4×10^8, 5×10^8, 1×10^9, 2×10^9, or 5×10^9 cells, e.g., CAR positive cells.

[0018] In another aspect, the invention provides a pharmaceutical composition including (i) a cell, e.g., a population of immune effector cells, including, e.g., expressing, a chimeric antigen receptor (CAR) (e.g., as described herein), wherein the CAR includes a tumor antigen binding domain, a transmembrane domain, and an intracellular signaling domain; and (ii) an inhibitor of a pro-M2 macrophage molecule (e.g., as described herein).

[0019] In another aspect, the invention provides a pharmaceutical composition including (i) a cell, e.g., a population of immune effector cells, including, e.g., expressing, a chimeric antigen receptor (CAR) (e.g., described herein), wherein the CAR includes a tumor antigen binding domain, a transmembrane domain, and an intracellular signaling domain; and (ii) an inhibitor of a pro-M2 macrophage molecule, (e.g., as described herein), for use in treating a disease or disorder described herein.

[0020] In another aspect, the invention provides a method for stimulating a T cell-mediated immune response to a solid tumor cell in a mammal, the method including administering to a mammal an effective amount of a composition of the previous aspects.

[0021] In another aspect, the invention provides a method of providing an anti-tumor, e.g., an anti-solid tumor, immunity in a mammal, including administering to the mammal an effective amount of the composition

[0022] In another aspect, the invention provides a method of treating a mammal having a disease associated with expression of a tumor antigen, e.g., a solid tumor antigen, said method including administering an effective amount of the composition of the previous aspects.

[0023] In embodiments, including in any of the method embodiments above, the cell, e.g., the population of immune effector cells, and the inhibitor of a pro-M2 macrophage molecule are provided for separate administration (e.g., in two separate compositions). In other embodiments, including in any of the method embodiments above, the cell, e.g., the population of immune effector cells, and the inhibitor of a pro-M2 macrophage molecule are provided for simultaneous administration (e.g., in one composition).

[0024] The following aspects of the inhibitor of the pro-M2 macrophage molecule may be utilized with any of the aforementioned aspects and embodiments.

[0025] In embodiments, the inhibitor of a pro-M2 macrophage molecule is an IL-13 inhibitor, an IL-4 inhibitor, an IL-13Rα1 inhibitor, an IL-4Rα inhibitor, an IL-10 inhibitor, a CSF-1 inhibitor, a TGF beta inhibitor, or combinations thereof, e.g., as described herein. In embodiments, the inhibitor of a pro-M2 macrophage molecule is an IL-13 inhibitor, an IL-4 inhibitor, an IL-13Rα1 inhibitor, an IL-4Rα inhibitor or combinations thereof, e.g., as described herein. In some embodiments, the inhibitor of a pro-M2 macrophage molecule is a small molecule, an antibody or antigen-binding fragment thereof, a protein (e.g., a fusion protein), a nucleic acid (e.g., an shRNA or siRNA), or a gene editing system. In some embodiment, the inhibitor of a pro-M2 macrophage molecule is an antibody or antigen-biding fragment thereof.

[0026] In some embodiments, the inhibitor of a pro-M2 macrophage molecule is an IL-13 inhibitor, an IL-4 inhibitor, an IL-13Rα1 inhibitor, an IL-4Rα inhibitor, an IL-10 inhibitor, a CSF-1 inhibitor, a TGF beta inhibitor, a JAK2 inhibitor, a cell surface molecule, an iron oxide, a small molecule inhibitor, a PI3K inhibitor, an HDAC inhibitor, an inhibitor of the glycolytic pathway, a mitochondria-targeted antioxidant, or a combination thereof, e.g., as described herein.

[0027] In one embodiment, the inhibitor of a pro-M2 macrophage molecule is an IL-13 inhibitor (e.g., fenretinide (4-HPR)).

[0028] In another embodiment, the inhibitor of a pro-M2 macrophage molecule is an IL-4 inhibitor (e.g., 4-HPR).

[0029] In another embodiment, the inhibitor of a pro-M2 macrophage molecule is an an IL-13Rα1 inhibitor.

[0030] In another embodiment, the inhibitor of a pro-M2 macrophage molecule is an IL-4Rα inhibitor.

[0031] In another embodiment, the inhibitor of a pro-M2 macrophage molecule is a CSF-1 inhibitor (e.g., nintedanib).

[0032] In another embodiment, the inhibitor of a pro-M2 macrophage molecule is a TGF beta inhibitor.

[0033] In another embodiment, the inhibitor of a pro-M2 macrophage molecule is a JAK2 inhibitor (e.g., ruxolitinib).

[0034] In another embodiment, the inhibitor of a pro-M2 macrophage molecule is a cell surface molecule (e.g., Dipeptidyl peptidase 4 (DPP4) or CD26).

[0035] In another embodiment, the inhibitor of a pro-M2 macrophage molecule is an iron oxide (e.g., ferumoxytol).

[0036] In another embodiment, the inhibitor of a pro-M2 macrophage molecule is a small molecule inhibitor (e.g., pterostilbene).

[0037] In another embodiment, the inhibitor of a pro-M2 macrophage molecule is a phosphoinositide 3-kinase (PI3K) inhibitor (e.g., tenalisib (RP6530)).

[0038] In another embodiment, the inhibitor of a pro-M2 macrophage molecule is an HDAC inhibitor (e.g., SAHA).

[0039] In another embodiment, the inhibitor of a pro-M2 macrophage molecule is an inhibitor of the glycolytic pathway (e.g., 2-deoxy-d-glucose (2-DG)).

[0040] In another embodiment, the inhibitor of a pro-M2 macrophage molecule is a mitochondria-targeted antioxidant (e.g., MitoQ).

[0041] In another aspect, the invention provides a method of treating a subject having a disease associated with expression of a tumor antigen (e.g., a subject having a cancer (e.g., a solid tumor or a tumor associated with tumor-associated macrophages)). The method includes administering to the subject (i) a CAR therapy including a cell, e.g., a population of immune effector cells, including (e.g., expressing) a chimeric antigen receptor (CAR), wherein the CAR includes a tumor antigen binding domain that binds to CD123, a transmembrane domain, and an intracellular signaling domain; and (ii) a tumor targeting therapy. In some embodiments, the CD123 CAR is administered in an amount and/or time sufficient to result in inhibition of an

M2 macrophage activity. In embodiments, the inhibition of the M2 macrophage activity comprises inhibition of polarization of a macrophage to an M2 phenotype, and/or reversal of a phenotype of an M2 macrophage.

[0042] In another aspect, the invention provides a CAR therapy including a cell, e.g., a population of immune effector cells, comprising (e.g., expressing) a chimeric antigen receptor (CAR) for use in combination with a tumor targeting therapy in treating a subject having a disease associated with expression of a tumor antigen (e.g., a subject having cancer (e.g., a solid tumor or a tumor associated with tumor-associated macrophages)). The CAR includes a tumor antigen binding domain that binds CD123, a transmembrane domain, and an intracellular signaling domain. In some embodiments, the CD123 CAR is administered in an amount and/or time sufficient to result in inhibition of an M2 macrophage activity. In embodiments, the inhibition of the M2 macrophage activity comprises inhibition of polarization of a macrophage to an M2 phenotype, and/or reversal of a phenotype of an M2 macrophage.

[0043] In some embodiments of the methods and the CAR therapies for use disclosed herein, the tumor targeting therapy is a second CAR therapy that includes a cell, e.g., a population of immune effector cells, including (e.g., expressing) a CAR including a tumor antigen binding domain that binds to a tumor antigen other than CD123 (e.g., a CAR that binds to a solid tumor antigen or a hematologic tumor antigen other than CD123). In one embodiment, the tumor antigen binding domain binds to CD19, mesothelin, or EGFRviii.

[0044] In some embodiments of the methods and the CAR therapies for use disclosed herein, the tumor targeting therapy is or includes a CD19-inhibiting or depleting therapy, e.g., a therapy that includes a CD19 inhibitor. In some embodiments, the tumor targeting therapy includes a CD19 CAR-expressing cell, e.g., a CD19 CART cell, or an anti-CD19 antibody (e.g., an anti-CD19 mono- or bispecific antibody) or a fragment or conjugate thereof. In one embodiment, the CD19 inhibitor is a CD19 antibody, e.g., a CD19 bispecific antibody (e.g., a bispecific T cell engager that targets CD19, e.g., blinatumomab).

[0045] In other embodiments, including in any of the aforementioned aspects and embodiments, the CAR therapy and the tumor targeting therapy are administered sequentially.

[0046] In other embodiments, including in any of the aforementioned aspects and embodiments, the tumor targeting therapy is administered prior to the CAR therapy.

[0047] In other embodiments, including in any of the aforementioned aspects and embodiments, the CD123 CAR therapy is administered prior to the tumor targeting therapy. In some embodiments, the CD123 CAR therapy is administered at least 5 days, at least 7 days, at least 10 days, at least 15 days, at least 20 days, at least 1 month, at least 2 months, at least 3 months, at least 4 months, at least 5 months, at least 6 months, at least 7 months, at least 8 months, at least 9 months or at least 10 months, prior to administration of the tumor targeting therapy.

[0048] In other embodiments, including in any of the aforementioned aspects and embodiments, the tumor targeting therapy and the CAR therapy are administered simultaneously or concurrently.

[0049] In other embodiments, including in any of the aforementioned aspects and embodiments, the CAR therapy is administered as (a) single infusion or (b) multiple infusions (e.g., a single dose split into multiple infusions), and the tumor targeting therapy is administered as (a) a single dose, or (b) multiple doses (e.g., a first and second, and optionally one or more subsequent doses).

[0050] In other embodiments, including in any of the aforementioned aspects and embodiments, a dose of the CAR therapy is administered after (e.g., at least 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 1 week, 2 weeks, 3 weeks, 4 weeks, 5 weeks, or more, after) administration of a first dose of the tumor targeting therapy, e.g., but before administration of the second dose of the tumor targeting therapy.

[0051] In other embodiments, a dose of the CAR therapy is administered concurrently with (e.g., within 2 days (e.g., within 2 days, 1 day, 24 hours, 12 hours, 6 hours, 4 hours, 2 hours, or less) of), the administration of a first dose of the tumor targeting therapy.

[0052] In other embodiments, one or more subsequent doses of the tumor targeting therapy are administered after a second dose of the tumor targeting therapy.

[0053] In other embodiments, the tumor targeting therapy is administered in more than one dose, and the doses are administered twice a day (BID), once a day, once a week, once every 14 days, or once every month.

[0054] In other embodiments, the administering of the tumor targeting therapy includes multiple doses comprising a duration of at least 7 days, e.g., at least 7 days, 8 days, 9 days, 10 days, 1 week, 2 weeks, 3 weeks, 4 weeks, 5 weeks, 6 weeks, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, or more.

[0055] In other embodiments, the CAR therapy or the tumor targeting therapy is administered at a dose comprising at least about 5 x 10^6, 1 x 10^7, 1.5 x 10^7, 2 x 10^7, 2.5 x 10^7, 3 x 10^7, 3.5 x 10^7, 4 x 10^7, 5 x 10^7, 1 x 10^8, 1.5 x 10^8, 2 x 10^8, 2.5 x 10^8, 3 x 10^8, 3.5 x 10^8, 4 x 10^8, 5 x 10^8, 1 x 10^9, 2 x 10^9, or 5 x 10^9 cells, e.g., CAR positive cells.

[0056] In some embodiments, the CAR therapy and the tumor targeting therapy are formulated in a pharmaceutical composition (e.g., comprising a pharmaceutical excipient).

[0057] The following aspects of the CAR and CAR-expressing cell, e.g., population of immune effector cells, may be utilized with any of the aforementioned aspects and embodiments.

[0058] In an aspect, the tumor antigen binding domain of the CAR binds CD123.

[0059] In embodiments, the tumor antigen binding domain of the CAR includes a heavy chain complementary determining region 1 (HC CDR1), a heavy chain complementary determining region 2 (HC CDR2), and a heavy chain complementary determining region 3 (HC CDR3) of any CD123 heavy chain binding domain amino acid sequence listed in Table 16, Table 18, Table 20, Table 22, Table 24, Table 25, Table 26, Table 27 or Table 28; and a light chain complementary determining region 1 (LC CDR1), a light chain complementary determining region 2 (LC CDR2), and a light chain complementary determining region 3 (LC CDR3) of any CD123 light chain binding domain amino acid sequence listed in Table 17, Table 19, Table 21, Table 23, Table 24, Table 25, Table 26, Table 27 or Table 28. In embodiments, the CD123 binding domain includes a CD123 binding domain (e.g., scFv) amino acid sequence listed in Table 26, Table 27 or Table 28. In embodiments, the CAR includes (e.g., consists of) a CAR amino acid sequence listed in Table 26 or Table 27.

[0060] In another aspect, the tumor antigen binding domain of the CAR binds mesothelin. In embodiments, the tumor antigen binding domain of the CAR includes a heavy chain complementary determining region 1 (HC CDR1), a heavy chain complementary determining region 2 (HC CDR2), and a heavy chain complementary determining region 3 (HC CDR3) of any mesothelin heavy chain binding domain amino acid sequence listed in Table 2, Table 3 or Table 11; and a light chain complementary determining region 1 (LC CDR1), a light chain complementary determining region 2 (LC CDR2), and a light chain complementary determining region 3 (LC CDR3) of any mesothelin light chain binding domain amino acid sequence listed in Table 2, Table 4 or Table 11. In embodiments, the mesothelin binding domain includes a mesothelin binding domain (e.g., scFv) amino acid sequence listed in Table 2 or Table 11. In embodiments, the CAR includes (e.g., consists of) a CAR amino acid sequence listed in Table 11.

[0061] In another aspect, the tumor antigen binding domain of the CAR binds EGFRvIII. In embodiments, the tumor antigen binding domain of the CAR includes a heavy chain complementary determining region 1 (HC CDR1), a heavy chain complementary determining region 2 (HC CDR2), and a heavy chain complementary determining region 3 (HC CDR3) of any EGFRvIII heavy chain binding domain amino acid sequence listed in Table 5; and a light chain complementary determining region 1 (LC CDR1), a light chain complementary determining region 2 (LC CDR2), and a light chain complementary determining region 3 (LC CDR3) of any EGFRvIII light chain binding domain amino acid sequence listed in Table 5. In embodiments, the EGFRvIII binding domain includes a EGFRvIII binding domain (e.g., scFv) amino acid sequence listed in Table 5. In embodiments, the CAR includes (e.g., consists of) a CAR amino acid sequence listed in Table 30.

[0062] In another aspect, the tumor antigen binding domain of the CAR binds CD19. In some embodiments, the tumor antigen binding domain of the CAR includes a heavy chain complementary determining region 1 (HC CDR1), a heavy chain complementary determining region 2 (HC CDR2), and a heavy chain complementary determining region 3 (HC CDR3) of any CD19 heavy chain binding domain amino acid sequence listed in Table 6, Table 7, or Table 9; and a light chain complementary determining region 1 (LC CDR1), a light chain complementary determining region 2 (LC CDR2), and a light chain complementary determining region 3 (LC CDR3) of any CD19 light chain binding domain amino acid sequence listed in Table 6, Table 8, or Table 9. In particular embodiments, the CD19 binding domain includes a CD19 binding domain (e.g., scFv) amino acid sequence listed in Table 6 or Table 9. In certain embodiments, the CD19 binding domain includes an amino acid sequence selected from the group consisting of SEQ ID NO: 83; SEQ ID NO: 84, SEQ ID NO: 85; SEQ

ID NO: 86; SEQ ID NO: 87; SEQ ID NO: 88; SEQ ID NO: 89, SEQ ID NO: 90, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, and SEQ ID NO: 112.

[0063] In another aspect, the tumor antigen binding domain of the CAR binds a solid tumor antigen. In another aspect, the tumor antigen binding domain of the CAR binds an antigen expressed on a tumor associated with tumor-associated macrophages (TAMs) and/or myeloid derived suppressor cells (MDSCs). In embodiments, the solid tumor antigen or the antigen expressed on a tumor associated with tumor-associated macrophages (TAMs) and/or myeloid derived suppressor cells (MDSCs) is CD123, EGFRvIII, mesothelin, GD2, Tn antigen, sTn antigen, Tn-O-Glycopeptides, sTn-O-Glycopeptides, PSMA, CD97, TAG72, CD44v6, CEA, EPCAM, KIT, IL-13Ra2, leguman, GD3, CD171, IL-11Ra, PSCA, MAD-CT-1, MAD-CT-2, VEGFR2, LewisY, CD24, PDGFR-beta, SSEA-4, folate receptor alpha, ERBBs (e.g., ERBB2), Her2/neu, MUC1, EGFR, NCAM, Ephrin B2, CAIX, LMP2, sLe, HMWMAA, o-acetyl-GD2, folate receptor beta, TEM1/CD248, TEM7R, FAP, Legumain, HPV E6 or E7, ML-IAP, CLDN6, TSHR, GPRC5D, ALK, Polysialic acid, Fos-related antigen, neutrophil elastase, TRP-2, CYP1B1, sperm protein 17, beta human chorionic gonadotropin, AFP, thyroglobulin, PLAC1, globoH, RAGE1, MN-CA IX, human telomerase reverse transcriptase, intestinal carboxyl esterase, mut hsp 70-2, NA-17, NY-BR-1, UPK2, HAVCR1, ADRB3, PANX3, NY-ESO-1, GPR20, Ly6k, OR51E2, TARP, GFRα4, or a peptide of any of these antigens presented on MHC.

[0064] In another aspect, the tumor antigen binding domain of the CAR binds to a hematological cancer, e.g., as described herein. In some embodiments, the tumor antigen binding domain of the CAR binds to CD19. Any of the aforesaid CARs binding to CD19 can be used to treat a disease associated with expression of CD19, e.g., a CD19-expressing B cell malignancy as described herein.

[0065] In embodiments, including in any of the aforementioned aspects and embodiments, the intracellular signaling domain includes a primary signaling domain including a CD3-zeta stimulatory domain.

[0066] In embodiments, including in any of the aforementioned aspects and embodiments, the intracellular signaling domain includes a costimulatory domain which is an intracellular domain of a costimulatory protein selected from the group consisting of CD27, CD28, 4-1BB

(CD137), OX40, GITR, CD30, CD40, ICOS, BAFFR, HVEM, ICAM-1, lymphocyte function-associated antigen-1 (LFA-1), CD2, CDS, CD7, CD287, LIGHT, NKG2C, NKG2D, SLAMF7, NKp80, NKp30, NKp44, NKp46, CD160, B7-H3, and a ligand that specifically binds with CD83. In embodiments, including in any of the aforementioned aspects and embodiments, the costimulatory domain includes an intracellular domain of 4-1BB. In embodiments, including in any of the aforementioned aspects and embodiments, the costimulatory domain includes an intracellular domain of CD28. In embodiments, including in any of the aforementioned aspects and embodiments, the intracellular signaling domain includes two costimulatory domains, e.g., a 4-1BB costimulatory domain and a CD28 costimulatory domain.

[0067] In embodiments, including in any of the aforementioned aspects and embodiments, the disease associated with expression of a tumor antigen is cancer. In embodiments, including in any of the aforementioned aspects and embodiments, the cancer is Hodgkin lymphoma. In embodiments where the cancer is Hodgkin lymphoma, the antigen binding domain of the CAR binds CD19 or CD123, e.g., binds CD123.

[0068] In embodiments, including in any of the aforementioned aspects and embodiments, the cancer is a solid cancer.

[0069] In embodiments, including in any of the aforementioned aspects and embodiments, the cell including a CAR includes a nucleic acid encoding the CAR. In embodiments, the nucleic acid encoding the CAR is a lentiviral vector. In embodiments, the nucleic acid encoding the CAR is introduced into the cells by lentiviral transduction.

[0070] In embodiments, including in any of the aforementioned aspects and embodiments, the nucleic acid encoding the CAR is an RNA, e.g., an in vitro transcribed RNA. In embodiments, the nucleic acid encoding the CAR is introduced into the cells by electroporation.

[0071] In embodiments, including in any of the aforementioned aspects and embodiments, the cell is a T cell or an NK cell. In embodiments, the T cell is an autologous or allogeneic T cell.

[0072] In embodiments, including in any of the aforementioned aspects and embodiments, the subject is a mammal, e.g., a human.

[0073] Headings, sub-headings or numbered or lettered elements, e.g., (a), (b), (i) etc, are presented merely for ease of reading. The use of headings or numbered or lettered elements in this document does not require the steps or elements be performed in alphabetical order or that the steps or elements are necessarily discrete from one another.

[0074] All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety.

[0075] The disclosure includes all combinations of any one or more of the foregoing aspects and/or embodiments, as well as combinations with any one or more of the embodiments set forth in the detailed description and examples.

[0076] Other features, objects, and advantages of the invention will be apparent from the description and drawings, and from the claims.

BRIEF DESCRIPTION OF THE DRAWINGS

[0077] The following detailed description of preferred embodiments of the invention will be better understood when read in conjunction with the appended drawings. For the purpose of illustrating the invention, there are shown in the drawings embodiments which are presently preferred. It should be understood, however, that the invention is not limited to the precise arrangements and instrumentalities of the embodiments shown in the drawings.

[0078] FIG. 1A shows Primary samples of Hodgkin lymphoma stained by immunohistochemistry for CD30 and CD123. Expression of CD123 was found of the HL Reed-sternberg cells but also in the tumor microenvironment, as opposed to CD30 that was only positive on HRS. FIG. 1B shows RNA expression of CD123 in 4 standard HL cell lines (MOLM-14 and A357 used as positive and negative controls). FIG. 1C shows CD123 was found to be also expressed on the surface of the HL cell lines (CD30 used as standard marker of HL).

[0079] FIG. 2A shows human normal donor macrophages differentiated from peripheral blood monocytes were co-cultured with HDLM-2 cells or IL-4 (M2 positive control) or a control acute lymphoblastic leukemia cell line (NALM-6). HL lymphoma cells (HDLM-2) can polarize macrophages to an M2 phenotype (CD163+CD206+) after a 24-hour culture. FIG. 2B shows M2-polarized macrophages (IL-4) are CD123+ by flow cytometry. FIG. 2C shows M2-polarized macrophages (IL-4) can inhibit anti-CD19 chimeric antigen receptor proliferation, as shown by CFSE dilution assay. FIG. 2D shows HL-polarized macrophages strongly inhibit CART19 proliferation, as shown by CFSE dilution assay and absolute T cell numbers at day 5 (FIG. 2E). FIG. 2F shows Luminex analysis of cytokines present in the supernatant of co-cultures of HL cells (HDLM-2) with macrophages reveales high levels of IL-13 as compared to controls. FIG. 2G shows blocking IL-13 with an anti-IL13 antibody reverted the HL-drived M2 polarization as shown by reduced PD-L1 expression.

[0080] FIG. 3A shows HL cells (HDLM-2) were co-cultured with CART123 for 4-6 hours. CAR+ but not CAR- T cells expressed high levels of the degranulation marker CD107A and produced intra-cellular cytokines like IFNγ, IL-2 and TNFα. FIG. 3B shows CART123 exert potent cytotoxicity against HL cells in a dose-dependent manner. FIG. 3C shows HL cells (HDLM-2) were co-cultured at long term with CART123 or control UTD. At day 20, CART123 but not UTD killed HL cells and proliferated. FIG. 3D shows CART123 or UTD were co-cultured with HL cell lines (or positive and negative controls) for 5 days. CART123 but not UTD controls showed significant proliferation as absolute number and CFSE dilution (FIG. 3E). FIG. 3F shows HL cells stimulated CART123 but not UTD cells to release multiple cytokines including GM-CSF, IFNγ, MIP1β and TNFα. In these Figures, E:T = effector:target cell ratio.

[0081] FIG. 4A shows the experimental schema for mouse experiments testing CD123 CART against HL. 2 x106 Luciferase-positive HDLM-2 cells were injected i.v. in NSG mice and tumor engraftment was monitored by bioluminescence imaging. At day 42 mice were randomized to receive no treatment, 2 x106 control untransduced T cells (UTD) or 2 x106 CART123. FIG. 4B shows mice receiving CART123, but not controls, experienced complete response with long term remission of disease (>250 days). FIG. 4C shows CART123-treated mice have a significantly longer overall survival as compared to controls. FIG. 4D shows CAR123 T cells engraft, expand and disappear from the peripheral blood after clearing the tumor. T cells in the PB of CART123-treated mice were both CD8 and CD4 with high expression of the CAR.

[0082] FIG. 5A shows the experiment schema for establishment of long-term immunological memory in mice with HL: mice previously treated with CART123 and experiencing a long-term remission were rechallenged at day 250 with HL cells (HDLM-2). As a control a tumor-naïve group of mice were also injected with tumor. FIG. 5B shows HL cells only engrafted and grew in tumor-naïve mice while long-term surviving mice were able to control disease growth. FIG. 5C shows a re-expansion of CART123 cells observed in mice previously treated with CART123. FIG. 5D shows an improved overall survival was observed in mice with previous exposure to CART123.

[0083] FIG. 6A shows that in a 5-day CFSE proliferation CART123 are completely resistant to HL-polarized macrophages. FIG. 6B shows CART123 cells rapidly (day 1) recognize M2-macrophages, clustering around them and clearing them by day 5, as shown by phase contrast microscopy (20X) and flow cytometry, respectively. FIG. 6C shows CART123 were also able to secrete cytokines in the presence of HL-polarized M2 macrophages as opposed to control CART19 cells.

DETAILED DESCRIPTION

Definitions

[0084] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which the invention pertains.

[0085] The term "pro-M2 macrophage molecule" refers to a molecule that, alone or in combination with other molecules, contributes to the polarization of macrophages to an M2 phenotype. Non-limiting examples of pro-M2 macrophage molecules include the cytokines IL-13 (OMIM Acc. No. 147683; Entrez No. 3596; Swiss Prot. Acc. No. P35225), IL-4 (OMIM Acc. No. 147780; Entrez No. 3565; Swiss Prot. Acc. No. P05112), CSF-1 (Entrez No. 1435; Swiss Prot. Acc. No. P09603) and/or IL-10 (OMIM Acc. No. 124092; Entrez No. 3586; Swiss Prot. Acc. No. P22301).

[0086] The term "inhibitor of a pro-M2 macrophage molecule" refers to a molecule that inhibits the expression or function, e.g., receptor binding function, of a pro-M2 macrophage molecule. Inhibitors of pro-M2 macrophage molecules include a small molecule, an antibody molecule, a polypeptide, e.g., a fusion protein, an inhibitory nucleic acid, e.g., a siRNA or shRNA, or a gene editing system, e.g., a CRISPR/Cas9 system. An example of an inhibitor of pro-M2 macrophage molecule includes an inhibitor of IL-13. Another example of an inhibitor of pro-M2 macrophage molecule includes an inhibitor of IL-4. Another example of an inhibitor of pro-M2 macrophage molecule includes an inhibitor of IL-13Rα1 (Entrez No. 3597; Swiss Prot. Acc. No. P78552). Another example of an inhibitor of pro-M2 macrophage molecule includes an inhibitor of IL-10. Another example of an inhibitor of pro-M2 macrophage molecule includes an inhibitor of CSF-1. Additional detail regarding an inhibitor of pro-M2 macrophage molecule is provided below. In embodiments, the inhibitor of a pro-M2 macrophage inhibits a function, e.g., an inhibitory function, of a myeloid derived suppressor cell (MDSC).

[0087] The term "tumor associated macrophage" or "TAM" refers to cells of macrophage lineage, typically derived from monocytes or resident tissue macrophages, which are found in close proximity or within tumor masses, e.g., within the tumor stroma.

[0088] The term "myeloid derived supresssor cells" or "MDSCs" refer to myeloid derived cells which are found in close proximity or within tumor masses, e.g., within the tumor stroma.

[0089] The term "a" and "an" refers to one or to more than one (i.e., to at least one) of the grammatical object of the article. By way of example, "an element" means one element or more than one element.

[0090] The term "about" when referring to a measurable value such as an amount, a temporal duration, and the like, is meant to encompass variations of ±20% or in some instances ±10%, or in some instances ±5%, or in some instances ±1%, or in some instances ±0.1% from the specified value, as such variations are appropriate to perform the disclosed methods.

[0091] The term "Chimeric Antigen Receptor" or alternatively a "CAR" refers to a set of polypeptides, typically two in the simplest embodiments, which when in an immune effector cell, provides the cell with specificity for a target cell, typically a cancer cell, and with intracellular signal generation. In some embodiments, a CAR comprises at least an extracellular antigen binding domain, a transmembrane domain and a cytoplasmic signaling domain (also referred to herein as "an intracellular signaling domain") comprising a functional signaling domain derived from a stimulatory molecule and/or costimulatory molecule as defined below. In some aspects, the set of polypeptides are contiguous with each other, e.g., are in the same polypeptide chain (e.g., comprise a chimeric fusion protein). In some embodiments, the set of polypeptides are not contiguous with each other, e.g., are in different polypeptide chains. In some embodiments, the set of polypeptides include a dimerization switch that, upon the presence of a dimerization molecule, can couple the polypeptides to one another, e.g., can couple an antigen binding domain to an intracellular signaling domain. In one aspect, the stimulatory molecule is the zeta chain associated with the T cell receptor complex. In one aspect, the cytoplasmic signaling domain further comprises one or more functional signaling domains derived from at least one costimulatory molecule as defined below. In one aspect, the costimulatory molecule is chosen from the costimulatory molecules described herein, e.g., 4-1BB (i.e., CD137), CD27 and/or CD28. In one aspect, the CAR comprises a chimeric fusion protein comprising an extracellular antigen binding domain, a transmembrane domain and an intracellular signaling domain comprising a functional signaling domain derived from a stimulatory molecule. In one aspect, the CAR comprises a chimeric fusion protein comprising an extracellular antigen binding domain, a transmembrane domain and an intracellular signaling domain comprising a functional signaling domain derived from a costimulatory molecule and a functional signaling domain derived from a stimulatory molecule. In one aspect, the CAR comprises a chimeric fusion protein comprising an extracellular antigen binding domain, a transmembrane domain and an intracellular signaling domain comprising two functional signaling domains derived from one or more costimulatory molecule(s) and a functional signaling domain derived from a stimulatory molecule. In one aspect, the CAR comprises a chimeric fusion protein comprising an extracellular antigen binding domain, a transmembrane domain and an intracellular signaling domain comprising at least two functional signaling domains derived from one or more costimulatory molecule(s) and a functional signaling domain derived from a stimulatory molecule. In one aspect the CAR comprises an optional leader sequence at the amino-terminus (N-ter) of the CAR fusion protein. In one aspect, the CAR further comprises a leader sequence at the N-terminus of the extracellular antigen binding domain, wherein the leader sequence is optionally cleaved from the antigen binding domain (e.g., a scFv) during cellular processing and localization of the CAR to the cellular membrane.

[0092] The term “signaling domain” refers to the functional portion of a protein which acts by transmitting information within the cell to regulate cellular activity via defined signaling pathways by generating second messengers or functioning as effectors by responding to such messengers.

[0093] As used herein, the terms “alpha subunit of the IL-3 receptor,” “IL3Rα,” “CD123,” “IL3Rα chain” and “IL3Rα subunit” refer interchangeably to an antigenic determinant known to be detectable on leukemia precursor cells. The human and murine amino acid and nucleic acid sequences can be found in a public database, such as GenBank, UniProt and Swiss-Prot. For example, the amino acid sequence of human IL3Rα can be found at Accession No. NP 002174 and the nucleotide sequence encoding of the human IL3Rα can be found at Accession No. NM 005191. In one aspect the antigen-binding portion of the CAR recognizes and binds an epitope within the extracellular domain of the CD123 protein. In one aspect, the CD123 protein is expressed on a cancer cell. As used herein, “CD123” includes proteins comprising mutations, e.g., point mutations, fragments, insertions, deletions and splice variants of full length wild-type CD123.

[0094] As used herein, the term “CD19” refers to the Cluster of Differentiation 19 protein, which is an antigenic de terminant detectable on leukemia precursor cells. The human and murine amino acid and nucleic acid sequences can be found in a public database, such as GenBank, UniProt and Swiss-Prot. For example, the amino acid sequence of human CD19 can be found as UniProt/Swiss-Prot Accession No. P15391 and the nucleotide sequence encoding of the human CD19 can be found at Accession No. NM_001178098. As used herein, “CD19” includes proteins comprising mutations, e.g., point mutations, fragments, insertions, deletions and splice variants of full length wild-type CD19. CD19 is expressed on most B lineage cancers, including, e.g., acute lymphoblastic leukaemia, chronic lymphocyte leukaemia and non-Hodgkin lymphoma. Other cells with express CD19 are provided below in the definition of “disease associated with expression of CD19.” It is also an early marker of B cell progenitors. See, e.g., Nicholson et al. Mol. Immun. 34 (16-17): 1157-1165 (1997). In one aspect the antigen-binding portion of the CART recognizes and binds an antigen within the extracellular domain of the CD19 protein. In one aspect, the CD19 protein is expressed on a cancer cell.

[0095] As used herein, the term “CD20” refers to an antigenic determinant known to be detectable on B cells. Human CD20 is also called membrane-spanning 4-domains, subfamily A, member 1 (MS4A1). The human and murine amino acid and nucleic acid sequences can be found in a public database, such as GenBank, UniProt and Swiss-Prot. For example, the amino acid sequence of human CD20 can be found at Accession Nos. NP_690605.1 and NP_068769.2, and the nucleotide sequence encoding transcript variants 1 and 3 of the human CD20 can be found at Accession No. NM_152866.2 and NM_021950.3, respectively. In one aspect the antigen-binding portion of the CAR recognizes and binds an antigen within the extracellular domain of the CD20 protein. In one aspect, the CD20 protein is expressed on a cancer cell.

[0096] As used herein, the term "CD22," refers to an antigenic determinant known to be detectable on leukemia precursor cells. The human and murine amino acid and nucleic acid sequences can be found in a public database, such as GenBank, UniProt and Swiss-Prot. For example, the amino acid sequences of isoforms 1-5 human CD22 can be found at Accession Nos. NP 001762.2, NP 001172028.1, NP 001172029.1, NP 001172030.1, and NP 001265346.1, respectively, and the nucleotide sequence encoding variants 1-5 of the human CD22 can be found at Accession No. NM 001771.3, NM 001185099.1, NM 001185100.1, NM 001185101.1, and NM 001278417.1, respectively. In one aspect the antigen-binding portion of the CAR recognizes and binds an antigen within the extracellular domain of the CD22 protein. In one aspect, the CD22 protein is expressed on a cancer cell.

[0097] As used herein, the term "ROR1" refers to an antigenic determinant known to be detectable on leukemia precursor cells. The human and murine amino acid and nucleic acid sequences can be found in a public database, such as GenBank, UniProt and Swiss-Prot. For example, the amino acid sequences of isoforms 1 and 2 precursors of human ROR1 can be found at Accession Nos. NP_005003.2 and NP_001077061.1, respectively, and the mRNA sequences encoding them can be found at Accession Nos. NM_005012.3 and NM_001083592.1, respectively. In one aspect the antigen-binding portion of the CAR recognizes and binds an antigen within the extracellular domain of the ROR1 protein. In one aspect, the ROR1 protein is expressed on a cancer cell.

[0098] As used herein, the term "CD33" refers to the Cluster of Differentiation 33 protein, which is an antigenic determinant detectable on leukemia cells as well on normal precursor cells of the myeloid lineage. The human and murine amino acid and nucleic acid sequences can be found in a public database, such as GenBank, UniProt and Swiss-Prot. For example, the amino acid sequence of human CD33 can be found as UniProt/Swiss-Prot Accession No.

P20138 and the nucleotide sequence encoding of the human CD33 can be found at Accession No. NM_001772.3. In one aspect the antigen-binding portion of the CAR recognizes and binds an epitope within the extracellular domain of the CD33 protein or fragments thereof. In one aspect, the CD33 protein is expressed on a cancer cell. As used herein, “CD33” includes proteins comprising mutations, e.g., point mutations, fragments, insertions, deletions and splice variants of full length wild-type CD33.

[0099] As used herein, the term “BCMA” refers to B-cell maturation antigen. BCMA (also known as TNFRSF17, BCM or CD269) is a member of the tumor necrosis receptor (TNFR) family and is predominantly expressed on terminally differentiated B cells, e.g., memory B cells, and plasma cells. Its ligand is called B-cell activator of the TNF family (BAFF) and a proliferation inducing ligand (APRIL). BCMA is involved in mediating the survival of plasma cells for mataining long-term humoral immunity. The gene for BCMA is encoded on chromosome 16 producing a primary mRNA transcript of 994 nucleotides in length (NCBI accession NM_001192.2) that encodes a protein of 184 amino acids (NP_001183.2). A second antisense transcript derived from the BCMA locus has been described, which may play a role in regulating BCMA expression. (Laabi Y. et al., Nucleic Acids Res., 1994, 22:1147-1154). Additional transcript variants have been described with unknown significance (Smirnova AS et al. Mol Immunol., 2008, 45(4):1179-1183. A second isoform, also known as TV4, has been identified (Uniprot identifier Q02223-2). As used herein, “BCMA” includes proteins comprising mutations, e.g., point mutations, fragments, insertions, deletions and splice variants of full length wild-type BCMA.

[00100] As used herein, the term “CLL-1” refers to C-type lectin-like molecule-1, which is an antigenic determinant detectable on leukemia precursor cells and on normal immune cells. C-type lectin-like-1 (CLL-1) is also known as MICL, CLEC12A, CLEC-1, Dendritic Cell-Associated Lectin 1, and DCAL-2. The human and murine amino acid and nucleic acid sequences can be found in a public database, such as GenBank, UniProt and Swiss-Prot. For example, the amino acid sequence of human CLL-1 can be found as UniProt/Swiss-Prot Accession No. Q5QGZ9 and the nucleotide sequence encoding of the human CLL-1 can be found at Accession Nos. NM 001207010.1, NM 138337.5, NM 201623.3, and NM 201625.1. In one embodiment, the antigen-binding portion of the CAR recognizes and binds an epitope

within the extracellular domain of the CLL-1 protein or a fragment thereof. In one embodiment, the CLL-1 protein is expressed on a cancer cell.

[00101] The term "EGFR" refers to any mammalian mature full-length epidermal growth factor receptor, including human and non-human forms. The 1186 amino acid human EGFR is described in Ullrich *et al.*, Nature 309:418-425 (1984)) and GenBank Accession No. AF125253 and SwissProt Acc No P00533-2.

[00102] The term "EGFRvIII" refers to Epidermal growth factor receptor variant III. EGFRvIII is the most common variant of EGFR observed in human tumors but is rarely observed in normal tissue. This protein results from the in-frame deletion of exons 2-7 and the generation of a novel glycine residue at the junction of exons 1 and 8 within the extra-cellular domain of the EGFR, thereby creating a tumor specific epitope. EGFRvIII is expressed in 24% to 67% of GBM, but not in normal tissues. EGFRvIII is also known as type III mutant, delta-EGFR, EGFRde2-7, and ΔEGFR and is described in U.S. Pat. Nos. 6,455,498, 6,127,126, 5,981,725, 5,814,317, 5,710,010, 5,401,828, and 5,212,290. Expression of EGFRvIII may result from a chromosomal deletion, and may also result from aberrant alternative splicing. See Sugawa *et al.*, 1990, Proc. Natl. Acad. Sci. 87:8602-8606.

[00103] As used herein, the term "mesothelin" refers to the 40-kDa protein, mesothelin, which is anchored at the cell membrane by a glycosylphosphatidyl inositol (GPI) linkage and an amino-terminal 31-kDa shed fragment, called megkaryocyte potentiating factor (MPF). Both fragments contain N-glycosylation sites. The term also refers to a soluble splice variant of the 40-kDa carboxyl-terminal fragment also called "soluble mesothelin/MPF-related". Preferably, the term refers to a human mesothelin of GenBank accession number AAH03512.1, and naturally cleaved portions thereof, e.g., as expressed on a cell membrane, e.g., a cancer cell membrane.

[00104] The term "antibody," as used herein, refers to a protein, or polypeptide sequence derived from an immunoglobulin molecule which specifically binds with an antigen. Antibodies can be polyclonal or monoclonal, multiple or single chain, or intact immunoglobulins, and may be derived from natural sources or from recombinant sources. Antibodies can be tetramers of immunoglobulin molecules.

[00105] The term "antibody fragment" refers to at least one portion of an antibody, that retains the ability to specifically interact with (e.g., by binding, steric hinderance, stabilizing/destabilizing, spatial distribution) an epitope of an antigen. Examples of antibody fragments include, but are not limited to, Fab, Fab', $F(ab')_2$, Fv fragments, scFv antibody fragments, disulfide-linked Fvs (sdFv), a Fd fragment consisting of the VH and CH1 domains, linear antibodies, single domain antibodies such as sdAb (either VL or VH), camelid VHH domains, multi-specific antibodies formed from antibody fragments such as a bivalent fragment comprising two Fab fragments linked by a disulfide brudge at the hinge region, and an isolated CDR or other epitope binding fragments of an antibody. An antigen binding fragment can also be incorporated into single domain antibodies, maxibodies, minibodies, nanobodies, intrabodies, diabodies, triabodies, tetrabodies, v-NAR and bis-scFv (see, e.g., Hollinger and Hudson, Nature Biotechnology 23:1126-1136, 2005). Antigen binding fragments can also be grafted into scaffolds based on polypeptides such as a fibronectin type III (Fn3)(see U.S. Patent No.: 6,703,199, which describes fibronectin polypeptide minibodies).

[00106] The term "scFv" refers to a fusion protein comprising at least one antibody fragment comprising a variable region of a light chain and at least one antibody fragment comprising a variable region of a heavy chain, wherein the light and heavy chain variable regions are contiguously linked, e.g., via a synthetic linker, e.g., a short flexible polypeptide linker, and capable of being expressed as a single chain polypeptide, and wherein the scFv retains the specificity of the intact antibody from which it is derived. Unless specified, as used herein an scFv may have the VL and VH variable regions in either order, e.g., with respect to the N-terminal and C-terminal ends of the polypeptide, the scFv may comprise VL-linker-VH or may comprise VH-linker-VL.

[00107] The portion of the CAR of the invention comprising an antibody or antibody fragment thereof may exist in a variety of forms where the antigen binding domain is expressed as part of a contiguous polypeptide chain including, for example, a single domain antibody fragment (sdAb), a single chain antibody (scFv), a humanized antibody or bispecific antibody (Harlow et al., 1999, In: Using Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory Press, NY; Harlow et al., 1989, In: Antibodies: A Laboratory Manual, Cold Spring Harbor, New York; Houston et al., 1988, Proc. Natl. Acad. Sci. USA 85:5879-5883; Bird et al., 1988, Science 242:423-426). In one aspect, the antigen binding domain of a CAR composition

of the invention comprises an antibody fragment. In a further aspect, the CAR comprises an antibody fragment that comprises a scFv. The precise amino acid sequence boundaries of a given CDR can be determined using any of a number of well-known schemes, including those described by Kabat et al. (1991), "Sequences of Proteins of Immunological Interest," 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD ("Kabat" numbering scheme), Al-Lazikani et al., (1997) JMB 273,927-948 ("Chothia" numbering scheme), or a combination thereof.

[00108] As used herein, the term "binding domain" or "antibody molecule" refers to a protein, e.g., an immunoglobulin chain or fragment thereof, comprising at least one immunoglobulin variable domain sequence. The term "binding domain" or "antibody molecule" encompasses antibodies and antibody fragments. In an embodiment, an antibody molecule is a multispecific antibody molecule, e.g., it comprises a plurality of immunoglobulin variable domain sequences, wherein a first immunoglobulin variable domain sequence of the plurality has binding specificity for a first epitope and a second immunoglobulin variable domain sequence of the plurality has binding specificity for a second epitope. In an embodiment, a multispecific antibody molecule is a bispecific antibody molecule. A bispecific antibody has specificity for no more than two antigens. A bispecific antibody molecule is characterized by a first immunoglobulin variable domain sequence which has binding specificity for a first epitope and a second immunoglobulin variable domain sequence that has binding specificity for a second epitope.

[00109] The portion of the CAR of the invention comprising an antibody or antibody fragment thereof may exist in a variety of forms where the antigen binding domain is expressed as part of a contiguous polypeptide chain including, for example, a single domain antibody fragment (sdAb), a single chain antibody (scFv), a humanized antibody, or bispecific antibody (Harlow et al., 1999, In: Using Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory Press, NY; Harlow et al., 1989, In: Antibodies: A Laboratory Manual, Cold Spring Harbor, New York; Houston et al., 1988, Proc. Natl. Acad. Sci. USA 85:5879-5883; Bird et al., 1988, Science 242:423-426). In one aspect, the antigen binding domain of a CAR composition of the invention comprises an antibody fragment. In a further aspect, the CAR comprises an antibody fragment that comprises a scFv.

[00110] The term “antibody heavy chain,” refers to the larger of the two types of polypeptide chains present in antibody molecules in their naturally occurring conformations, and which normally determines the class to which the antibody belongs.

[00111] The term “antibody light chain,” refers to the smaller of the two types of polypeptide chains present in antibody molecules in their naturally occurring conformations. Kappa (κ) and lambda (λ) light chains refer to the two major antibody light chain isotypes.

[00112] The term “recombinant antibody” refers to an antibody which is generated using recombinant DNA technology, such as, for example, an antibody expressed by a bacteriophage or yeast expression system. The term should also be construed to mean an antibody which has been generated by the synthesis of a DNA molecule encoding the antibody and which DNA molecule expresses an antibody protein, or an amino acid sequence specifying the antibody, wherein the DNA or amino acid sequence has been obtained using recombinant DNA or amino acid sequence technology which is available and well known in the art.

[00113] The term “antigen” or “Ag” refers to a molecule that provokes an immune response. This immune response may involve either antibody production, or the activation of specific immunologically-competent cells, or both. The skilled artisan will understand that any macromolecule, including virtually all proteins or peptides, can serve as an antigen. Furthermore, antigens can be derived from recombinant or genomic DNA. A skilled artisan will understand that any DNA, which comprises a nucleotide sequences or a partial nucleotide sequence encoding a protein that elicits an immune response therefore encodes an “antigen” as that term is used herein. Furthermore, one skilled in the art will understand that an antigen need not be encoded solely by a full length nucleotide sequence of a gene. It is readily apparent that the present invention includes, but is not limited to, the use of partial nucleotide sequences of more than one gene and that these nucleotide sequences are arranged in various combinations to encode polypeptides that elicit the desired immune response. Moreover, a skilled artisan will understand that an antigen need not be encoded by a “gene” at all. It is readily apparent that an antigen can be generated synthesized or can be derived from a biological sample, or might be macromolecule besides a polypeptide. Such a biological sample can include, but is not limited to a tissue sample, a tumor sample, a cell or a fluid with other biological components.

The term “anti-cancer effect” refers to a biological effect which can be manifested by various means, including but not limited to, e.g., a decrease in tumor volume, a decrease in the number of cancer cells, a decrease in the number of metastases, an increase in life expectancy, decrease in cancer cell proliferation, decrease in cancer cell survival, or amelioration of various physiological symptoms associated with the cancerous condition. An “anti-cancer effect” can also be manifested by the ability of the peptides, polynucleotides, cells and antibodies in prevention of the occurrence of cancer in the first place. The term “anti-tumor effect” refers to a biological effect which can be manifested by various means, including but not limited to, e.g., a decrease in tumor volume, a decrease in the number of tumor cells, a decrease in tumor cell proliferation, or a decrease in tumor cell survival.

[00114] The term “autologous” refers to any material derived from the same individual to whom it is later to be re-introduced into the individual.

[00115] The term “allogeneic” refers to any material derived from a different animal of the same species as the individual to whom the material is introduced. Two or more individuals are said to be allogeneic to one another when the genes at one or more loci are not identical. In some aspects, allogeneic material from individuals of the same species may be sufficiently unlike genetically to interact antigenically

[00116] The term “xenogeneic” refers to a graft derived from an animal of a different species.

[00117] The term “cancer” refers to a disease characterized by the uncontrolled growth of aberrant cells. Cancer cells can spread locally or through the bloodstream and lymphatic system to other parts of the body. Examples of various cancers are described herein and include but are not limited to, breast cancer, prostate cancer, ovarian cancer, cervical cancer, skin cancer, pancreatic cancer, colorectal cancer, renal cancer, liver cancer, brain cancer, lymphoma, leukemia, lung cancer and the like. The terms “tumor” and “cancer” are used interchangeably herein, e.g., both terms encompass solid and liquid, e.g., diffuse or circulating, tumors. As used herein, the term “cancer” or “tumor” includes premalignant, as well as malignant cancers and tumors.

[00118] The phrase “disease associated with expression of CD19” includes, but is not limited to, a disease associated with expression of CD19 or condition associated with cells

which express, or at any time expressed, CD19 including, e.g., proliferative diseases such as a cancer or malignancy or a precancerous condition such as a myelodysplasia, a myelodysplastic syndrome or a preleukemia; or a noncancer related indication associated with cells which express CD19. For the avoidance of doubt, a disease associated with expression of CD19 may include a condition associated with cells which do not presently express CD19, e.g., because CD19 expression has been downregulated, e.g., due to treatment with a molecule targeting CD19, e.g., a CD19 CAR, but which at one time expressed CD19. In one aspect, a cancer associated with expression of CD19 is a hematological cancer. In one aspect, the hematological cancer is a leukemia or a lymphoma. In one aspect, a cancer associated with expression of CD19 includes cancers and malignancies including, but not limited to, e.g., one or more acute leukemias including but not limited to, e.g., B-cell acute Lymphoid Leukemia (BALL), T-cell acute Lymphoid Leukemia (TALL), acute lymphoid leukemia (ALL); one or more chronic leukemias including but not limited to, e.g., chronic myelogenous leukemia (CML), Chronic Lymphoid Leukemia (CLL). Additional cancers or hematologic conditions associated with expression of CD19 comprise, but are not limited to, e.g., B cell prolymphocytic leukemia, blastic plasmacytoid dendritic cell neoplasm, Burkitt's lymphoma, diffuse large B cell lymphoma, Follicular lymphoma, Hairy cell leukemia, small cell- or a large cell-follicular lymphoma, malignant lymphoproliferative conditions, MALT lymphoma, mantle cell lymphoma (MCL), Marginal zone lymphoma, multiple myeloma, myelodysplasia and myelodysplastic syndrome, non-Hodgkin lymphoma, Hodgkin lymphoma, plasmablastic lymphoma, plasmacytoid dendritic cell neoplasm, Waldenstrom macroglobulinemia, and “preleukemia” which are a diverse collection of hematological conditions united by ineffective production (or dysplasia) of myeloid blood cells, and the like. Further diseases associated with expression of CD19 expression include, but not limited to, e.g., atypical and/or non-classical cancers, malignancies, precancerous conditions or proliferative diseases associated with expression of CD19. Non-cancer related indications associated with expression of CD19 include, but are not limited to, e.g., autoimmune disease, (e.g., lupus), inflammatory disorders (allergy and asthma) and transplantation. In some embodiments, the tumor antigen-expressing cells express, or at any time expressed, mRNA encoding the tumor antigen. In an embodiment, the tumor antigen -expressing cells produce the tumor antigen protein (e.g., wild-type or mutant), and the tumor antigen protein may be present at normal levels or reduced levels. In an embodiment, the tumor antigen -expressing cells produced detectable levels of a tumor antigen protein at one point, and subsequently produced substantially no detectable tumor antigen protein.

[00119] The phrase “disease associated with expression of a B-cell antigen” includes, but is not limited to, a disease associated with expression of one or more of CD19, CD20, CD22 or ROR1, or a condition associated with cells which express, or at any time expressed, one or more of CD19, CD20, CD22 or ROR1, including, e.g., proliferative diseases such as a cancer or malignancy or a precancerous condition such as a myelodysplasia, a myelodysplastic syndrome or a preleukemia; or a noncancer related indication associated with cells which express one or more of CD19, CD20, CD22 or ROR1. For the avoidance of doubt, a disease associated with expression of the B-cell antigen may include a condition associated with cells which do not presently express the B-cell antigen, e.g., because the antigen expression has been downregulated, e.g., due to treatment with a molecule targeting the B-cell antigen, e.g., a B-cell targeting CAR, but which at one time expressed the antigen. The phrase “disease associated with expression of a B-cell antigen” includes a disease associated with expression of CD19, as described herein.

The phrase “disease associated with expression of CD123” as used herein includes but is not limited to, a disease associated with expression of CD123 or condition associated with a cell which expresses CD123 (e.g., wild-type or mutant CD123) including, e.g., a proliferative disease such as a cancer or malignancy; a precancerous condition such as a myelodysplasia, a myelodysplastic syndrome or a preleukemia; or a non-cancer related indication associated with a cell which expresses CD123 (e.g., wild-type or mutant CD123). In one aspect, a cancer associated with expression of CD123 (e.g., wild-type or mutant CD123) is a hematological cancer. In one aspect, the disease includes AML, ALL, hairy cell leukemia, Prolymphocytic leukemia, Chronic myeloid leukemia (CML), Hodgkin lymphoma, Blastic plasmacytoid dendritic cell neoplasm, lymphoblastic B-cell leukemia (B-cell acute lymphoid leukemia, BALL), acute lymphoblastic T-cell leukemia (T-cell acute lymphoid leukemia (TALL); myelodysplastic syndrome; a myeloproliferative neoplasm; a histiocytic disorder (e.g., a mast cell disorder or a blastic plasmacytoid dendritic cell neoplasm); a mast cell disorder, e.g., systemic mastocytosis or mast cell leukemia, and the like. Further disease associated with expression of CD123 expression include, but are not limited to, e.g., atypical and/or non-classical cancers, malignancies, precancerous conditions or proliferative diseases associated with expression of CD123. Non-cancer related indications associated with expression of CD123 may also be included.

The phrase “disease associated with expression of CD33” as used herein includes but is not limited to, a disease associated with a cell which expresses CD33 (e.g., wild-type or mutant CD33) or condition associated with a cell which expresses CD33 (e.g., wild-type or mutant CD33) including, e.g., a proliferative disease such as a cancer or malignancy or a precancerous condition such as a myelodysplasia, a myelodysplastic syndrome or a preleukemia; or a noncancer related indication associated with a cell which expresses CD33 (e.g., wild-type or mutant CD33). For the avoidance of doubt, a disease associated with expression of CD33 may include a condition associated with a cell which do not presently express CD33, e.g., because CD33 expression has been downregulated, e.g., due to treatment with a molecule targeting CD33, e.g., a CD33 inhibitor described herein, but which at one time expressed CD33. In one aspect, a cancer associated with expression of CD33 (e.g., wild-type or mutant CD33) is a hematological cancer. In one aspect, a hematological cancer includes but is not limited to acute myeloid leukemia (AML), myelodysplasia and myelodysplastic syndrome, myelofibrosis and myeloproliferative neoplasms, acute lymphoid leukemia (ALL), hairy cell leukemia, Prolymphocytic leukemia, chronic myeloid leukemia (CML), Blastic plasmacytoid dendritic cell neoplasm, and the like. Further disease associated with expression of CD33 (e.g., wild-type or mutant CD33) expression include, but are not limited to, e.g., atypical and/or non-classical cancers, malignancies, precancerous conditions or proliferative diseases associated with expression of CD33 (e.g., wild-type or mutant CD33). Non-cancer related indications associated with expression of CD33 (e.g., wild-type or mutant CD33) may also be included. In embodiments, a non-cancer related indication associated with expression of CD33 includes but is not limited to, e.g., autoimmune disease, (e.g., lupus), inflammatory disorders (allergy and asthma) and transplantation. In some embodiments, the tumor antigen-expressing cell expresses, or at any time expressed, mRNA encoding the tumor antigen. In an embodiment, the tumor antigen-expressing cell produces the tumor antigen protein (e.g., wild-type or mutant), and the tumor antigen protein may be present at normal levels or reduced levels. In an embodiment, the tumor antigen-expressing cell produced detectable levels of a tumor antigen protein at one point, and subsequently produced substantially no detectable tumor antigen protein.

The phrase “disease associated with expression of BCMA” includes, but is not limited to, a disease associated with a cell which expresses BCMA (e.g., wild-type or mutant BCMA) or condition associated with a cell which expresses BCMA (e.g., wild-type or mutant BCMA) including, e.g., proliferative diseases such as a cancer or malignancy or a precancerous condition such as a myelodysplasia, a myelodysplastic syndrome or a preleukemia; or a noncancer related indication associated with a cell which expresses BCMA (e.g., wild-type or mutant BCMA). For the avoidance of doubt, a disease associated with expression of BCMA may include a condition associated with a cell which does not presently express BCMA, e.g., because BCMA expression has been downregulated, e.g., due to treatment with a molecule targeting BCMA, e.g., a BCMA inhibitor described herein, but which at one time expressed BCMA. In one aspect, a cancer associated with expression of BCMA (e.g., wild-type or mutant BCMA) is a hematological cancer. In one aspect, the hematogical cancer is a leukemia or a lymphoma. In one aspect, a cancer associated with expression of BCMA (e.g., wild-type or mutant BCMA) is a malignancy of differentiated plasma B cells. In one aspect, a cancer associated with expression of BCMA(e.g., wild-type or mutant BCMA) includes cancers and malignancies including, but not limited to, e.g., one or more acute leukemias including but not limited to, e.g., B-cell acute Lymphoid Leukemia ("BALL"), T-cell acute Lymphoid Leukemia ("TALL"), acute lymphoid leukemia (ALL); one or more chronic leukemias including but not limited to, e.g., chronic myelogenous leukemia (CML), Chronic Lymphoid Leukemia (CLL). Additional cancers or hematologic conditions associated with expression of BMCA (e.g., wild-type or mutant BCMA) comprise, but are not limited to, e.g., B cell prolymphocytic leukemia, blastic plasmacytoid dendritic cell neoplasm, Burkitt's lymphoma, diffuse large B cell lymphoma, Follicular lymphoma, Hairy cell leukemia, small cell- or a large cell-follicular lymphoma, malignant lymphoproliferative conditions, MALT lymphoma, mantle cell lymphoma, Marginal zone lymphoma, multiple myeloma, myelodysplasia and myelodysplastic syndrome, non-Hodgkin's lymphoma, plasmablastic lymphoma, plasmacytoid dendritic cell neoplasm, Waldenstrom macroglobulinemia, and "preleukemia" which are a diverse collection of hematological conditions united by ineffective production (or dysplasia) of myeloid blood cells, and the like. In some embodiments, the cancer is multiple myeloma, Hodgkin's lymphoma, non-Hodgkin's lymphoma, or glioblastoma. In embodiments, a disease associated with expression of BCMA includes a plasma cell proliferative disorder, e.g., asymptomatic myeloma (smoldering multiple myeloma or indolent myeloma), monoclonal gammapathy of undetermined significance (MGUS), Waldenstrom's macroglobulinemia, plasmacytomas (e.g., plasma cell dyscrasia, solitary myeloma, solitary plasmacytoma, extramedullary plasmacytoma, and multiple plasmacytoma), systemic amyloid light chain amyloidosis, and POEMS syndrome (also known as Crow-Fukase syndrome, Takatsuki disease, and PEP syndrome). Further diseases associated with expression of BCMA (e.g., wild-type or mutant BCMA) expression include, but not limited to, e.g., atypical and/or non-classical cancers, malignancies, precancerous conditions or proliferative diseases associated with expression of BCMA (e.g., wild-type or mutant BCMA), e.g., a cancer described herein, e.g., a prostate cancer (e.g., castrate-resistant or therapy-resistant prostate cancer, or metastatic prostate cancer), pancreatic cancer, or lung cancer.

Non-cancer related conditions that are associated with BCMA (e.g., wild-type or mutant BCMA) include viral infections; e.g., HIV, fungal invections, e.g., *C. neoformans*; autoimmune disease; e.g. rheumatoid arthritis, system lupus erythematosus (SLE or lupus), pemphigus vulgaris, and Sjogren's syndrome; inflammatory bowel disease, ulcerative colitis; transplant-related allospecific immunity disorders related to mucosal immunity; and unwanted immune responses towards biologics (e.g., Factor VIII) where humoral immunity is important. In embodiments, a non-cancer related indication associated with expression of BCMA includes but is not limited to, e.g., autoimmune disease, (e.g., lupus), inflammatory disorders (allergy and asthma) and transplantation. In some embodiments, the tumor antigen-expressing cell expresses, or at any time expressed, mRNA encoding the tumor antigen. In an embodiment, the tumor antigen -expressing cell produces the tumor antigen protein (e.g., wild-type or mutant), and the tumor antigen protein may be present at normal levels or reduced levels. In an embodiment, the tumor antigen -expressing cell produced detectable levels of a tumor antigen protein at one point, and subsequently produced substantially no detectable tumor antigen protein.

The phrase "disease associated with expression of CLL-1" includes, but is not limited to, a disease associated with a cell which expresses CLL-1 or condition associated with a cell which expresses CLL-1 including, e.g., proliferative diseases such as a cancer or malignancy or a precancerous condition such as a myelodysplasia, a myelodysplastic syndrome or a preleukemia; or a noncancer related indication associated with a cell which expresses CLL-1 (e.g., wild-type or mutant CLL-1). For the avoidance of doubt, a disease associated with expression of CLL-1 may include a condition associated with a cell which do not presently express CLL-1, e.g., because CLL-1 expression has been downregulated, e.g., due to treatment with a molecule targeting CLL-1, e.g., a CLL-1 inhibitor described herein, but which at one time expressed CLL-1. In one aspect, a cancer associated with expression of CLL-1 is a hematological cancer. In one aspect, a hematological cancer includes but is not limited to leukemia (such as acute myelogenous leukemia, chronic myelogenous leukemia, acute lymphoid leukemia, chronic lymphoid leukemia and myelodysplastic syndrome) and malignant lymphoproliferative conditions, including lymphoma (such as multiple myeloma, non-Hodgkin's lymphoma, Burkitt's lymphoma, and small cell- and large cell-follicular lymphoma). Further diseases associated with expression of CLL-1 expression include, but not limited to, e.g., atypical and/or non-classical cancers, malignancies, precancerous conditions or proliferative diseases associated with expression of CLL-1. Non-cancer related indications associated with expression of CLL-1 may also be included. In some embodiments, the tumor antigen-expressing cell expresses, or at any time expressed, mRNA encoding the tumor antigen. In an embodiment, the tumor antigen-expressing cell produces the tumor antigen protein (e.g., wild-type or mutant), and the tumor antigen protein may be present at normal levels or reduced levels. In an embodiment, the tumor antigen-expressing cell produced detectable levels of a tumor antigen protein at one point, and subsequently produced substantially no detectable tumor antigen protein.

The term “disease associated with expression of EGFRvIII” as used herein includes, but is not limited to, a disease associated with expression of EGFRvIII or condition associated with cells which express EGFRvIII including, tumor cells of various cancers such as, e.g., glioblastoma (including glioblastoma stem cells); breast, ovarian, and non-small cell lung carcinomas; head and neck squamous cell carcinoma; medulloblastoma, colorectal cancer, prostate cancer, and bladder carcinoma. Without being bound to a particular theory or mechanism, it is believed that by eliciting an antigen-specific response against EGFRvIII, the CARs disclosed herein provide for one or more of the following: targeting and destroying EGFRvIII-expressing tumor cells, reducing or eliminating tumors, facilitating infiltration of immune cells to the tumor site, and enhancing/extending anti-tumor responses. Because EGFRvIII is not expressed at detectable levels in normal (i.e., non-cancerous) tissue, it is contemplated that the inventive CARs advantageously substantially avoid targeting/destroying normal tissues and cells.

[00120] The phrase “disease associated with expression of mesothelin” as used herein includes, but is not limited to, a disease associated with expression of mesothelin or condition associated with cells which express mesothelin including, e.g., proliferative diseases such as a cancer or malignancy or a precancerous condition such as a mesothelial hyperplasia; or a noncancer related indication associated with cells which express mesothelin. Examples of various cancers that express mesothelin include but are not limited to, mesothelioma, ovarian cancer, pancreatic cancer, and the like.

[00121] The term “conservative sequence modifications” refers to amino acid modifications that do not significantly affect or alter the binding characteristics of the antibody or antibody fragment containing the amino acid sequence. Such conservative modifications include amino acid substitutions, additions and deletions. Modifications can be introduced into an antibody or antibody fragment of the invention by standard techniques known in the art, such as site-directed mutagenesis and PCR-mediated mutagenesis. Conservative amino acid substitutions are ones in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine, tryptophan), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Thus, one or more amino acid residues within a CAR of the invention can be replaced with other amino acid residues from the same side chain family and the altered CAR can be tested using the functional assays described herein.

[00122] The term “stimulation,” refers to a primary response induced by binding of a stimulatory molecule (e.g., a TCR/CD3 complex or CAR) with its cognate ligand (or tumor antigen in the case of a CAR) thereby mediating a signal transduction event, such as, but not limited to, signal transduction via the TCR/CD3 complex or signal transduction via the appropriate NK receptor or signaling domains of the CAR. Stimulation can mediate altered expression of certain molecules.

[00123] The term "stimulatory molecule," refers to a molecule expressed by an immune cell (e.g., T cell, NK cell, B cell) that provides the cytoplasmic signaling sequence(s) that regulate activation of the immune cell in a stimulatory way for at least some aspect of the immune cell signaling pathway. In one aspect, the signal is a primary signal that is initiated by, for instance, binding of a TCR/CD3 complex with an MHC molecule loaded with peptide, and which leads to mediation of a T cell response, including, but not limited to, proliferation, activation, differentiation, and the like. A primary cytoplasmic signaling sequence (also referred to as a "primary signaling domain") that acts in a stimulatory manner may contain a signaling motif which is known as immunoreceptor tyrosine-based activation motif or ITAM. Examples of an ITAM containing cytoplasmic signaling sequence that is of particular use in the invention includes, but is not limited to, those derived from CD3 zeta, common FcR gamma (FCER1G), Fc gamma RIIa, FcR beta (Fc Epsilon R1b), CD3 gamma, CD3 delta, CD3 epsilon, CD79a, CD79b, DAP10, and DAP12. In a specific CAR of the invention, the intracellular signaling domain in any one or more CARS of the invention comprises an intracellular signaling sequence, e.g., a primary signaling sequence of CD3-zeta. In a specific CAR of the invention, the primary signaling sequence of CD3-zeta is the sequence provided as SEQ ID NO: 17, or the equivalent residues from a non-human species, e.g., mouse, rodent, monkey, ape and the like. In a specific CAR of the invention, the primary signaling sequence of CD3-zeta is the sequence as provided in SEQ ID NO: 43, or the equivalent residues from a non-human species, e.g., mouse, rodent, monkey, ape and the like.

[00124] The term "antigen presenting cell" or "APC" refers to an immune system cell such as an accessory cell (e.g., a B-cell, a dendritic cell, and the like) that displays a foreign antigen complexed with major histocompatibility complexes (MHC's) on its surface. T-cells may recognize these complexes using their T-cell receptors (TCRs). APCs process antigens and present them to T-cells.

[00125] An "intracellular signaling domain," as the term is used herein, refers to an intracellular portion of a molecule. The intracellular signaling domain generates a signal that promotes an immune effector function of the CAR containing cell, e.g., a CART cell. Examples of immune effector function, e.g., in a CART cell, include cytolytic activity and helper activity, including the secretion of cytokines.

[00126] In an embodiment, the intracellular signaling domain can comprise a primary intracellular signaling domain. Exemplary primary intracellular signaling domains include those derived from the molecules responsible for primary stimulation, or antigen dependent simulation. In an embodiment, the intracellular signaling domain can comprise a costimulatory intracellular domain. Exemplary costimulatory intracellular signaling domains include those derived from molecules responsible for costimulatory signals, or antigen independent stimulation. For example, in the case of a CART, a primary intracellular signaling domain can comprise a cytoplasmic sequence of a T cell receptor, and a costimulatory intracellular signaling domain can comprise cytoplasmic sequence from co-receptor or costimulatory molecule.

[00127] A primary intracellular signaling domain can comprise a signaling motif which is known as an immunoreceptor tyrosine-based activation motif or ITAM. Examples of ITAM containing primary cytoplasmic signaling sequences include, but are not limited to, those derived from CD3 zeta, common FcR gamma (FCER1G), Fc gamma RIIa, FcR beta (Fc Epsilon R1b), CD3 gamma, CD3 delta, CD3 epsilon, CD79a, CD79b, DAP10, and DAP12.

[00128] The term "zeta" or alternatively "zeta chain", "CD3-zeta" or "TCR-zeta" is defined as the protein provided as GenBan Acc. No. BAG36664.1, or the equivalent residues from a non-human species, e.g., mouse, rodent, monkey, ape and the like, and a "zeta stimulatory domain" or alternatively a "CD3-zeta stimulatory domain" or a "TCR-zeta stimulatory domain" is defined as the amino acid residues from the cytoplasmic domain of the zeta chain, or functional derivatives thereof, that are sufficient to functionally transmit an initial signal necessary for T cell activation. In one aspect the cytoplasmic domain of zeta comprises residues 52 through 164 of GenBank Acc. No. BAG36664.1 or the equivalent residues from a non-human species, e.g., mouse, rodent, monkey, ape and the like, that are functional orthologs thereof. In one aspect, the "zeta stimulatory domain" or a "CD3-zeta stimulatory domain" is the sequence provided as SEQ ID NO:17. In one aspect, the "zeta stimulatory domain" or a "CD3-zeta stimulatory domain" is the sequence provided as SEQ ID NO:43.

[00129] The term "costimulatory molecule" refers to the cognate binding partner on a T cell that specifically binds with a costimulatory ligand, thereby mediating a costimulatory response by the T cell, such as, but not limited to, proliferation. Costimulatory molecules are cell surface molecules other than antigen receptors or their ligands that are contribute to an efficient

immune response. Costimulatory molecules include, but are not limited to an MHC class I molecule, BTLA and a Toll ligand receptor, as well as OX40, CD27, CD28, CDS, ICAM-1, LFA-1 (CD11a/CD18) , ICOS (CD278), and 4-1BB (CD137). Further examples of such costimulatory molecules include CDS, ICAM-1, GITR, BAFFR, HVEM (LIGHTR), SLAMF7, NKp80 (KLRF1), NKp44, NKp30, NKp46, CD160, CD19, CD4, CD8alpha, CD8beta, IL2R beta, IL2R gamma, IL7R alpha, ITGA4, VLA1, CD49a, ITGA4, IA4, CD49D, ITGA6, VLA-6, CD49f, ITGAD, CD11d, ITGAE, CD103, ITGAL, CD11a, LFA-1, ITGAM, CD11b, ITGAX, CD11c, ITGB1, CD29, ITGB2, CD18, LFA-1, ITGB7, NKG2D, NKG2C, TNFR2, TRANCE/RANKL, DNAM1 (CD226), SLAMF4 (CD244, 2B4), CD84, CD96 (Tactile), CEACAM1, CRTAM, Ly9 (CD229), CD160 (BY55), PSGL1, CD100 (SEMA4D), CD69, SLAMF6 (NTB-A, Ly108), SLAM (SLAMF1, CD150, IPO-3), BLAME (SLAMF8), SELPLG (CD162), LTBR, LAT, GADS, SLP-76, PAG/Cbp, CD19a, and a ligand that specifically binds with CD83.

[00130] A costimulatory intracellular signaling domain can be the intracellular portion of a costimulatory molecule. A costimulatory molecule can be represented in the following protein families: TNF receptor proteins, Immunoglobulin-like proteins, cytokine receptors, integrins, signaling lymphocytic activation molecules (SLAM proteins), and activating NK cell receptors. Examples of such molecules include CD27, CD28, 4-1BB (CD137), OX40, GITR, CD30, CD40, ICOS, BAFFR, HVEM, ICAM-1, lymphocyte function-associated antigen-1 (LFA-1), CD2, CDS, CD7, CD287, LIGHT, NKG2C, NKG2D, SLAMF7, NKp80, NKp30, NKp44, NKp46, CD160, B7-H3, and a ligand that specifically binds with CD83, and the like.

[00131] The intracellular signaling domain can comprise the entire intracellular portion, or the entire native intracellular signaling domain, of the molecule from which it is derived, or a functional fragment or derivative thereof.

[00132] The term “4-1BB” refers to a member of the TNFR superfamily with an amino acid sequence provided as GenBank Acc. No. AAA62478.2, or the equivalent residues from a non-human species, e.g., mouse, rodent, monkey, ape and the like; and a “4-1BB costimulatory domain” is defined as amino acid residues 214-255 of GenBank accno. AAA62478.2, or the equivalent residues from a non-human species, e.g., mouse, rodent, monkey, ape and the like. In one aspect, the “4-1BB costimulatory domain” is the sequence provided as SEQ ID NO:16

or the equivalent residues from a non-human species, e.g., mouse, rodent, monkey, ape and the like.

[00133] "Immune effector cell," as that term is used herein, refers to a cell that is involved in an immune response, e.g., in the promotion of an immune effector response. Examples of immune effector cells include T cells, e.g., alpha/beta T cells and gamma/delta T cells, B cells, natural killer (NK) cells, natural killer T (NKT) cells, mast cells, and myeloic-derived phagocytes. Immune effector cells, e.g., T cells or NK cells, may be derived directly from a subject, or may be differentiated from cells derived from a subject (e.g., may be differentiated from stem cells, e.g., embryonic stem cells or induced pluripotent stem cells (iPSCs)).

[00134] "Immune effector function or immune effector response," as that term is used herein, refers to function or response, e.g., of an immune effector cell, that enhances or promotes an immune attack of a target cell. E.g., an immune effector function or response refers a property of a T or NK cell that promotes killing or the inhibition of growth or proliferation, of a target cell. In the case of a T cell, primary stimulation and co-stimulation are examples of immune effector function or response.

[00135] The term "encoding" refers to the inherent property of specific sequences of nucleotides in a polynucleotide, such as a gene, a cDNA, or an mRNA, to serve as templates for synthesis of other polymers and macromolecules in biological processes having either a defined sequence of nucleotides (e.g., rRNA, tRNA and mRNA) or a defined sequence of amino acids and the biological properties resulting therefrom. Thus, a gene, cDNA, or RNA, encodes a protein if transcription and translation of mRNA corresponding to that gene produces the protein in a cell or other biological system. Both the coding strand, the nucleotide sequence of which is identical to the mRNA sequence and is usually provided in sequence listings, and the non-coding strand, used as the template for transcription of a gene or cDNA, can be referred to as encoding the protein or other product of that gene or cDNA.

[00136] Unless otherwise specified, a "nucleotide sequence encoding an amino acid sequence" includes all nucleotide sequences that are degenerate versions of each other and that encode the same amino acid sequence. The phrase nucleotide sequence that encodes a protein or a RNA may also include introns to the extent that the nucleotide sequence encoding the protein may in some version contain an intron(s).

[00137] The term “effective amount” or “therapeutically effective amount” are used interchangeably herein, and refer to an amount of a compound, formulation, material, or composition, as described herein effective to achieve a particular biological result. In one non-limiting embodiment, the term “a therapeutically effective amount” refers to the amount of the compound described herein that, when administered to a subject, is effective to (1) at least partially alleviate, inhibit, preventand/or ameliorate a condition, or a disorder or a disease (i) mediated by BTK, or (ii) associated with BTK activity, or (iii) characterized by activity (normal or abnormal) of BTK; or (2) reducing or inhibiting the activity of BTK; or (3) reducing or inhibiting the expression of BTK. In another non-limiting embodiment, the term “a therapeutically effective amount” refers to the amount of the compound described herein, that when administered to a cell, or a tissue, or a non-cellular biological material, or a medium, is effective to at least partially reducing or inhibiting the activity of BTK; or reducing or inhibiting the expression of BTK partially or completely.

[00138] The term “endogenous” refers to any material from or produced inside an organism, cell, tissue or system.

[00139] The term “exogenous” refers to any material introduced from or produced outside an organism, cell, tissue or system.

[00140] The term “expression” refers to the transcription and/or translation of a particular nucleotide sequence driven by a promoter.

[00141] The term “transfer vector” refers to a composition of matter which comprises an isolated nucleic acid and which can be used to deliver the isolated nucleic acid to the interior of a cell. Numerous vectors are known in the art including, but not limited to, linear polynucleotides, polynucleotides associated with ionic or amphiphilic compounds, plasmids, and viruses. Thus, the term “transfer vector” includes an autonomously replicating plasmid or a virus. The term should also be construed to further include non-plasmid and non-viral compounds which facilitate transfer of nucleic acid into cells, such as, for example, a polylysine compound, liposome, and the like. Examples of viral transfer vectors include, but are not limited to, adenoviral vectors, adeno-associated virus vectors, retroviral vectors, lentiviral vectors, and the like.

[00142] The term “expression vector” refers to a vector comprising a recombinant polynucleotide comprising expression control sequences operatively linked to a nucleotide sequence to be expressed. An expression vector comprises sufficient cis-acting elements for expression; other elements for expression can be supplied by the host cell or in an in vitro expression system. Expression vectors include all those known in the art, including cosmids, plasmids (e.g., naked or contained in liposomes) and viruses (e.g., lentiviruses, retroviruses, adenoviruses, and adeno-associated viruses) that incorporate the recombinant polynucleotide.

[00143] The term “lentivirus” refers to a genus of the Retroviridae family. Lentiviruses are unique among the retroviruses in being able to infect non-dividing cells; they can deliver a significant amount of genetic information into the DNA of the host cell, so they are one of the most efficient methods of a gene delivery vector. HIV, SIV, and FIV are all examples of lentiviruses.

[00144] The term “lentiviral vector” refers to a vector derived from at least a portion of a lentivirus genome, including especially a self-inactivating lentiviral vector as provided in Milone et al., Mol. Ther. 17(8): 1453–1464 (2009). Other examples of lentivirus vectors that may be used in the clinic, include but are not limited to, e.g., the LENTIVECTOR® gene delivery technology from Oxford BioMedica, the LENTIMAX™ vector system from Lentigen and the like. Nonclinical types of lentiviral vectors are also available and would be known to one skilled in the art.

[00145] The term “homologous” or “identity” refers to the subunit sequence identity between two polymeric molecules, e.g., between two nucleic acid molecules, such as, two DNA molecules or two RNA molecules, or between two polypeptide molecules. When a subunit position in both of the two molecules is occupied by the same monomeric subunit; e.g., if a position in each of two DNA molecules is occupied by adenine, then they are homologous or identical at that position. The homology between two sequences is a direct function of the number of matching or homologous positions; e.g., if half (e.g., five positions in a polymer ten subunits in length) of the positions in two sequences are homologous, the two sequences are 50% homologous; if 90% of the positions (e.g., 9 of 10), are matched or homologous, the two sequences are 90% homologous.

[00146] "Humanized" forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. For the most part, humanized antibodies and antibody fragments thereof are human immunoglobulins (recipient antibody or antibody fragment) in which residues from a complementary-determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework region (FR) residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, a humanized antibody/antibody fragment can comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. These modifications can further refine and optimize antibody or antibody fragment performance. In general, the humanized antibody or antibody fragment thereof will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or a significant portion of the FR regions are those of a human immunoglobulin sequence. The humanized antibody or antibody fragment can also comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details, see Jones et al., Nature, 321: 522-525, 1986; Reichmann et al., Nature, 332: 323-329, 1988; Presta, Curr. Op. Struct. Biol., 2: 593-596, 1992.

[00147] "Fully human" refers to an immunoglobulin, such as an antibody or antibody fragment, where the whole molecule is of human origin or consists of an amino acid sequence identical to a human form of the antibody or immunoglobulin.

[00148] The term "isolated" means altered or removed from the natural state. For example, a nucleic acid or a peptide naturally present in a living animal is not "isolated," but the same nucleic acid or peptide partially or completely separated from the coexisting materials of its natural state is "isolated." An isolated nucleic acid or protein can exist in substantially purified form, or can exist in a non-native environment such as, for example, a host cell.

[00149] In the context of the present invention, the following abbreviations for the commonly occurring nucleic acid bases are used. "A" refers to adenosine, "C" refers to cytosine, "G" refers to guanosine, "T" refers to thymidine, and "U" refers to uridine.

[00150] The term "operably linked" or "transcriptional control" refers to functional linkage between a regulatory sequence and a heterologous nucleic acid sequence resulting in expression of the latter. For example, a first nucleic acid sequence is operably linked with a second nucleic acid sequence when the first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Operably linked DNA sequences can be contiguous with each other and, e.g., where necessary to join two protein coding regions, are in the same reading frame.

[00151] The term "parenteral" administration of an immunogenic composition includes, e.g., subcutaneous (s.c.), intravenous (i.v.), intramuscular (i.m.), or intrasternal injection, intratumoral, or infusion techniques.

[00152] The term "nucleic acid" or "polynucleotide" refers to deoxyribonucleic acids (DNA) or ribonucleic acids (RNA) and polymers thereof in either single- or double-stranded form. Unless specifically limited, the term encompasses nucleic acids containing known analogues of natural nucleotides that have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions), alleles, orthologs, SNPs, and complementary sequences as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzer et al., Nucleic Acid Res. 19:5081 (1991); Ohtsuka et al., J. Biol. Chem. 260:2605-2608 (1985); and Rossolini et al., Mol. Cell. Probes 8:91-98 (1994)).

[00153] The terms "peptide," "polypeptide," and "protein" are used interchangeably, and refer to a compound comprised of amino acid residues covalently linked by peptide bonds. A protein or peptide must contain at least two amino acids, and no limitation is placed on the maximum number of amino acids that can comprise a protein's or peptide's sequence. Polypeptides include any peptide or protein comprising two or more amino acids joined to each other by peptide bonds. As used herein, the term refers to both short chains, which also commonly are referred to in the art as peptides, oligopeptides and oligomers, for example, and to longer chains, which generally are referred to in the art as proteins, of which there are many

types. “Polypeptides” include, for example, biologically active fragments, substantially homologous polypeptides, oligopeptides, homodimers, heterodimers, variants of polypeptides, modified polypeptides, derivatives, analogs, fusion proteins, among others. A polypeptide includes a natural peptide, a recombinant peptide, or a combination thereof.

[00154] The term “promoter” refers to a DNA sequence recognized by the synthetic machinery of the cell, or introduced synthetic machinery, required to initiate the specific transcription of a polynucleotide sequence.

[00155] The term “promoter/regulatory sequence” refers to a nucleic acid sequence which is required for expression of a gene product operably linked to the promoter/regulatory sequence. In some instances, this sequence may be the core promoter sequence and in other instances, this sequence may also include an enhancer sequence and other regulatory elements which are required for expression of the gene product. The promoter/regulatory sequence may, for example, be one which expresses the gene product in a tissue specific manner.

[00156] The term “constitutive” promoter refers to a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a cell under most or all physiological conditions of the cell.

[00157] The term “inducible” promoter refers to a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a cell substantially only when an inducer which corresponds to the promoter is present in the cell.

[00158] The term “tissue-specific” promoter refers to a nucleotide sequence which, when operably linked with a polynucleotide encodes or specified by a gene, causes the gene product to be produced in a cell substantially only if the cell is a cell of the tissue type corresponding to the promoter.

[00159] The term “flexible polypeptide linker” or “linker” as used in the context of a scFv refers to a peptide linker that consists of amino acids such as glycine and/or serine residues used alone or in combination, to link variable heavy and variable light chain regions together. In one embodiment, the flexible polypeptide linker is a Gly/Ser linker and comprises the amino acid sequence (Gly-Gly-Gly-Ser)$_n$, where n is a positive integer equal to or greater than 1 (SEQ ID NO: 31). For example, n=1, n=2, n=3. n=4, n=5 and n=6, n=7, n=8, n=9 and n=10 (SEQ ID

NO: 28). In one embodiment, the flexible polypeptide linkers include, but are not limited to, $(Gly_4 Ser)_4$ (SEQ ID NO: 29) or $(Gly_4 Ser)_3$ (SEQ ID NO: 30). In another embodiment, the linkers include multiple repeats of (Gly_2Ser), (GlySer) or (Gly_3Ser) (SEQ ID NO: 31). Also included within the scope of the invention are linkers described in WO2012/138475, incorporated herein by reference).

[00160] As used herein, a 5' cap (also termed an RNA cap, an RNA 7-methylguanosine cap or an RNA m^7G cap) is a modified guanine nucleotide that has been added to the "front" or 5' end of a eukaryotic messenger RNA shortly after the start of transcription. The 5' cap consists of a terminal group which is linked to the first transcribed nucleotide. Its presence is critical for recognition by the ribosome and protection from RNases. Cap addition is coupled to transcription, and occurs co-transcriptionally, such that each influences the other. Shortly after the start of transcription, the 5' end of the mRNA being synthesized is bound by a cap-synthesizing complex associated with RNA polymerase. This enzymatic complex catalyzes the chemical reactions that are required for mRNA capping. Synthesis proceeds as a multi-step biochemical reaction. The capping moiety can be modified to modulate functionality of mRNA such as its stability or efficiency of translation.

[00161] As used herein, "in vitro transcribed RNA" refers to RNA, preferably mRNA, that has been synthesized in vitro. Generally, the in vitro transcribed RNA is generated from an in vitro transcription vector. The in vitro transcription vector comprises a template that is used to generate the in vitro transcribed RNA.

[00162] As used herein, a "poly(A)" is a series of adenosines attached by polyadenylation to the mRNA. In the preferred embodiment of a construct for transient expression, the polyA is between 50 and 5000 (SEQ ID NO: 2589), preferably greater than 64, more preferably greater than 100, most preferably greater than 300 or 400. poly(A) sequences can be modified chemically or enzymatically to modulate mRNA functionality such as localization, stability or efficiency of translation.

[00163] As used herein, "polyadenylation" refers to the covalent linkage of a polyadenylyl moiety, or its modified variant, to a messenger RNA molecule. In eukaryotic organisms, most messenger RNA (mRNA) molecules are polyadenylated at the 3' end. The 3' poly(A) tail is a long sequence of adenine nucleotides (often several hundred) added to the pre-mRNA through

the action of an enzyme, polyadenylate polymerase. In higher eukaryotes, the poly(A) tail is added onto transcripts that contain a specific sequence, the polyadenylation signal. The poly(A) tail and the protein bound to it aid in protecting mRNA from degradation by exonucleases. Polyadenylation is also important for transcription termination, export of the mRNA from the nucleus, and translation. Polyadenylation occurs in the nucleus immediately after transcription of DNA into RNA, but additionally can also occur later in the cytoplasm. After transcription has been terminated, the mRNA chain is cleaved through the action of an endonuclease complex associated with RNA polymerase. The cleavage site is usually characterized by the presence of the base sequence AAUAAA near the cleavage site. After the mRNA has been cleaved, adenosine residues are added to the free 3' end at the cleavage site.

[00164] As used herein, "transient" refers to expression of a non-integrated transgene for a period of hours, days or weeks, wherein the period of time of expression is less than the period of time for expression of the gene if integrated into the genome or contained within a stable plasmid replicon in the host cell.

[00165] The term "signal transduction pathway" refers to the biochemical relationship between a variety of signal transduction molecules that play a role in the transmission of a signal from one portion of a cell to another portion of a cell. The phrase "cell surface receptor" includes molecules and complexes of molecules capable of receiving a signal and transmitting signal across the membrane of a cell.

[00166] The term "subject" is intended to include living organisms in which an immune response can be elicited (e.g., mammals, human).

[00167] The term, a "substantially purified" cell refers to a cell that is essentially free of other cell types. A substantially purified cell also refers to a cell which has been separated from other cell types with which it is normally associated in its naturally occurring state. In some instances, a population of substantially purified cells refers to a homogenous population of cells. In other instances, this term refers simply to cell that have been separated from the cells with which they are naturally associated in their natural state. In some aspects, the cells are cultured in vitro. In other aspects, the cells are not cultured in vitro.

[00168] The term "therapeutic" as used herein means a treatment. A therapeutic effect is obtained by reduction, suppression, remission, or eradication of a disease state.

[00169] The term “prophylaxis” as used herein means the prevention of or protective treatment for a disease or disease state.

[00170] In the context of the present invention, "tumor antigen" or "hyperproliferative disorder antigen" or "antigen associated with a hyperproliferative disorder" refers to antigens that are common to specific hyperproliferative disorders. In certain aspects, the hyperproliferative disorder antigens of the present invention are derived from, cancers including but not limited to primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, non-Hodgkin lymphoma, Hodgkin lymphoma, leukemias, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast cancer, prostate cancer, ovarian cancer, pancreatic cancer, and the like.

[00171] The term “transfected” or “transformed” or “transduced” refers to a process by which exogenous nucleic acid is transferred or introduced into the host cell. A “transfected” or “transformed” or “transduced” cell is one which has been transfected, transformed or transduced with exogenous nucleic acid. The cell includes the primary subject cell and its progeny.

[00172] The term “specifically binds,” refers to an antibody, or a ligand, which recognizes and binds with a binding partner (e.g., a stimulatory tumor antigen) protein present in a sample, but which antibody or ligand does not substantially recognize or bind other molecules in the sample.

[00173] “Regulatable chimeric antigen receptor (RCAR),”as that term is used herein, refers to a set of polypeptides, typically two in the simplest embodiments, which when in a RCARX cell, provides the RCARX cell with specificity for a target cell, typically a cancer cell, and with regulatable intracellular signal generation or proliferation, which can optimize an immune effector property of the RCARX cell. An RCARX cell relies at least in part, on an antigen binding domain to provide specificity to a target cell that comprises the antigen bound by the antigen binding domain. In an embodiment, an RCAR includes a dimerization switch that, upon the presence of a dimerization molecule, can couple an intracellular signaling domain to the antigen binding domain.

[00174] "Membrane anchor" or "membrane tethering domain", as that term is used herein, refers to a polypeptide or moiety, e.g., a myristoyl group, sufficient to anchor an extracellular or intracellular domain to the plasma membrane.

[00175] "Switch domain," as that term is used herein, e.g., when referring to an RCAR, refers to an entity, typically a polypeptide-based entity, that, in the presence of a dimerization molecule, associates with another switch domain. The association results in a functional coupling of a first entity linked to, e.g., fused to, a first switch domain, and a second entity linked to, e.g., fused to, a second switch domain. A first and second switch domain are collectively referred to as a dimerization switch. In embodiments, the first and second switch domains are the same as one another, e.g., they are polypeptides having the same primary amino acid sequence, and are referred to collectively as a homodimerization switch. In embodiments, the first and second switch domains are different from one another, e.g., they are polypeptides having different primary amino acid sequences, and are referred to collectively as a heterodimerization switch. In embodiments, the switch is intracellular. In embodiments, the switch is extracellular. In embodiments, the switch domain is a polypeptide-based entity, e.g., FKBP or FRB-based, and the dimerization molecule is small molecule, e.g., a rapalogue. In embodiments, the switch domain is a polypeptide-based entity, e.g., an scFv that binds a myc peptide, and the dimerization molecule is a polypeptide, a fragment thereof, or a multimer of a polypeptide, e.g., a myc ligand or multimers of a myc ligand that bind to one or more myc scFvs. In embodiments, the switch domain is a polypeptide-based entity, e.g., myc receptor, and the dimerization molecule is an antibody or fragments thereof, e.g., myc antibody.

[00176] "Dimerization molecule," as that term is used herein, e.g., when referring to an RCAR, refers to a molecule that promotes the association of a first switch domain with a second switch domain. In embodiments, the dimerization molecule does not naturally occur in the subject, or does not occur in concentrations that would result in significant dimerization. In embodiments, the dimerization molecule is a small molecule, e.g., rapamycin or a rapalogue, e.g, RAD001.

[00177] "Refractory" as used herein refers to a disease, e.g., cancer, that does not respond to a treatment. In embodiments, a refractory cancer can be resistant to a treatment before or at the beginning of the treatment. In other embodiments, the refractory cancer can become refractory during a treatment.

[00178] A "complete responder" as used herein refers to a subject having a disease, e.g., a cancer, who exhibits a complete response, e.g., a complete remission, to a treatment. A complete response may be identified, e.g., using the Cheson criteria as described herein.

[00179] A "partial responder" as used herein refers to a subject having a disease, e.g., a cancer, who exhibits a partial response, e.g., a partial remission, to a treatment. A partial response may be identified, e.g., using the Cheson criteria.

[00180] A "non-responder" as used herein refers to a subject having a disease, e.g., a cancer, who does not exhibit a response to a treatment, e.g., the patient has stable disease or progressive disease. A non-responder may be identified, e.g., using the Cheson criteria as described herein.

[00181] The term "relapse" as used herein refers to reappearance of a disease (e.g., cancer) after an initial period of responsiveness (e.g., complete response or partial response). The initial period of responsiveness may involve the level of cancer cells falling below a certain threshold, e.g., below 20%, 1%, 10%, 5%, 4%, 3%, 2%, or 1%. The reappearance may involve the level of cancer cells rising above a certain threshold, e.g., above 20%, 1%, 10%, 5%, 4%, 3%, 2%, or 1%. Relapse may be identified, e.g., using the Cheson criteria as described herein.

[00182] Ranges: throughout this disclosure, various aspects of the invention can be presented in a range format. It should be understood that the description in range format is merely for convenience and brevity and should not be construed as an inflexible limitation on the scope of the invention. Accordingly, the description of a range should be considered to have specifically disclosed all the possible subranges as well as individual numerical values within that range. For example, description of a range such as from 1 to 6 should be considered to have specifically disclosed subranges such as from 1 to 3, from 1 to 4, from 1 to 5, from 2 to 4, from 2 to 6, from 3 to 6 etc., as well as individual numbers within that range, for example, 1, 2, 2.7, 3, 4, 5, 5.3, and 6. As another example, a range such as 95-99% identity, includes something with 95%, 96%, 97%, 98% or 99% identity, and includes subranges such as 96-99%, 96-98%, 96-97%, 97-99%, 97-98% and 98-99% identity. This applies regardless of the breadth of the range.

Description

[00183] Provided herein are compositions of matter and methods of use for the treatment of a disease such as cancer (e.g., a solid tumor or tumor associated with tumor associated macrophages) using immune effector cells (e.g., T cells or NK cells) that express a chimeric antigen receptor (CAR) (e.g., a CAR that targets an antigen on a solid tumor or antigen on a tumor associated with tumor associated macrophages). The methods include, inter alia, administering immune effector cells (e.g., T cells or NK cells) expressing a CAR described herein in combination with another agent such as an inhibitor of a pro-M2 macrophage molecule, e.g., an inhibitor of a pro-M2 macrophage molecule described herein, e.g., an anti-IL-13 antibody, an anti-IL-4 antibody or an anti-IL-13Rα1 antibody.

[00184] The present invention provides, at least in part, experiments supporting the high efficacy of a combination of a CAR therapy (e.g., a CAR that targets an antigen on a solid tumor or antigen on a tumor associated with tumor associated macrophages) and an inhibitor of a pro-M2 macrophage molecule. The combination of an inhibitor of a pro-M2 macrophage molecule, with a CAR therapy can increase efficacy of the combination therapy relative to a monotherapy of the inhibitor of a pro-M2 macrophage molecule, or a dose of CAR-expressing cells, or both. These beneficial effects can, for example, allow for a lower dose of the inhibitor of a pro-M2 macrophage molecule or the CAR-expressing cells, or both, while maintaining efficacy. The results herein are applicable to a wide range of cancers, e.g., solid tumors or tumors associated with tumor assoiciated macrophages. For example, lymphomas, such as Hodgkin lymphoma are known to be associated with MDSCs or TAMs, which may inhibit the function of the CAR-expressing immune effector cell against said lymphoma, e.g., a CD123 CAR. An immune effector cell (e.g., T cell or NK cell) that expresses a CD123 CAR, e.g., as described herein, targets cancers with CD123 surface expression (such as Hodgkin lymphoma). Alternatively or in combination with CD123 CAR, any other lymphoma-targeting CAR can be used in the combination therapies described herein. Therefore, the combination of a CAR therapy (e.g., one or more of a CD123 CAR, or other CAR targeting a lymphoma antigen) with an inhibitor of a pro-M2 macrophage molecule (e.g., as described herein) is suitable for treating a wide range of lymphomas (e.g., Hodgkin lymphoma). Similarly, an immune effector cell (e.g., T cell or NK cell) that expresses a CAR which targets an antigen on a solid tumor, e.g., as described herein, e.g., mesothelin or EGFRvIII, targets cancers with surface expression of the

antigen. Therefore, the combination of a CAR therapy (e.g., one or more of a solid tumor-targeting CAR, e.g., a CAR targeting mesothelin or EGFRvIII, e.g., as described herein) with an inhibitor of a pro-M2 macrophage molecule (e.g., as described herein) is suitable for treating a wide range of solid tumors, e.g., a disease associated with expression on mesothelin or a disease associated with expression of EGFRvIII.

[00185] According to the present invention, an inhibitor of a pro-M2 macrophage molecule can reduce inhibition, e.g., macrophage-mediated inhibition, of immune effector cells, e.g., CAR-expressing tumor effector cells, e.g., as described herein, against a cancer, e.g., a solid tumor or tumor associated with MDSCs or TAMs. Without wishing to be bound by theory, certain lymphomas, such as Hodgkin lymphoma, and solid tumors are characterized by masses of cancerous cells associated with MDSCs or TAMs. CAR-expressing immune effector cells sometimes have difficulty penetrating these densely packed masses and their anti-cancer function may be impaired by the inhibitory tumor microenvironment, e.g., inhibited by MDSCs or TAMs. Thus, an inhibitor of a pro-M2 macrophage molecule may be administered in combination with a CAR-expressing cell therapy, making the cancer cells more vulnerable to the CAR-expressing cells.

[00186] In one aspect, the invention provides a number of chimeric antigen receptors (CAR) comprising an antibody or antibody fragment engineered for specific binding to an antigen expressed on a solid tumor or tumor associated with MDSCs or TAMs (e.g., in the case of Hodgkin lymphoma, the antigen being, e.g., CD123). In one aspect, the invention provides a cell (e.g., T cell) engineered to express a CAR, wherein the CAR T cell ("CART") exhibits an anticancer property. In one aspect a cell is transformed with the CAR and the CAR is expressed on the cell surface. In some embodiments, the cell (e.g., T cell) is transduced with a viral vector encoding a CAR. In some embodiments, the viral vector is a retroviral vector. In some embodiments, the viral vector is a lentiviral vector. In some such embodiments, the cell may stably express the CAR. In another embodiment, the cell (e.g., T cell) is transfected with a nucleic acid, e.g., mRNA, cDNA, DNA, encoding a CAR. In some such embodiments, the cell may transiently express the CAR.

[00187] In one aspect, the antigen binding portion of the CAR is a scFv antibody fragment. In one aspect such antibody fragments are functional in that they retain the equivalent binding affinity, e.g., they bind the same antigen with comparable affinity, as the IgG antibody from

which it is derived. In one aspect such antibody fragments are functional in that they provide a biological response that can include, but is not limited to, activation of an immune response, inhibition of signal-transduction origination from its target antigen, inhibition of kinase activity, and the like, as will be understood by a skilled artisan. In one aspect, the antigen binding domain of the CAR is a scFv antibody fragment that is humanized compared to the murine sequence of the scFv from which it is derived. In some aspects, the antibodies of the invention are incorporated into a chimeric antigen receptor (CAR).

[00188] In one aspect, the CAR or binding domain, e.g., a humanized scFv, portion of a CAR of the invention is encoded by a transgene whose sequence has been codon optimized for expression in a mammalian cell. In one aspect, entire CAR construct of the invention is encoded by a transgene whose entire sequence has been codon optimized for expression in a mammalian cell. Codon optimization refers to the discovery that the frequency of occurrence of synonymous codons (i.e., codons that code for the same amino acid) in coding DNA is biased in different species. Such codon degeneracy allows an identical polypeptide to be encoded by a variety of nucleotide sequences. A variety of codon optimization methods is known in the art, and include, e.g., methods disclosed in at least US Patent Numbers 5,786,464 and 6,114,148.

[00189] In one aspect, the CARs of the invention combine an antigen binding domain of a specific antibody with an intracellular signaling molecule. For example, in some aspects, the intracellular signaling molecule includes, but is not limited to, CD3-zeta chain, 4-1BB and CD28 signaling modules and combinations thereof.

[00190] Furthermore, the present invention provides CAR compositions and their use in medicaments or methods for treating, among other diseases, cancer or any malignancy or autoimmune diseases involving cells or tissues which express the target antigen recognized by the CAR.

[00191] In one aspect, the CAR of the invention can be used to eradicate target antigen-expressing normal cells, thereby applicable for use as a cellular conditioning therapy prior to cell transplantation. In one aspect, the target antigen-expressing normal cell is a CD19-expressing normal stem cell and the cell transplantation is a stem cell transplantation.

[00192] In one aspect, the invention provides a cell (e.g., T cell) engineered to express a chimeric antigen receptor (CAR), wherein the CAR-expressing cell, e.g., CAR T cell ("CART"), exhibits an anticancer property. With respect to anticancer peroperties against, e.g., Hodgkin lymphoma, a preferred antigen is CD123. In one aspect, the antigen binding domain of the CAR comprises a plurality of antigen-binding fragments. In one aspect, the antigen binding domain of the CAR comprises a plurality of antibody fragments comprising a scFv.

[00193] In one aspect, the CAR comprises at least one intracellular domain selected from the group of a CD137 (4-1BB) signaling domain, a CD28 signaling domain, a CD3zeta signaling domain, and any combination thereof. In one aspect, the CAR comprises at least one intracellular signaling domain is from one or more co-stimulatory molecule(s) other than a CD137 (4-1BB) or CD28.

Chimeric Antigen Receptor (CAR)

[00194] The present invention encompasses a recombinant DNA construct comprising sequences encoding a CAR, wherein the CAR comprises an antibody or antibody fragment that binds specifically to an antigen (e.g., an antigen expressed on a solid tumor or tumor associated with MDSCs or TAMs), wherein the sequence of the antibody fragment is contiguous with and in the same reading frame as a nucleic acid sequence encoding an intracellular signaling domain. The intracellular signaling domain can comprise a costimulatory signaling domain and/or a primary signaling domain, e.g., a zeta chain. The costimulatory signaling domain refers to a portion of the CAR comprising at least a portion of the intracellular domain of a costimulatory molecule. In one embodiment, the antigen binding domain is a murine antibody or antibody fragment described herein. In one embodiment, the antigen binding domain is a humanized antibody or antibody fragment.

[00195] In one aspect an exemplary CAR construct, e.g., as described herein, comprises an optional leader sequence, an extracellular antigen binding domain, a hinge, a transmembrane domain, and an intracellular stimulatory domain. In one aspect an exemplary CAR construct comprises an optional leader sequence, an extracellular antigen binding domain, a hinge, a transmembrane domain, an intracellular costimulatory domain and an intracellular stimulatory

domain. Specific CAR constructs containing murine, fully human and/or humanized scFv domains of the invention are provided below.

[00196] An exemplary leader sequence is provided as SEQ ID NO: 2. An exemplary hinge/spacer sequence is provided as SEQ ID NO: 4 or SEQ ID NO:6 or SEQ ID NO:8 or SEQ ID NO:10. An exemplary transmembrane domain sequence is provided as SEQ ID NO:12. An exemplary sequence of the intracellular signaling domain of the 4-1BB protein is provided as SEQ ID NO: 14. An exemplary sequence of the intracellular signaling domain of CD27 is provided as SEQ ID NO:16. An exemplary CD3zeta domain sequence is provided as SEQ ID NO: 18 or SEQ ID NO:20.

[00197] In one aspect, the present invention encompasses a recombinant nucleic acid construct comprising a nucleic acid molecule encoding a CAR, wherein the nucleic acid molecule comprises the nucleic acid sequence encoding an antigen binding domain, e.g., described herein, that is contiguous with and in the same reading frame as a nucleic acid sequence encoding an intracellular signaling domain. In one aspect, the present invention encompasses a recombinant nucleic acid construct comprising a transgene encoding a CAR, wherein the nucleic acid molecule comprises a nucleic acid sequence encoding an antigen binding domain, described herein. An exemplary intracellular signaling domain that can be used in the CAR includes, but is not limited to, one or more intracellular signaling domains of, e.g., CD3-zeta, CD28, 4-1BB, and the like. In some instances, the CAR can comprise any combination of CD3-zeta, CD28, 4-1BB, and the like.

[00198] The nucleic acid sequences coding for the desired molecules can be obtained using recombinant methods known in the art, such as, for example by screening libraries from cells expressing the gene, by deriving the gene from a vector known to include the same, or by isolating directly from cells and tissues containing the same, using standard techniques. Alternatively, the nucleic acid of interest can be produced synthetically, rather than cloned.

[00199] The present invention includes retroviral and lentiviral vector constructs expressing a CAR that can be directly transduced into a cell.

[00200] The present invention also includes an RNA construct that can be directly transfected into a cell. A method for generating mRNA for use in transfection involves in vitro transcription (IVT) of a template with specially designed primers, followed by polyA addition,

to produce a construct containing 3’ and 5’ untranslated sequence (“UTR”), a 5’ cap and/or Internal Ribosome Entry Site (IRES), the nucleic acid to be expressed, and a polyA tail, typically 50-2000 bases in length (SEQ ID NO: 32) (e.g., SEQ ID NO:32-34 or SEQ ID NO:37-38). RNA so produced can efficiently transfect different kinds of cells. In one embodiment, the template includes sequences for the CAR. In an embodiment, an RNA CAR vector is transduced into a T cell by electroporation.

[00201] Sequences of non-limiting examples of various components that can be part of a CAR molecule described herein, are listed in Table 1, where “aa” stands for amino acids, and “na” stands for nucleic acids that encode the corresponding peptide.

[00202] **Table 1.** Sequences of various components of CAR (aa – amino acids, na – nucleic acids that encodes the corresponding protein)

SEQ ID NO	Description	Sequence
1	EF-1 promoter (na)	CGTGAGGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCC CACAGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACC GGTGCCTAGAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATG TCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCG TATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGG GTTTGCCGCCAGAACACAGGTAAGTGCCGTGTGTGGTTCCCGCG GGCCTGGCCTCTTTACGGGTTATGGCCCTTGCGTGCCTTGAATT ACTTCCACCTGGCTGCAGTACGTGATTCTTGATCCCGAGCTTCG GGTTGGAAGTGGGTGGGAGAGTTCGAGGCCTTGCGCTTAAGGA GCCCCTTCGCCTCGTGCTTGAGTTGAGGCCTGGCCTGGGCGCTG GGGCCGCCGCGTGCGAATCTGGTGGCACCTTCGCGCCTGTCTCG CTGCTTTCGATAAGTCTCTAGCCATTTAAAATTTTTGATGACCTG CTGCGACGCTTTTTTTCTGGCAAGATAGTCTTGTAAATGCGGGC CAAGATCTGCACACTGGTATTTCGGTTTTTGGGGCCGCGGGCGG CGACGGGGCCCGTGCGTCCCAGCGCACATGTTCGGCGAGGCGG GGCCTGCGAGCGCGGCCACCGAGAATCGGACGGGGGTAGTCTC AAGCTGGCCGGCCTGCTCTGGTGCCTGGCCTCGCGCCGCCGTGT ATCGCCCCGCCCTGGGCGGCAAGGCTGGCCCGGTCGGCACCAG TTGCGTGAGCGGAAAGATGGCCGCTTCCCGGCCCTGCTGCAGG GAGCTCAAAATGGAGGACGCGGCGCTCGGGAGAGCGGGCGGG TGAGTCACCCACACAAAGGAAAAGGGCCTTTCCGTCCTCAGCC GTCGCTTCATGTGACTCCACGGAGTACCGGGCGCCGTCCAGGCA CCTCGATTAGTTCTCGAGCTTTTGGAGTACGTCGTCTTTAGGTTG GGGGGAGGGGTTTTATGCGATGGAGTTTCCCCACACTGAGTGG GTGGAGACTGAAGTTAGGCCAGCTTGGCACTTGATGTAATTCTC CTTGGAATTTGCCCTTTTTGAGTTTGGATCTTGGTTCATTCTCAA GCCTCAGACAGTGGTTCAAAGTTTTTTTCTTCCATTTCAGGTGTC GTGA
2	Leader (aa)	MALPVTALLLPLALLLHAARP

3	Leader (na)	ATGGCCCTGCCTGTGACAGCCCTGCTGCTGCCTCTGGCTCTGCT GCTGCATGCCGCTAGACCC
	Leader codon optimized (na)	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTG CTCCACGCCGCTCGGCCC
4	CD 8 hinge (aa)	TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACD
5	CD8 hinge (na)	ACCACGACGCCAGCGCCGCGACCACCAACACCGGCGCCCACCA TCGCGTCGCAGCCCCTGTCCCTGCGCCCAGAGGCGTGCCGGCCA GCGGCGGGGGGCGCAGTGCACACGAGGGGGCTGGACTTCGCCT GTGAT
6	Ig4 hinge (aa)	ESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQ EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS DGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSL GKM
7	Ig4 hinge (na)	GAGAGCAAGTACGGCCCTCCCTGCCCCCCTTGCCCTGCCCCCGA GTTCCTGGGCGGACCCAGCGTGTTCCTGTTCCCCCCCAAGCCCA AGGACACCCTGATGATCAGCCGGACCCCCGAGGTGACCTGTGT GGTGGTGGACGTGTCCCAGGAGGACCCCGAGGTCCAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCACAACGCCAAGACCAAGC CCCGGGAGGAGCAGTTCAATAGCACCTACCGGGTGGTGTCCGT GCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAGGAATAC AAGTGTAAGGTGTCCAACAAGGGCCTGCCCAGCAGCATCGAGA AAACCATCAGCAAGGCCAAGGGCCAGCCTCGGGAGCCCCAGGT GTACACCCTGCCCCCTAGCCAAGAGGAGATGACCAAGAACCAG GTGTCCCTGACCTGCCTGGTGAAGGGCTTCTACCCCAGCGACAT CGCCGTGGAGTGGGAGAGCAACGGCCAGCCCGAGAACAACTAC AAGACCACCCCCCCTGTGCTGGACAGCGACGGCAGCTTCTTCCT GTACAGCCGGCTGACCGTGGACAAGAGCCGGTGGCAGGAGGGC AACGTCTTTAGCTGCTCCGTGATGCACGAGGCCCTGCACAACCA CTACACCCAGAAGAGCCTGAGCCTGTCCCTGGGCAAGATG
8	IgD hinge (aa)	RWPESPKAQASSVPTAQPQAEGSLAKATTAPATTRNTGRGGEEKK KEKEKEEQEERETKTPECPSHTQPLGVYLLTPAVQDLWLRDKATF TCFVVGSDLKDAHLTWEVAGKVPTGGVEEGLLERHSNGSQSQHS RLTLPRSLWNAGTSVTCTLNHPSLPPQRLMALREPAAQAPVKLSL NLLASSDPPEAASWLLCEVSGFSPPNILLMWLEDQREVNTSGFAPA RPPPQPGSTTFWAWSVLRVPAPPSPQPATYTCVVSHEDSRTLLNAS RSLEVSYVTDH
9	IgD hinge (na)	AGGTGGCCCGAAAGTCCCAAGGCCCAGGCATCTAGTGTTCCTA CTGCACAGCCCCAGGCAGAAGGCAGCCTAGCCAAAGCTACTAC TGCACCTGCCACTACGCGCAATACTGGCCGTGGCGGGGAGGAG AAGAAAAAGGAGAAAGAGAAAGAAGAACAGGAAGAGAGGGA GACCAAGACCCCTGAATGTCCATCCCATACCCAGCCGCTGGGC GTCTATCTCTTGACTCCCGCAGTACAGGACTTGTGGCTTAGAGA TAAGGCCACCTTTACATGTTTCGTCGTGGGCTCTGACCTGAAGG ATGCCCATTTGACTTGGGAGGTTGCCGGAAAGGTACCCACAGG GGGGGTTGAGGAAGGGTTGCTGGAGCGCCATTCCAATGGCTCT CAGAGCCAGCACTCAAGACTCACCCTTCCGAGATCCCTGTGGA ACGCCGGGACCTCTGTCACATGTACTCTAAATCATCCTAGCCTG CCCCCACAGCGTCTGATGGCCCTTAGAGAGCCAGCCGCCCAGG

		CACCAGTTAAGCTTAGCCTGAATCTGCTCGCCAGTAGTGATCCC CCAGAGGCCGCCAGCTGGCTCTTATGCGAAGTGTCCGGCTTTAG CCCGCCCAACATCTTGCTCATGTGGCTGGAGGACCAGCGAGAA GTGAACACCAGCGGCTTCGCTCCAGCCCGGCCCCCACCCCAGCC GGGTTCTACCACATTCTGGGCCTGGAGTGTCTTAAGGGTCCCAG CACCACCTAGCCCCCAGCCAGCCACATACACCTGTGTTGTGTCC CATGAAGATAGCAGGACCCTGCTAAATGCTTCTAGGAGTCTGG AGGTTTCCTACGTGACTGACCATT
10	GS hinge/linker (aa)	GGGGSGGGGS
11	GS hinge/linker (na)	GGTGGCGGAGGTTCTGGAGGTGGAGGTTCC
12	CD8TM (aa)	IYIWAPLAGTCGVLLLSLVITLYC
13	CD8 TM (na)	ATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCCTTCT CCTGTCACTGGTTATCACCCTTTACTGC
	CD8 TM, codon optimized (na)	ATCTACATTTGGGCCCCTCTGGCTGGTACTTGCGGGGTCCTGCT GCTTTCACTCGTGATCACTCTTTACTGT
14	4-1BB intracellular domain (aa)	KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL
15	4-1BB intracellular domain (na)	AAACGGGGCAGAAAGAAACTCCTGTATATATTCAAACAACCAT TTATGAGACCAGTACAAACTACTCAAGAGGAAGATGGCTGTAG CTGCCGATTTCCAGAAGAAGAAGAAGGAGGATGTGAACTG
	4-1BB intracellular domain, codon optimized (na)	AAGCGCGGTCGGAAGAAGCTGCTGTACATCTTTAAGCAACCCTT CATGAGGCCTGTGCAGACTACTCAAGAGGAGGACGGCTGTTCA TGCCGGTTCCCAGAGGAGGAGGAAGGCGGCTGCGAACTG
16	CD27 intracellular domain (aa)	QRRKYRSNKGESPVEPAEPCRYSCPREEEGSTIPIQEDYRKPEPACS P
17	CD27 intracellular domain (na)	AGGAGTAAGAGGAGCAGGCTCCTGCACAGTGACTACATGAACA TGACTCCCCGCCGCCCCGGGCCCACCCGCAAGCATTACCAGCCC TATGCCCCACCACGCGACTTCGCAGCCTATCGCTCC
18	CD3-zeta (aa)	RVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHD GLYQGLSTATKDTYDALHMQALPPR
19	CD3-zeta (na)	AGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGCGTACAAGC AGGGCCAGAACCAGCTCTATAACGAGCTCAATCTAGGACGAAG AGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCCT GAGATGGGGGGAAAGCCGAGAAGGAAGAACCCTCAGGAAGGC CTGTACAATGAACTGCAGAAAGATAAGATGGCGGAGGCCTACA GTGAGATTGGGATGAAAGGCGAGCGCCGGAGGGGCAAGGGGC ACGATGGCCTTTACCAGGGTCTCAGTACAGCCACCAAGGACAC CTACGACGCCCTTCACATGCAGGCCCTGCCCCCTCGC
20	CD3-zeta (aa)	RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHD GLYQGLSTATKDTYDALHMQALPPR
21	CD3-zeta (na)	AGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGCGTACCAGC

		AGGGCCAGAACCAGCTCTATAACGAGCTCAATCTAGGACGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGAACCCTCAGGAAGGCCTGTACAATGAACTGCAGAAAGATAAGATGGCGGAGGCCTACAGTGAGATTGGGATGAAAGGCGAGCGCCGGAGGGGCAAGGGGCACGATGGCCTTTACCAGGGTCTCAGTACAGCCACCAAGGACACCTACGACGCCCTTCACATGCAGGCCCTGCCCCCTCGC
	CD3-zeta, codon optimized (na)	CGCGTGAAATTCAGCCGCAGCGCAGATGCTCCAGCCTACAAGCAGGGGCAGAACCAGCTCTACAACGAACTCAATCTTGGTCGGAGAGAGGAGTACGACGTGCTGGACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGGAAGCCGCGCAGAAAGAATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAAGATGGCAGAAGCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGAAGAGGCAAAGGCCACGACGGACTGTACCAGGGACTCAGCACCGCCACCAAGGACACCTATGACGCTCTTCACATGCAGGCCCTGCCGCCTCGG
22	linker	GGGGS
23	linker	GGTGGCGGAGGTTCTGGAGGTGGAGGTTCC
24	PD-1 extracellular domain (aa)	Pgwfldspdrpwnpptfspallvvtegdnatftcsfsntsesfvlnwyrmspsnqtdklaafpedrsqpgqdcrfrvtqlpngrdfhmsvvrarrndsgtylcgaislapkaqikeslraelrvterraevptahpspsprpagqfqtlv
25	PD-1 extracellular domain (na)	Cccggatggtttctggactctccggatcgcccgtggaatcccccaaccttctcaccggcactcttggttgtgactgagggcgataatgcgaccttcacgtgctcgttctccaacacctccgaatcattcgtgctgaactggtaccgcatgagcccgtcaaaccagaccgacaagctcgccgcgtttccggaagatcggtcgcaaccgggacaggattgtcggttccgcgtgactcaactgccgaatggcagagacttccacatgagcgtggtccgcgctaggcgaaacgactccgggacctacctgtgcggagccatctcgctggcgcctaaggcccaaatcaaagagagcttgagggccgaactgagagtgaccgagcgcagagctgaggtgccaactgcacatccatccccatcgcctcggcctgcggggcagtttcagaccctggtc
26	PD-1 CAR (aa) with signal	Malpvtalllplalllhaarppgwfldspdrpwnpptfspallvvtegdnatftcsfsntsesfvlnwyrmspsnqtdklaafpedrsqpgqdcrfrvtqlpngrdfhmsvvrarrndsgtylcgaislapkaqikeslraelrvterraevptahpspsprpagqfqtlvtttpaprpptpaptiasqplslrpeacrpaaggavhtrgldfacdiyiwaplagtcgvlllslvitlyckrgrkkllyifkqpfmrpvqttqeedgcscrfpeeeeggcelrvkfsrsadapaykqgqnqlynelnlgrreeydvldkrrgrdpemggkprrknpqeglynelqkdkmaeayseigmkgerrrgkghdglyqglstatkdtydalhmqalppr
27	PD-1 CAR (na)	Atggccctccctgtcactgccctgcttctccccctcgcactcctgctccacgccgctagaccacccggatggtttctggactctccggatcgcccgtggaatcccccaaccttctcaccggcactcttggttgtgactgagggcgataatgcgaccttcacgtgctcgttctccaacacctccgaatcattcgtgctgaactggtaccgcatgagcccgtcaaaccagaccgacaagctcgccgcgtttccggaagatcggtcgcaaccgggacaggattgtcggttccgcgtgactcaactgccgaatggcagagacttccacatgagcgtggtccgcgctaggcgaaacgactccgggacctacctgtgcggagccatctcgctggcgcctaaggcccaaatcaaagagagcttgagggccgaactgagagtgaccgagcgcagagctgaggtgccaactgcacatccatccccatcgcctcggcctgcggggcagtttcagaccctggtcacgaccactccggcgccgcgcccaccgactccggccccaactatcgcgagccagcccctgtcgctgaggccggaagcatgccgccctgccgccggaggtgctgtgcatacccggggattggacttcgcatgcgacatctacatttgggctcctctcgccggaacttgtggcgtgctccttctgtccctggtcatcaccctgtactgcaagcggggtcggaaaaagcttctgtacattttcaagcagcccttcatgaggcccgtgcaaaccacccaggaggaggacggttgctcctgccggttccccgaagaggaagaaggaggttgcgagctgcgcgtgaagttctcccggagcgccgacgcccccgcctataagcagggccagaaccagctgtacaacgaactgaacctgggacggcgggaagagtacgatgtgctggacaagcggcgcggccgggaccccgaaatgggcgggaagcctagaagaaagaaccctcaggaaggcctgtataacgagctgcagaaggacaagatggccgaggcctactccgaaattgggatgaagggagagcggcggaggggaaaggggcacgacggcctgtaccaaggactgtccaccgccaccaaggacacatacgatgccctgcacatgcaggcccttccccctcgc

28	linker	(Gly-Gly-Gly-Ser)$_n$, where n = 1-10
29	linker	(Gly$_4$ Ser)$_4$
30	linker	(Gly$_4$ Ser)3
31	linker	(Gly$_3$Ser)
32	polyA (2000 A's)	[a]$_{2000}$
33	polyA (150 A's)	[a]$_{150}$
34	polyA (5000 A's)	[a]$_{5000}$
35	polyA (100 T's)	[t]$_{100}$
36	polyA (500 T's)	[t]$_{500}$
37	polyA (64 A's)	[a]$_{64}$
38	polyA (400 A's)	[a]$_{400}$
39	PD1 CAR (aa)	Pgwfldspdrpwnpptfspallvvtegdnatftcsfsntsesfvlnwyrmspsnqtdklaafpedrsqpgqdcrfrvtqlpngrdfhmsvvrarrndsgtylcgaislapkaqikeslraelrvterraevptahpspsprpagqfqtlvtttpaprpptpaptiasqplslrpeacrpaaggavhtrgldfacdiyiwaplagtcgvlllslvitlyckrgrkkllyifkqpfmrpvqttqeedgcscrfpeeeeggcelrvkfsrsadapaykqgqnqlynelnlgrreeydvldkrrgrdpemggkprrknpqeglynelqkdkmaeayseigmkgerrrgkghdglyqglstatkdtydalhmqalppr
40	ICOS intracellular domain (aa)	T K K K Y S S S V H D P N G E Y M F M R A V N T A K K S R L T D V T L
41	ICOS intracellular domain (na)	ACAAAAAAGAAGTATTCATCCAGTGTGCACGACCCTAACGGTGAATACATGTTCATGAGAGCAGTGAACACAGCCAAAAAATCCAGACTCACAGATGTGACCCTA
42	ICOS TM domain (aa)	T T T P A P R P P T P A P T I A S Q P L S L R P E A C R P A A G G A V H T R G L D F A C D F W L P I G C A A F V V V C I L G C I L I C W L
43	ICOS TM domain (na)	ACCACGACGCCAGCGCCGCGACCACCAACACCGGCGCCCACCATCGCGTCGCAGCCCCTGTCCCTGCGCCCAGAGGCGTGCCGGCCAGCGGCGGGGGGCGCAGTGCACACGAGGGGGCTGGACTTCGCCTGTGATTTCTGGTTACCCATAGGATGTGCAGCCTTTGTTGTAGTCTGCATTTTGGGATGCATACTTATTTGTTGGCTT
44	CD28 intracellular domain (aa)	RSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS
45	CD28 intracellular domain (na)	AGGAGTAAGAGGAGCAGGCTCCTGCACAGTGACTACATGAACATGACTCCCCGCCGCCCCGGGCCCACCCGCAAGCATTACCAGCCCTATGCCCCACCACGCGACTTCGCAGCCTATCGCTCC

Antigen binding domains and CARs

[00203] In one aspect, the CAR of the invention comprises a target-specific binding element otherwise referred to as an antigen binding domain. The choice of moiety depends upon the

type and number of ligands that define the surface of a target cell. For example, the antigen binding domain may be chosen to recognize a ligand that acts as a cell surface marker on target cells associated with a particular disease state. Thus examples of cell surface markers that may act as ligands for the antigen binding domain in a CAR of the invention include those associated with viral, bacterial and parasitic infections, autoimmune disease and cancer cells.

[00204] In one aspect, the CAR-mediated T-cell response can be directed to an antigen of interest by way of engineering an antigen binding domain that specifically binds a desired antigen into the CAR.

[00205] In one aspect, the CAR comprises an antigen binding domain which targets a solid tumor antigen. In one aspect the CAR comprises an antigen binding domain which targets a tumor antigen expressed on a tumor associated with MDSCs or TAMs, e.g., Hodgkin lymphoma.

[00206] The antigen binding domain can be any domain that binds to the antigen including but not limited to a monoclonal antibody, a polyclonal antibody, a recombinant antibody, a murine antibody, a human antibody, a humanized antibody, and a functional fragment thereof, including but not limited to a single-domain antibody such as a heavy chain variable domain (VH), a light chain variable domain (VL) and a variable domain (VHH) of camelid derived nanobody, and to an alternative scaffold known in the art to function as antigen binding domain, such as a recombinant fibronectin domain, and the like.

[00207] In an embodiment, the antigen binding domain of a CAR binds to human mesothelin. In an embodiment, the antigen binding domain is a murine scFv domain that binds to human mesothelin, e.g., SS1 or SEQ ID NO: 46. In an embodiment, the antigen binding domain is a humanized antibody or antibody fragment, e.g., scFv domain, derived from the murine SS1 scFv. In an embodiment, the antigen binding domain is a human antibody or antibody fragment that binds to human mesothelin. Exemplary human scFv domains (and their sequences) and the murine SS1 scFv that bind to mesothelin are provided in Table 2. CDR sequences are underlined. The scFv domain sequences provided in Table 2 include a light chain variable region (VL) and a heavy chain variable region (VH). The VL and VH are attached by a linker comprising the sequence GGGGSGGGGSGGGGS (SEQ ID NO: 30) (e.g., as shown in SS1 scFv domains) or GGGGSGGGGSGGGGSGGGGS (SEQ ID NO: 29) (e.g.,

as shown in M1, M2, M3, M4, M5, M6, M7, M8, M9, M10, M11, M12, M13, M14, M15, M16, M17, M18, M19, M20, M21, M22, M23, or M24 scFv domains). The scFv domains listed in Table 2 are in the following orientation: VL-linker-VH.

Table 2. Examples of antigen binding domains that bind to mesothelin

Tumor antigen	Name	Amino acid sequence	SEQ ID NO:
mesothelin	M5 (human)	QVQLVQSGAEVEKPGASVKVSCKASGYTFTDYYMHWVRQAPGQGLEWMGW INPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCASGW DFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIVMTQSPSSLSASV GDRVTITCRASQSIRYYLSWYQQKPGKAPKLLIYTASILQNGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCLQTYTTPDFGPGTKVEIK	51
mesothelin	M11 (human)	QVQLQQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGW INPNSGGTNYAQNFQGRVTMTRDTSISTAYMELRRLRSDDTAVYYCASGW DFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIRMTQSPSSLSASV GDRVTITCRASQSIRYYLSWYQQKPGKAPKLLIYTASILQNGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCLQTYTTPDFGPGTKVEIK	57
mesothelin	ss1 (murine)	Q V Q L Q Q S G P E L E K P G A S V K I S C K A S G Y S F T G Y T M N W V K Q S H G K S L E W I G L I T P Y N G A S S Y N Q K F R G K A T L T V D K S S S T A Y M D L L S L T S E D S A V Y F C A R G G Y D G R G F D Y W G Q G T T V T V S S G G G G S G G G G S G G G G S D I E L T Q S P A I M S A S P G E K V T M T C S A S S S V S Y M H W Y Q Q K S G T S P K R W I Y D T S K L A S G V P G R F S G S G S G N S Y S L T I S S V E A E D D A T Y Y C Q Q W S G Y P L T F G A G T K L E I	46
mesothelin	M1 (human)	QVQLQQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGR INPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGR YYGMDVWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPATLSL SPGERATISCRASQSVSSNFAWYQQRPGQAPRLLIYDASNRATGIPPRFS GSGSGTDFTLTISSLEPEDFAAYYCHQRSNWLYTFGQGTKVDIK	47
mesothelin	M2 (human)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGW INPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARDL RRTVVTPRAYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDIQL TQSPSTLSASVGDRVTITCQASQDISNSLNWYQQKAGKAPKLLIYDASTL ETGVPSRFSGSGSGTDFSFTISSLQPEDIATYYCQQHDNLPLTFGQGTKV EIK	48
mesothelin	M3 (human)	QVQLVQSGAEVKKPGAPVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGW INPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGE WDGSYYYDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIVLTQTPSS LSASVGDRVTITCRASQSINTYLNWYQHKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQSFSPLTFGGGTKLEIK	49
mesothelin	M4 (human)	QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMHWVRQVPGKGLVWVSR INTDGSTTTYADSVEGRFTISRDNAKNTLYLQMNSLRDDDTAVYYCVGGH WAVWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSTLSASVG DRVTITCRASQSISDRLAWYQQKPGKAPKLLIYKASSLESGVPSRFSGSG SGTEFTLTISSLQPDDFAVYYCQQYGHLPMYTFGQGTKVEIK	50
mesothelin	M6 (human)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGI INPSGGSTSYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARYR	52

		LIAVAGDYYYYGMDVWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSDIQM TQSPSSVASVGDRVTITCRASQGVGRWLAWYQQKPGTAPKLLIYAASTLQ SGVPSRFSGSGSGTDFTLTINNLQPEDFATYYCQQANSFPLTFGGGTRLE IK	
mesothelin	M7 (human)	QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAV ISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARWK VSSSSPAFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPA TLSLSPGERAILSCRASQSVYTKYLGWYQQKPGQAPRLLIYDASTRATGI PDRFSGSGSGTDFTLTINRLEPEDFAVYYCQHYGGSPLITFGQGTRLEIK	53
mesothelin	M8 (human)	QVQLQQSGAEVKKPGASVKVSCKTSGYPFTGYSLHWVRQAPGQGLEWMGW INPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARDH YGGNSLFYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSSI SASVGDTVSITCRASQDSGTWLAWYQQKPGKAPNLLMYDASTLEDGVPSR FSGSASGTEFTLTVNRLQPEDSATYYCQQYNSYPLTFGGGTKVDIK	54
mesothelin	M9 (human)	QVQLVQSGAEVKKPGASVEVSCKASGYTFTSYYMHWVRQAPGQGLEWMGI INPSGGSTGYAQKFQGRVTMTRDTSTSTVHMELSSLRSEDTAVYYCARGG YSSSSDAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPP SLSASVGDRVTITCRASQDISSALAWYQQKPGTPPKLLIYDASSLESGVP SRFSGSGSGTDFTLTISSLQPEDFATYYCQQFSSYPLTFGGGTRLEIK	55
mesothelin	M10 (human)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGW ISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARVA GGIYYYYGMDVWGQGTTITVSSGGGGSGGGGSGGGGSGGGGSDIVMTQTP DSLAVSLGERATISCKSSHSVLYNRNNKNYLAWYQQKPGQPPKLLFYWAS TRKSGVPDRFSGSGSGTDFTLTISSLQPEDFATYFCQQTQTFPLTFGQGT RLEIN	56
mesothelin	M12 (human)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGR INPNSGGTNYAQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARTT TSYAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSTLS ASVGDRVTITCRASQSISTWLAWYQQKPGKAPNLLIYKASTLESGVPSRF SGSGSGTEFTLTISSLQPDDFATYYCQQYNTYSPYTFGQGTKLEIK	58
mesothelin	M13 (human)	QVQLVQSGGGLVKPGGSLRLSCEASGFIFSDYYMGWIRQAPGKGLEWVSY IGRSGSSMYYADSVKGRFTFSRDNAKNSLYLQMNSLRAEDTAVYYCAASP VVAATEDFQHWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIVMTQTPA TLSLSPGERATLSCRASQSVTSNYLAWYQQKPGQAPRLLLFGASTRATGI PDRFSGSGSGTDFTLTINRLEPEDFAMYYCQQYGSAPVTFGQGTKLEIK	59
mesothelin	M14 (human)	QVQLVQSGAEVRAPGASVKISCKASGFTFRGYYIHWVRQAPGQGLEWMGI INPSGGSRAYAQKFQGRVTMTRDTSTSTVYMELSSLRSDDTAMYYCARTA SCGGDCYYLDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSP PTLSASVGDRVTITCRASENVNIWLAWYQQKPGKAPKLLIYKSSSLASGV PSRFSGSGSGAEFTLTISSLQPDDFATYYCQQYQSYPLTFGGGTKVDIK	60
mesothelin	M15 (human)	QVQLVQSGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSG ISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAKDG SSSWSWGYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSSSELTQDPAVSVA LGQTVRTTCQGDALRSYYASWYQQKPGQAPMLVIYGKNNRPSGIPDRFSG SDSGDTASLTITGAQAEDEADYYCNSRDSSGYPVFGTGTKVTVL	61
mesothelin	M16 (human)	EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSG ISWNSGSTGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAKDS SSWYGGGSAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSSSELTQEPAVSV ALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIFGRSRRPSGIPDRFS GSSSGNTASLIITGAQAEDEADYYCNSRDNTANHYVFGTGTKLTVL	62
mesothelin	M17 (human)	EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSG ISWNSGSTGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAKDS SSWYGGGSAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSSSELTQDPAVSV ALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFS GSSSGNTASLTITGAQAEDEADYYCNSRGSSGNHYVFGTGTKVTVL	63
mesothelin	M18	QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYWMHWVRQAPGKGLVWVSR INSDGSSTSYADSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCVRTG	64

	(human)	WVGSYYYYMDVWGKGTTVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSNYLAWYQQKPGQPPRLLIYDVSTRATGIPARFSGGGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPWTFGQGTKVEIK	
mesothelin	M19 (human)	QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGYSRYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSEIVMTQSPATLSLSPGERAILSCRASQSVYTKYLGWYQQKPGQAPRLLIYDASTRATGIPDRFSGSGSGTDFTLTINRLEPEDFAVYYCQHYGGSPLITFGQGTKVDIK	65
mesothelin	M20 (human)	QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKREAAAGHDWYFDLWGRGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIRVTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSIPLTFGQGTKVEIK	66
mesothelin	M21 (human)	QVQLVQSWAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGSTSYAQKFQGRVTMTRDTSTSTVYMELSNLRSEDTAVYYCARSPRVTTGYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYKASSLESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYSSYPLTFGGGTRLEIK	67
mesothelin	M22 (human)	QVQLVQSGAEVRRPGASVKISCRASGDTSTRHYIHWLRQAPGQGPEWMGVINPTTGPATGSPAYAQMLQGRVTMTRDTSTRTVYMELRSLRFEDTAVYYCARSVVGRSAPYYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQGISDYSAWYQQKPGKAPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISYLQSEDFATYYCQQYYSYPLTFGGGTKVDIK	68
mesothelin	M23 (human)	QVQLQQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGQGLEWMGIINPSGGYTTYAQKFQGRLTMTRDTSTSTVYMELSSLRSEDTAVYYCARIRSCGGDCYYFDNWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSTLSASVGDRVTITCRASENVNIWLAWYQQKPGKAPKLLIYKSSSLASGVPSRFSGSGSGAEFTLTISSLQPDDFATYYCQQYQSYPLTFGGGTKVDIK	69
mesothelin	M24 (human)	QITLKESGPALVKPTQTLTLTCTFSGFSLSTAGVHVGWIRQPPGKALEWLALISWADDKRYRPSLRSRLDITRVTSKDQVVLSMTNMQPEDTATYYCALQGFDGYEANWGPGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIVMTQSPSSLSASAGDRVTITCRASRGISSALAWYQQKPGKPPKLLIYDASSLESGVPSRFSGSGSGTDFTLTIDSLEPEDFATYYCQQSYSTPWTFGQGTKVDIK	70

[00208] The sequences of the CDR sequences of the scFv domains of the mesothelin antigen binding domains provided in Table 2 are shown in Table 3 for the heavy chain variable domains and in Table 4 for the light chain variable domains.

Table 3. Amino acid sequences for the heavy chain (HC) CDR1, CDR2, and CDR3 regions of human anti-mesothelin scFvs

Descrip.	HC-CDR1	SEQ ID NO:	HC-CDR2	SEQ ID NO:	HC-CDR3	SEQ ID NO:
M5	GYTFTDYYMH	115	WINPNSGGTNYAQKFQG	134	GWDFDY	159
M11	GYTFTGYYMH	121	WINPNSGGTNYAQNFQG	141	GWDFDY	165
Ss1	GYSFTGYTMN	132	LITPYNGASSYNQKFRG	154	GGYDGRGFDY	179
M1	GYTFTGYYMH	113	RINPNSGGTNYAQKFQG	133	GRYYGMDV	155
M2	GYTFTGYYMH	113	WINPNSGGTNYAQKFQG	134	DLRRTVVTPRAYYGMDV	156
M3	GYTFTGYYMH	113	WINPNSGGTNYAQKFQG	134	GEWDGSYYYDY	157

M4	GFTFSSYWMH	114	RINTDGSTTTYADSVEG	135	GHWAV	158
M6	GYTFTSYYMH	116	IINPSGGSTSYAQKFQ	136	YRLIAVAGDYYYYG MDV	160
M7	GFTFSSYAMH	117	VISYDGSNKYYADSVKG	137	WKVSSSSPAFDY	161
M8	GYPFTGYSLH	118	WINPNSGGTNYAQKFQG	138	DHYGGNSLFY	162
M9	GYTFTSYYMH	119	IINPSGGSTGYAQKFQG	139	GGYSSSSDAFDI	163
M10	GYTFTSYGIS	120	WISAYNGNTNYAQKLQ	140	VAGGIYYYYGMDV	164
M12	GYTFTGYYMH	121	RINPNSGGTNYAQKFQG	142	TTTSYAFDI	166
M13	GFIFSDYYMG	122	YIGRSGSSMYYADSVKG	143	SPVVAATEDFQH	167
M14	GFTFRGYYIH	123	IINPSGGSRAYAQKFQG	144	TASCGGDCYYLDY	168
M15	GFTFDDYAMH	124	GISWNSGSIGYADSVK	145	DGSSSWSWGYFDY	169
M16	GFTFDDYAMH	124	GISWNSGSTGYADSVKG	146	DSSSWYGGGSAFDI	170
M17	GFTFDDYAMH	124	GISWNSGSTGYADSVKG	146	DSSSWYGGGSAFDI	171
M18	GFTFSSYWMH	125	RINSDGSSTSYADSVKG	147	TGWVGSYYYYMDV	172
M19	GFTFSSYGMH	126	VISYDGSNKYYADSVKG	148	GYSRYYYYGMDV	173
M20	GFTFSSYAMS	127	AISGSGGSTYYADSVKG	149	REAAAGHDWYFDL	174
M21	GYTFTSYYMH	128	IINPSGGSTSYAQKFQG	150	SPRVTTGYFDY	175
M22	GDTSTRHYIH	129	VINPTTGPATGSPAYAQMLQ G	151	SVVGRSAPYYFDY	176
M23	GYTFTNYYMH	130	IINPSGGYTTYAQKFQG	152	IRSCGGDCYYFDN	177
M24	GFSLSTAGVHVG	131	LISWADDKRYRPSLRS	153	QGFDGYEAN	178

Table 4. Amino acid sequences for the light chain (LC) CDR1, CDR2, and CDR3 regions of human anti-mesothelin scFvs

Description	LC-CDR1	SEQ ID NO:	LC-CDR2	SEQ ID NO:	LC-CDR3	SEQ ID NO:
M5	RASQSIRYYLS	184	TASILQN	209	LQTYTTPD	234
M11	RASQSIRYYLS	190	TASILQN	215	LQTYTTPD	240
Ss1	SASSSVSYMH	204	DTSKLAS	229	QQWSGYPLT	254
M1	RASQSVSSNFA	180	DASNRAT	205	HQRSNWLYT	230
M2	QASQDISNSLN	181	DASTLET	206	QQHDNLPLT	231
M3	RASQSINTYLN	182	AASSLQS	207	QQSFSPLT	232
M4	RASQSISDRLA	183	KASSLES	208	QQYGHLPMYT	233
M6	RASQGVGRWLA	185	AASTLQS	210	QQANSFPLT	235
M7	RASQSVYTKYLG	186	DASTRAT	211	QHYGGSPLIT	236
M8	RASQDSGTWLA	187	DASTLED	212	QQYNSYPLT	237
M9	RASQDISSALA	188	DASSLES	213	QQFSSYPLT	238
M10	KSSHSVLYNRNNKNYLA	189	WASTRKS	214	QQTQTFPLT	239
M12	RASQSISTWLA	191	KASTLES	216	QQYNTYSPYT	241
M13	RASQSVTSNYLA	192	GASTRAT	217	QQYGSAPVT	242
M14	RASENVNIWLA	193	KSSSLAS	218	QQYQSYPLT	243
M15	QGDALRSYYAS	194	GKNNRPS	219	NSRDSSGYPV	244

M16	QGDSLRSYYAS	195	GRSRRPS	220	NSRDNTANHYV	245
M17	QGDSLRSYYAS	196	GKNNRPS	221	NSRGSSGNHYV	246
M18	RASQSVSSNYLA	197	DVSTRAT	222	QQRSNWPPWT	247
M19	RASQSVYTKYLG	198	DASTRAT	223	QHYGGSPLIT	248
M20	RASQSISSYLN	199	AASSLQS	224	QQSYSIPLT	249
M21	RASQSISSWLA	200	KASSLES	225	QQYSSYPLT	250
M22	RASQGISDYS	201	AASTLQS	226	QQYYSYPLT	251
M23	RASENVNIWLA	202	KSSSLAS	227	QQYQSYPLT	252
M24	RASRGISSALA	203	DASSLES	228	QQSYSTPWT	253

[00209] Any known anti-mesothelin binding domain, from, for example, a known antibody, bispecific molecule or CAR, may be suitable for use in the CAR of the present invention. For example, the antigen binding domain against mesothelin is or may be derived from an antigen binding, e.g., CDRs or VH and VL, of an antibody, antigen-binding fragment or CAR described in, e.g., PCT publication WO2015/090230. In embodiments, the antigen binding domain against mesothelin is or is derived from an antigen binding portion, e.g., CDRs or VH and VL, of an antibody, antigen-binding fragment, or CAR described in, e.g., PCT publication WO1997/025068, WO1999/028471, WO2005/014652, WO2006/099141, WO2009/045957, WO2009/068204, WO2013/142034, WO2013/040557, or WO2013/063419.

[00210] In one embodiment, the mesothelin binding domain comprises one or more (e.g., all three) light chain complementary determining region 1 (LC CDR1), light chain complementary determining region 2 (LC CDR2), and light chain complementary determining region 3 (LC CDR3) of a mesothelin binding domain described herein, e.g., provided in Table 2 or 4, and/or one or more (e.g., all three) heavy chain complementary determining region 1 (HC CDR1), heavy chain complementary determining region 2 (HC CDR2), and heavy chain complementary determining region 3 (HC CDR3) of a mesothelin binding domain described herein, e.g., provided in Table 2 or 3. In one embodiment, the mesothelin binding domain comprises one, two, or all of LC CDR1, LC CDR2, and LC CDR3 of any amino acid sequences as provided in Table 4; and one, two or three of all of HC CDR1, HC CDR2 and HC CDR3, of any amino acid acid sequences as provided in Table 3.

[00211] In one embodiment, the mesothelin antigen binding domain comprises:

(i) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 184, a LC CDR2 amino acid sequence of SEQ ID NO: 209, and a LC CDR3 amino acid sequence of SEQ ID NO: 234; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 115, a HC CDR2 amino acid sequence of SEQ ID NO: 134, and a HC CDR3 amino acid sequence of SEQ ID NO: 159;

(ii) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 190, a LC CDR2 amino acid sequence of SEQ ID NO: 215, and a LC CDR3 amino acid sequence of SEQ ID NO: 240; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 121, a HC CDR2 amino acid sequence of SEQ ID NO: 141, and a HC CDR3 amino acid sequence of SEQ ID NO: 165;

(iii) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 204, a LC CDR2 amino acid sequence of SEQ ID NO: 229, and a LC CDR3 amino acid sequence of SEQ ID NO: 254; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 132, a HC CDR2 amino acid sequence of SEQ ID NO: 154, and a HC CDR3 amino acid sequence of SEQ ID NO: 179;

(iv) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 180, a LC CDR2 amino acid sequence of SEQ ID NO: 205, and a LC CDR3 amino acid sequence of SEQ ID NO: 230; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 113, a HC CDR2 amino acid sequence of SEQ ID NO: 133, and a HC CDR3 amino acid sequence of SEQ ID NO: 155;

(v) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 181, a LC CDR2 amino acid sequence of SEQ ID NO: 206, and a LC CDR3 amino acid sequence of SEQ ID NO: 231; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 113, a HC CDR2 amino acid sequence of SEQ ID NO: 134, and a HC CDR3 amino acid sequence of SEQ ID NO: 156;

(vi) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 182, a LC CDR2 amino acid sequence of SEQ ID NO: 207, and a LC CDR3 amino acid sequence of SEQ ID NO: 232; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 113, a HC CDR2 amino acid sequence of SEQ ID NO: 134, and a HC CDR3 amino acid sequence of SEQ ID NO: 157;

(vii) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 183, a LC CDR2 amino acid sequence of SEQ ID NO: 208, and a LC CDR3 amino acid sequence of SEQ ID NO: 233; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 114, a HC CDR2 amino acid sequence of SEQ ID NO: 135, and a HC CDR3 amino acid sequence of SEQ ID NO: 158;

(viii) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 186, a LC CDR2 amino acid sequence of SEQ ID NO: 210, and a LC CDR3 amino acid sequence of SEQ ID NO: 235; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 116, a HC CDR2 amino acid sequence of SEQ ID NO: 136, and a HC CDR3 amino acid sequence of SEQ ID NO: 160;

(ix) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 186, a LC CDR2 amino acid sequence of SEQ ID NO: 211, and a LC CDR3 amino acid sequence of SEQ ID NO: 236; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 117, a HC CDR2 amino acid sequence of SEQ ID NO: 137, and a HC CDR3 amino acid sequence of SEQ ID NO: 161;

(x) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 187, a LC CDR2 amino acid sequence of SEQ ID NO: 212, and a LC CDR3 amino acid sequence of SEQ ID NO: 237; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 118, a HC CDR2 amino acid sequence of SEQ ID NO: 138, and a HC CDR3 amino acid sequence of SEQ ID NO: 162;

(xi) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 188, a LC CDR2 amino acid sequence of SEQ ID NO: 213, and a LC CDR3 amino acid sequence of SEQ ID NO: 238; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 119, a HC CDR2 amino acid sequence of SEQ ID NO: 139, and a HC CDR3 amino acid sequence of SEQ ID NO: 163;

(xii) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 189, a LC CDR2 amino acid sequence of SEQ ID NO: 214, and a LC CDR3 amino acid sequence of SEQ ID NO: 239; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 120, a HC CDR2 amino acid sequence of SEQ ID NO: 140, and a HC CDR3 amino acid sequence of SEQ ID NO: 164;

(xiii) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 191, a LC CDR2 amino acid sequence of SEQ ID NO: 216, and a LC CDR3 amino acid sequence of SEQ ID NO: 241; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 121, a HC CDR2 amino acid sequence of SEQ ID NO: 142, and a HC CDR3 amino acid sequence of SEQ ID NO: 166;

(xiv) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 192, a LC CDR2 amino acid sequence of SEQ ID NO: 217, and a LC CDR3 amino acid sequence of SEQ ID NO: 242; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 122, a HC CDR2 amino acid sequence of SEQ ID NO: 143, and a HC CDR3 amino acid sequence of SEQ ID NO: 167;

(xv) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 193, a LC CDR2 amino acid sequence of SEQ ID NO: 218, and a LC CDR3 amino acid sequence of SEQ ID NO: 243; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 123, a HC CDR2 amino acid sequence of SEQ ID NO: 144, and a HC CDR3 amino acid sequence of SEQ ID NO: 168;

(xvi) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 194, a LC CDR2 amino acid sequence of SEQ ID NO: 219, and a LC CDR3 amino acid sequence of SEQ ID NO: 244; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 124, a HC CDR2 amino acid sequence of SEQ ID NO: 145, and a HC CDR3 amino acid sequence of SEQ ID NO: 169;

(xvii) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 195, a LC CDR2 amino acid sequence of SEQ ID NO: 220, and a LC CDR3 amino acid sequence of SEQ ID NO: 245; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 124, a HC CDR2 amino acid sequence of SEQ ID NO: 146, and a HC CDR3 amino acid sequence of SEQ ID NO: 170;

(xviii) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 196, a LC CDR2 amino acid sequence of SEQ ID NO: 221, and a LC CDR3 amino acid sequence of SEQ ID NO: 246; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 124, a HC CDR2 amino acid sequence of SEQ ID NO: 146, and a HC CDR3 amino acid sequence of SEQ ID NO: 171;

(xix) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 197, a LC CDR2 amino acid sequence of SEQ ID NO: 222, and a LC CDR3 amino acid sequence of SEQ ID NO: 247; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 125, a HC CDR2 amino acid sequence of SEQ ID NO: 147, and a HC CDR3 amino acid sequence of SEQ ID NO: 172;

(xx) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 198, a LC CDR2 amino acid sequence of SEQ ID NO: 223, and a LC CDR3 amino acid sequence of SEQ ID NO: 248; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 126, a HC CDR2 amino acid sequence of SEQ ID NO: 148, and a HC CDR3 amino acid sequence of SEQ ID NO: 173;

(xxi) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 199, a LC CDR2 amino acid sequence of SEQ ID NO: 224, and a LC CDR3 amino acid sequence of SEQ ID NO: 249; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 127, a HC CDR2 amino acid sequence of SEQ ID NO: 149, and a HC CDR3 amino acid sequence of SEQ ID NO: 174;

(xxii) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 200, a LC CDR2 amino acid sequence of SEQ ID NO: 225, and a LC CDR3 amino acid sequence of SEQ ID NO: 250; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 128, a HC CDR2 amino acid sequence of SEQ ID NO: 150, and a HC CDR3 amino acid sequence of SEQ ID NO: 175;

(xxiii) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 201, a LC CDR2 amino acid sequence of SEQ ID NO: 226, and a LC CDR3 amino acid sequence of SEQ ID NO: 251; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 129, a HC CDR2 amino acid sequence of SEQ ID NO: 151, and a HC CDR3 amino acid sequence of SEQ ID NO: 176;

(xxiv) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 202, a LC CDR2 amino acid sequence of SEQ ID NO: 227, and a LC CDR3 amino acid sequence of SEQ ID NO: 252; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 130, a HC CDR2 amino acid sequence of SEQ ID NO: 152, and a HC CDR3 amino acid sequence of SEQ ID NO: 177; or

(xxv) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 203, a LC CDR2 amino acid sequence of SEQ ID NO: 228, and a LC CDR3 amino acid sequence of SEQ ID NO: 253; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 131, a HC CDR2 amino acid sequence of SEQ ID NO: 153, and a HC CDR3 amino acid sequence of SEQ ID NO: 178.

[00212] In one embodiment, the mesothelin binding domain comprises a light chain variable region described herein (e.g., in Table 2) and/or a heavy chain variable region described herein (e.g., in Table 2). In one embodiment, the mesothelin binding domain is a scFv comprising a light chain and a heavy chain of an amino acid sequence listed in Table 2. In an embodiment,

the mesothelin binding domain (e.g., an scFv) comprises: a light chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence of a light chain variable region provided in Table 2, or a sequence with 95-99% identity with an amino acid sequence provided in Table 2; and/or a heavy chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence of a heavy chain variable region provided in Table 2, or a sequence with 95-99% identity to an amino acid sequence provided in Table 2.

[00213] In one embodiment, the mesothelin binding domain comprises an amino acid sequence selected from a group consisting of SEQ ID NO: 46; SEQ ID NO: 47; SEQ ID NO: 48; SEQ ID NO: 49; SEQ ID NO: 50; SEQ ID NO: 51; SEQ ID NO: 52; SEQ ID NO: 53; SEQ ID NO: 54; SEQ ID NO: 55; SEQ ID NO: 56; SEQ ID NO: 57; SEQ ID NO: 58; SEQ ID NO: 59; SEQ ID NO: 60; SEQ ID NO: 61; SEQ ID NO: 62; SEQ ID NO: 63; SEQ ID NO: 64; SEQ ID NO: 65; SEQ ID NO: 66; SEQ ID NO: 67, SEQ ID NO: 68; SEQ ID NO: 69; and SEQ ID NO: 70; or an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) to any of the aforesaid sequences; or a sequence with 95-99% identity to any of the aforesaid sequences. In one embodiment, the mesothelin binding domain is a scFv, and a light chain variable region comprising an amino acid sequence described herein, e.g., in Table 2, is attached to a heavy chain variable region comprising an amino acid sequence described herein, e.g., in Table 2, via a linker, e.g., a linker described herein. In one embodiment, the mesothelin binding domain includes a (Gly4-Ser)n linker, wherein n is 1, 2, 3, 4, 5, or 6, preferably 4 (SEQ ID NO: 80). The light chain variable region and heavy chain variable region of a scFv can be, e.g., in any of the following orientations: light chain variable region-linker-heavy chain variable region or heavy chain variable region-linker-light chain variable region.

[00214] Such antigen binding domains which bind mesothelin, e.g., as described herein, are useful, for example, in embodiments of the invention in which a disease associated with the expression of mesothelin, e.g., as described herein, is treated.

[00215] In an embodiment, the antigen binding domain of a CAR, e.g., a CAR expressed by a cell of the invention, binds to human EGFRvIII. In an embodiment, the antigen binding domain is a murine scFv domain that binds to human EGFRvIII such as, e.g., mu310C. In an embodiment, the antigen binding domain is a humanized antibody or antibody fragment, e.g., scFv domain, derived from the murine mu310C scFv. Exemplary humanized scFv domains (and their sequences) that bind to EGFRvIII are provided in Table 5.

[00216] In an embodiment, the antigen binding domain of a CAR, e.g., a CAR expressed by a cell of the inveniton, binds to human claudin 6 (CLDN6). In an embodiment, the antigen binding domain is a murine scFv domain that binds to human CLDN6. In an embodiment, the antigen binding domain is a humanized antibody or antibody fragment. Exemplary scFv domains (and their sequences) that bind to CLDN6 are provided in Table 5. The scFv domain sequences provided in Table 5 include a light chain variable region (VL) and a heavy chain variable region (VH). The VL and VH are attached by a linker comprising the sequence GGGGSGGGGSGGGGSGGGGS (SEQ ID NO: 29), e.g., in the following orientation: VL-linker-VH.

Table 5. Examples of antigen binding domains that bind to the tumor antigen EGFRvIII or CLDN6 (as indicated)

Tumor antigen	Name	Amino acid sequence	SEQ ID NO:
EGFR vIII	huscFv1	Eiqlvqsgaevkkpgatvkisckgsgfniedyyihwvqqapgkglewmgridpendetkygpif qgrvtitadtstntvymelsslrsedtavyycafrggvywgqgttvtvssggggsggggsggggsgg ggsdvvmtqspdslavslgeratinckssqslldsdgktylnwlqqkpgqppkrlislvskldsgvp drfsgsgsgtdftltisslqaedvavyycwqgthfpgtfgggtkveik	71
EGFR vIII	huscFv2	Dvvmtqspdslavslgeratinckssqslldsdgktylnwlqqkpgqppkrlislvskldsgvpdrfs gsgsgtdftltisslqaedvavyycwqgthfpgtfgggtkveikggggsggggsggggsggggsei qlvqsgaevkkpgatvkisckgsgfniedyyihwvqqapgkglewmgridpendetkygpifqg rvtitadtstntvymelsslrsedtavyycafrggvywgqgttvtvss	72
EGFR vIII	huscFv3	Eiqlvqsgaevkkpgeslrisckgsgfniedyyihwvrqmpgkglewmgridpendetkygpif qghvtisadtsintvylqwsslkasdtamyycafrggvywgqgttvtvssggggsggggsggggs ggggsdvvmtqsplslpvtlgqpasisckssqslldsdgktylnwlqqrpgqsprrlislvskldsgv pdrfsgsgsgtdftlkisrveaedvgvyycwqgthfpgtfgggtkveik	73
EGFR vIII	huscFv4	Dvvmtqsplslpvtlgqpasisckssqslldsdgktylnwlqqrpgqsprrlislvskldsgvpdrfsg sgsgtdftlkisrveaedvgvyycwqgthfpgtfgggtkveikggggsggggsggggsggggseiq lvqsgaevkkpgeslrisckgsgfniedyyihwvrqmpgkglewmgridpendetkygpifqgh vtisadtsintvylqwsslkasdtamyycafrggvywgqgttvtvss	74

EGFR vIII	huscFv5	Eiqlvqsgaevkkpgatvkisckgsgfniedyyihwvqqapgkglewmgridpendetkygpifqgrvtitadtstntvymelsslrsedtavyycafrggvywgqgttvtvssggggsggggsggggsggggsdvvmtqsplslpvtlgqpasisckssqslldsdgktylnwlqqrpgqsprrlislvskldsgvpdrfsgsgsgtdftlkisrveaedvgvyycwqgthfpgtfgggtkveik	75
EGFR vIII	huscFv6	Eiqlvqsgaevkkpgeslrisckgsgfniedyyihwvrqmpgkglewmgridpendetkygpifqghvtisadtsintvylqwsslkasdtamyycafrggvywgqgttvtvssggggsggggsggggsggggsdvvmtqspdslavslgeratinckssqslldsdgktylnwlqqkpgqppkrlislvskldsgvpdrfsgsgsgtdftltisslqaedvavyycwqgthfpgtfgggtkveik	76
EGFR vIII	huscFv7	Dvvmtqspdslavslgeratinckssqslldsdgktylnwlqqkpgqppkrlislvskldsgvpdrfsgsgsgtdftltisslqaedvavyycwqgthfpgtfgggtkveikggggsggggsggggsggggseiqlvqsgaevkkpgeslrisckgsgfniedyyihwvrqmpgkglewmgridpendetkygpifqghvtisadtsintvylqwsslkasdtamyycafrggvywgqgttvtvss	77
EGFR vIII	huscFv8	Dvvmtqsplslpvtlgqpasisckssqslldsdgktylnwlqqrpgqsprrlislvskldsgvpdrfsgsgsgtdftlkisrveaedvgvyycwqgthfpgtfgggtkveikggggsggggsggggsggggseiqlvqsgaevkkpgatvkisckgsgfniedyyihwvqqapgkglewmgridpendetkygpifqgrvtitadtstntvymelsslrsedtavyycafrggvywgqgttvtvss	78
EGFR vIII	Mu310C	eiqlqqsgaelvkpgasvklsctgsgfniedyyihwvkqrteqglewigridpendetkygpifqgratitadtssntvylqlssltsedtavyycafrggvywgpgttltvssggggsggggsggggshmdvvmtqspltlsvaigqsasisckssqslldsdgktylnwllqrpgqspkrlislvskldsgvpdrftgsgsgtdftlrisrveaedlgiyycwqgthfpgtfgggtkleik	79
Claudin6	muMAB 64A	EVQLQQSGPELVKPGASMKISCKASGYSFTGYTMNWVKQSHGKNLEWIGLINPYNGGTIYNQKFKGKATLTVDKSSSTAYMELLSLTSEDSAVYYCARDYGFVLDYWGQGTTLTVSSGGGGSGGGGSGGGGSGGGGSQIVLTQSPSIMSVSPGEKVTITCSASSSVSYMHWFQQKPGTSPKLCIYSTSNLASGVPARFSGRGSGTSYSLTISRVAAEDAATYYCQQRSNYPPWTFGGGTKLEIK	98
Claudin6	mAb206-LCC	EVQLQQSGPELVKPGASMKISCKASGYSFTGYTMNWVKQSHGKNLEWIGLINPYNGGTIYNQKFKGKATLTVDKSSSTAYMELLSLTSEDSAVYYCARDYGFVLDYWGQGTTLTVSSGGGGSGGGGSGGGGSGGGGSQIVLTQSPAIMSASPGEKVTITCSASSSVSYLHWFQQKPGTSPKLWVYSTSNLPSGVPARFGGSGSGTSYSLTISRMEAEDAATYYCQQRSIYPPWTFGGGTKLEIK	99
Claudin6	mAb206-SUBG	EVQLQQSGPELVKPGASMKISCKASGYSFTGYTMNWVKQSHGKNLEWIGLINPYNGGTIYNQKFKGKATLTVDKSSSTAYMELLSLTSEDSAVYYCARDYGFVLDYWGQGTTLTVSSGGGGSGGGGSGGGGSGGGGSQIVLTQSPSIMSVSPGEKVTITCSASSSVSYMHWFQQKPGTSPKLGIYSTSNLASGVPARFSGRGSGTSYSLTISRVAAEDAATYYCQQRSNYPPWTFGGGTKLEIK	100

[00217] In one embodiment, the EGFRvIII binding domain comprises one or more (e.g., all three) light chain complementary determining region 1 (LC CDR1), light chain complementary determining region 2 (LC CDR2), and light chain complementary determining region 3 (LC CDR3) of an EGFRvIII binding domain described herein, e.g., provided in Table 5, and/or one or more (e.g., all three) heavy chain complementary determining region 1 (HC CDR1), heavy

chain complementary determining region 2 (HC CDR2), and heavy chain complementary determining region 3 (HC CDR3) of an EGFRvIII binding domain described herein, e.g., provided in Table 5.

[00218] In one embodiment, the EGFRvIII binding domain comprises a light chain variable region described herein (e.g., in Table 5) and/or a heavy chain variable region described herein (e.g., in Table 5). In one embodiment, the EGFRvIII binding domain is a scFv comprising a light chain and a heavy chain of an amino acid sequence listed in Table 5. In an embodiment, the EGFRvIII binding domain (e.g., an scFv) comprises: a light chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence of a light chain variable region provided in Table 5, or a sequence with 95-99% identity with an amino acid sequence provided in Table 5; and/or a heavy chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence of a heavy chain variable region provided in Table 5, or a sequence with 95-99% identity to an amino acid sequence provided in Table 5.

[00219] In one embodiment, the EGFRvIII binding domain comprises an amino acid sequence selected from a group consisting of SEQ ID NO: 71; SEQ ID NO: 72; SEQ ID NO: 73; SEQ ID NO: 74; SEQ ID NO: 75; SEQ ID NO: 76; SEQ ID NO: 77; SEQ ID NO: 78; and SEQ ID NO: 79; or an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) to any of the aforesaid sequences; or a sequence with 95-99% identity to any of the aforesaid sequences. In one embodiment, the EGFRvIII binding domain is a scFv, and a light chain variable region comprising an amino acid sequence described herein, e.g., in Table 5, is attached to a heavy chain variable region comprising an amino acid sequence described herein, e.g., in Table 5, via a linker, e.g., a linker described herein. In one embodiment, the EGFRvIII binding domain includes a (Gly4-Ser)n linker, wherein n is 1, 2, 3, 4, 5, or 6, preferably 4 (SEQ ID NO: 80). The light chain variable region and heavy chain variable region of a scFv can be, e.g., in any of

the following orientations: light chain variable region-linker-heavy chain variable region or heavy chain variable region-linker-light chain variable region.

[00220] In one embodiment, the claudin-6 binding domain comprises one or more (e.g., all three) light chain complementary determining region 1 (LC CDR1), light chain complementary determining region 2 (LC CDR2), and light chain complementary determining region 3 (LC CDR3) of an EGFRvIII binding domain described herein, e.g., provided in Table 5, and/or one or more (e.g., all three) heavy chain complementary determining region 1 (HC CDR1), heavy chain complementary determining region 2 (HC CDR2), and heavy chain complementary determining region 3 (HC CDR3) of an claudin-6 binding domain described herein, e.g., provided in Table 5.

[00221] In one embodiment, the claudin-6 binding domain comprises a light chain variable region described herein (e.g., in Table 5) and/or a heavy chain variable region described herein (e.g., in Table 5). In one embodiment, the claudin-6 binding domain is a scFv comprising a light chain and a heavy chain of an amino acid sequence listed in Table 5. In an embodiment, the claudin-6 binding domain (e.g., an scFv) comprises: a light chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence of a light chain variable region provided in Table 5, or a sequence with 95-99% identity with an amino acid sequence provided in Table 5; and/or a heavy chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence of a heavy chain variable region provided in Table 5, or a sequence with 95-99% identity to an amino acid sequence provided in Table 5.

[00222] Such antigen binding domains which bind EGFRvIII, e.g., as described herein, are useful, for example, in embodiments of the invention in which a disease associated with the expression of EGFRvIII, e.g., as described herein, is treated.

[00223] In one embodiment, the claudin-6 binding domain comprises an amino acid sequence selected from a group consisting of SEQ ID NO: 98; SEQ ID NO: 99; and SEQ ID

NO: 100; or an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) to any of the aforesaid sequences; or a sequence with 95-99% identity to any of the aforesaid sequences. In one embodiment, the claudin-6 binding domain is a scFv, and a light chain variable region comprising an amino acid sequence described herein, e.g., in Table 5, is attached to a heavy chain variable region comprising an amino acid sequence described herein, e.g., in Table 5, via a linker, e.g., a linker described herein. In one embodiment, the claudin-6 binding domain includes a (Gly4-Ser)n linker, wherein n is 1, 2, 3, 4, 5, or 6, preferably 4 (SEQ ID NO: 80). The light chain variable region and heavy chain variable region of a scFv can be, e.g., in any of the following orientations: light chain variable region-linker-heavy chain variable region or heavy chain variable region-linker-light chain variable region.

[00224] In one embodiment, an antigen binding domain against GD2 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Mujoo et al., Cancer Res. 47(4):1098-1104 (1987); Cheung et al., Cancer Res 45(6):2642-2649 (1985), Cheung et al., J Clin Oncol 5(9):1430-1440 (1987), Cheung et al., J Clin Oncol 16(9):3053-3060 (1998), Handgretinger et al., Cancer Immunol Immunother 35(3):199-204 (1992). In some embodiments, an antigen binding domain against GD2 is an antigen binding portion of an antibody selected from mAb 14.18, 14G2a, ch14.18, hu14.18, 3F8, hu3F8, 3G6, 8B6, 60C3, 10B8, ME36.1, and 8H9, see e.g., WO2012033885, WO2013040371, WO2013192294, WO2013061273, WO2013123061, WO2013074916, and WO201385552. In some embodiments, an antigen binding domain against GD2 is an antigen binding portion of an antibody described in US Publication No.: 20100150910 or PCT Publication No.: WO 2011160119.

[00225] In one embodiment, an antigen binding domain against the Tn antigen, the sTn antigen, a Tn-O-glycopeptide antigen, or a sTn-O-glycopeptide antigen is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., US 2014/0178365, US8,440,798, EP 2083868 A2, Brooks et al., PNAS 107(22):10056-10061 (2010), and Stone et al., OncoImmunology 1(6):863-873(2012).

[00226] In one embodiment, an antigen binding domain against PSMA is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Parker et al., Protein Expr Purif 89(2):136-145 (2013), US 20110268656 (J591 ScFv); Frigerio et al, European J Cancer

49(9):2223-2232 (2013) (scFvD2B); WO 2006125481 (mAbs 3/A12, 3/E7 and 3/F11) and single chain antibody fragments (scFv A5 and D7).

[00227] In one embodiment, an antigen binding domain against CD97 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., US6,846,911;de Groot et al., J Immunol 183(6):4127-4134 (2009); or an antibody from R&D:MAB3734.

[00228] In one embodiment, an antigen binding domain against TAG72 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Hombach et al., Gastroenterology 113(4):1163-1170 (1997); and Abcam ab691.

[00229] In one embodiment, an antigen binding domain against CD44v6 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Casucci et al., Blood 122(20):3461-3472 (2013).

[00230] In one embodiment, an antigen binding domain against CEA is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Chmielewski et al., Gastoenterology 143(4):1095-1107 (2012).

[00231] In one embodiment, an antigen binding domain against EPCAM is an antigen binding portion, e.g., CDRS, of an antibody selected from MT110, EpCAM-CD3 bispecific Ab (see, e.g., clinicaltrials.gov/ct2/show/NCT00635596); Edrecolomab; 3622W94; ING-1; and adecatumumab (MT201).

[00232] In one embodiment, an antigen binding domain against KIT is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., US7915391, US20120288506, and several commercial catalog antibodies.

[00233] In one embodiment, an antigen binding domain against IL-13Ra2 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., WO2008/146911, WO2004087758, several commercial catalog antibodies, and WO2004087758.

[00234] In one embodiment, an antigen binding domain against CD171 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Hong et al., J Immunother 37(2):93-104 (2014).

[00235] In one embodiment, an antigen binding domain against PSCA is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Morgenroth et al., Prostate 67(10):1121-

1131 (2007) (scFv 7F5); Nejatollahi et al., J of Oncology 2013(2013), article ID 839831 (scFv C5-II); and US Pat Publication No. 20090311181.

[00236] In one embodiment, an antigen binding domain against MAD-CT-2 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., PMID: 2450952; US7635753.

[00237] In one embodiment, an antigen binding domain against Folate receptor alpha is an antigen binding portion, e.g., CDRs, of the antibody IMGN853, or an antibody described in US20120009181; US4851332, LK26: US5952484.

[00238] In one embodiment, an antigen binding domain against ERBB2 (Her2/neu) is an antigen binding portion, e.g., CDRs, of the antibody trastuzumab, or pertuzumab.

[00239] In one embodiment, an antigen binding domain against MUC1 is an antigen binding portion, e.g., CDRs, of the antibody SAR566658.

[00240] In one embodiment, the antigen binding domain against EGFR is antigen binding portion, e.g., CDRs, of the antibody cetuximab, panitumumab, zalutumumab, nimotuzumab, or matuzumab.

[00241] In one embodiment, an antigen binding domain against NCAM is an antigen binding portion, e.g., CDRs, of the antibody clone 2-2B: MAB5324 (EMD Millipore)

[00242] In one embodiment, an antigen binding domain against CAIX is an antigen binding portion, e.g., CDRs, of the antibody clone 303123 (R&D Systems).

[00243] In one embodiment, an antigen binding domain against Fos-related antigen 1 is an antigen binding portion, e.g., CDRs, of the antibody 12F9 (Novus Biologicals).

[00244] In one embodiment, an antigen binding domain against SSEA-4 is an antigen binding portion, e.g., CDRs, of antibody MC813 (Cell Signaling), or other commercially available antibodies.

[00245] In one embodiment, an antigen binding domain against PDGFR-beta is an antigen binding portion, e.g., CDRs, of an antibody Abcam ab32570.

[00246] In one embodiment, an antigen binding domain against ALK is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Mino-Kenudson et al., Clin Cancer Res 16(5):1561-1571 (2010).

[00247] In one embodiment, an antigen binding domain against plysialic acid is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Nagae et al., J Biol Chem 288(47):33784-33796 (2013).

[00248] In one embodiment, an antigen binding domain against PLAC1 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Ghods et al., Biotechnol Appl Biochem 2013 doi:10.1002/bab.1177.

[00249] In one embodiment, an antigen binding domain against GloboH is an antigen binding portion of the antibody VK9; or an antibody described in, e.g., Kudryashov V et al, Glycoconj J.15(3):243-9 (1998), Lou et al., Proc Natl Acad Sci USA 111(7):2482-2487 (2014) ; MBr1: Bremer E-G et al. J Biol Chem 259:14773–14777 (1984).

[00250] In one embodiment, an antigen binding domain against NY-BR-1 is an antigen binding portion, e.g., CDRs of an antibody described in, e.g., Jager et al., Appl Immunohistochem Mol Morphol 15(1):77-83 (2007).

[00251] In one embodiment, an antigen binding domain against sperm protein 17 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Song et al., Target Oncol 2013 Aug 14 (PMID: 23943313); Song et al., Med Oncol 29(4):2923-2931 (2012).

[00252] In one embodiment, an antigen binding domain against TRP-2 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Wang et al, J Exp Med. 184(6):2207-16 (1996).

[00253] In one embodiment, an antigen binding domain against CYP1B1 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Maecker et al, Blood 102 (9): 3287-3294 (2003).

[00254] In one embodiment, an antigen binding domain against RAGE-1 is an antigen binding portion, e.g., CDRs, of the antibody MAB5328 (EMD Millipore).

[00255] In one embodiment, an antigen binding domain against human telomerase reverse transcriptase is an antigen binding portion, e.g., CDRs, of the antibody cat no: LS-B95-100 (Lifespan Biosciences)

[00256] In one embodiment, an antigen binding domain against intestinal carboxyl esterase is an antigen binding portion, e.g., CDRs, of the antibody 4F12: cat no: LS-B6190-50 (Lifespan Biosciences).

[00257] In one embodiment, an antigen binding domain against mut hsp70-2 is an antigen binding portion, e.g., CDRs, of the antibody Lifespan Biosciences: monoclonal: cat no: LS-C133261-100 (Lifespan Biosciences).

[00258] In one embodiment, an antigen binding domain against MAD-CT-2 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., PMID: 2450952; US7635753.

[00259] In one embodiment, the antigen binding domain comprises one, two three (e.g., all three) heavy chain CDRs, HC CDR1, HC CDR2 and HC CDR3, from an antibody listed above, and/or one, two, three (e.g., all three) light chain CDRs, LC CDR1, LC CDR2 and LC CDR3, from an antibody listed above. In one embodiment, the antigen binding domain comprises a heavy chain variable region and/or a variable light chain region of an antibody listed above.

[00260] In one embodiment, the antigen-binding domain of a CAR, e.g., the CAR expressed by a cell of the invention, can be chosen such that a myeloid tumor population is targeted. Alternatively, when targeting of more than one type of myeloid tumor is desired, an antigen binding domain that targets a myeloid tumor antigen that is expressed by more than one, e.g., all, of the myeloid tumors to be targeted can be selected.

[00261] In one aspect, the antigen-binding domain of a CAR, e.g., the CAR expressed by a cell of the invention, binds to CD123, e.g., human CD123. Any known CD123 binding domain may be used in the invention. In one embodiment, an antigen binding domain against CD123 is an antigen binding portion, e.g., CDRs or VH and VL, of an antibody, antigen-binding fragment or CAR described in, e.g., PCT publication WO2014/130635. In one embodiment, an antigen binding domain against CD123 is an antigen binding portion, e.g., CDRs or VH and VL, of an antibody, antigen-binding fragment or CAR described in, e.g., PCT publication WO2016/028896. In one embodiment, an antigen binding domain against CD123 is an antigen binding portion, e.g., CDRs, of an antibody, antigen-binding fragment, or CAR described in, e.g., PCT publication WO1997/024373, WO2008/127735 (e.g., a CD123 binding domain of 26292, 32701, 37716 or 32703), WO2014/138805 (e.g., a CD123 binding domain of CSL362), WO2014/138819, WO2013/173820, WO2014/144622, WO2001/66139,

WO2010/126066 (e.g., the CD123 binding domain of any of Old4, Old5, Old17, Old19, New102, or Old6), WO2014/144622, or US2009/0252742. In embodiments, the antigen binding domain is or is derived from a murine anti-human CD123 binding domain. In embodiments, the antigen binding domain is a humanized antibody or antibody fragment, e.g., scFv domain. In an embodiment, the antigen binding domain is a human antibody or antibody fragment that binds to human CD123. In embodiments, the antigen binding domain is an scFv domain which includes a light chain variable region (VL) and a heavy chain variable region (VH). The VL and VH may attached by a linker described herein, e.g., comprising the sequence GGGGSGGGGSGGGGS (SEQ ID NO: 30), and may be in any orientation, e.g., VL-linker-VH, or VH-linker-VL.

[00262] In one embodiment, the human CD123 binding domain comprises one or more (e.g., all three) light chain complementary determining region 1 (LC CDR1), light chain complementary determining region 2 (LC CDR2), and light chain complementary determining region 3 (LC CDR3) of a human CD123 binding domain described herein, and/or one or more (e.g., all three) heavy chain complementary determining region 1 (HC CDR1), heavy chain complementary determining region 2 (HC CDR2), and heavy chain complementary determining region 3 (HC CDR3) of a human CD123 binding domain described herein, e.g., a human CD123 binding domain comprising one or more, e.g., all three, LC CDRs and one or more, e.g., all three, HC CDRs. In one embodiment, the human CD123 binding domain comprises one or more (e.g., all three) heavy chain complementary determining region 1 (HC CDR1), heavy chain complementary determining region 2 (HC CDR2), and heavy chain complementary determining region 3 (HC CDR3) of a human CD123 binding domain described herein, e.g., the human CD123 binding domain has two variable heavy chain regions, each comprising a HC CDR1, a HC CDR2 and a HC CDR3 described herein. In one embodiment, the human CD123 binding domain comprises a human light chain variable region described herein (e.g., in Table 26 or 28) and/or a human heavy chain variable region described herein (e.g., in Table 26 or 28). In one embodiment, the human CD123 binding domain comprises a human heavy chain variable region described herein (e.g., in Table 26 or 28), e.g., at least two human heavy chain variable regions described herein (e.g., in Table 26 or 28). In one embodiment, the CD123 binding domain is a scFv comprising a light chain and a heavy chain of an amino acid sequence of Table 26 or 28. In an embodiment, the CD123 binding

domain (e.g., an scFv) comprises: a light chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions) of an amino acid sequence of a light chain variable region provided in Table 26 or 28, or a sequence with at least 95% identity, e.g., 95-99% identity, with an amino acid sequence of Table 26; and/or a heavy chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions) of an amino acid sequence of a heavy chain variable region provided in Table 26 or 28, or a sequence with at least 95% identity, e.g., 95-99% identity, to an amino acid sequence of Table 26 or 28. In one embodiment, the human CD123 binding domain comprises a sequence selected from a group consisting of SEQ ID NO:2157-2160, 2478, 2480, 2483, and 2485, or a sequence with at least 95% identity, e.g., 95-99% identity, thereof. In one embodiment, the human CD123 binding domain is a scFv, and a light chain variable region comprising an amino acid sequence described herein, e.g., in Table 26 or 28, is attached to a heavy chain variable region comprising an amino acid sequence described herein, e.g., in Table 26, via a linker, e.g., a linker described herein. In one embodiment, the human CD123 binding domain includes a (Gly_4-Ser)n linker, wherein n is 1, 2, 3, 4, 5, or 6, preferably 3 or 4 (SEQ ID NO: 80). The light chain variable region and heavy chain variable region of a scFv can be, e.g., in any of the following orientations: light chain variable region-linker-heavy chain variable region or heavy chain variable region-linker-light chain variable region.

[00263] In some aspects, a non-human antibody is humanized, where specific sequences or regions of the antibody are modified to increase similarity to an antibody naturally produced in a human or fragment thereof. Thus, in one aspect, the antigen binding domain comprises a humanized antibody or an antibody fragment. In one embodiment, the humanized CD123 binding domain comprises one or more (e.g., all three) light chain complementary determining region 1 (LC CDR1), light chain complementary determining region 2 (LC CDR2), and light chain complementary determining region 3 (LC CDR3) of a humanized CD123 binding domain described herein, and/or one or more (e.g., all three) heavy chain complementary determining region 1 (HC CDR1), heavy chain complementary determining region 2 (HC CDR2), and heavy chain complementary determining region 3 (HC CDR3) of a humanized CD123 binding domain described herein, e.g., a humanized CD123 binding domain comprising one or more,

e.g., all three, LC CDRs and one or more, e.g., all three, HC CDRs. In one embodiment, the humanized CD123 binding domain comprises one or more (e.g., all three) heavy chain complementary determining region 1 (HC CDR1), heavy chain complementary determining region 2 (HC CDR2), and heavy chain complementary determining region 3 (HC CDR3) of a humanized CD123 binding domain described herein, e.g., the humanized CD123 binding domain has two variable heavy chain regions, each comprising a HC CDR1, a HC CDR2 and a HC CDR3 described herein. In one embodiment, the humanized CD123 binding domain comprises a humanized light chain variable region described herein (e.g., in Table 27) and/or a humanized heavy chain variable region described herein (e.g., in Table 27). In one embodiment, the humanized CD123 binding domain comprises a humanized heavy chain variable region described herein (e.g., in Table 27), e.g., at least two humanized heavy chain variable regions described herein (e.g., in Table 27). In one embodiment, the CD123 binding domain is a scFv comprising a light chain and a heavy chain of an amino acid sequence of Table 27. In an embodiment, the CD123 binding domain (e.g., an scFv) comprises: a light chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions) of an amino acid sequence of a light chain variable region provided in Table 27, or a sequence with at least 95% identity, e.g., 95-99% identity, with an amino acid sequence of Table 27; and/or a heavy chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions) of an amino acid sequence of a heavy chain variable region provided in Table 27, or a sequence with at least 95% identity, e.g., 95-99% identity, to an amino acid sequence of Table 27. In one embodiment, the humanized CD123 binding domain comprises a sequence selected from a group consisting of SEQ ID NO:2184-2215 and 2302-2333, or a sequence with at least 95% identity, e.g., 95-99% identity, thereof. In one embodiment, the humanized CD123 binding domain is a scFv, and a light chain variable region comprising an amino acid sequence described herein, e.g., in Table 27, is attached to a heavy chain variable region comprising an amino acid sequence described herein, e.g., in Table 27, via a linker, e.g., a linker described herein. In one embodiment, the humanized CD123 binding domain includes a (Gly4-Ser)n linker, wherein n is 1, 2, 3, 4, 5, or 6, preferably 3 or 4 (SEQ ID NO: 80). The light chain variable region and heavy chain variable region of a scFv can be, e.g., in any of the following orientations: light chain variable region-linker-heavy chain variable region or heavy chain variable region-linker-light chain variable region.

[00264] Exemplary CD123 CAR constructs disclose herein comprise an scFv (e.g., a human scFv as disclosed in Tables 26, 27 and 28 herein, optionally preceded with an optional leader sequence (e.g., SEQ ID NO:2 and SEQ ID NO:3 for exemplary leader amino acid and nucleotide sequences, respectively). The sequences of the human scFv fragments (amino acid sequences of SEQ ID NOs:2157-2160) are provided herein in Table 26. The sequences of human scFv fragments, without the leader sequence, are provided herein in Table 28 (SEQ ID NOs: 2479, 2481, 2482, and 2484 for the nucleotide sequences, and SEQ ID NOs: 2478, 2480, 2483, and 2485 for the amino acid sequences). The CD123 CAR construct can further include an optional hinge domain, e.g., a CD8 hinge domain (e.g., including the amino acid sequence of SEQ ID NO: 4 or encoded by a nucleic acid sequence of SEQ ID NO:5); a transmembrane domain, e.g., a CD8 transmembrane domain (e.g., including the amino acid sequence of SEQ ID NO: 12 or encoded by the nucleotide sequence of SEQ ID NO: 13); an intracellular domain, e.g., a 4-1BB intracellular domain (e.g., including the amino acid sequence of SEQ ID NO: 14 or encoded by the nucleotide sequence of SEQ ID NO: 15; and a functional signaling domain, e.g., a CD3 zeta domain (e.g., including amino acid sequence of SEQ ID NO: 18 or 20, or encoded by the nucleotide sequence of SEQ ID NO: 19 or 21). In certain embodiments, the domains are contiguous with and in the same reading frame to form a single fusion protein. In other embodiments, the domain are in separate polypeptides, e.g., as in an RCAR molecule as described herein.

[00265] In certain embodiments, the full length CD123 CAR molecule includes the amino acid sequence of, or is encoded by the nucleotide sequence of, CD123-1, CD123-2, CD123-3, CD123-4, hzCD123-1, hzCD123-2, hzCD123-3, hzCD123-4, hzCD123-5, hzCD123-6, hzCD123-7, hzCD123-8, hzCD123-9, hzCD123-10, hzCD123-11, hzCD123-12, hzCD123-13, hzCD123-14, hzCD123-15, hzCD123-16, hzCD123-17, hzCD123-18, hzCD123-19, hzCD123-20, hzCD123-21, hzCD123-22, hzCD123-23, hzCD123-24, hzCD123-25, hzCD123-26, hzCD123-27, hzCD123-28, hzCD123-29, hzCD123-30, hzCD123-31, or hzCD123-32, provided in Table 26, 27, or 28, or a sequence substantially identical (e.g., with at least 95% identity, e.g., 95-99% identity) thereto.

[00266] In certain embodiments, the CD123 CAR molecule, or the CD123 antigen binding domain, includes the scFv amino acid sequence of CD123-1, CD123-2, CD123-3, CD123-4, hzCD123-1, hzCD123-2, hzCD123-3, hzCD123-4, hzCD123-5, hzCD123-6, hzCD123-7, hzCD123-8, hzCD123-9, hzCD123-10, hzCD123-11, hzCD123-12, hzCD123-13, hzCD123-14, hzCD123-15, hzCD123-16, hzCD123-17, hzCD123-18, hzCD123-19, hzCD123-20, hzCD123-21, hzCD123-22, hzCD123-23, hzCD123-24, hzCD123-25, hzCD123-26, hzCD123-27, hzCD123-28, hzCD123-29, hzCD123-30, hzCD123-31, or hzCD123-32, provided in Table 26, 27, or 28; or includes the scFv amino acid sequence of, or is encoded by the nucleotide sequence of, CD123-1, CD123-2, CD123-3, CD123-4, hzCD123-1, hzCD123-2, hzCD123-3, hzCD123-4, hzCD123-5, hzCD123-6, hzCD123-7, hzCD123-8, hzCD123-9, hzCD123-10, hzCD123-11, hzCD123-12, hzCD123-13, hzCD123-14, hzCD123-15, hzCD123-16, hzCD123-17, hzCD123-18, hzCD123-19, hzCD123-20, hzCD123-21, hzCD123-22, hzCD123-23, hzCD123-24, hzCD123-25, hzCD123-26, hzCD123-27, hzCD123-28, hzCD123-29, hzCD123-30, hzCD123-31, or hzCD123-32, or a sequence substantially identical (e.g., with at least 95% identity, e.g., 95-99% identity, or up to 20, 15, 10, 8, 6, 5, 4, 3, 2, or 1 amino acid changes) to any of the aforesaid sequences.

[00267] In certain embodiments, the CD123 CAR molecule, or the CD123 antigen binding domain, includes the heavy chain variable region and/or the light chain variable region of CD123-1, CD123-2, CD123-3, CD123-4, hzCD123-1, hzCD123-2, hzCD123-3, hzCD123-4, hzCD123-5, hzCD123-6, hzCD123-7, hzCD123-8, hzCD123-9, hzCD123-10, hzCD123-11, hzCD123-12, hzCD123-13, hzCD123-14, hzCD123-15, hzCD123-16, hzCD123-17, hzCD123-18, hzCD123-19, hzCD123-20, hzCD123-21, hzCD123-22, hzCD123-23, hzCD123-24, hzCD123-25, hzCD123-26, hzCD123-27, hzCD123-28, hzCD123-29, hzCD123-30, hzCD123-31, or hzCD123-32, provided in Table 26 or 27, or a sequence substantially identical (e.g., with at least 95% identity, e.g., 95-99% identity, or up to 20, 15, 10, 8, 6, 5, 4, 3, 2, or 1 amino acid changes) to any of the aforesaid sequences.

[00268] In certain embodiments, the CD123 CAR molecule, or the CD123 antigen binding domain, includes one, two or three CDRs from the heavy chain variable region (e.g., HCDR1, HCDR2 and/or HCDR3), provided in Table 16 or 18; and/or one, two or three CDRs from the light chain variable region (e.g., LCDR1, LCDR2 and/or LCDR3) of CD123-1, CD123-2, CD123-3, CD123-4, hzCD123-1, hzCD123-2, hzCD123-3, hzCD123-4, hzCD123-5,

hzCD123-6, hzCD123-7, hzCD123-8, hzCD123-9, hzCD123-10, hzCD123-11, hzCD123-12, hzCD123-13, hzCD123-14, hzCD123-15, hzCD123-16, hzCD123-17, hzCD123-18, hzCD123-19, hzCD123-20, hzCD123-21, hzCD123-22, hzCD123-23, hzCD123-24, hzCD123-25, hzCD123-26, hzCD123-27, hzCD123-28, hzCD123-29, hzCD123-30, hzCD123-31, or hzCD123-32, provided in Table 17 or 19; or a sequence substantially identical (e.g., at least 95% identical, e.g., 95-99% identical, or up to 5, 4, 3, 2, or 1 amino acid changes) to any of the aforesaid sequences.

[00269] In certain embodiments, the CD123 CAR molecule, or the CD123 antigen binding domain, includes one, two or three CDRs from the heavy chain variable region (e.g., HCDR1, HCDR2 and/or HCDR3), provided in Table 20; and/or one, two or three CDRs from the light chain variable region (e.g., LCDR1, LCDR2 and/or LCDR3) of CD123-1, CD123-2, CD123-3, CD123-4, hzCD123-1, hzCD123-2, hzCD123-3, hzCD123-4, hzCD123-5, hzCD123-6, hzCD123-7, hzCD123-8, hzCD123-9, hzCD123-10, hzCD123-11, hzCD123-12, hzCD123-13, hzCD123-14, hzCD123-15, hzCD123-16, hzCD123-17, hzCD123-18, hzCD123-19, hzCD123-20, hzCD123-21, hzCD123-22, hzCD123-23, hzCD123-24, hzCD123-25, hzCD123-26, hzCD123-27, hzCD123-28, hzCD123-29, hzCD123-30, hzCD123-31, or hzCD123-32, provided in Table 21; or a sequence substantially identical (e.g., at least 95% identical, e.g., 95-99% identical, or up to 5, 4, 3, 2, or 1 amino acid changes) to any of the aforesaid sequences.

[00270] In certain embodiments, the CD123 molecule, or the CD123 antigen binding domain, includes one, two or three CDRs from the heavy chain variable region (e.g., HCDR1, HCDR2 and/or HCDR3), provided in Table 22; and/or one, two or three CDRs from the light chain variable region (e.g., LCDR1, LCDR2 and/or LCDR3) of CD123-1, CD123-2, CD123-3, CD123-4, hzCD123-1, hzCD123-2, hzCD123-3, hzCD123-4, hzCD123-5, hzCD123-6, hzCD123-7, hzCD123-8, hzCD123-9, hzCD123-10, hzCD123-11, hzCD123-12, hzCD123-13, hzCD123-14, hzCD123-15, hzCD123-16, hzCD123-17, hzCD123-18, hzCD123-19, hzCD123-20, hzCD123-21, hzCD123-22, hzCD123-23, hzCD123-24, hzCD123-25, hzCD123-26, hzCD123-27, hzCD123-28, hzCD123-29, hzCD123-30, hzCD123-31, or hzCD123-32, provided in Table 23; or a sequence substantially identical (e.g., at least 95% identical, e.g., 95-99% identical, or up to 5, 4, 3, 2, or 1 amino acid changes) to any of the aforesaid sequences.

[00271] The sequences of CDR sequences of the scFv domains are shown in Tables 16, 18, 20, and 22 for the heavy chain variable domains and in Tables 17, 19, 21, and 23 for the light chain variable domains. "ID" stands for the respective SEQ ID NO for each CDR.

[00272] The CDRs provided in Tables 16, 17, 18, and 19 are according to a combination of the Kabat and Chothia numbering scheme.

Table 16. Heavy Chain Variable Domain CDRs

Candidate	HCDR1	SEQ ID NO:	HCDR2	SEQ ID NO:	HCDR3	SEQ ID NO:
CAR123-2	GYTFTGYYMH	2335	WINPNSGGTNYAQKFQG	2363	DMNILATVPFDI	2391
CAR123-3	GYIFTGYYIH	2337	WINPNSGGTNYAQKFQG	2364	DMNILATVPFDI	2392
CAR123-4	GYTFTGYYMH	2336	WINPNSGGTNYAQKFQG	2365	DMNILATVPFDI	2393
CAR123-1	GYTFTDYYMH	2334	WINPNSGDTNYAQKFQG	2362	DMNILATVPFDI	2390

Table 17. Light Chain Variable Domain CDRs

Candidate	LCDR1	SEQ ID NO:	LCDR2	SEQ ID NO:	LCDR3	SEQ ID NO:
CAR123-2	RASQSISSYLN	2419	AAFSLQS	2447	QQGDSVPLT	2475
CAR123-3	RASQSISSYLN	2420	AASSLQS	2448	QQGDSVPLT	2476
CAR123-4	RASQSISSYLN	2421	AASSLQS	2449	QQGDSVPLT	2477
CAR123-1	RASQSISTYLN	2418	AASSLQS	2446	QQGDSVPLT	2474

Table 18. Heavy Chain Variable Domain CDR

	HCDR1	SEQ ID NO:	HCDR2	SEQ ID NO:	HCDR3	SEQ ID NO:
hzCAR123	GYTFTSYWMN	2361	RIDPYDSETHYNQKFKD	2389	GNWDDY	2417

Table 19. Light Chain Variable Domain CDR

	LCDR1	SEQ ID NO:	LCDR2	SEQ ID NO:	LCDR3	SEQ ID NO:
hzCAR123	RASKSISKDLA	2445	SGSTLQS	2473	QQHNKYPYT	2515

Table 20. Heavy Chain Variable Domain CDRs according to the Kabat numbering scheme (Kabat et al. (1991), "Sequences of Proteins of Immunological Interest," 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD)

Candidate	HCDR1	SEQ ID NO:	HCDR2	SEQ ID NO:	HCDR3	SEQ ID NO:
CAR123-2	GYYMH	2487	WINPNSGGTNYAQKFQG	2492	DMNILATVPFDI	2497
CAR123-3	GYYIH	2488	WINPNSGGTNYAQKFQG	2493	DMNILATVPFDI	2498
CAR123-4	DYYMH	2489	WINPNSGDTNYAQKFQG	2494	DMNILATVPFDI	2499
CAR123-1	GYYMH	2486	WINPNSGGTNYAQKFQG	2491	DMNILATVPFDI	2496
hzCAR123-1	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-2	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-3	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-4	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-5	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-6	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-7	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-8	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-9	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-10	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-11	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-12	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-13	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-14	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-15	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-16	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-17	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-18	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-19	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-20	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-21	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500

hzCAR123-22	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-23	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-24	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-25	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-26	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-27	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-28	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-29	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-30	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-31	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500
hzCAR123-32	SYWMN	2490	RIDPYDSETHYNQKFKD	2495	GNWDDY	2500

Table 21. Light Chain Variable Domain CDRs according to the Kabat numbering scheme (Kabat et al. (1991), "Sequences of Proteins of Immunological Interest," 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD)

Candidate	LCDR1	SEQ ID NO:	LCDR2	SEQ ID NO:	LCDR3	SEQ ID NO:
CAR123-2	RASQSISSYLN	2502	AASSLQS	2507	QQGDSVPLT	2512
CAR123-3	RASQSISSYLN	2503	AASSLQS	2508	QQGDSVPLT	2513
CAR123-4	RASQSISSYLN	2504	AASSLQS	2509	QQGDSVPLT	2514
CAR123-1	RASQSISTYLN	1501	AAFSLQS	2506	QQGDSVPLT	2511
hzCAR123-1	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-2	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-3	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-4	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-5	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-6	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-7	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-8	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-10	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-10	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-11	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-12	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-13	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-14	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515

hzCAR123-15	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-16	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-17	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-18	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-19	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-20	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-21	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-22	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-23	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-24	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-25	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-26	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-27	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-28	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-29	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-30	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-31	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515
hzCAR123-32	RASKSISKDLA	2505	SGSTLQS	2510	QQHNKYPYT	2515

Table 22. Heavy Chain Variable Domain CDRs according to the Chothia numbering scheme (Al-Lazikani et al., (1997) JMB 273,927-948)

Candidate	**HCDR1**	SEQ ID NO:	**HCDR2**	SEQ ID NO:	**HCDR3**	SEQ ID NO:
CAR123-2	GYTFTGY	2517	NPNSGG	2522	DMNILATVPFDI	2527
CAR123-3	GYIFTGY	2518	NPNSGG	2523	DMNILATVPFDI	2528
CAR123-4	GYTFTDY	2519	NPNSGD	2524	DMNILATVPFDI	2529
CAR123-1	GYTFTGY	2516	NPNSGG	2521	DMNILATVPFDI	2526
hzCAR123-1	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-2	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-3	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-4	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-5	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-6	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-7	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-8	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-9	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530

hzCAR123-10	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-11	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-12	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-13	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-14	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-15	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-16	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-17	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-18	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-19	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-20	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-21	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-22	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-23	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-24	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-25	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-26	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-27	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-28	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-29	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-30	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-31	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530
hzCAR123-32	GYTFTSY	2520	DPYDSE	2525	GNWDDY	2530

Table 23. Light Chain Variable Domain CDRs according to the Chothia numbering scheme (Al-Lazikani et al., (1997) JMB 273,927-948)

Candidate	LCDR1	SEQ ID NO:	LCDR2	SEQ ID NO:	LCDR3	SEQ ID NO:
CAR123-2	SQSISSY	2532	AAS	2537	GDSVPL	2542
CAR123-3	SQSISSY	2533	AAS	2538	GDSVPL	2543
CAR123-4	SQSISSY	2534	AAS	2539	GDSVPL	2544
CAR123-1	SQSISTY	2531	AAF	2536	GDSVPL	2541
hzCAR123-1	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-2	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-3	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-4	SKSISKD	2535	SGS	2540	HNKYPY	2555

hzCAR123-5	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-6	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-7	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-8	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-10	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-10	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-11	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-12	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-13	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-14	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-15	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-16	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-17	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-18	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-19	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-20	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-21	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-22	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-23	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-24	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-25	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-26	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-27	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-28	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-29	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-30	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-31	SKSISKD	2535	SGS	2540	HNKYPY	2555
hzCAR123-32	SKSISKD	2535	SGS	2540	HNKYPY	2555

[00273] In embodiments, CD123 single chain variable fragments are generated and cloned into lentiviral CAR expression vectors with the intracellular CD3zeta domain and the intracellular co-stimulatory domain of 4-1BB. Names of exemplary fully human CD123 scFvs are depicted in Table 24. Names of exemplary humanized CD123 scFvs are depicted in Table 25.

Table 24: CAR-CD123 constructs

Construct ID	CAR Nickname
EBB-C1357-F11	CAR123-1
EBB-C1358-B10	CAR123-2
EBB-C1358-D5	CAR123-3
EBB-C1357-C4	CAR123-4

Table 25: CAR-CD123 constructs

Construct ID	CAR Nickname
VH1_1-46_X_VK1_L8	hzCAR-1
VH1_1-46_X_VK3_L6	hzCAR-2
VH1_1-46_X_VK6_A14	hzCAR-3
VH1_1-46_X_VK4_B3	hzCAR-4
VK1_L8_X_VH1_1-46	hzCAR-5
VK3_L6_X_VH1_1-46	hzCAR-6
VK6_A14_X_VH1_1-46	hzCAR-7
VK4_B3_X_VH1_1-46	hzCAR-8
VH7_7-4.1_X_VK1_L8	hzCAR-9
VH7_7-4.1_X_VK3_L6	hzCAR-10
VH7_7-4.1_X_VK6_A14	hzCAR-11
VH7_7-4.1_X_VK4_B3	hzCAR-12
VK1_L8_X_VH7_7-4.1	hzCAR-13
VK3_L6_X_VH7_7-4.1	hzCAR-14
VK6_A14_X_VH7_7-4.1	hzCAR-15
VK4_B3_X_VH7_7-4.1	hzCAR-16
VH5_5-A_X_VK1_L8	hzCAR-17
VH5_5-A_X_VK3_L6	hzCAR-18
VH5_5-A_X_VK6_A14	hzCAR-19
VH5_5-A_X_VK4_B3	hzCAR-20
VK1_L8_X_VH5_5-A	hzCAR-21
VK3_L6_X_VH5_5-A	hzCAR-22
VK6_A14_X_VH5_5-A	hzCAR-23
VK4_B3_X_VH5_5-A	hzCAR-24
VH3_3-74_X_VK1_L8	hzCAR-25
VH3_3-74_X_VK3_L6	hzCAR-26
VH3_3-74_X_VK6_A14	hzCAR-27
VH3_3-74_X_VK4_B3	hzCAR-28
VK1_L8_X_VH3_3-74	hzCAR-29
VK3_L6_X_VH3_3-74	hzCAR-30
VK6_A14_X_VH3_3-74	hzCAR-31
VK4_B3_X_VH3_3-74	hzCAR-32

[00274] In embodiments, the order in which the VL and VH domains appear in the scFv is varied (i.e., VL-VH, or VH-VL orientation), and where either three (SEQ ID NO: 30) or four (SEQ ID NO: 29) copies of the “G4S” (SEQ ID NO: 22) subunit, in which each subunit comprises the sequence GGGGS (SEQ ID NO: 22) (e.g., $(G4S)_3$ (SEQ ID NO:30) or $(G4S)_4$ (SEQ ID NO:29)), connect the variable domains to create the entirety of the scFv domain, as shown in Table 26, Table 27, and Table 28.

[00275] The amino acid and nucleic acid sequences of the CD123 scFv domains and CD123 CAR molecules are provided in Table 26, Table 27, and Table 28. The amino acid sequences for the variable heavy chain and variable light chain for each scFv is also provided in Table 26 and Table 27. It is noted that the scFv fragments (SEQ ID NOs: 2157-2160, and 2184-2215) with a leader sequence (e.g., the amino acid sequence of SEQ ID NO: 2 or the nucleotide sequence of SEQ ID NO: 3) and without a leader sequence (SEQ ID NOs: 2478, 2480, 2483, 2485, and 2556-2587) are also encompassed by the present invention.

[00276] In embodiments, these clones in Table 26 and 27 all contained a Q/K residue change in the signal domain of the co-stimulatory domain derived from CD3zeta chain.

Table 26. Exemplary CD123 CAR sequences

Name	SEQ ID NO:	Sequence
CAR123-2 NT	2040	atggccctccctgtcaccgccctgctgcttccgctggctcttctgctccacgccgctcggccccaagtgcaactcgtccaaagcggagcggaagtcaagaaacccggagcgagcgtgaaagtgtcctgcaaagcctccggctacacctttacgggctactacatgcactgggtgcgccaggcaccaggacagggtcttgaatggatgggatggatcaaccctaattcgggcggaactaactacgcacagaagttccaggggagagtgactctgactcgggatacctccatctcaactgtctacatggaactctcccgcttgcggtcagatgatacggcagtgtactactgcgcccgcgacatgaatatcctggctaccgtgccgttcgacatctggggacaggggactatggttactgtctcatcgggcggtggaggttcaggaggaggcggctcgggaggcggaggttcggacattcagatgacccagtccccatcctctctgtcggccagcgtcggagatagggtgaccattacctgtcgggcctcgcaaagcatctcctcgtacctcaactggtatcagcaaaagccgggaaaggcgcctaagctgctgatctacgccgcttcgagcttgcaaagcggggtgccatccagattctcgggatcaggctcaggaaccgacttcaccctgaccgtgaacagcctccagccggaggactttgccacttactactgccagcagggagactccgtgccgcttactttcggggggggtacccgcctggagatcaagaccactaccccagcaccgaggccacccaccccggctcctaccatcgcctcccagcctctgtccctgcgtccggaggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc

		gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctg ctgctttcactcgtgatcactctttactgtaagcgcggtcggaagaagctg ctgtacatctttaagcaacccttcatgaggcctgtgcagactactcaagag gaggacggctgttcatgccggttcccagaggaggaggaaggcggctgcgaa ctgcgcgtgaaattcagccgcagcgcagatgctccagcctacaagcagggg cagaaccagctctacaacgaactcaatcttggtcggagagaggagtacgac gtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgc agaaagaatccccaagagggcctgtacaacgagctccaaaaggataagatg gcagaagcctatagcgagattggtatgaaaggggaacgcagaagaggcaaa ggccacgacggactgtaccagggactcagcaccgccaccaaggacacctat gacgctcttcacatgcaggccctgccgcctcgg
CAR123-2 AA	2099	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFT GYYMHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTLTRDTSISTVYM ELSRLRSDDTAVYYCARDMNILATVPFDIWGQGTMVTVSSGGGGSGGGGSG GGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTVNSLQPEDFATYYCQQGDSVPLTF GGGTRLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDF ACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQE EDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
CAR123-2 scFv	2158	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFT GYYMHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTLTRDTSISTVYM ELSRLRSDDTAVYYCARDMNILATVPFDIWGQGTMVTVSSGGGGSGGGGSG GGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTVNSLQPEDFATYYCQQGDSVPLTF GGGTRLEIK
CAR123-2 VH	2217	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWI NPNSGGTNYAQKFQGRVTLTRDTSISTVYMELSRLRSDDTAVYYCARDMNI LATVPFDIWGQGTMVTVSS
CAR123-2 VL	2276	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAA SSLQSGVPSRFSGSGSGTDFTLTVNSLQPEDFATYYCQQGDSVPLTFGGGT RLEIK
CAR123-3 NT	2041	atggccctccctgtcaccgccctgctgcttccgctggctcttctgctccac gccgctcggccccaagtccaactcgttcaatccggcgcagaagtcaagaag ccaggagcatcagtgaaagtgtcctgcaaagcctcaggctacatcttcacg ggatactacatccactgggtgcgccaggctccgggccagggccttgagtgg atgggctggatcaaccctaactctgggggaaccaactacgctcagaagttc caggggagggtcactatgactcgcgatacctccatctccactgcgtacatg gaactctcgggactgagatccgacgatcctgccgtgtactactgcgcccgg gacatgaacatcttggcgaccgtgccgtttgacatttggggacagggcacc ctcgtcactgtgtcgagcggtggaggaggctcgggggggtggcggatcagga gggggaggaagcgacatccagctgactcagagcccatcgtcgttgtccgcg tcggtgggggatagagtgaccattacttgccgcgccagccagagcatctca tcatatctgaattggtaccagcagaagcccggaaaggccccaaaactgctg

		atctacgctgcaagcagcctccaatcgggagtgccgtcacggttctccggg tccggttcgggaactgactttaccctgaccgtgaattcgctgcaaccggag gatttcgccacgtactactgtcagcaaggagactccgtgccgctgaccttc ggtggaggcaccaaggtcgaaatcaagaccactaccccagcaccgaggcca cccaccccggctcctaccatcgcctcccagcctctgtccctgcgtccggag gcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctg ctgctttcactcgtgatcactctttactgtaagcgcggtcggaagaagctg ctgtacatctttaagcaacccttcatgaggcctgtgcagactactcaagag gaggacggctgttcatgccggttcccagaggaggaggaaggcggctgcgaa ctgcgcgtgaaattcagccgcagcgcagatgctccagcctacaagcagggg cagaaccagctctacaacgaactcaatcttggtcggagagaggagtacgac gtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgc agaaagaatccccaagagggcctgtacaacgagctccaaaaggataagatg gcagaagcctatagcgagattggtatgaaaggggaacgcagaagaggcaaa ggccacgacggactgtaccagggactcagcaccgccaccaaggacacctat gacgctcttcacatgcaggccctgccgcctcgg
CAR123-3 AA	2100	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYIFT GYYIHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSISTAYM ELSGLRSDDPAVYYCARDMNILATVPFDIWGQGTLVTVSSGGGGSGGGGSG GGGSDIQLTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTVNSLQPEDFATYYCQQGDSVPLTF GGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDF ACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQE EDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
CAR123-3 scFv	2159	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYIFT GYYIHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSISTAYM ELSGLRSDDPAVYYCARDMNILATVPFDIWGQGTLVTVSSGGGGSGGGGSG GGGSDIQLTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTVNSLQPEDFATYYCQQGDSVPLTF GGGTKVEIK
CAR123-3 VH	2218	QVQLVQSGAEVKKPGASVKVSCKASGYIFTGYYIHWVRQAPGQGLEWMGWI NPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSGLRSDDPAVYYCARDMNI LATVPFDIWGQGTLVTVSS
CAR123-3 VL	2277	DIQLTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAA SSLQSGVPSRFSGSGSGTDFTLTVNSLQPEDFATYYCQQGDSVPLTFGGGT KVEIK
CAR123-4 NT	2042	atggccctccctgtcaccgccctgctgcttccgctggctcttctgctccac gccgctcggccccaagtccaactccaacagtcaggcgcagaagtgaaaaag agcggtgcatcggtgaaagtgtcatgcaaagcctcgggctacaccttcact gactactatatgcactggctgcggcaggcaccgggacagggacttgagtgg atgggatggatcaacccgaattcaggggacactaactacgcgcagaagttc caggggagagtgaccctgacgagggacacctcaatttcgaccgtctacatg

		gaattgtcgcgcctgagatcggacgatactgctgtgtactactgtgcccgc gacatgaacatcctcgcgactgtgccttttgatatctggggacaggggact atggtcaccgtttcctccgcttccggtggcggaggctcgggaggccgggcc tccggtggaggaggcagcgacatccagatgactcagagcccttcctcgctg agcgcctcagtgggagatcgcgtgaccatcacttgccgggccagccagtcc atttcgtcctacctcaattggtaccagcagaagccgggaaaggcgcccaag ctcttgatctacgctgcgagctccctgcaaagcggggtgccgagccgattc tcgggttccggctcgggaaccgacttcactctgaccatctcatccctgcaa ccagaggactttgccacctactactgccaacaaggagattctgtcccactg acgttcggcggaggaaccaaggtcgaaatcaagaccactaccccagcaccg aggccacccaccccggctcctaccatcgcctcccagcctctgtccctgcgt ccggaggcatgtagacccgcagctggtggggccgtgcatacccggggtctt gacttcgcctgcgatatctacatttgggcccctctggctggtacttgcggg gtcctgctgctttcactcgtgatcactctttactgtaagcgcggtcggaag aagctgctgtacatctttaagcaacccttcatgaggcctgtgcagactact caagaggaggacggctgttcatgccggttcccagaggaggaggaaggcggc tgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcctacaag caggggcagaaccagctctacaacgaactcaatcttggtcggagagaggag tacgacgtgctggacaagcggagaggacgggacccagaaatgggcgggaag ccgcgcagaaagaatccccaagagggcctgtacaacgagctccaaaaggat aagatggcagaagcctatagcgagattggtatgaaaggggaacgcagaaga ggcaaaggccacgacggactgtaccagggactcagcaccgccaccaaggac acctatgacgctcttcacatgcaggccctgccgcctcgg
CAR123-4 AA	2101	MALPVTALLLPLALLLHAARPQVQLQQSGAEVKKSGASVKVSCKASGYTFT DYYMHWLRQAPGQGLEWMGWINPNSGDTNYAQKFQGRVTLTRDTSISTVYM ELSRLRSDDTAVYYCARDMNILATVPFDIWGQGTMVTVSSASGGGGSGGRA SGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPK LLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGDSVPL TFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGL DFACDIYIWAPLAGTCGVLLLSLVITLYCK
CAR123-4 scFv	2160	MALPVTALLLPLALLLHAARPQVQLQQSGAEVKKSGASVKVSCKASGYTFT DYYMHWLRQAPGQGLEWMGWINPNSGDTNYAQKFQGRVTLTRDTSISTVYM ELSRLRSDDTAVYYCARDMNILATVPFDIWGQGTMVTVSSASGGGGSGGRA SGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPK LLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGDSVPL TFGGGTKVEIK
CAR123-4 VH	2219	QVQLQQSGAEVKKSGASVKVSCKASGYTFTDYYMHWLRQAPGQGLEWMGWI NPNSGDTNYAQKFQGRVTLTRDTSISTVYMELSRLRSDDTAVYYCARDMNI LATVPFD**I**WGQGTMVTVSS
CAR123-4 VL	2278	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAA SSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGDSVPLTFGGGT KVEIK
CAR123-1 NT	2039	atggccctccctgtcaccgccctgctgcttccgctggctcttctgctccac gccgctcggccccaagtccaactcgtccagtcaggagcggaagtcaagaag cccggagcgtcagtcaaagtgtcatgcaaagcctcgggctacactttcact

		gggtactacatgcactgggtgcgccaggctccaggacagggactggaatgg atgggatggatcaacccgaactccggtggcaccaattacgcccagaagttc caggggagggtgaccatgactcgcgacacgtcgatcagcaccgcatacatg gagctgtcaagactccggtccgacgatactgccgtgtactactgcgcacgg gacatgaacattctggccaccgtgccttttgacatctggggtcagggaact atggttaccgtgtcctctggtggaggcggctccggcgggggggggaagcgga ggcggtggaagcgacattcagatgacccagtcgccttcatccctttcggcg agcgtgggagatcgcgtcactatcacttgtcgggcctcgcagtccatctcc acctacctcaattggtaccagcagaagccaggaaaagcaccgaatctgctg atctacgccgcgttttccttgcaatcgggagtgccaagcagattcagcgga tcgggatcaggcactgatttcaccctcaccatcaactcgctgcaaccggag gatttcgctacgtactattgccaacaaggagacagcgtgccgctcaccttc ggcggagggactaagctggaaatcaagaccactaccccagcaccgaggcca cccaccccggctcctaccatcgcctcccagcctctgtccctgcgtccggag gcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctg ctgctttcactcgtgatcactctttactgtaagcgcggtcggaagaagctg ctgtacatctttaagcaacccttcatgaggcctgtgcagactactcaagag gaggacggctgttcatgccggttcccagaggaggaggaaggcggctgcgaa ctgcgcgtgaaattcagccgcagcgcagatgctccagcctacaagcagggg cagaaccagctctacaacgaactcaatcttggtcggagagaggagtacgac gtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgc agaaagaatccccaagagggcctgtacaacgagctccaaaaggataagatg gcagaagcctatagcgagattggtatgaaaggggaacgcagaagaggcaaa ggccacgacggactgtaccagggactcagcaccgccaccaaggacacctat gacgctcttcacatgcaggccctgccgcctcgg
CAR123-1 AA	2098	malpvtalllplalllhaarpqvqlvqsgaevkkpgasvkvsckasgytft gyymhwvrqapgqglewmgwinpnsggtnyaqkfqgrvtmtrdtsistaym elsrlrsddtavyycardmnilatvpfdiwgqgtmvtvssggggsggggsg gggsdiqmtqspsslsasvgdrvtitcrasqsistylnwyqqkpgkapnll iyaafslqsgvpsrfsgsgsgtdftltinslqpedfatyycqqgdsvpltf gggtkleiktttpaprpptpaptiasqplslrpeacrpaaggavhtrgldf acdiyiwaplagtcgvllllslvitlyckrgrkkllyifkqpfmrpvqttqe edgcscrfpeeeeggcelrvkfsrsadapaykqgqnqlynelnlgrreeyd vldkrrgrdpemggkprrknpqeglynelqkdkmaeayseigmkgerrrgk ghdglyqglstatkdtydalhmqalppr
CAR123-1 scFv	2157	malpvtalllplalllhaarpqvqlvqsgaevkkpgasvkvsckasgytft gyymhwvrqapgqglewmgwinpnsggtnyaqkfqgrvtmtrdtsistaym elsrlrsddtavyycardmnilatvpfdiwgqgtmvtvssggggsggggsg gggsdiqmtqspsslsasvgdrvtitcrasqsistylnwyqqkpgkapnll iyaafslqsgvpsrfsgsgsgtdftltinslqpedfatyycqqgdsvpltf gggtkleik
CAR123-1 VH	2216	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWI NPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARDMNI LATVPFDIWGQGTMVTVSS

CAR123-1 VL	2275	DIQMTQSPSSLSASVGDRVTITCRASQSISTYLNWYQQKPGKAPNLLIYAA FSLQSGVPSRFSGSGSGTDFTLTINSLQPEDFATYYCQQGDSVPLTFGGGT KLEIK

Table 27: Humanized CD123 CAR Sequences

Name	SEQ ID NO:	Sequence
hzCAR123-1 NT	2066	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCCAAGTGCAGCTGGTCCAGTCGGGAGCCGAAGTCAAGAAGCCCGGCGCTAGCGTGAAAGT GTCCTGCAAAGCCTCCGGGTACACATTCACCTCCTACTGGATGAATTGGGTCAGACAGGCG CCCGGCCAGGGACTCGAGTGGATGGGAAGGATTGATCCTTACGACTCCGAAACCCATTACA ACCAGAAGTTCAAGGACCGCGTGACCATGACTGTGGATAAGTCCACTTCCACCGCTTACAT GGAGCTGTCCAGCCTGCGCTCCGAGGATACCGCAGTGTACTACTGCGCCCGGGGAAACTGG GACGACTATTGGGGACAGGGAACTACCGTGACCGTGTCAAGCGGGGGTGGCGGTAGCGGAG GAGGGGGCTCCGGCGGCGGCGGCTCAGGGGGCGGAGGAAGCGACGTGCAGCTCACCCAGTC GCCCTCATTTCTGTCGGCCTCAGTGGGAGACAGAGTGACCATTACTTGTCGGGCCTCCAAG AGCATCTCCAAGGACCTGGCCTGGTATCAGCAGAAGCCAGGAAAGGCGCCTAAGTTGCTCA TCTACTCGGGGTCGACCCTGCAATCTGGCGTGCCGTCCCGGTTCTCCGGTTCGGGAAGCGG TACCGAATTCACCCTTACTATCTCCTCCCTGCAACCGGAGGACTTCGCCACCTACTACTGC CAACAGCACAACAAGTACCCGTACACTTTCGGGGGTGGCACGAAGGTCGAAATCAAGACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR123-1 AA	2125	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQA PGQGLEWMGRIDPYDSETHYNQKFKDRVTMTVDKSTSTAYMELSSLRSEDTAVYYCARGNW DDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVQLTQSPSFLSASVGDRVTITCRASK SISKDLAWYQQKPGKAPKLLIYSGSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYC QQHNKYPYTFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDF ACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPE EEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKN PQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
hzCAR123-1 scFv	2184	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQA PGQGLEWMGRIDPYDSETHYNQKFKDRVTMTVDKSTSTAYMELSSLRSEDTAVYYCARGNW DDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVQLTQSPSFLSASVGDRVTITCRASK SISKDLAWYQQKPGKAPKLLIYSGSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYC QQHNKYPYTFGGGTKVEIK
hzCAR12	2243	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQGLEWMGRIDPYDSETHYN QKFKDRVTMTVDKSTSTAYMELSSLRSEDTAVYYCARGNWDDYWGQGTTVTVSS

3-1 VH		
hzCAR12 3-1 VL	2302	DVQLTQSPSFLSASVGDRVTITCRASKSISKDLAWYQQKPGKAPKLLIYSGSTLQSGVPSR FSGSGSGTEFTLTISSLQPEDFATYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-2 NT	2067	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCCAAGTGCAGCTGGTCCAGTCGGGAGCCGAAGTCAAGAAGCCCGGCGCTAGCGTGAAAGT GTCCTGCAAAGCCTCCGGGTACACATTCACCTCCTACTGGATGAATTGGGTCAGACAGGCG CCCGGCCAGGGACTCGAGTGGATGGGAAGGATTGATCCTTACGACTCCGAAACCCATTACA ACCAGAAGTTCAAGGACCGCGTGACCATGACTGTGGATAAGTCCACTTCCACCGCTTACAT GGAGCTGTCCAGCCTGCGCTCCGAGGATACCGCAGTGTACTACTGCGCCCGGGGAAACTGG GACGACTATTGGGGACAGGGAACTACCGTGACCGTGTCAAGCGGGGGTGGCGGTAGCGGAG GAGGGGGCTCCGGCGGCGGCGGCTCAGGGGGCGGAGGAAGCGAAGTGGTGCTGACCCAGTC GCCCGCAACCCTCTCTCTGTCGCCGGGAGAACGCGCCACTCTTTCCTGTCGGGCGTCCAAG AGCATCTCAAAGGACCTCGCCTGGTACCAGCAGAAGCCTGGTCAAGCCCCGCGGCTGCTGA TCTACTCCGGCTCCACGCTGCAATCAGGAATCCCAGCCAGATTTTCCGGTTCGGGGTCGGG GACTGACTTCACCTTGACCATTAGCTCGCTGGAACCTGAGGACTTCGCCGTGTATTACTGC CAGCAGCACAACAAGTACCCGTACACCTTCGGAGGCGGTACTAAGGTCGAGATCAAGACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-2 AA	2126	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQ APGQGLEWMGRIDPYDSETHYNQKFKDRVTMTVDKSTSTAYMELSSLRSEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSEVVLTQSPATLSLSPGERATLSCR ASKSISKDLAWYQQKPGQAPRLLIYSGSTLQSGIPARFSGSGSGTDFTLTISSLEPEDFA VYYCQQHNKYPYTFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-2 scFv	2185	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQ APGQGLEWMGRIDPYDSETHYNQKFKDRVTMTVDKSTSTAYMELSSLRSEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSEVVLTQSPATLSLSPGERATLSCR ASKSISKDLAWYQQKPGQAPRLLIYSGSTLQSGIPARFSGSGSGTDFTLTISSLEPEDFA VYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-2 VH	2244	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQGLEWMGRIDPYDSETHYN QKFKDRVTMTVDKSTSTAYMELSSLRSEDTAVYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-2 VL	2303	EVVLTQSPATLSLSPGERATLSCRASKSISKDLAWYQQKPGQAPRLLIYSGSTLQSGIPAR FSGSGSGTDFTLTISSLEPEDFAVYYCQQHNKYPYTFGGGTKVEIK
hzCAR12	2068	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC

3-3 NT		CCCAAGTGCAGCTGGTCCAGTCGGGAGCCGAAGTCAAGAAGCCCGGCGCTAGCGTGAAAGT GTCCTGCAAAGCCTCCGGGTACACATTCACCTCCTACTGGATGAATTGGGTCAGACAGGCG CCCGGCCAGGGACTCGAGTGGATGGGAAGGATTGATCCTTACGACTCCGAAACCCATTACA ACCAGAAGTTCAAGGACCGCGTGACCATGACTGTGGATAAGTCCACTTCCACCGCTTACAT GGAGCTGTCCAGCCTGCGCTCCGAGGATACCGCAGTGTACTACTGCGCCCGGGGAAACTGG GACGACTATTGGGGACAGGGAACTACCGTGACCGTGTCAAGCGGGGGTGGCGGTAGCGGAG GAGGGGGCTCCGGCGGCGGCGGCTCAGGGGGCGGAGGAAGCGACGTCGTGATGACCCAGTC ACCGGCATTCCTGTCCGTGACTCCCGGAGAAAAGGTCACGATTACTTGCCGGGCGTCCAAG AGCATCTCCAAGGACCTCGCCTGGTACCAACAGAAGCCGGACCAGGCCCCTAAGCTGTTGA TCTACTCGGGGTCCACCCTTCAATCGGGAGTGCCATCGCGGTTTAGCGGTTCGGGTTCTGG GACCGACTTCACTTTCACCATCTCCTCACTGGAAGCCGAGGATGCCGCCACTTACTACTGT CAGCAGCACAACAAGTATCCGTACACCTTCGGAGGCGGTACCAAAGTGGAGATCAAGACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-3 AA	2127	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQ APGQGLEWMGRIDPYDSETHYNQKFKDRVTMTVDKSTSTAYMELSSLRSEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVVMTQSPAFLSVTPGEKVTITCR ASKSISKDLAWYQQKPDQAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTFTISSLEAEDAA TYYCQQHNKYPYTFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-3 scFv	2186	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQ APGQGLEWMGRIDPYDSETHYNQKFKDRVTMTVDKSTSTAYMELSSLRSEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVVMTQSPAFLSVTPGEKVTITCR ASKSISKDLAWYQQKPDQAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTFTISSLEAEDAA TYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-3 VH	2245	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQGLEWMGRIDPYDSETHYN QKFKDRVTMTVDKSTSTAYMELSSLRSEDTAVYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-3 VL	2304	DVVMTQSPAFLSVTPGEKVTITCRASKSISKDLAWYQQKPDQAPKLLIYSGSTLQSGVPSR FSGSGSGTDFTFTISSLEAEDAATYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-4 NT	2069	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCCAAGTGCAGCTGGTCCAGTCGGGAGCCGAAGTCAAGAAGCCCGGCGCTAGCGTGAAAGT GTCCTGCAAAGCCTCCGGGTACACATTCACCTCCTACTGGATGAATTGGGTCAGACAGGCG CCCGGCCAGGGACTCGAGTGGATGGGAAGGATTGATCCTTACGACTCCGAAACCCATTACA ACCAGAAGTTCAAGGACCGCGTGACCATGACTGTGGATAAGTCCACTTCCACCGCTTACAT GGAGCTGTCCAGCCTGCGCTCCGAGGATACCGCAGTGTACTACTGCGCCCGGGGAAACTGG GACGACTATTGGGGACAGGGAACTACCGTGACCGTGTCAAGCGGGGGTGGCGGTAGCGGAG

		GAGGGGGCTCCGGCGGCGGCGGCTCAGGGGGCGGAGGAAGCGACGTGGTCATGACTCAGTC CCCGGACTCACTCGCGGTGTCGCTTGGAGAGAGAGCGACCATCAACTGTCGGGCCTCAAAG AGCATCAGCAAGGACCTGGCCTGGTACCAGCAGAAGCCGGGACAGCCGCCAAAGCTGCTGA TCTACTCCGGGTCCACCTTGCAATCTGGTGTCCCTGACCGGTTCTCCGGTTCCGGGTCGGG TACCGACTTCACGCTCACTATTTCGTCGCTGCAAGCCGAAGATGTGGCCGTGTACTATTGC CAACAGCACAACAAGTACCCCTACACTTTTGGCGGAGGCACCAAGGTGGAAATCAAGACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-4 AA	2128	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQ APGQGLEWMGRIDPYDSETHYNQKFKDRVTMTVDKSTSTAYMELSSLRSEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVVMTQSPDSLAVSLGERATINCR ASKSISKDLAWYQQKPGQPPKLLIYSGSTLQSGVPDRFSGSGSGTDFTLTISSLQAEDVA VYYCQQHNKYPYTFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-4 scFv	2187	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQ APGQGLEWMGRIDPYDSETHYNQKFKDRVTMTVDKSTSTAYMELSSLRSEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVVMTQSPDSLAVSLGERATINCR ASKSISKDLAWYQQKPGQPPKLLIYSGSTLQSGVPDRFSGSGSGTDFTLTISSLQAEDVA VYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-4 VH	2246	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQGLEWMGRIDPYDSETHYN QKFKDRVTMTVDKSTSTAYMELSSLRSEDTAVYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-4 VL	2305	DVVMTQSPDSLAVSLGERATINCRASKSISKDLAWYQQKPGQPPKLLIYSGSTLQSGVPDR FSGSGSGTDFTLTISSLQAEDVAVYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-5 NT	2070	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCGACGTGCAGCTCACCCAGTCGCCCTCATTTCTGTCGGCCTCAGTGGGAGACAGAGTGAC CATTACTTGTCGGGCCTCCAAGAGCATCTCCAAGGACCTGGCCTGGTATCAGCAGAAGCCA GGAAAGGCGCCTAAGTTGCTCATCTACTCGGGGTCGACCCTGCAATCTGGCGTGCCGTCCC GGTTCTCCGGTTCGGGAAGCGGTACCGAATTCACCCTTACTATCTCCTCCCTGCAACCGGA GGACTTCGCCACCTACTACTGCCAACAGCACAACAAGTACCCGTACACTTTCGGGGGTGGC ACGAAGGTCGAAATCAAGGGGGGTGGCGGTAGCGGAGGAGGGGGCTCCGGCGGCGGCGGCT CAGGGGGCGGAGGAAGCCAAGTGCAGCTGGTCCAGTCGGGAGCCGAAGTCAAGAAGCCCGG CGCTAGCGTGAAAGTGTCCTGCAAAGCCTCCGGGTACACATTCACCTCCTACTGGATGAAT TGGGTCAGACAGGCGCCCGGCCAGGGACTCGAGTGGATGGGAAGGATTGATCCTTACGACT CCGAAACCCATTACAACCAGAAGTTCAAGGACCGCGTGACCATGACTGTGGATAAGTCCAC TTCCACCGCTTACATGGAGCTGTCCAGCCTGCGCTCCGAGGATACCGCAGTGTACTACTGC GCCCGGGGAAACTGGGACGACTATTGGGGACAGGGAACTACCGTGACCGTGTCAAGCACCA

		CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-5 AA	2129	MALPVTALLLPLALLLHAARPDVQLTQSPSFLSASVGDRVTITCRASKSISKDLAWYQQK PGKAPKLLIYSGSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSY WMNWVRQAPGQGLEWMGRIDPYDSETHYNQKFKDRVTMTVDKSTSTAYMELSSLRSEDTA VYYCARGNWDDYWGQGTTVTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-5 scFv	2188	MALPVTALLLPLALLLHAARPDVQLTQSPSFLSASVGDRVTITCRASKSISKDLAWYQQK PGKAPKLLIYSGSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSY WMNWVRQAPGQGLEWMGRIDPYDSETHYNQKFKDRVTMTVDKSTSTAYMELSSLRSEDTA VYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-5 VH	2247	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQGLEWMGRIDPYDSETHYN QKFKDRVTMTVDKSTSTAYMELSSLRSEDTAVYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-5 VL	2306	DVQLTQSPSFLSASVGDRVTITCRASKSISKDLAWYQQKPGKAPKLLIYSGSTLQSGVPSR FSGSGSGTEFTLTISSLQPEDFATYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-6 NT	2071	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCGAAGTGGTGCTGACCCAGTCGCCCGCAACCCTCTCTCTGTCGCCGGGAGAACGCGCCAC TCTTTCCTGTCGGGCGTCCAAGAGCATCTCAAAGGACCTCGCCTGGTACCAGCAGAAGCCT GGTCAAGCCCCGCGGCTGCTGATCTACTCCGGCTCCACGCTGCAATCAGGAATCCCAGCCA GATTTTCCGGTTCGGGGTCGGGGACTGACTTCACCTTGACCATTAGCTCGCTGGAACCTGA GGACTTCGCCGTGTATTACTGCCAGCAGCACAACAAGTACCCGTACACCTTCGGAGGCGGT ACTAAGGTCGAGATCAAGGGGGGTGGCGGTAGCGGAGGAGGGGGCTCCGGCGGCGGCGGCT CAGGGGGCGGAGGAAGCCAAGTGCAGCTGGTCCAGTCGGGAGCCGAAGTCAAGAAGCCCGG CGCTAGCGTGAAAGTGTCCTGCAAAGCCTCCGGGTACACATTCACCTCCTACTGGATGAAT TGGGTCAGACAGGCGCCCGGCCAGGGACTCGAGTGGATGGGAAGGATTGATCCTTACGACT CCGAAACCCATTACAACCAGAAGTTCAAGGACCGCGTGACCATGACTGTGGATAAGTCCAC TTCCACCGCTTACATGGAGCTGTCCAGCCTGCGCTCCGAGGATACCGCAGTGTACTACTGC GCCCGGGGAAACTGGGACGACTATTGGGGACAGGGAACTACCGTGACCGTGTCAAGCACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct

		acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-6 AA	2130	MALPVTALLLPLALLLHAARPEVVLTQSPATLSLSPGERATLSCRASKSISKDLAWYQQK PGQAPRLLIYSGSTLQSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSY WMNWVRQAPGQGLEWMGRIDPYDSETHYNQKFKDRVTMTVDKSTSTAYMELSSLRSEDTA VYYCARGNWDDYWGQGTTVTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-6 scFv	2189	MALPVTALLLPLALLLHAARPEVVLTQSPATLSLSPGERATLSCRASKSISKDLAWYQQK PGQAPRLLIYSGSTLQSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSY WMNWVRQAPGQGLEWMGRIDPYDSETHYNQKFKDRVTMTVDKSTSTAYMELSSLRSEDTA VYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-6 VH	2248	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQGLEWMGRIDPYDSETHYN QKFKDRVTMTVDKSTSTAYMELSSLRSEDTAVYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-6 VL	2307	EVVLTQSPATLSLSPGERATLSCRASKSISKDLAWYQQKPGQAPRLLIYSGSTLQSGIPAR FSGSGSGTDFTLTISSLEPEDFAVYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-7 NT	2072	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCGACGTCGTGATGACCCAGTCACCGGCATTCCTGTCCGTGACTCCCGGAGAAAAGGTCAC GATTACTTGCCGGGCGTCCAAGAGCATCTCCAAGGACCTCGCCTGGTACCAACAGAAGCCG GACCAGGCCCCTAAGCTGTTGATCTACTCGGGGTCCACCCTTCAATCGGGAGTGCCATCGC GGTTTAGCGGTTCGGGTTCTGGGACCGACTTCACTTTCACCATCTCCTCACTGGAAGCCGA GGATGCCGCCACTTACTACTGTCAGCAGCACAACAAGTATCCGTACACCTTCGGAGGCGGT ACCAAAGTGGAGATCAAGGGGGGTGGCGGTAGCGGAGGAGGGGGCTCCGGCGGCGGCGGCT CAGGGGGCGGAGGAAGCCAAGTGCAGCTGGTCCAGTCGGGAGCCGAAGTCAAGAAGCCCGG CGCTAGCGTGAAAGTGTCCTGCAAAGCCTCCGGGTACACATTCACCTCCTACTGGATGAAT TGGGTCAGACAGGCGCCCGGCCAGGGACTCGAGTGGATGGGAAGGATTGATCCTTACGACT CCGAAACCCATTACAACCAGAAGTTCAAGGACCGCGTGACCATGACTGTGGATAAGTCCAC TTCCACCGCTTACATGGAGCTGTCCAGCCTGCGCTCCGAGGATACCGCAGTGTACTACTGC GCCCGGGGAAACTGGGACGACTATTGGGGACAGGGAACTACCGTGACCGTGTCAAGCACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg

hzCAR12 3-7 AA	2131	MALPVTALLLPLALLLHAARPDVVMTQSPAFLSVTPGEKVTITCRASKSISKDLAWYQQK PDQAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSY WMNWVRQAPGQGLEWMGRIDPYDSETHYNQKFKDRVTMTVDKSTSTAYMELSSLRSEDTA VYYCARGNWDDYWGQGTTVTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-7 scFv	2190	MALPVTALLLPLALLLHAARPDVVMTQSPAFLSVTPGEKVTITCRASKSISKDLAWYQQK PDQAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSY WMNWVRQAPGQGLEWMGRIDPYDSETHYNQKFKDRVTMTVDKSTSTAYMELSSLRSEDTA VYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-7 VH	2249	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQGLEWMGRIDPYDSETHYN QKFKDRVTMTVDKSTSTAYMELSSLRSEDTAVYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-7 VL	2308	DVVMTQSPAFLSVTPGEKVTITCRASKSISKDLAWYQQKPDQAPKLLIYSGSTLQSGVPSR FSGSGSGTDFTFTISSLEAEDAATYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-8 NT	2073	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCGACGTGGTCATGACTCAGTCCCCGGACTCACTCGCGGTGTCGCTTGGAGAGAGAGCGAC CATCAACTGTCGGGCCTCAAAGAGCATCAGCAAGGACCTGGCCTGGTACCAGCAGAAGCCG GGACAGCCGCCAAAGCTGCTGATCTACTCCGGGTCCACCTTGCAATCTGGTGTCCCTGACC GGTTCTCCGGTTCCGGGTCGGGTACCGACTTCACGCTCACTATTTCGTCGCTGCAAGCCGA AGATGTGGCCGTGTACTATTGCCAACAGCACAACAAGTACCCCTACACTTTTGGCGGAGGC ACCAAGGTGGAAATCAAGGGGGGTGGCGGTAGCGGAGGAGGGGGCTCCGGCGGCGGCGGCT CAGGGGGCGGAGGAAGCCAAGTGCAGCTGGTCCAGTCGGGAGCCGAAGTCAAGAAGCCCGG CGCTAGCGTGAAAGTGTCCTGCAAAGCCTCCGGGTACACATTCACCTCCTACTGGATGAAT TGGGTCAGACAGGCGCCCGGCCAGGGACTCGAGTGGATGGGAAGGATTGATCCTTACGACT CCGAAACCCATTACAACCAGAAGTTCAAGGACCGCGTGACCATGACTGTGGATAAGTCCAC TTCCACCGCTTACATGGAGCTGTCCAGCCTGCGCTCCGAGGATACCGCAGTGTACTACTGC GCCCGGGGAAACTGGGACGACTATTGGGGACAGGGAACTACCGTGACCGTGTCAAGCACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-8 AA	2132	MALPVTALLLPLALLLHAARPDVVMTQSPDSLAVSLGERATINCRASKSISKDLAWYQQK PGQPPKLLIYSGSTLQSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSY WMNWVRQAPGQGLEWMGRIDPYDSETHYNQKFKDRVTMTVDKSTSTAYMELSSLRSEDTA VYYCARGNWDDYWGQGTTVTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC

		SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-8 scFv	2191	MALPVTALLLPLALLLHAARPDVVMTQSPDSLAVSLGERATINCRASKSISKDLAWYQQK PGQPPKLLIYSGSTLQSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSY WMNWVRQAPGQGLEWMGRIDPYDSETHYNQKFKDRVTMTVDKSTSTAYMELSSLRSEDTA VYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-8 VH	2250	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQGLEWMGRIDPYDSETHYN QKFKDRVTMTVDKSTSTAYMELSSLRSEDTAVYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-8 VL	2309	DVVMTQSPDSLAVSLGERATINCRASKSISKDLAWYQQKPGQPPKLLIYSGSTLQSGVPDR FSGSGSGTDFTLTISSLQAEDVAVYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-9 NT	2074	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCCAAGTGCAGCTGGTGCAGTCAGGCAGCGAACTGAAGAAGCCCGGAGCCTCCGTCAAAGT GTCCTGCAAAGCCTCGGGATACACCTTCACCTCCTACTGGATGAACTGGGTCCGCCAGGCA CCTGGACAGGGGCTGGAGTGGATGGGAAGGATCGATCCCTACGATTCCGAAACCCATTACA ATCAGAAGTTCAAGGACCGGTTTGTGTTCTCCGTGGACAAGTCCGTGTCCACCGCCTACCT CCAAATTAGCAGCCTGAAGGCGGAGGATACAGCTGTCTACTACTGCGCTCGCGGAAACTGG GATGACTATTGGGGCCAGGGAACTACCGTGACTGTGTCCTCCGGGGGTGGCGGTAGCGGAG GAGGGGGCTCCGGCGGCGGCGGCTCAGGGGGCGGAGGAAGCGACGTGCAGCTCACCCAGTC GCCCTCATTTCTGTCGGCCTCAGTGGGAGACAGAGTGACCATTACTTGTCGGGCCTCCAAG AGCATCTCCAAGGACCTGGCCTGGTATCAGCAGAAGCCAGGAAAGGCGCCTAAGTTGCTCA TCTACTCGGGGTCGACCCTGCAATCTGGCGTGCCGTCCCGGTTCTCCGGTTCGGGAAGCGG TACCGAATTCACCCTTACTATCTCCTCCCTGCAACCGGAGGACTTCGCCACCTACTACTGC CAACAGCACAACAAGTACCCGTACACTTTCGGGGGTGGCACGAAGGTCGAAATCAAGACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-9 AA	2133	MALPVTALLLPLALLLHAARPQVQLVQSGSELKKPGASVKVSCKASGYTFTSYWMNWVRQ APGQGLEWMGRIDPYDSETHYNQKFKDRFVFSVDKSVSTAYLQISSLKAEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVQLTQSPSFLSASVGDRVTITCR ASKSISKDLAWYQQKPGKAPKLLIYSGSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFA TYYCQQHNKYPYTFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-9	2192	MALPVTALLLPLALLLHAARPQVQLVQSGSELKKPGASVKVSCKASGYTFTSYWMNWVRQ APGQGLEWMGRIDPYDSETHYNQKFKDRFVFSVDKSVSTAYLQISSLKAEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVQLTQSPSFLSASVGDRVTITCR

scFv		ASKSISKDLAWYQQKPGKAPKLLIYSGSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFA TYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-9 VH	2251	QVQLVQSGSELKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQGLEWMGRIDPYDSETHYN QKFKDRFVFSVDKSVSTAYLQISSLKAEDTAVYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-10 VL	2310	DVQLTQSPSFLSASVGDRVTITCRASKSISKDLAWYQQKPGKAPKLLIYSGSTLQSGVPSR FSGSGSGTEFTLTISSLQPEDFATYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-10 NT	2075	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCCAAGTGCAGCTGGTGCAGTCAGGCAGCGAACTGAAGAAGCCCGGAGCCTCCGTCAAAGT GTCCTGCAAAGCCTCGGGATACACCTTCACCTCCTACTGGATGAACTGGGTCCGCCAGGCA CCTGGACAGGGGCTGGAGTGGATGGGAAGGATCGATCCCTACGATTCCGAAACCCATTACA ATCAGAAGTTCAAGGACCGGTTTGTGTTCTCCGTGGACAAGTCCGTGTCCACCGCCTACCT CCAAATTAGCAGCCTGAAGGCGGAGGATACAGCTGTCTACTACTGCGCTCGCGGAAACTGG GATGACTATTGGGGCCAGGGAACTACCGTGACTGTGTCCTCCGGGGGTGGCGGTAGCGGAG GAGGGGGCTCCGGCGGCGGCGGCTCAGGGGGCGGAGGAAGCGAAGTGGTGCTGACCCAGTC GCCCGCAACCCTCTCTCTGTCGCCGGGAGAACGCGCCACTCTTTCCTGTCGGGCGTCCAAG AGCATCTCAAAGGACCTCGCCTGGTACCAGCAGAAGCCTGGTCAAGCCCCGCGGCTGCTGA TCTACTCCGGCTCCACGCTGCAATCAGGAATCCCAGCCAGATTTTCCGGTTCGGGGTCGGG GACTGACTTCACCTTGACCATTAGCTCGCTGGAACCTGAGGACTTCGCCGTGTATTACTGC CAGCAGCACAACAAGTACCCGTACACCTTCGGAGGCGGTACTAAGGTCGAGATCAAGACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-10 AA	2134	MALPVTALLLPLALLLHAARPQVQLVQSGSELKKPGASVKVSCKASGYTFTSYWMNWVRQ APGQGLEWMGRIDPYDSETHYNQKFKDRFVFSVDKSVSTAYLQISSLKAEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSEVVLTQSPATLSLSPGERATLSCR ASKSISKDLAWYQQKPGQAPRLLIYSGSTLQSGIPARFSGSGSGTDFTLTISSLEPEDFA VYYCQQHNKYPYTFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-10 scFv	2193	MALPVTALLLPLALLLHAARPQVQLVQSGSELKKPGASVKVSCKASGYTFTSYWMNWVRQ APGQGLEWMGRIDPYDSETHYNQKFKDRFVFSVDKSVSTAYLQISSLKAEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSEVVLTQSPATLSLSPGERATLSCR ASKSISKDLAWYQQKPGQAPRLLIYSGSTLQSGIPARFSGSGSGTDFTLTISSLEPEDFA VYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-10 VH	2252	QVQLVQSGSELKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQGLEWMGRIDPYDSETHYN QKFKDRFVFSVDKSVSTAYLQISSLKAEDTAVYYCARGNWDDYWGQGTTVTVSS

hzCAR12 3-10 VL	2311	EVVLTQSPATLSLSPGERATLSCRASKSISKDLAWYQQKPGQAPRLLIYSGSTLQSGIPAR FSGSGSGTDFTLTISSLEPEDFAVYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-11 NT	2076	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCCAAGTGCAGCTGGTGCAGTCAGGCAGCGAACTGAAGAAGCCCGGAGCCTCCGTCAAAGT GTCCTGCAAAGCCTCGGGATACACCTTCACCTCCTACTGGATGAACTGGGTCCGCCAGGCA CCTGGACAGGGGCTGGAGTGGATGGGAAGGATCGATCCCTACGATTCCGAAACCCATTACA ATCAGAAGTTCAAGGACCGGTTTGTGTTCTCCGTGGACAAGTCCGTGTCCACCGCCTACCT CCAAATTAGCAGCCTGAAGGCGGAGGATACAGCTGTCTACTACTGCGCTCGCGGAAACTGG GATGACTATTGGGGCCAGGGAACTACCGTGACTGTGTCCTCCGGGGGTGGCGGTAGCGGAG GAGGGGGCTCCGGCGGCGGCGGCTCAGGGGGCGGAGGAAGCGACGTCGTGATGACCCAGTC ACCGGCATTCCTGTCCGTGACTCCCGGAGAAAAGGTCACGATTACTTGCCGGGCGTCCAAG AGCATCTCCAAGGACCTCGCCTGGTACCAACAGAAGCCGGACCAGGCCCCTAAGCTGTTGA TCTACTCGGGGTCCACCCTTCAATCGGGAGTGCCATCGCGGTTTAGCGGTTCGGGTTCTGG GACCGACTTCACTTTCACCATCTCCTCACTGGAAGCCGAGGATGCCGCCACTTACTACTGT CAGCAGCACAACAAGTATCCGTACACCTTCGGAGGCGGTACCAAAGTGGAGATCAAGACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-11 AA	2135	MALPVTALLLPLALLLHAARPQVQLVQSGSELKKPGASVKVSCKASGYTFTSYWMNWVRQ APGQGLEWMGRIDPYDSETHYNQKFKDRFVFSVDKSVSTAYLQISSLKAEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVVMTQSPAFLSVTPGEKVTITCR ASKSISKDLAWYQQKPDQAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTFTISSLEAEDAA TYYCQQHNKYPYTFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-11 scFv	2194	MALPVTALLLPLALLLHAARPQVQLVQSGSELKKPGASVKVSCKASGYTFTSYWMNWVRQ APGQGLEWMGRIDPYDSETHYNQKFKDRFVFSVDKSVSTAYLQISSLKAEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVVMTQSPAFLSVTPGEKVTITCR ASKSISKDLAWYQQKPDQAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTFTISSLEAEDAA TYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-11 VH	2253	QVQLVQSGSELKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQGLEWMGRIDPYDSETHYN QKFKDRFVFSVDKSVSTAYLQISSLKAEDTAVYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-11 VL	2312	DVVMTQSPAFLSVTPGEKVTITCRASKSISKDLAWYQQKPDQAPKLLIYSGSTLQSGVPSR FSGSGSGTDFTFTISSLEAEDAATYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-12 NT	2077	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCCAAGTGCAGCTGGTGCAGTCAGGCAGCGAACTGAAGAAGCCCGGAGCCTCCGTCAAAGT GTCCTGCAAAGCCTCGGGATACACCTTCACCTCCTACTGGATGAACTGGGTCCGCCAGGCA

		CCTGGACAGGGGCTGGAGTGGATGGGAAGGATCGATCCCTACGATTCCGAAACCCATTACA ATCAGAAGTTCAAGGACCGGTTTGTGTTCTCCGTGGACAAGTCCGTGTCCACCGCCTACCT CCAAATTAGCAGCCTGAAGGCGGAGGATACAGCTGTCTACTACTGCGCTCGCGGAAACTGG GATGACTATTGGGGCCAGGGAACTACCGTGACTGTGTCCTCCGGGGGTGGCGGTAGCGGAG GAGGGGGCTCCGGCGGCGGCGGCTCAGGGGGCGGAGGAAGCGACGTGGTCATGACTCAGTC CCCGGACTCACTCGCGGTGTCGCTTGGAGAGAGAGCGACCATCAACTGTCGGGCCTCAAAG AGCATCAGCAAGGACCTGGCCTGGTACCAGCAGAAGCCGGGACAGCCGCCAAAGCTGCTGA TCTACTCCGGGTCCACCTTGCAATCTGGTGTCCCTGACCGGTTCTCCGGTTCCGGGTCGGG TACCGACTTCACGCTCACTATTTCGTCGCTGCAAGCCGAAGATGTGGCCGTGTACTATTGC CAACAGCACAACAAGTACCCCTACACTTTTGGCGGAGGCACCAAGGTGGAAATCAAGACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-12 AA	2136	MALPVTALLLPLALLLHAARPQVQLVQSGSELKKPGASVKVSCKASGYTFTSYWMNWVRQ APGQGLEWMGRIDPYDSETHYNQKFKDRFVFSVDKSVSTAYLQISSLKAEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVVMTQSPDSLAVSLGERATINCR ASKSISKDLAWYQQKPGQPPKLLIYSGSTLQSGVPDRFSGSGSGTDFTLTISSLQAEDVA VYYCQQHNKYPYTFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-12 scFv	2195	MALPVTALLLPLALLLHAARPQVQLVQSGSELKKPGASVKVSCKASGYTFTSYWMNWVRQ APGQGLEWMGRIDPYDSETHYNQKFKDRFVFSVDKSVSTAYLQISSLKAEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVVMTQSPDSLAVSLGERATINCR ASKSISKDLAWYQQKPGQPPKLLIYSGSTLQSGVPDRFSGSGSGTDFTLTISSLQAEDVA VYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-12 VH	2254	QVQLVQSGSELKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQGLEWMGRIDPYDSETHYN QKFKDRFVFSVDKSVSTAYLQISSLKAEDTAVYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-12 VL	2313	DVVMTQSPDSLAVSLGERATINCRASKSISKDLAWYQQKPGQPPKLLIYSGSTLQSGVPDR FSGSGSGTDFTLTISSLQAEDVAVYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-13 NT	2078	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCGACGTGCAGCTCACCCAGTCGCCCTCATTTCTGTCGGCCTCAGTGGGAGACAGAGTGAC CATTACTTGTCGGGCCTCCAAGAGCATCTCCAAGGACCTGGCCTGGTATCAGCAGAAGCCA GGAAAGGCGCCTAAGTTGCTCATCTACTCGGGGTCGACCCTGCAATCTGGCGTGCCGTCCC GGTTCTCCGGTTCGGGAAGCGGTACCGAATTCACCCTTACTATCTCCTCCCTGCAACCGGA GGACTTCGCCACCTACTACTGCCAACAGCACAACAAGTACCCGTACACTTTCGGGGGTGGC ACGAAGGTCGAAATCAAGGGGGGTGGCGGTAGCGGAGGAGGGGGCTCCGGCGGCGGCGGCT CAGGGGGCGGAGGAAGCCAAGTGCAGCTGGTGCAGTCAGGCAGCGAACTGAAGAAGCCCGG AGCCTCCGTCAAAGTGTCCTGCAAAGCCTCGGGATACACCTTCACCTCCTACTGGATGAAC

		TGGGTCCGCCAGGCACCTGGACAGGGGCTGGAGTGGATGGGAAGGATCGATCCCTACGATT CCGAAACCCATTACAATCAGAAGTTCAAGGACCGGTTTGTGTTCTCCGTGGACAAGTCCGT GTCCACCGCCTACCTCCAAATTAGCAGCCTGAAGGCGGAGGATACAGCTGTCTACTACTGC GCTCGCGGAAACTGGGATGACTATTGGGGCCAGGGAACTACCGTGACTGTGTCCTCCACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-13 AA	2137	MALPVTALLLPLALLLHAARPDVQLTQSPSFLSASVGDRVTITCRASKSISKDLAWYQQK PGKAPKLLIYSGSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGSELKKPGASVKVSCKASGYTFTSY WMNWVRQAPGQGLEWMGRIDPYDSETHYNQKFKDRFVFSVDKSVSTAYLQISSLKAEDTA VYYCARGNWDDYWGQGTTVTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-13 scFv	2196	MALPVTALLLPLALLLHAARPDVQLTQSPSFLSASVGDRVTITCRASKSISKDLAWYQQK PGKAPKLLIYSGSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGSELKKPGASVKVSCKASGYTFTSY WMNWVRQAPGQGLEWMGRIDPYDSETHYNQKFKDRFVFSVDKSVSTAYLQISSLKAEDTA VYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-13 VH	2255	QVQLVQSGSELKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQGLEWMGRIDPYDSETHYN QKFKDRFVFSVDKSVSTAYLQISSLKAEDTAVYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-13 VL	2314	DVQLTQSPSFLSASVGDRVTITCRASKSISKDLAWYQQKPGKAPKLLIYSGSTLQSGVPSR FSGSGSGTEFTLTISSLQPEDFATYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-14 NT	2079	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCGAAGTGGTGCTGACCCAGTCGCCCGCAACCCTCTCTCTGTCGCCGGGAGAACGCGCCAC TCTTTCCTGTCGGGCGTCCAAGAGCATCTCAAAGGACCTCGCCTGGTACCAGCAGAAGCCT GGTCAAGCCCCGCGGCTGCTGATCTACTCCGGCTCCACGCTGCAATCAGGAATCCCAGCCA GATTTTCCGGTTCGGGGTCGGGGACTGACTTCACCTTGACCATTAGCTCGCTGGAACCTGA GGACTTCGCCGTGTATTACTGCCAGCAGCACAACAAGTACCCGTACACCTTCGGAGGCGGT ACTAAGGTCGAGATCAAGGGGGGTGGCGGTAGCGGAGGAGGGGGCTCCGGCGGCGGCGGCT CAGGGGGCGGAGGAAGCCAAGTGCAGCTGGTGCAGTCAGGCAGCGAACTGAAGAAGCCCGG AGCCTCCGTCAAAGTGTCCTGCAAAGCCTCGGGATACACCTTCACCTCCTACTGGATGAAC TGGGTCCGCCAGGCACCTGGACAGGGGCTGGAGTGGATGGGAAGGATCGATCCCTACGATT CCGAAACCCATTACAATCAGAAGTTCAAGGACCGGTTTGTGTTCTCCGTGGACAAGTCCGT GTCCACCGCCTACCTCCAAATTAGCAGCCTGAAGGCGGAGGATACAGCTGTCTACTACTGC GCTCGCGGAAACTGGGATGACTATTGGGGCCAGGGAACTACCGTGACTGTGTCCTCCACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc

		gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-14 AA	2138	MALPVTALLLPLALLLHAARPEVVLTQSPATLSLSPGERATLSCRASKSISKDLAWYQQK PGQAPRLLIYSGSTLQSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGSELKKPGASVKVSCKASGYTFTSY WMNWVRQAPGQGLEWMGRIDPYDSETHYNQKFKDRFVFSVDKSVSTAYLQISSLKAEDTA VYYCARGNWDDYWGQGTTVTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-14 scFv	2197	MALPVTALLLPLALLLHAARPEVVLTQSPATLSLSPGERATLSCRASKSISKDLAWYQQK PGQAPRLLIYSGSTLQSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGSELKKPGASVKVSCKASGYTFTSY WMNWVRQAPGQGLEWMGRIDPYDSETHYNQKFKDRFVFSVDKSVSTAYLQISSLKAEDTA VYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-14 VH	2256	QVQLVQSGSELKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQGLEWMGRIDPYDSETHYN QKFKDRFVFSVDKSVSTAYLQISSLKAEDTAVYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-14 VL	2315	EVVLTQSPATLSLSPGERATLSCRASKSISKDLAWYQQKPGQAPRLLIYSGSTLQSGIPAR FSGSGSGTDFTLTISSLEPEDFAVYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-15 NT	2080	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCGACGTCGTGATGACCCAGTCACCGGCATTCCTGTCCGTGACTCCCGGAGAAAAGGTCAC GATTACTTGCCGGGCGTCCAAGAGCATCTCCAAGGACCTCGCCTGGTACCAACAGAAGCCG GACCAGGCCCCTAAGCTGTTGATCTACTCGGGGTCCACCCTTCAATCGGGAGTGCCATCGC GGTTTAGCGGTTCGGGTTCTGGGACCGACTTCACTTTCACCATCTCCTCACTGGAAGCCGA GGATGCCGCCACTTACTACTGTCAGCAGCACAACAAGTATCCGTACACCTTCGGAGGCGGT ACCAAAGTGGAGATCAAGGGGGGTGGCGGTAGCGGAGGAGGGGGCTCCGGCGGCGGCGGCT CAGGGGGCGGAGGAAGCCAAGTGCAGCTGGTGCAGTCAGGCAGCGAACTGAAGAAGCCCGG AGCCTCCGTCAAAGTGTCCTGCAAAGCCTCGGGATACACCTTCACCTCCTACTGGATGAAC TGGGTCCGCCAGGCACCTGGACAGGGGCTGGAGTGGATGGGAAGGATCGATCCCTACGATT CCGAAACCCATTACAATCAGAAGTTCAAGGACCGGTTTGTGTTCTCCGTGGACAAGTCCGT GTCCACCGCCTACCTCCAAATTAGCAGCCTGAAGGCGGAGGATACAGCTGTCTACTACTGC GCTCGCGGAAACTGGGATGACTATTGGGGCCAGGGAACTACCGTGACTGTGTCCTCCACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat

		ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-15 AA	2139	MALPVTALLLPLALLLHAARPDVVMTQSPAFLSVTPGEKVTITCRASKSISKDLAWYQQK PDQAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGSELKKPGASVKVSCKASGYTFTSY WMNWVRQAPGQGLEWMGRIDPYDSETHYNQKFKDRFVFSVDKSVSTAYLQISSLKAEDTA VYYCARGNWDDYWGQGTTVTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-15 scFv	2198	MALPVTALLLPLALLLHAARPDVVMTQSPAFLSVTPGEKVTITCRASKSISKDLAWYQQK PDQAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGSELKKPGASVKVSCKASGYTFTSY WMNWVRQAPGQGLEWMGRIDPYDSETHYNQKFKDRFVFSVDKSVSTAYLQISSLKAEDTA VYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-15 VH	2257	QVQLVQSGSELKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQGLEWMGRIDPYDSETHYN QKFKDRFVFSVDKSVSTAYLQISSLKAEDTAVYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-15 VL	2316	DVVMTQSPAFLSVTPGEKVTITCRASKSISKDLAWYQQKPDQAPKLLIYSGSTLQSGVPSR FSGSGSGTDFTFTISSLEAEDAATYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-16 NT	2081	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCGACGTGGTCATGACTCAGTCCCCGGACTCACTCGCGGTGTCGCTTGGAGAGAGAGCGAC CATCAACTGTCGGGCCTCAAAGAGCATCAGCAAGGACCTGGCCTGGTACCAGCAGAAGCCG GGACAGCCGCCAAAGCTGCTGATCTACTCCGGGTCCACCTTGCAATCTGGTGTCCCTGACC GGTTCTCCGGTTCCGGGTCGGGTACCGACTTCACGCTCACTATTTCGTCGCTGCAAGCCGA AGATGTGGCCGTGTACTATTGCCAACAGCACAACAAGTACCCCTACACTTTTGGCGGAGGC ACCAAGGTGGAAATCAAGGGGGGTGGCGGTAGCGGAGGAGGGGGCTCCGGCGGCGGCGGCT CAGGGGGCGGAGGAAGCCAAGTGCAGCTGGTGCAGTCAGGCAGCGAACTGAAGAAGCCCGG AGCCTCCGTCAAAGTGTCCTGCAAAGCCTCGGGATACACCTTCACCTCCTACTGGATGAAC TGGGTCCGCCAGGCACCTGGACAGGGGCTGGAGTGGATGGGAAGGATCGATCCCTACGATT CCGAAACCCATTACAATCAGAAGTTCAAGGACCGGTTTGTGTTCTCCGTGGACAAGTCCGT GTCCACCGCCTACCTCCAAATTAGCAGCCTGAAGGCGGAGGATACAGCTGTCTACTACTGC GCTCGCGGAAACTGGGATGACTATTGGGGCCAGGGAACTACCGTGACTGTGTCCTCCACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-16 AA	2140	MALPVTALLLPLALLLHAARPDVVMTQSPDSLAVSLGERATINCRASKSISKDLAWYQQK PGQPPKLLIYSGSTLQSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGSELKKPGASVKVSCKASGYTFTSY

		WMNWVRQAPGQGLEWMGRIDPYDSETHYNQKFKDRFVFSVDKSVSTAYLQISSLKAEDTA VYYCARGNWDDYWGQGTTVTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-16 scFv	2199	MALPVTALLLPLALLLHAARPDVVMTQSPDSLAVSLGERATINCRASKSISKDLAWYQQK PGQPPKLLIYSGSTLQSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGSELKKPGASVKVSCKASGYTFTSY WMNWVRQAPGQGLEWMGRIDPYDSETHYNQKFKDRFVFSVDKSVSTAYLQISSLKAEDTA VYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-16 VH	2258	QVQLVQSGSELKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQGLEWMGRIDPYDSETHYN QKFKDRFVFSVDKSVSTAYLQISSLKAEDTAVYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-16 VL	2317	DVVMTQSPDSLAVSLGERATINCRASKSISKDLAWYQQKPGQPPKLLIYSGSTLQSGVPDR FSGSGSGTDFTLTISSLQAEDVAVYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-17 NT	2082	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCGAGGTGCAGCTGGTGCAGAGCGGAGCCGAGGTCAAGAAGCCTGGAGAATCCCTGAGGAT CAGCTGCAAAGGCAGCGGGTATACCTTCACCTCCTACTGGATGAATTGGGTCCGCCAGATG CCCGGAAAAGGCCTGGAGTGGATGGGACGGATTGACCCCTACGACTCGGAAACCCATTACA ACCAGAAGTTCAAGGATCACGTGACCATCTCCGTGGACAAGTCCATTTCCACTGCGTACCT CCAGTGGTCAAGCCTGAAGGCCTCCGACACTGCTATGTACTACTGCGCACGCGGAAACTGG GATGATTACTGGGGACAGGGAACAACCGTGACTGTGTCCTCCGGGGGTGGCGGTAGCGGAG GAGGGGGCTCCGGCGGCGGCGGCTCAGGGGGCGGAGGAAGCGACGTGCAGCTCACCCAGTC GCCCTCATTTCTGTCGGCCTCAGTGGGAGACAGAGTGACCATTACTTGTCGGGCCTCCAAG AGCATCTCCAAGGACCTGGCCTGGTATCAGCAGAAGCCAGGAAAGGCGCCTAAGTTGCTCA TCTACTCGGGGTCGACCCTGCAATCTGGCGTGCCGTCCCGGTTCTCCGGTTCGGGAAGCGG TACCGAATTCACCCTTACTATCTCCTCCCTGCAACCGGAGGACTTCGCCACCTACTACTGC CAACAGCACAACAAGTACCCGTACACTTTCGGGGGTGGCACGAAGGTCGAAATCAAGACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-17 AA	2141	MALPVTALLLPLALLLHAARPEVQLVQSGAEVKKPGESLRISCKGSGYTFTSYWMNWVRQ MPGKGLEWMGRIDPYDSETHYNQKFKDHVTISVDKSISTAYLQWSSLKASDTAMYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVQLTQSPSFLSASVGDRVTITCR ASKSISKDLAWYQQKPGKAPKLLIYSGSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFA TYYCQQHNKYPYTFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR

hzCAR12 3-17 scFv	2200	MALPVTALLLPLALLLHAARPEVQLVQSGAEVKKPGESLRISCKGSGYTFTSYWMNWVRQMPGKGLEWMGRIDPYDSETHYNQKFKDHVTISVDKSISTAYLQWSSLKASDTAMYYCARGNWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVQLTQSPSFLSASVGDRVTITCRASKSISKDLAWYQQKPGKAPKLLIYSGSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-17 VH	2259	EVQLVQSGAEVKKPGESLRISCKGSGYTFTSYWMNWVRQMPGKGLEWMGRIDPYDSETHYNQKFKDHVTISVDKSISTAYLQWSSLKASDTAMYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-17 VL	2318	DVQLTQSPSFLSASVGDRVTITCRASKSISKDLAWYQQKPGKAPKLLIYSGSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-18 NT	2083	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGCCCGAGGTGCAGCTGGTGCAGAGCGGAGCCGAGGTCAAGAAGCCTGGAGAATCCCTGAGGATCAGCTGCAAAGGCAGCGGGTATACCTTCACCTCCTACTGGATGAATTGGGTCCGCCAGATGCCCGGAAAAGGCCTGGAGTGGATGGGACGGATTGACCCCTACGACTCGGAAACCCATTACAACCAGAAGTTCAAGGATCACGTGACCATCTCCGTGGACAAGTCCATTTCCACTGCGTACCTCCAGTGGTCAAGCCTGAAGGCCTCCGACACTGCTATGTACTACTGCGCACGCGGAAACTGGGATGATTACTGGGGACAGGGAACAACCGTGACTGTGTCCTCCGGGGGTGGCGGTAGCGGAGGAGGGGGCTCCGGCGGCGGCGGCTCAGGGGGCGGAGGAAGCGAAGTGGTGCTGACCCAGTCGCCCGCAACCCTCTCTCTGTCGCCGGGAGAACGCGCCACTCTTTCCTGTCGGGCGTCCAAGAGCATCTCAAAGGACCTCGCCTGGTACCAGCAGAAGCCTGGTCAAGCCCCGCGGCTGCTGATCTACTCCGGCTCCACGCTGCAATCAGGAATCCCAGCCAGATTTTCCGGTTCGGGGTCGGGGACTGACTTCACCTTGACCATTAGCTCGCTGGAACCTGAGGACTTCGCCGTGTATTACTGCCAGCAGCACAACAAGTACCCGTACACCTTCGGAGGCGGTACTAAGGTCGAGATCAAGACCACTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTGCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttcgcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcactcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacccttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagaggaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcctacaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacgacgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaatccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgagattggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcagcaccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-18 AA	2142	MALPVTALLLPLALLLHAARPEVQLVQSGAEVKKPGESLRISCKGSGYTFTSYWMNWVRQMPGKGLEWMGRIDPYDSETHYNQKFKDHVTISVDKSISTAYLQWSSLKASDTAMYYCARGNWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSEVVLTQSPATLSLSPGERATLSCRASKSISKDLAWYQQKPGQAPRLLIYSGSTLQSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQHNKYPYTFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
hzCAR12 3-18 scFv	2201	MALPVTALLLPLALLLHAARPEVQLVQSGAEVKKPGESLRISCKGSGYTFTSYWMNWVRQMPGKGLEWMGRIDPYDSETHYNQKFKDHVTISVDKSISTAYLQWSSLKASDTAMYYCARGNWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSEVVLTQSPATLSLSPGERATLSCRASKSISKDLAWYQQKPGQAPRLLIYSGSTLQSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQHNKYPYTFGGGTKVEIK

hzCAR12 3-18 VH	2260	EVQLVQSGAEVKKPGESLRISCKGSGYTFTSYWMNWVRQMPGKGLEWMGRIDPYDSETHYN QKFKDHVTISVDKSISTAYLQWSSLKASDTAMYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-18 VL	2319	EVVLTQSPATLSLSPGERATLSCRASKSISKDLAWYQQKPGQAPRLLIYSGSTLQSGIPAR FSGSGSGTDFTLTISSLEPEDFAVYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-19 NT	2084	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCGAGGTGCAGCTGGTGCAGAGCGGAGCCGAGGTCAAGAAGCCTGGAGAATCCCTGAGGAT CAGCTGCAAAGGCAGCGGGTATACCTTCACCTCCTACTGGATGAATTGGGTCCGCCAGATG CCCGGAAAAGGCCTGGAGTGGATGGGACGGATTGACCCCTACGACTCGGAAACCCATTACA ACCAGAAGTTCAAGGATCACGTGACCATCTCCGTGGACAAGTCCATTTCCACTGCGTACCT CCAGTGGTCAAGCCTGAAGGCCTCCGACACTGCTATGTACTACTGCGCACGCGGAAACTGG GATGATTACTGGGGACAGGGAACAACCGTGACTGTGTCCTCCGGGGGTGGCGGTAGCGGAG GAGGGGGCTCCGGCGGCGGCGGCTCAGGGGGCGGAGGAAGCGACGTCGTGATGACCCAGTC ACCGGCATTCCTGTCCGTGACTCCCGGAGAAAAGGTCACGATTACTTGCCGGGCGTCCAAG AGCATCTCCAAGGACCTCGCCTGGTACCAACAGAAGCCGGACCAGGCCCCTAAGCTGTTGA TCTACTCGGGGTCCACCCTTCAATCGGGAGTGCCATCGCGGTTTAGCGGTTCGGGTTCTGG GACCGACTTCACTTTCACCATCTCCTCACTGGAAGCCGAGGATGCCGCCACTTACTACTGT CAGCAGCACAACAAGTATCCGTACACCTTCGGAGGCGGTACCAAAGTGGAGATCAAGACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-19 AA	2143	MALPVTALLLPLALLLHAARPEVQLVQSGAEVKKPGESLRISCKGSGYTFTSYWMNWVRQ MPGKGLEWMGRIDPYDSETHYNQKFKDHVTISVDKSISTAYLQWSSLKASDTAMYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVVMTQSPAFLSVTPGEKVTITCR ASKSISKDLAWYQQKPDQAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTFTISSLEAEDAA TYYCQQHNKYPYTFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-19 scFv	2202	MALPVTALLLPLALLLHAARPEVQLVQSGAEVKKPGESLRISCKGSGYTFTSYWMNWVRQ MPGKGLEWMGRIDPYDSETHYNQKFKDHVTISVDKSISTAYLQWSSLKASDTAMYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVVMTQSPAFLSVTPGEKVTITCR ASKSISKDLAWYQQKPDQAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTFTISSLEAEDAA TYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-19 VH	2261	EVQLVQSGAEVKKPGESLRISCKGSGYTFTSYWMNWVRQMPGKGLEWMGRIDPYDSETHYN QKFKDHVTISVDKSISTAYLQWSSLKASDTAMYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-19 VL	2320	DVVMTQSPAFLSVTPGEKVTITCRASKSISKDLAWYQQKPDQAPKLLIYSGSTLQSGVPSR FSGSGSGTDFTFTISSLEAEDAATYYCQQHNKYPYTFGGGTKVEIK

hzCAR12 3-20 NT	2085	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCGAGGTGCAGCTGGTGCAGAGCGGAGCCGAGGTCAAGAAGCCTGGAGAATCCCTGAGGAT CAGCTGCAAAGGCAGCGGGTATACCTTCACCTCCTACTGGATGAATTGGGTCCGCCAGATG CCCGGAAAAGGCCTGGAGTGGATGGGACGGATTGACCCCTACGACTCGGAAACCCATTACA ACCAGAAGTTCAAGGATCACGTGACCATCTCCGTGGACAAGTCCATTTCCACTGCGTACCT CCAGTGGTCAAGCCTGAAGGCCTCCGACACTGCTATGTACTACTGCGCACGCGGAAACTGG GATGATTACTGGGGACAGGGAACAACCGTGACTGTGTCCTCCGGGGGTGGCGGTAGCGGAG GAGGGGGCTCCGGCGGCGGCGGCTCAGGGGGCGGAGGAAGCGACGTGGTCATGACTCAGTC CCCGGACTCACTCGCGGTGTCGCTTGGAGAGAGAGCGACCATCAACTGTCGGGCCTCAAAG AGCATCAGCAAGGACCTGGCCTGGTACCAGCAGAAGCCGGGACAGCCGCCAAAGCTGCTGA TCTACTCCGGGTCCACCTTGCAATCTGGTGTCCCTGACCGGTTCTCCGGTTCCGGGTCGGG TACCGACTTCACGCTCACTATTTCGTCGCTGCAAGCCGAAGATGTGGCCGTGTACTATTGC CAACAGCACAACAAGTACCCCTACACTTTTGGCGGAGGCACCAAGGTGGAAATCAAGACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-20 AA	2144	MALPVTALLLPLALLLHAARPEVQLVQSGAEVKKPGESLRISCKGSGYTFTSYWMNWVRQ MPGKGLEWMGRIDPYDSETHYNQKFKDHVTISVDKSISTAYLQWSSLKASDTAMYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVVMTQSPDSLAVSLGERATINCR ASKSISKDLAWYQQKPGQPPKLLIYSGSTLQSGVPDRFSGSGSGTDFTLTISSLQAEDVA VYYCQQHNKYPYTFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-20 scFv	2203	MALPVTALLLPLALLLHAARPEVQLVQSGAEVKKPGESLRISCKGSGYTFTSYWMNWVRQ MPGKGLEWMGRIDPYDSETHYNQKFKDHVTISVDKSISTAYLQWSSLKASDTAMYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVVMTQSPDSLAVSLGERATINCR ASKSISKDLAWYQQKPGQPPKLLIYSGSTLQSGVPDRFSGSGSGTDFTLTISSLQAEDVA VYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-20 VH	2262	EVQLVQSGAEVKKPGESLRISCKGSGYTFTSYWMNWVRQMPGKGLEWMGRIDPYDSETHYN QKFKDHVTISVDKSISTAYLQWSSLKASDTAMYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-20 VL	2321	DVVMTQSPDSLAVSLGERATINCRASKSISKDLAWYQQKPGQPPKLLIYSGSTLQSGVPDR FSGSGSGTDFTLTISSLQAEDVAVYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-21 NT	2086	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCGACGTGCAGCTCACCCAGTCGCCCTCATTTCTGTCGGCCTCAGTGGGAGACAGAGTGAC CATTACTTGTCGGGCCTCCAAGAGCATCTCCAAGGACCTGGCCTGGTATCAGCAGAAGCCA GGAAAGGCGCCTAAGTTGCTCATCTACTCGGGGTCGACCCTGCAATCTGGCGTGCCGTCCC GGTTCTCCGGTTCGGGAAGCGGTACCGAATTCACCCTTACTATCTCCTCCCTGCAACCGGA GGACTTCGCCACCTACTACTGCCAACAGCACAACAAGTACCCGTACACTTTCGGGGGTGGC

		ACGAAGGTCGAAATCAAGGGGGGTGGCGGTAGCGGAGGAGGGGGCTCCGGCGGCGGCGGCT CAGGGGGCGGAGGAAGCGAGGTGCAGCTGGTGCAGAGCGGAGCCGAGGTCAAGAAGCCTGG AGAATCCCTGAGGATCAGCTGCAAAGGCAGCGGGTATACCTTCACCTCCTACTGGATGAAT TGGGTCCGCCAGATGCCCGGAAAAGGCCTGGAGTGGATGGGACGGATTGACCCCTACGACT CGGAAACCCATTACAACCAGAAGTTCAAGGATCACGTGACCATCTCCGTGGACAAGTCCAT TTCCACTGCGTACCTCCAGTGGTCAAGCCTGAAGGCCTCCGACACTGCTATGTACTACTGC GCACGCGGAAACTGGGATGATTACTGGGGACAGGGAACAACCGTGACTGTGTCCTCCACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-21 AA	2145	MALPVTALLLPLALLLHAARPDVQLTQSPSFLSASVGDRVTITCRASKSISKDLAWYQQK PGKAPKLLIYSGSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVQSGAEVKKPGESLRISCKGSGYTFTSY WMNWVRQMPGKGLEWMGRIDPYDSETHYNQKFKDHVTISVDKSISTAYLQWSSLKASDTA MYYCARGNWDDYWGQGTTVTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-21 scFv	2204	MALPVTALLLPLALLLHAARPDVQLTQSPSFLSASVGDRVTITCRASKSISKDLAWYQQK PGKAPKLLIYSGSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVQSGAEVKKPGESLRISCKGSGYTFTSY WMNWVRQMPGKGLEWMGRIDPYDSETHYNQKFKDHVTISVDKSISTAYLQWSSLKASDTA MYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-21 VH	2263	EVQLVQSGAEVKKPGESLRISCKGSGYTFTSYWMNWVRQMPGKGLEWMGRIDPYDSETHYN QKFKDHVTISVDKSISTAYLQWSSLKASDTAMYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-21 VL	2322	DVQLTQSPSFLSASVGDRVTITCRASKSISKDLAWYQQKPGKAPKLLIYSGSTLQSGVPSR FSGSGSGTEFTLTISSLQPEDFATYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-22 NT	2087	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCGAAGTGGTGCTGACCCAGTCGCCCGCAACCCTCTCTCTGTCGCCGGGAGAACGCGCCAC TCTTTCCTGTCGGGCGTCCAAGAGCATCTCAAAGGACCTCGCCTGGTACCAGCAGAAGCCT GGTCAAGCCCCGCGGCTGCTGATCTACTCCGGCTCCACGCTGCAATCAGGAATCCCAGCCA GATTTTCCGGTTCGGGGTCGGGGACTGACTTCACCTTGACCATTAGCTCGCTGGAACCTGA GGACTTCGCCGTGTATTACTGCCAGCAGCACAACAAGTACCCGTACACCTTCGGAGGCGGT ACTAAGGTCGAGATCAAGGGGGGTGGCGGTAGCGGAGGAGGGGGCTCCGGCGGCGGCGGCT CAGGGGGCGGAGGAAGCGAGGTGCAGCTGGTGCAGAGCGGAGCCGAGGTCAAGAAGCCTGG AGAATCCCTGAGGATCAGCTGCAAAGGCAGCGGGTATACCTTCACCTCCTACTGGATGAAT TGGGTCCGCCAGATGCCCGGAAAAGGCCTGGAGTGGATGGGACGGATTGACCCCTACGACT CGGAAACCCATTACAACCAGAAGTTCAAGGATCACGTGACCATCTCCGTGGACAAGTCCAT TTCCACTGCGTACCTCCAGTGGTCAAGCCTGAAGGCCTCCGACACTGCTATGTACTACTGC

		GCACGCGGAAACTGGGATGATTACTGGGGACAGGGAACAACCGTGACTGTGTCCTCCACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-22 AA	2146	MALPVTALLLPLALLLHAARPEVVLTQSPATLSLSPGERATLSCRASKSISKDLAWYQQK PGQAPRLLIYSGSTLQSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVQSGAEVKKPGESLRISCKGSGYTFTSY WMNWVRQMPGKGLEWMGRIDPYDSETHYNQKFKDHVTISVDKSISTAYLQWSSLKASDTA MYYCARGNWDDYWGQGTTVTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-22 scFv	2205	MALPVTALLLPLALLLHAARPEVVLTQSPATLSLSPGERATLSCRASKSISKDLAWYQQK PGQAPRLLIYSGSTLQSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVQSGAEVKKPGESLRISCKGSGYTFTSY WMNWVRQMPGKGLEWMGRIDPYDSETHYNQKFKDHVTISVDKSISTAYLQWSSLKASDTA MYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-22 VH	2264	EVQLVQSGAEVKKPGESLRISCKGSGYTFTSYWMNWVRQMPGKGLEWMGRIDPYDSETHYN QKFKDHVTISVDKSISTAYLQWSSLKASDTAMYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-22 VL	2323	EVVLTQSPATLSLSPGERATLSCRASKSISKDLAWYQQKPGQAPRLLIYSGSTLQSGIPAR FSGSGSGTDFTLTISSLEPEDFAVYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-23 NT	2088	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCGACGTCGTGATGACCCAGTCACCGGCATTCCTGTCCGTGACTCCCGGAGAAAAGGTCAC GATTACTTGCCGGGCGTCCAAGAGCATCTCCAAGGACCTCGCCTGGTACCAACAGAAGCCG GACCAGGCCCCTAAGCTGTTGATCTACTCGGGGTCCACCCTTCAATCGGGAGTGCCATCGC GGTTTAGCGGTTCGGGTTCTGGGACCGACTTCACTTTCACCATCTCCTCACTGGAAGCCGA GGATGCCGCCACTTACTACTGTCAGCAGCACAACAAGTATCCGTACACCTTCGGAGGCGGT ACCAAAGTGGAGATCAAGGGGGGTGGCGGTAGCGGAGGAGGGGGCTCCGGCGGCGGCGGCT CAGGGGGCGGAGGAAGCGAGGTGCAGCTGGTGCAGAGCGGAGCCGAGGTCAAGAAGCCTGG AGAATCCCTGAGGATCAGCTGCAAAGGCAGCGGGTATACCTTCACCTCCTACTGGATGAAT TGGGTCCGCCAGATGCCCGGAAAAGGCCTGGAGTGGATGGGACGGATTGACCCCTACGACT CGGAAACCCATTACAACCAGAAGTTCAAGGATCACGTGACCATCTCCGTGGACAAGTCCAT TTCCACTGCGTACCTCCAGTGGTCAAGCCTGAAGGCCTCCGACACTGCTATGTACTACTGC GCACGCGGAAACTGGGATGATTACTGGGGACAGGGAACAACCGTGACTGTGTCCTCCACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag

		gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-23 AA	2147	MALPVTALLLPLALLLHAARPDVVMTQSPAFLSVTPGEKVTITCRASKSISKDLAWYQQK PDQAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVQSGAEVKKPGESLRISCKGSGYTFTSY WMNWVRQMPGKGLEWMGRIDPYDSETHYNQKFKDHVTISVDKSISTAYLQWSSLKASDTA MYYCARGNWDDYWGQGTTVTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-23 scFv	2206	MALPVTALLLPLALLLHAARPDVVMTQSPAFLSVTPGEKVTITCRASKSISKDLAWYQQK PDQAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVQSGAEVKKPGESLRISCKGSGYTFTSY WMNWVRQMPGKGLEWMGRIDPYDSETHYNQKFKDHVTISVDKSISTAYLQWSSLKASDTA MYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-23 VH	2265	EVQLVQSGAEVKKPGESLRISCKGSGYTFTSYWMNWVRQMPGKGLEWMGRIDPYDSETHYN QKFKDHVTISVDKSISTAYLQWSSLKASDTAMYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-23 VL	2324	DVVMTQSPAFLSVTPGEKVTITCRASKSISKDLAWYQQKPDQAPKLLIYSGSTLQSGVPSR FSGSGSGTDFTFTISSLEAEDAATYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-24 NT	2089	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCGACGTGGTCATGACTCAGTCCCCGGACTCACTCGCGGTGTCGCTTGGAGAGAGAGCGAC CATCAACTGTCGGGCCTCAAAGAGCATCAGCAAGGACCTGGCCTGGTACCAGCAGAAGCCG GGACAGCCGCCAAAGCTGCTGATCTACTCCGGGTCCACCTTGCAATCTGGTGTCCCTGACC GGTTCTCCGGTTCCGGGTCGGGTACCGACTTCACGCTCACTATTTCGTCGCTGCAAGCCGA AGATGTGGCCGTGTACTATTGCCAACAGCACAACAAGTACCCCTACACTTTTGGCGGAGGC ACCAAGGTGGAAATCAAGGGGGGTGGCGGTAGCGGAGGAGGGGGCTCCGGCGGCGGCGGCT CAGGGGGCGGAGGAAGCGAGGTGCAGCTGGTGCAGAGCGGAGCCGAGGTCAAGAAGCCTGG AGAATCCCTGAGGATCAGCTGCAAAGGCAGCGGGTATACCTTCACCTCCTACTGGATGAAT TGGGTCCGCCAGATGCCCGGAAAAGGCCTGGAGTGGATGGGACGGATTGACCCCTACGACT CGGAAACCCATTACAACCAGAAGTTCAAGGATCACGTGACCATCTCCGTGGACAAGTCCAT TTCCACTGCGTACCTCCAGTGGTCAAGCCTGAAGGCCTCCGACACTGCTATGTACTACTGC GCACGCGGAAACTGGGATGATTACTGGGGACAGGGAACAACCGTGACTGTGTCCTCCACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg

hzCAR12 3-24 AA	2148	MALPVTALLLPLALLLHAARPDVVMTQSPDSLAVSLGERATINCRASKSISKDLAWYQQK PGQPPKLLIYSGSTLQSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVQSGAEVKKPGESLRISCKGSGYTFTSY WMNWVRQMPGKGLEWMGRIDPYDSETHYNQKFKDHVTISVDKSISTAYLQWSSLKASDTA MYYCARGNWDDYWGQGTTVTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-24 scFv	2207	MALPVTALLLPLALLLHAARPDVVMTQSPDSLAVSLGERATINCRASKSISKDLAWYQQK PGQPPKLLIYSGSTLQSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVQSGAEVKKPGESLRISCKGSGYTFTSY WMNWVRQMPGKGLEWMGRIDPYDSETHYNQKFKDHVTISVDKSISTAYLQWSSLKASDTA MYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-24 VH	2266	EVQLVQSGAEVKKPGESLRISCKGSGYTFTSYWMNWVRQMPGKGLEWMGRIDPYDSETHYN QKFKDHVTISVDKSISTAYLQWSSLKASDTAMYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-24 VL	2325	DVVMTQSPDSLAVSLGERATINCRASKSISKDLAWYQQKPGQPPKLLIYSGSTLQSGVPDR FSGSGSGTDFTLTISSLQAEDVAVYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-25 NT	2090	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCGAAGTGCAGCTCGTCGAGAGCGGAGGGGGACTGGTGCAGCCCGGAGGAAGCCTGAGGCT GTCCTGCGCTGCCTCCGGCTACACCTTCACCTCCTACTGGATGAACTGGGTCAGACAGGCA CCTGGAAAGGGACTGGTCTGGGTGTCGCGCATTGACCCCTACGACTCCGAAACCCATTACA ATCAGAAATTCAAGGACCGCTTCACCATCTCCGTGGACAAAGCCAAGAGCACCGCGTACCT CCAAATGAACTCCCTGCGCGCTGAGGATACAGCAGTGTACTATTGCGCCCGGGGAAACTGG GATGATTACTGGGGCCAGGGAACTACTGTGACTGTGTCATCCGGGGGTGGCGGTAGCGGAG GAGGGGGCTCCGGCGGCGGCGGCTCAGGGGGCGGAGGAAGCGACGTGCAGCTCACCCAGTC GCCCTCATTTCTGTCGGCCTCAGTGGGAGACAGAGTGACCATTACTTGTCGGGCCTCCAAG AGCATCTCCAAGGACCTGGCCTGGTATCAGCAGAAGCCAGGAAAGGCGCCTAAGTTGCTCA TCTACTCGGGGTCGACCCTGCAATCTGGCGTGCCGTCCCGGTTCTCCGGTTCGGGAAGCGG TACCGAATTCACCCTTACTATCTCCTCCCTGCAACCGGAGGACTTCGCCACCTACTACTGC CAACAGCACAACAAGTACCCGTACACTTTCGGGGGTGGCACGAAGGTCGAAATCAAGACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-25 AA	2149	MALPVTALLLPLALLLHAARPEVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMNWVRQ APGKGLVWVSRIDPYDSETHYNQKFKDRFTISVDKAKSTAYLQMNSLRAEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVQLTQSPSFLSASVGDRVTITCR ASKSISKDLAWYQQKPGKAPKLLIYSGSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFA TYYCQQHNKYPYTFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC

		SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-25 scFv	2208	MALPVTALLLPLALLLHAARPEVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMNWVRQ APGKGLVWVSRIDPYDSETHYNQKFKDRFTISVDKAKSTAYLQMNSLRAEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVQLTQSPSFLSASVGDRVTITCR ASKSISKDLAWYQQKPGKAPKLLIYSGSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFA TYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-25 VH	2267	EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMNWVRQAPGKGLVWVSRIDPYDSETHYN QKFKDRFTISVDKAKSTAYLQMNSLRAEDTAVYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-25 VL	2326	DVQLTQSPSFLSASVGDRVTITCRASKSISKDLAWYQQKPGKAPKLLIYSGSTLQSGVPSR FSGSGSGTEFTLTISSLQPEDFATYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-26 NT	2091	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCGAAGTGCAGCTCGTCGAGAGCGGAGGGGGACTGGTGCAGCCCGGAGGAAGCCTGAGGCT GTCCTGCGCTGCCTCCGGCTACACCTTCACCTCCTACTGGATGAACTGGGTCAGACAGGCA CCTGGAAAGGGACTGGTCTGGGTGTCGCGCATTGACCCCTACGACTCCGAAACCCATTACA ATCAGAAATTCAAGGACCGCTTCACCATCTCCGTGGACAAAGCCAAGAGCACCGCGTACCT CCAAATGAACTCCCTGCGCGCTGAGGATACAGCAGTGTACTATTGCGCCCGGGGAAACTGG GATGATTACTGGGGCCAGGGAACTACTGTGACTGTGTCATCCGGGGGTGGCGGTAGCGGAG GAGGGGGCTCCGGCGGCGGCGGCTCAGGGGGCGGAGGAAGCGAAGTGGTGCTGACCCAGTC GCCCGCAACCCTCTCTCTGTCGCCGGGAGAACGCGCCACTCTTTCCTGTCGGGCGTCCAAG AGCATCTCAAAGGACCTCGCCTGGTACCAGCAGAAGCCTGGTCAAGCCCCGCGGCTGCTGA TCTACTCCGGCTCCACGCTGCAATCAGGAATCCCAGCCAGATTTTCCGGTTCGGGGTCGGG GACTGACTTCACCTTGACCATTAGCTCGCTGGAACCTGAGGACTTCGCCGTGTATTACTGC CAGCAGCACAACAAGTACCCGTACACCTTCGGAGGCGGTACTAAGGTCGAGATCAAGACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-26 AA	2150	MALPVTALLLPLALLLHAARPEVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMNWVRQ APGKGLVWVSRIDPYDSETHYNQKFKDRFTISVDKAKSTAYLQMNSLRAEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSEVVLTQSPATLSLSPGERATLSCR ASKSISKDLAWYQQKPGQAPRLLIYSGSTLQSGIPARFSGSGSGTDFTLTISSLEPEDFA VYYCQQHNKYPYTFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-26	2209	MALPVTALLLPLALLLHAARPEVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMNWVRQ APGKGLVWVSRIDPYDSETHYNQKFKDRFTISVDKAKSTAYLQMNSLRAEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSEVVLTQSPATLSLSPGERATLSCR

scFv		ASKSISKDLAWYQQKPGQAPRLLIYSGSTLQSGIPARFSGSGSGTDFTLTISSLEPEDFA VYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-26 VH	2268	EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMNWVRQAPGKGLVWVSRIDPYDSETHYN QKFKDRFTISVDKAKSTAYLQMNSLRAEDTAVYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-26 VL	2327	EVVLTQSPATLSLSPGERATLSCRASKSISKDLAWYQQKPGQAPRLLIYSGSTLQSGIPAR FSGSGSGTDFTLTISSLEPEDFAVYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-27 NT	2092	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCGAAGTGCAGCTCGTCGAGAGCGGAGGGGGACTGGTGCAGCCCGGAGGAAGCCTGAGGCT GTCCTGCGCTGCCTCCGGCTACACCTTCACCTCCTACTGGATGAACTGGGTCAGACAGGCA CCTGGAAAGGGACTGGTCTGGGTGTCGCGCATTGACCCCTACGACTCCGAAACCCATTACA ATCAGAAATTCAAGGACCGCTTCACCATCTCCGTGGACAAAGCCAAGAGCACCGCGTACCT CCAAATGAACTCCCTGCGCGCTGAGGATACAGCAGTGTACTATTGCGCCCGGGGAAACTGG GATGATTACTGGGGCCAGGGAACTACTGTGACTGTGTCATCCGGGGGTGGCGGTAGCGGAG GAGGGGGCTCCGGCGGCGGCGGCTCAGGGGGCGGAGGAAGCGACGTCGTGATGACCCAGTC ACCGGCATTCCTGTCCGTGACTCCCGGAGAAAAGGTCACGATTACTTGCCGGGCGTCCAAG AGCATCTCCAAGGACCTCGCCTGGTACCAACAGAAGCCGGACCAGGCCCCTAAGCTGTTGA TCTACTCGGGGTCCACCCTTCAATCGGGAGTGCCATCGCGGTTTAGCGGTTCGGGTTCTGG GACCGACTTCACTTTCACCATCTCCTCACTGGAAGCCGAGGATGCCGCCACTTACTACTGT CAGCAGCACAACAAGTATCCGTACACCTTCGGAGGCGGTACCAAAGTGGAGATCAAGACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-27 AA	2151	MALPVTALLLPLALLLHAARPEVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMNWVRQ APGKGLVWVSRIDPYDSETHYNQKFKDRFTISVDKAKSTAYLQMNSLRAEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVVMTQSPAFLSVTPGEKVTITCR ASKSISKDLAWYQQKPDQAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTFTISSLEAEDAA TYYCQQHNKYPYTFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-27 scFv	2210	MALPVTALLLPLALLLHAARPEVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMNWVRQ APGKGLVWVSRIDPYDSETHYNQKFKDRFTISVDKAKSTAYLQMNSLRAEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVVMTQSPAFLSVTPGEKVTITCR ASKSISKDLAWYQQKPDQAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTFTISSLEAEDAA TYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-27 VH	2269	EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMNWVRQAPGKGLVWVSRIDPYDSETHYN QKFKDRFTISVDKAKSTAYLQMNSLRAEDTAVYYCARGNWDDYWGQGTTVTVSS

hzCAR12 3-27 VL	2328	DVVMTQSPAFLSVTPGEKVTITCRASKSISKDLAWYQQKPDQAPKLLIYSGSTLQSGVPSR FSGSGSGTDFTFTISSLEAEDAATYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-28 NT	2093	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCGAAGTGCAGCTCGTCGAGAGCGGAGGGGGACTGGTGCAGCCCGGAGGAAGCCTGAGGCT GTCCTGCGCTGCCTCCGGCTACACCTTCACCTCCTACTGGATGAACTGGGTCAGACAGGCA CCTGGAAAGGGACTGGTCTGGGTGTCGCGCATTGACCCCTACGACTCCGAAACCCATTACA ATCAGAAATTCAAGGACCGCTTCACCATCTCCGTGGACAAAGCCAAGAGCACCGCGTACCT CCAAATGAACTCCCTGCGCGCTGAGGATACAGCAGTGTACTATTGCGCCCGGGGAAACTGG GATGATTACTGGGGCCAGGGAACTACTGTGACTGTGTCATCCGGGGGTGGCGGTAGCGGAG GAGGGGGCTCCGGCGGCGGCGGCTCAGGGGGCGGAGGAAGCGACGTGGTCATGACTCAGTC CCCGGACTCACTCGCGGTGTCGCTTGGAGAGAGAGCGACCATCAACTGTCGGGCCTCAAAG AGCATCAGCAAGGACCTGGCCTGGTACCAGCAGAAGCCGGGACAGCCGCCAAAGCTGCTGA TCTACTCCGGGTCCACCTTGCAATCTGGTGTCCCTGACCGGTTCTCCGGTTCCGGGTCGGG TACCGACTTCACGCTCACTATTTCGTCGCTGCAAGCCGAAGATGTGGCCGTGTACTATTGC CAACAGCACAACAAGTACCCCTACACTTTTGGCGGAGGCACCAAGGTGGAAATCAAGACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-28 AA	2152	MALPVTALLLPLALLLHAARPEVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMNWVRQ APGKGLVWVSRIDPYDSETHYNQKFKDRFTISVDKAKSTAYLQMNSLRAEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVVMTQSPDSLAVSLGERATINCR ASKSISKDLAWYQQKPGQPPKLLIYSGSTLQSGVPDRFSGSGSGTDFTLTISSLQAEDVA VYYCQQHNKYPYTFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-28 scFv	2211	MALPVTALLLPLALLLHAARPEVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMNWVRQ APGKGLVWVSRIDPYDSETHYNQKFKDRFTISVDKAKSTAYLQMNSLRAEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVVMTQSPDSLAVSLGERATINCR ASKSISKDLAWYQQKPGQPPKLLIYSGSTLQSGVPDRFSGSGSGTDFTLTISSLQAEDVA VYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-28 VH	2270	EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMNWVRQAPGKGLVWVSRIDPYDSETHYN QKFKDRFTISVDKAKSTAYLQMNSLRAEDTAVYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-28 VL	2329	DVVMTQSPDSLAVSLGERATINCRASKSISKDLAWYQQKPGQPPKLLIYSGSTLQSGVPDR FSGSGSGTDFTLTISSLQAEDVAVYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-29 NT	2094	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCGACGTGCAGCTCACCCAGTCGCCCTCATTTCTGTCGGCCTCAGTGGGAGACAGAGTGAC CATTACTTGTCGGGCCTCCAAGAGCATCTCCAAGGACCTGGCCTGGTATCAGCAGAAGCCA

		GGAAAGGCGCCTAAGTTGCTCATCTACTCGGGGTCGACCCTGCAATCTGGCGTGCCGTCCC GGTTCTCCGGTTCGGGAAGCGGTACCGAATTCACCCTTACTATCTCCTCCCTGCAACCGGA GGACTTCGCCACCTACTACTGCCAACAGCACAACAAGTACCCGTACACTTTCGGGGGTGGC ACGAAGGTCGAAATCAAGGGGGGTGGCGGTAGCGGAGGAGGGGGCTCCGGCGGCGGCGGCT CAGGGGGCGGAGGAAGCGAAGTGCAGCTCGTCGAGAGCGGAGGGGGACTGGTGCAGCCCGG AGGAAGCCTGAGGCTGTCCTGCGCTGCCTCCGGCTACACCTTCACCTCCTACTGGATGAAC TGGGTCAGACAGGCACCTGGAAAGGGACTGGTCTGGGTGTCGCGCATTGACCCCTACGACT CCGAAACCCATTACAATCAGAAATTCAAGGACCGCTTCACCATCTCCGTGGACAAAGCCAA GAGCACCGCGTACCTCCAAATGAACTCCCTGCGCGCTGAGGATACAGCAGTGTACTATTGC GCCCGGGGAAACTGGGATGATTACTGGGGCCAGGGAACTACTGTGACTGTGTCATCCACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-29 AA	2153	MALPVTALLLPLALLLHAARPDVQLTQSPSFLSASVGDRVTITCRASKSISKDLAWYQQK PGKAPKLLIYSGSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGYTFTSY WMNWVRQAPGKGLVWVSRIDPYDSETHYNQKFKDRFTISVDKAKSTAYLQMNSLRAEDTA VYYCARGNWDDYWGQGTTVTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-29 scFv	2212	MALPVTALLLPLALLLHAARPDVQLTQSPSFLSASVGDRVTITCRASKSISKDLAWYQQK PGKAPKLLIYSGSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGYTFTSY WMNWVRQAPGKGLVWVSRIDPYDSETHYNQKFKDRFTISVDKAKSTAYLQMNSLRAEDTA VYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-29 VH	2271	EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMNWVRQAPGKGLVWVSRIDPYDSETHYN QKFKDRFTISVDKAKSTAYLQMNSLRAEDTAVYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-29 VL	2330	DVQLTQSPSFLSASVGDRVTITCRASKSISKDLAWYQQKPGKAPKLLIYSGSTLQSGVPSR FSGSGSGTEFTLTISSLQPEDFATYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-30 NT	2095	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCGAAGTGGTGCTGACCCAGTCGCCCGCAACCCTCTCTCTGTCGCCGGGAGAACGCGCCAC TCTTTCCTGTCGGGCGTCCAAGAGCATCTCAAAGGACCTCGCCTGGTACCAGCAGAAGCCT GGTCAAGCCCCGCGGCTGCTGATCTACTCCGGCTCCACGCTGCAATCAGGAATCCCAGCCA GATTTTCCGGTTCGGGGTCGGGGACTGACTTCACCTTGACCATTAGCTCGCTGGAACCTGA GGACTTCGCCGTGTATTACTGCCAGCAGCACAACAAGTACCCGTACACCTTCGGAGGCGGT ACTAAGGTCGAGATCAAGGGGGGTGGCGGTAGCGGAGGAGGGGGCTCCGGCGGCGGCGGCT CAGGGGGCGGAGGAAGCGAAGTGCAGCTCGTCGAGAGCGGAGGGGGACTGGTGCAGCCCGG AGGAAGCCTGAGGCTGTCCTGCGCTGCCTCCGGCTACACCTTCACCTCCTACTGGATGAAC

		TGGGTCAGACAGGCACCTGGAAAGGGACTGGTCTGGGTGTCGCGCATTGACCCCTACGACT CCGAAACCCATTACAATCAGAAATTCAAGGACCGCTTCACCATCTCCGTGGACAAAGCCAA GAGCACCGCGTACCTCCAAATGAACTCCCTGCGCGCTGAGGATACAGCAGTGTACTATTGC GCCCGGGGAAACTGGGATGATTACTGGGGCCAGGGAACTACTGTGACTGTGTCATCCACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-30 AA	2154	MALPVTALLLPLALLLHAARPEVVLTQSPATLSLSPGERATLSCRASKSISKDLAWYQQK PGQAPRLLIYSGSTLQSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGYTFTSY WMNWVRQAPGKGLVWVSRIDPYDSETHYNQKFKDRFTISVDKAKSTAYLQMNSLRAEDTA VYYCARGNWDDYWGQGTTVTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-30 scFv	2213	MALPVTALLLPLALLLHAARPEVVLTQSPATLSLSPGERATLSCRASKSISKDLAWYQQK PGQAPRLLIYSGSTLQSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGYTFTSY WMNWVRQAPGKGLVWVSRIDPYDSETHYNQKFKDRFTISVDKAKSTAYLQMNSLRAEDTA VYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-30 VH	2272	EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMNWVRQAPGKGLVWVSRIDPYDSETHYN QKFKDRFTISVDKAKSTAYLQMNSLRAEDTAVYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-30 VL	2331	EVVLTQSPATLSLSPGERATLSCRASKSISKDLAWYQQKPGQAPRLLIYSGSTLQSGIPAR FSGSGSGTDFTLTISSLEPEDFAVYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-31 NT	2096	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCGACGTCGTGATGACCCAGTCACCGGCATTCCTGTCCGTGACTCCCGGAGAAAAGGTCAC GATTACTTGCCGGGCGTCCAAGAGCATCTCCAAGGACCTCGCCTGGTACCAACAGAAGCCG GACCAGGCCCCTAAGCTGTTGATCTACTCGGGGTCCACCCTTCAATCGGGAGTGCCATCGC GGTTTAGCGGTTCGGGTTCTGGGACCGACTTCACTTTCACCATCTCCTCACTGGAAGCCGA GGATGCCGCCACTTACTACTGTCAGCAGCACAACAAGTATCCGTACACCTTCGGAGGCGGT ACCAAAGTGGAGATCAAGGGGGGTGGCGGTAGCGGAGGAGGGGGCTCCGGCGGCGGCGGCT CAGGGGGCGGAGGAAGCGAAGTGCAGCTCGTCGAGAGCGGAGGGGGACTGGTGCAGCCCGG AGGAAGCCTGAGGCTGTCCTGCGCTGCCTCCGGCTACACCTTCACCTCCTACTGGATGAAC TGGGTCAGACAGGCACCTGGAAAGGGACTGGTCTGGGTGTCGCGCATTGACCCCTACGACT CCGAAACCCATTACAATCAGAAATTCAAGGACCGCTTCACCATCTCCGTGGACAAAGCCAA GAGCACCGCGTACCTCCAAATGAACTCCCTGCGCGCTGAGGATACAGCAGTGTACTATTGC GCCCGGGGAAACTGGGATGATTACTGGGGCCAGGGAACTACTGTGACTGTGTCATCCACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc

		gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR12 3-31 AA	2155	MALPVTALLLPLALLLHAARPDVVMTQSPAFLSVTPGEKVTITCRASKSISKDLAWYQQK PDQAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGYTFTSY WMNWVRQAPGKGLVWVSRIDPYDSETHYNQKFKDRFTISVDKAKSTAYLQMNSLRAEDTA VYYCARGNWDDYWGQGTTVTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR12 3-31 scFv	2214	MALPVTALLLPLALLLHAARPDVVMTQSPAFLSVTPGEKVTITCRASKSISKDLAWYQQK PDQAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGYTFTSY WMNWVRQAPGKGLVWVSRIDPYDSETHYNQKFKDRFTISVDKAKSTAYLQMNSLRAEDTA VYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-31 VH	2273	EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMNWVRQAPGKGLVWVSRIDPYDSETHYN QKFKDRFTISVDKAKSTAYLQMNSLRAEDTAVYYCARGNWDDYWGQGTTVTVSS
hzCAR12 3-31 VL	2332	DVVMTQSPAFLSVTPGEKVTITCRASKSISKDLAWYQQKPDQAPKLLIYSGSTLQSGVPSR FSGSGSGTDFTFTISSLEAEDAATYYCQQHNKYPYTFGGGTKVEIK
hzCAR12 3-32 NT	2097	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGC CCGACGTGGTCATGACTCAGTCCCCGGACTCACTCGCGGTGTCGCTTGGAGAGAGAGCGAC CATCAACTGTCGGGCCTCAAAGAGCATCAGCAAGGACCTGGCCTGGTACCAGCAGAAGCCG GGACAGCCGCCAAAGCTGCTGATCTACTCCGGGTCCACCTTGCAATCTGGTGTCCCTGACC GGTTCTCCGGTTCCGGGTCGGGTACCGACTTCACGCTCACTATTTCGTCGCTGCAAGCCGA AGATGTGGCCGTGTACTATTGCCAACAGCACAACAAGTACCCCTACACTTTTGGCGGAGGC ACCAAGGTGGAAATCAAGGGGGGTGGCGGTAGCGGAGGAGGGGGCTCCGGCGGCGGCGGCT CAGGGGGCGGAGGAAGCGAAGTGCAGCTCGTCGAGAGCGGAGGGGGACTGGTGCAGCCCGG AGGAAGCCTGAGGCTGTCCTGCGCTGCCTCCGGCTACACCTTCACCTCCTACTGGATGAAC TGGGTCAGACAGGCACCTGGAAAGGGACTGGTCTGGGTGTCGCGCATTGACCCCTACGACT CCGAAACCCATTACAATCAGAAATTCAAGGACCGCTTCACCATCTCCGTGGACAAAGCCAA GAGCACCGCGTACCTCCAAATGAACTCCCTGCGCGCTGAGGATACAGCAGTGTACTATTGC GCCCGGGGAAACTGGGATGATTACTGGGGCCAGGGAACTACTGTGACTGTGTCATCCACCA CTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCT GCGTCCGGAggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttc gcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcac tcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacc cttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagag gaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcct acaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacga cgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaat

		ccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgaga ttggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcag caccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
hzCAR123-32 AA	2156	MALPVTALLLPLALLLHAARPDVVMTQSPDSLAVSLGERATINCRASKSISKDLAWYQQK PGQPPKLLIYSGSTLQSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGYTFTSY WMNWVRQAPGKGLVWVSRIDPYDSETHYNQKFKDRFTISVDKAKSTAYLQMNSLRAEDTA VYYCARGNWDDYWGQGTTVTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
hzCAR123-32 scFv	2215	MALPVTALLLPLALLLHAARPDVVMTQSPDSLAVSLGERATINCRASKSISKDLAWYQQK PGQPPKLLIYSGSTLQSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGYTFTSY WMNWVRQAPGKGLVWVSRIDPYDSETHYNQKFKDRFTISVDKAKSTAYLQMNSLRAEDTA VYYCARGNWDDYWGQGTTVTVSS
hzCAR123-32 VH	2274	EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMNWVRQAPGKGLVWVSRIDPYDSETHYN QKFKDRFTISVDKAKSTAYLQMNSLRAEDTAVYYCARGNWDDYWGQGTTVTVSS
hzCAR123-32 VL	2333	DVVMTQSPDSLAVSLGERATINCRASKSISKDLAWYQQKPGQPPKLLIYSGSTLQSGVPDR FSGSGSGTDFTLTISSLQAEDVAVYYCQQHNKYPYTFGGGTKVEIK

In embodiments, a CAR molecule described herein comprises a scFv that specifically binds to CD123, and does not contain a leader sequence, e.g., the amino acid sequence SEQ ID NO: 2. Table 28 below provides amino acid and nucleotide sequences for CD123 scFv sequences that do not contain a leader sequence SEQ ID NO: 2.

Table 28. CD123 CAR scFv sequences

Name	SEQ ID NO:	Sequence
CAR123-2 scFv - NT	2479	CAAGTGCAACTCGTCCAAAGCGGAGCGGAAGTCAAGAAACCCGGAGCGAGCGTGAAAGTG TCCTGCAAAGCCTCCGGCTACACCTTTACGGGCTACTACATGCACTGGGTGCGCCAGGCA CCAGGACAGGGTCTTGAATGGATGGGATGGATCAACCCTAATTCGGGCGGAACTAACTAC GCACAGAAGTTCCAGGGGAGAGTGACTCTGACTCGGGATACCTCCATCTCAACTGTCTAC ATGGAACTCTCCCGCTTGCGGTCAGATGATACGGCAGTGTACTACTGCGCCCGCGACATG AATATCCTGGCTACCGTGCCGTTCGACATCTGGGGACAGGGGACTATGGTTACTGTCTCA TCGGGCGGTGGAGGTTCAGGAGGAGGCGGCTCGGGAGGCGGAGGTTCGGACATTCAGATG ACCCAGTCCCCATCCTCTCTGTCGGCCAGCGTCGGAGATAGGGTGACCATTACCTGTCGG GCCTCGCAAAGCATCTCCTCGTACCTCAACTGGTATCAGCAAAAGCCGGGAAAGGCGCCT AAGCTGCTGATCTACGCCGCTTCGAGCTTGCAAAGCGGGGTGCCATCCAGATTCTCGGGA TCAGGCTCAGGAACCGACTTCACCCTGACCGTGAACAGCCTCCAGCCGGAGGACTTTGCC ACTTACTACTGCCAGCAGGGAGACTCCGTGCCGCTTACTTTCGGGGGGGGTACCCGCCTG GAGATCAAG

CAR123-2 scFv - AA	2480	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTLTRDTSISTVYMELSRLRSDDTAVYYCARDMNILATVPFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTVNSLQPEDFATYYCQQGDSVPLTFGGGTRLEIK
CAR123-2 ORF-free NT	2481	atggccctccctgtcaccgccctgctgcttccgctggctcttctgctccacgccgctcggccccaagtgcaactcgtccaaagcggagcggaagtcaagaaacccggagcgagcgtgaaagtgtcctgcaaagcctccggctacacctttacgggctactacatgcactgggtgcgccaggcaccaggacagggtcttgaatggatgggatggatcaaccctaattcgggcggaactaactacgcacagaagttccaggggagagtgactctgactcgggatacctccatctcaactgtctacatggaactctcccgcttgcggtcagatgatacggcagtgtactactgcgcccgcgacatgaatatcctggctaccgtgccgttcgacatctggggacaggggactatggttactgtctcatcgggcggtggaggttcaggaggaggcggctcgggaggcggaggttcggacattcagatgacccagtccccatcctctctgtcggccagcgtcggagatagggtgaccattacctgtcgggcctcgcaaagcatctcctcgtacctcaactggtatcagcaaaagccgggaaaggcgcctaagctgctgatctacgccgcttcgagcttgcaaagcggggtgccatccagattctcgggatcaggctcaggaaccgacttcaccctgaccgtgaacagcctccagccggaggactttgccacttactactgccagcagggagactccgtgccgcttactttcgggggggggtacccgcctggagatcaagaccactaccccagcaccgaggccacccaccccggctcctaccatcgcctcccagcctctgtccctgcgtccggaggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttcgcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcactcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacccttcatgaggcctgtgcagactactcaagaggaggacggctgttcttgccggttcccagaggaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagacgctccagcctacaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacgacgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaatccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgagattggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcagcaccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcggtaagtcgacagctcgctttcttgctgtccaatttctattaaaggttcctttgttccctaagtccaactactaaactgggggatattatgaagggccttgagcatctggattctgcctaataaaaaacatttattttcattgctgcgtcgagagctcgctttcttgctgtccaatttctattaaaggttcctttgttccctaagtccaactactaaactgggggatattatgaagggccttgagcatctggattctgcctaataaaaaacatttattttcattgctgcctcgacgaattc
CAR123-3 scFv - NT	2482	CAAGTCCAACTCGTTCAATCCGGCGCAGAAGTCAAGAAGCCAGGAGCATCAGTGAAAGTGTCCTGCAAAGCCTCAGGCTACATCTTCACGGGATACTACATCCACTGGGTGCGCCAGGCTCCGGGCCAGGGCCTTGAGTGGATGGGCTGGATCAACCCTAACTCTGGGGGAACCAACTACGCTCAGAAGTTCCAGGGGAGGGTCACTATGACTCGCGATACCTCCATCTCCACTGCGTACATGGAACTCTCGGGACTGAGATCCGACGATCCTGCCGTGTACTACTGCGCCCGGGACATGAACATCTTGGCGACCGTGCCGTTTGACATTTGGGGACAGGGCACCCTCGTCACTGTGTCGAGCGGTGGAGGAGGCTCGGGGGGTGGCGGATCAGGAGGGGGAGGAAGCGACATCCAGCTGACTCAGAGCCCATCGTCGTTGTCCGCGTCGGTGGGGGATAGAGTGACCATTACTTGCCGCGCCAGCCAGAGCATCTCATCATATCTGAATTGGTACCAGCAGAAGCCCGGAAAGGCCCCAAAACTGCTGATCTACGCTGCAAGCAGCCTCCAATCGGGAGTGCCGTCACGGTTCTCCGGGTCCGGTTCGGGAACTGACTTTACCCTGACCGTGAATTCGCTGCAACCGGAGGATTTCGCCACGTACTACTGTCAGCAAGGAGACTCCGTGCCGCTGACCTTCGGTGGAGGCACCAAGGTCGAAATCAAG
CAR123-3 scFv - AA	2483	QVQLVQSGAEVKKPGASVKVSCKASGYIFTGYYIHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSGLRSDDPAVYYCARDMNILATVPFDIWGQGTLVTVSSGGGGSGGGGSGGGGSDIQLTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTVNSLQPEDFATYYCQQGDSVPLTFGGGTKVEIK
CAR123-4 scFv - NT	2484	CAAGTCCAACTCCAACAGTCAGGCGCAGAAGTGAAAAAGAGCGGTGCATCGGTGAAAGTGTCATGCAAAGCCTCGGGCTACACCTTCACTGACTACTATATGCACTGGCTGCGGCAGGCACCGGGACAGGGACTTGAGTGGATGGGATGGATCAACCCGAATTCAGGGGACACTAACTACGCGCAGAAGTTCCAGGGGAGAGTGACCCTGACGAGGGACACCTCAATTTCGACCGTCTACATGGAATTGTCGCGCCTGAGATCGGACGATACTGCTGTGTACTACTGTGCCCGCGACATG

		AACATCCTCGCGACTGTGCCTTTTGATATCTGGGGACAGGGGACTATGGTCACCGTTTCC TCCGCTTCCGGTGGCGGAGGCTCGGGAGGCCGGGCCTCCGGTGGAGGAGGCAGCGACATC CAGATGACTCAGAGCCCTTCCTCGCTGAGCGCCTCAGTGGGAGATCGCGTGACCATCACT TGCCGGGCCAGCCAGTCCATTTCGTCCTACCTCAATTGGTACCAGCAGAAGCCGGGAAAG GCGCCCAAGCTCTTGATCTACGCTGCGAGCTCCCTGCAAAGCGGGGTGCCGAGCCGATTC TCGGGTTCCGGCTCGGGAACCGACTTCACTCTGACCATCTCATCCCTGCAACCAGAGGAC TTTGCCACCTACTACTGCCAACAAGGAGATTCTGTCCCACTGACGTTCGGCGGAGGAACC AAGGTCGAAATCAAG
CAR123-4 scFv - AA	2485	QVQLQQSGAEVKKSGASVKVSCKASGYTFTDYYMHWLRQAPGQGLEWMGWINPNSGDTNY AQKFQGRVTLTRDTSISTVYMELSRLRSDDTAVYYCARDMNILATVPFDIWGQGTMVTVS SASGGGGSGGRASGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGK APKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGDSVPLTFGGGT KVEIK
CAR123-1 scFv - AA	2478	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY AQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARDMNILATVPFDIWGQGTMVTVS SGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISTYLNWYQQKPGKAP NLLIYAAFSLQSGVPSRFSGSGSGTDFTLTINSLQPEDFATYYCQQGDSVPLTFGGGTKL EIK
hzCAR123-1 scFv	2556	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQAPGQGLEWMGRIDPYDSETHY NQKFKDRVTMTVDKSTSTAYMELSSLRSEDTAVYYCARGNWDDYWGQGTTVTVSSGGGGS GGGGSGGGGSGGGGSDVQLTQSPSFLSASVGDRVTITCRASKSISKDLAWYQQKPGKAPK LLIYSGSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQHNKYPYTFGGGTKVE IK
hzCAR123-2 scFv	2557	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQ APGQGLEWMGRIDPYDSETHYNQKFKDRVTMTVDKSTSTAYMELSSLRSEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSEVVLTQSPATLSLSPGERATLSCR ASKSISKDLAWYQQKPGQAPRLLIYSGSTLQSGIPARFSGSGSGTDFTLTISSLEPEDFA VYYCQQHNKYPYTFGGGTKVEIK
hzCAR123-3 scFv	2558	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQ APGQGLEWMGRIDPYDSETHYNQKFKDRVTMTVDKSTSTAYMELSSLRSEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVVMTQSPAFLSVTPGEKVTITCR ASKSISKDLAWYQQKPDQAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTFTISSLEAEDAA TYYCQQHNKYPYTFGGGTKVEIK
hzCAR123-4 scFv	2559	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMNWVRQ APGQGLEWMGRIDPYDSETHYNQKFKDRVTMTVDKSTSTAYMELSSLRSEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVVMTQSPDSLAVSLGERATINCR ASKSISKDLAWYQQKPGQPPKLLIYSGSTLQSGVPDRFSGSGSGTDFTLTISSLQAEDVA VYYCQQHNKYPYTFGGGTKVEIK
hzCAR123-5 scFv	2560	DVQLTQSPSFLSASVGDRVTITCRASKSISKDLAWYQQK PGKAPKLLIYSGSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSY WMNWVRQAPGQGLEWMGRIDPYDSETHYNQKFKDRVTMTVDKSTSTAYMELSSLRSEDTA VYYCARGNWDDYWGQGTTVTVSS
hzCAR123-6 scFv	2561	EVVLTQSPATLSLSPGERATLSCRASKSISKDLAWYQQK PGQAPRLLIYSGSTLQSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSY WMNWVRQAPGQGLEWMGRIDPYDSETHYNQKFKDRVTMTVDKSTSTAYMELSSLRSEDTA VYYCARGNWDDYWGQGTTVTVSS
hzCAR123-	2562	DVVMTQSPAFLSVTPGEKVTITCRASKSISKDLAWYQQK

7 scFv		PDQAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSY WMNWVRQAPGQGLEWMGRIDPYDSETHYNQKFKDRVTMTVDKSTSTAYMELSSLRSEDTA VYYCARGNWDDYWGQGTTVTVSS
hzCAR123- 8 scFv	2563	DVVMTQSPDSLAVSLGERATINCRASKSISKDLAWYQQK PGQPPKLLIYSGSTLQSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSY WMNWVRQAPGQGLEWMGRIDPYDSETHYNQKFKDRVTMTVDKSTSTAYMELSSLRSEDTA VYYCARGNWDDYWGQGTTVTVSS
hzCAR123- 9 scFv	2564	QVQLVQSGSELKKPGASVKVSCKASGYTFTSYWMNWVRQ APGQGLEWMGRIDPYDSETHYNQKFKDRFVFSVDKSVSTAYLQISSLKAEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVQLTQSPSFLSASVGDRVTITCR ASKSISKDLAWYQQKPGKAPKLLIYSGSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFA TYYCQQHNKYPYTFGGGTKVEIK
hzCAR123- 10 scFv	2565	QVQLVQSGSELKKPGASVKVSCKASGYTFTSYWMNWVRQ APGQGLEWMGRIDPYDSETHYNQKFKDRFVFSVDKSVSTAYLQISSLKAEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSEVVLTQSPATLSLSPGERATLSCR ASKSISKDLAWYQQKPGQAPRLLIYSGSTLQSGIPARFSGSGSGTDFTLTISSLEPEDFA VYYCQQHNKYPYTFGGGTKVEIK
hzCAR123- 11 scFv	2566	QVQLVQSGSELKKPGASVKVSCKASGYTFTSYWMNWVRQ APGQGLEWMGRIDPYDSETHYNQKFKDRFVFSVDKSVSTAYLQISSLKAEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVVMTQSPAFLSVTPGEKVTITCR ASKSISKDLAWYQQKPDQAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTFTISSLEAEDAA TYYCQQHNKYPYTFGGGTKVEIK
hzCAR123- 12 scFv	2567	QVQLVQSGSELKKPGASVKVSCKASGYTFTSYWMNWVRQ APGQGLEWMGRIDPYDSETHYNQKFKDRFVFSVDKSVSTAYLQISSLKAEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVVMTQSPDSLAVSLGERATINCR ASKSISKDLAWYQQKPGQPPKLLIYSGSTLQSGVPDRFSGSGSGTDFTLTISSLQAEDVA VYYCQQHNKYPYTFGGGTKVEIK
hzCAR123- 13 scFv	2568	DVQLTQSPSFLSASVGDRVTITCRASKSISKDLAWYQQK PGKAPKLLIYSGSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGSELKKPGASVKVSCKASGYTFTSY WMNWVRQAPGQGLEWMGRIDPYDSETHYNQKFKDRFVFSVDKSVSTAYLQISSLKAEDTA VYYCARGNWDDYWGQGTTVTVSS
hzCAR123- 14 scFv	2569	EVVLTQSPATLSLSPGERATLSCRASKSISKDLAWYQQK PGQAPRLLIYSGSTLQSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGSELKKPGASVKVSCKASGYTFTSY WMNWVRQAPGQGLEWMGRIDPYDSETHYNQKFKDRFVFSVDKSVSTAYLQISSLKAEDTA VYYCARGNWDDYWGQGTTVTVSS
hzCAR123- 15 scFv	2570	DVVMTQSPAFLSVTPGEKVTITCRASKSISKDLAWYQQK PDQAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGSELKKPGASVKVSCKASGYTFTSY WMNWVRQAPGQGLEWMGRIDPYDSETHYNQKFKDRFVFSVDKSVSTAYLQISSLKAEDTA VYYCARGNWDDYWGQGTTVTVSS
hzCAR123- 16 scFv	2571	DVVMTQSPDSLAVSLGERATINCRASKSISKDLAWYQQK PGQPPKLLIYSGSTLQSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGSELKKPGASVKVSCKASGYTFTSY WMNWVRQAPGQGLEWMGRIDPYDSETHYNQKFKDRFVFSVDKSVSTAYLQISSLKAEDTA VYYCARGNWDDYWGQGTTVTVSS

hzCAR123-17 scFv	2572	EVQLVQSGAEVKKPGESLRISCKGSGYTFTSYWMNWVRQ MPGKGLEWMGRIDPYDSETHYNQKFKDHVTISVDKSISTAYLQWSSLKASDTAMYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVQLTQSPSFLSASVGDRVTITCR ASKSISKDLAWYQQKPGKAPKLLIYSGSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFA TYYCQQHNKYPYTFGGGTKVEIK
hzCAR123-18 scFv	2573	EVQLVQSGAEVKKPGESLRISCKGSGYTFTSYWMNWVRQ MPGKGLEWMGRIDPYDSETHYNQKFKDHVTISVDKSISTAYLQWSSLKASDTAMYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSEVVLTQSPATLSLSPGERATLSCR ASKSISKDLAWYQQKPGQAPRLLIYSGSTLQSGIPARFSGSGSGTDFTLTISSLEPEDFA VYYCQQHNKYPYTFGGGTKVEIK
hzCAR123-19 scFv	2574	EVQLVQSGAEVKKPGESLRISCKGSGYTFTSYWMNWVRQ MPGKGLEWMGRIDPYDSETHYNQKFKDHVTISVDKSISTAYLQWSSLKASDTAMYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVVMTQSPAFLSVTPGEKVTITCR ASKSISKDLAWYQQKPDQAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTFTISSLEAEDAA TYYCQQHNKYPYTFGGGTKVEIK
hzCAR123-20 scFv	2575	EVQLVQSGAEVKKPGESLRISCKGSGYTFTSYWMNWVRQ MPGKGLEWMGRIDPYDSETHYNQKFKDHVTISVDKSISTAYLQWSSLKASDTAMYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVVMTQSPDSLAVSLGERATINCR ASKSISKDLAWYQQKPGQPPKLLIYSGSTLQSGVPDRFSGSGSGTDFTLTISSLQAEDVA VYYCQQHNKYPYTFGGGTKVEIK
hzCAR123-21 scFv	2576	DVQLTQSPSFLSASVGDRVTITCRASKSISKDLAWYQQK PGKAPKLLIYSGSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVQSGAEVKKPGESLRISCKGSGYTFTSY WMNWVRQMPGKGLEWMGRIDPYDSETHYNQKFKDHVTISVDKSISTAYLQWSSLKASDTA MYYCARGNWDDYWGQGTTVTVSS
hzCAR123-22 scFv	2577	EVVLTQSPATLSLSPGERATLSCRASKSISKDLAWYQQK PGQAPRLLIYSGSTLQSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVQSGAEVKKPGESLRISCKGSGYTFTSY WMNWVRQMPGKGLEWMGRIDPYDSETHYNQKFKDHVTISVDKSISTAYLQWSSLKASDTA MYYCARGNWDDYWGQGTTVTVSS
hzCAR123-23 scFv	2578	DVVMTQSPAFLSVTPGEKVTITCRASKSISKDLAWYQQK PDQAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVQSGAEVKKPGESLRISCKGSGYTFTSY WMNWVRQMPGKGLEWMGRIDPYDSETHYNQKFKDHVTISVDKSISTAYLQWSSLKASDTA MYYCARGNWDDYWGQGTTVTVSS
hzCAR123-24 scFv	2579	DVVMTQSPDSLAVSLGERATINCRASKSISKDLAWYQQK PGQPPKLLIYSGSTLQSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVQSGAEVKKPGESLRISCKGSGYTFTSY WMNWVRQMPGKGLEWMGRIDPYDSETHYNQKFKDHVTISVDKSISTAYLQWSSLKASDTA MYYCARGNWDDYWGQGTTVTVSS
hzCAR123-25 scFv	2580	EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMNWVRQ APGKGLVWVSRIDPYDSETHYNQKFKDRFTISVDKAKSTAYLQMNSLRAEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVQLTQSPSFLSASVGDRVTITCR ASKSISKDLAWYQQKPGKAPKLLIYSGSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFA TYYCQQHNKYPYTFGGGTKVEIK
hzCAR123-26 scFv	2581	EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMNWVRQ APGKGLVWVSRIDPYDSETHYNQKFKDRFTISVDKAKSTAYLQMNSLRAEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSEVVLTQSPATLSLSPGERATLSCR ASKSISKDLAWYQQKPGQAPRLLIYSGSTLQSGIPARFSGSGSGTDFTLTISSLEPEDFA

		VYYCQQHNKYPYTFGGGTKVEIK
hzCAR123-27 scFv	2582	EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMNWVRQ APGKGLVWVSRIDPYDSETHYNQKFKDRFTISVDKAKSTAYLQMNSLRAEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVVMTQSPAFLSVTPGEKVTITCR ASKSISKDLAWYQQKPDQAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTFTISSLEAEDAA TYYCQQHNKYPYTFGGGTKVEIK
hzCAR123-28 scFv	2583	EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMNWVRQ APGKGLVWVSRIDPYDSETHYNQKFKDRFTISVDKAKSTAYLQMNSLRAEDTAVYYCARG NWDDYWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDVVMTQSPDSLAVSLGERATINCR ASKSISKDLAWYQQKPGQPPKLLIYSGSTLQSGVPDRFSGSGSGTDFTLTISSLQAEDVA VYYCQQHNKYPYTFGGGTKVEIK
hzCAR123-29 scFv	2584	DVQLTQSPSFLSASVGDRVTITCRASKSISKDLAWYQQK PGKAPKLLIYSGSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGYTFTSY WMNWVRQAPGKGLVWVSRIDPYDSETHYNQKFKDRFTISVDKAKSTAYLQMNSLRAEDTA VYYCARGNWDDYWGQGTTVTVSS
hzCAR123-30 scFv	2585	EVVLTQSPATLSLSPGERATLSCRASKSISKDLAWYQQK PGQAPRLLIYSGSTLQSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGYTFTSY WMNWVRQAPGKGLVWVSRIDPYDSETHYNQKFKDRFTISVDKAKSTAYLQMNSLRAEDTA VYYCARGNWDDYWGQGTTVTVSS
hzCAR123-31 scFv	2586	DVVMTQSPAFLSVTPGEKVTITCRASKSISKDLAWYQQK PDQAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGYTFTSY WMNWVRQAPGKGLVWVSRIDPYDSETHYNQKFKDRFTISVDKAKSTAYLQMNSLRAEDTA VYYCARGNWDDYWGQGTTVTVSS
hzCAR123-32 scFv	2587	DVVMTQSPDSLAVSLGERATINCRASKSISKDLAWYQQK PGQPPKLLIYSGSTLQSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHNKYPYTFG GGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGYTFTSY WMNWVRQAPGKGLVWVSRIDPYDSETHYNQKFKDRFTISVDKAKSTAYLQMNSLRAEDTA VYYCARGNWDDYWGQGTTVTVSS

[00277] In one aspect, the antigen-binding domain of a CAR, e.g., the CAR expressed by a cell of the invention, binds to CD33, e.g., human CD33. Any known CD33 binding domain may be used in the invention. In one embodiment, an antigen binding domain against CD33 is an antigen binding portion, e.g., CDRs or VH and VL, of an antibody, antigen-binding fragment or CAR described in, e.g., PCT publication WO2016/014576, the contents of which are incorporated herein in their entirety. In one embodiment, an antigen binding domain against CD33 is an antigen binding portion of or derived from Gemtuzumab ozogamicin (e.g., comprising an antigen binding domain comprising one or more, e.g., one, two, or three, CDRs of the heavy chain variable domain and/or one or more, e.g., one, two, or three, CDRs of the light chain variable domain, or the VH or VL, or the scFv sequence, of the scFv sequence of Gemtuzumab ozogamicin) (previously marketed as Mylotarg), e.g., Bross et al., Clin Cancer

Res 7(6):1490-1496 (2001) (Gemtuzumab Ozogamicin, hP67.6). In one embodiment, an antigen binding domain against CD33 is an antigen binding portion of or derived from (e.g., comprising an antigen binding domain comprising one or more, e.g., one, two, or three, CDRs of the heavy chain variable domain and/or one or more, e.g., one, two, or three, CDRs of the light chain variable domain, or the VH or VL, or the scFv sequence) of the scFv sequence encoded by GenBank reference no. AM402974.1 (See, Wang et al., *Mol. Ther.*, vol. 23:1, pp. 184-191 (2015), hereby incorporated by reference. In one embodiment, an antigen binding domain against CD33 is an antigen binding portion, e.g., CDRs, of an antibody described in,, e.g., Caron et al., Cancer Res 52(24):6761-6767 (1992) (Lintuzumab, HuM195), Lapusan et al., Invest New Drugs 30(3):1121-1131 (2012) (AVE9633), Aigner et al., Leukemia 27(5): 1107-1115 (2013) (AMG330, CD33 BiTE), Dutour et al., Adv hematol 2012:683065 (2012), and Pizzitola et al., Leukemia doi:10.1038/Lue.2014.62 (2014). In embodiments, the antigen binding domain is or is derived from a murine anti-human CD33 binding domain. In embodiments, the antigen binding domain is a humanized antibody or antibody fragment, e.g., scFv domain. In an embodiment, the antigen binding domain is a human antibody or antibody fragment that binds to human CD33. In embodiments, the antigen binding domain is an scFv domain which includes a light chain variable region (VL) and a heavy chain variable region (VH). The VL and VH may attached by a linker described herein, e.g., comprising the sequence GGGGSGGGGSGGGGS (SEQ ID NO: 30), and may be in any orientation, e.g., VL-linker-VH, or VH-linker-VL.

[00278] In one aspect, the antigen-binding domain of a CAR, e.g., the CAR expressed by a cell of the invention, binds to CLL-1, e.g., human CLL-1. Any known CLL-1 binding domain may be used in the invention. In one embodiment, an antigen binding domain against CLL-1 is an antigen binding portion, e.g., CDRs or VH and VL, of an antibody, antigen-binding fragment or CAR described in, e.g., PCT publication WO2016/014535, the contents of which are incorporated herein in their entirety. In one embodiment, an antigen binding domain against CLL-1 is an antigen binding portion, e.g., CDRs, of an antibody available from R&D, ebiosciences, Abcam, for example, PE-CLL1-hu Cat# 353604 (BioLegend); and PE-CLL1 (CLEC12A) Cat# 562566 (BD). In embodiments, the antigen binding domain is or is derived from a murine anti-human CLL-1 binding domain. In embodiments, the antigen binding domain is a humanized antibody or antibody fragment, e.g., scFv domain. In an embodiment,

the antigen binding domain is a human antibody or antibody fragment that binds to human CLL-1. In embodiments, the antigen binding domain is an scFv domain which includes a light chain variable region (VL) and a heavy chain variable region (VH). The VL and VH may attached by a linker described herein, e.g., comprising the sequence GGGGSGGGGSGGGGS (SEQ ID NO: 30), and may be in any orientation, e.g., VL-linker-VH, or VH-linker-VL.

[00279] In one aspect, the antigen-binding domain of a CAR, e.g., the CAR expressed by a cell of the invention, binds to a B-cell antigen, e.g., a human B-cell antigen. Any known B-cell antigen binding domain may be used in the invention.

[00280] In an embodiment, the B cell antigen is an antigen that is preferentially or specifically expressed on the surface of the B cell. The antigen can be expressed on the surface of any one of the following types of B cells: progenitor B cells (e.g., pre-B cells or pro-B cells), early pro-B cells, late pro-B cells, large pre-B cells, small pre-B cells, immature B cells, e.g., naïve B cells, mature B cells, plama B cells, plasmablasts, memory B cells, B-1 cells, B-2 cells, marginal-zone B cells, follicular B cells, germinal center B cells, or regulatory B cells (Bregs).

[00281] The present disclosure provides CARs that can target the following B cell antigens: CD10, CD19, CD20, CD21, CD22, CD23, CD24, CD25, CD37, CD38, CD53, CD72, CD73, CD74, CD75, CD77, CD79a, CD79b, CD80, CD81, CD82, CD83, CD84, CD85, ROR1, BCMA, CD86, and CD179b. Other B cell antigens that can be targeted by a CAR described herein include: CD1a, CD1b, CD1c, CD1d, CD2, CD5, CD6, CD9, CD11a, CD11b, CD11c, CD17, CD18, CD26, CD27, CD29, CD30, CD31, CD32a, CD32b, CD35, CD38, CD39, CD40, CD44, CD45, CD45RA, CD45RB, CD45RC, CD45RO, CD46, CD47, CD48, CD49b, CD49c, CD49d, CD50, CD52, CD54, CD55, CD58, CD60a, CD62L, CD63, CD63, CD68 CD69, CD70, CD85E, CD85I, CD85J, CD92, CD95, CD97, CD98, CD99, CD100, CD102, CD108, CD119, CD120a, CD120b, CD121b, CD122, CD124, CD125, CD126, CD130, CD132, CD137, CD138, CD139, CD147, CD148, CD150, CD152, CD162, CD164, CD166, CD167a, CD170, CD175, CD175s, CD180, CD184, CD185, CD192, CD196, CD197, CD200, CD205, CD210a, CDw210b, CD212, CD213a1, CD213a2, CD215, CD217, CD218a, CD218b, CD220, CD221, CD224, CD225, CD226, CD227, CD229, CD230, CD232, CD252, CD253, CD257, CD258, CD261, CD262, CD263, CD264, CD267, CD268, CD269, CD270, CD272, CD274, CD275, CD277, CD279, CD283, CD289, CD290, CD295, CD298, CD300a, CD300c, CD305, CD306, CD307a, CD307b, CD307c, CD307d, CD307e, CD314, CD315, CD316, CD317,

CD319, CD321, CD327, CD328, CD329, CD338, CD351, CD352, CD353, CD354, CD355, CD357, CD358, CD360, CD361, CD362, and CD363.

[00282] In another embodiment, the B cell antigen targeted by the CAR is chosen from CD19, BCMA, CD20, CD22, FcRn5, FcRn2, CS-1 and CD138. In an embodiment, the B-Cell antigen targeted by the CAR is CD19. In an embodiment, the B-Cell antigen targeted by the CAR is CD20. In an embodiment, the B-Cell antigen targeted by the CAR is CD22. In an embodiment, the B-Cell antigen targeted by the CAR is BCMA. In an embodiment, the B-Cell antigen targeted by the CAR is FcRn5. In an embodiment, the B-Cell antigen targeted by the CAR is FcRn2. In an embodiment, the B-Cell antigen targeted by the CAR is CS-1. In an embodiment, the B-Cell antigen targeted by the CAR is CD138.

[00283] In one embodiment, the antigen-binding domain of a CAR, e.g., the CAR expressed by a cell of the invention, can be chosen such that a preferred B cell population is targeted. For example, in an embodiment where targeting of B regulatory cells is desired, an antigen binding domain is selected that targets a B cell antigen that is expressed on regulatory B cells and not on other B cell populations, e.g., plasma B cells and memory B cells. Cell surface markers expressed on regulatory B cells include: CD19, CD24, CD25, CD38, or CD86, or markers described in He et al., 2014, *J Immunology Research*, Article ID 215471. When targeting of more than one type of B cells is desired, an antigen binding domain that targets a B cell antigen that is expressed by all of the B cells to be targeted can be selected.

[00284] In an embodiment, the antigen-binding domain of a CAR, e.g., the CAR expressed by a cell of the invention, binds to CD19. CD19 is found on B cells throughout differentiation of the lineage from the pro/pre-B cell stage through the terminally differentiated plasma cell stage. In an embodiment, the antigen binding domain is a murine scFv domain that binds to human CD19, e.g., CTL019 (e.g., SEQ ID NO: 95). In an embodiment, the antigen binding domain is a humanized antibody or antibody fragment, e.g., scFv domain, derived from the murine CTL019 scFv. In an embodiment, the antigen binding domain is a human antibody or antibody fragment that binds to human CD19. Exemplary scFv domains (and their sequences, e.g., CDRs, VL and VH sequences) that bind to CD19 are provided in Table 6. The scFv domain sequences provided in Table 6 include a light chain variable region (VL) and a heavy chain variable region (VH). The VL and VH are attached by a linker comprising the sequence GGGGSGGGGSGGGGS (SEQ ID NO: 30), e.g., in the following orientation: VL-linker-VH.

Table 6. Antigen Binding domains that bind B cell antigen CD19

B cell antigen	Name	Amino Acid Sequence	SEQ ID NO:
CD19	muCTL019	DIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEITGGGGSGGGGSGGGGSEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQPPRKGLEWLGVIWGSETTYYNSALKSRLTIIKDNSKSQVFLKMNSLQTDDTAIYYCAKHYYYGGSYAMDYWGQGTSVTVSS	95
CD19	huscFv1	EIVMTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLIYHTSRLHSGIPARFSGSGSGTDYTLTISSLQPEDFAVYFCQQGNTLPYTFGQGTKLEIKGGGGSGGGGSGGGGSQVQLQESGPGLVKPSETLSLTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYYSSSLKSRVTISKDNSKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYAMDYWGQGTLVTVSS	83
CD19	huscFv2	EIVMTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLIYHTSRLHSGIPARFSGSGSGTDYTLTISSLQPEDFAVYFCQQGNTLPYTFGQGTKLEIKGGGGSGGGGSGGGGSQVQLQESGPGLVKPSETLSLTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYYQSSLKSRVTISKDNSKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYAMDYWGQGTLVTVSS	84
CD19	huscFv3	QVQLQESGPGLVKPSETLSLTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYYSSSLKSRVTISKDNSKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYAMDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVMTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLIYHTSRLHSGIPARFSGSGSGTDYTLTISSLQPEDFAVYFCQQGNTLPYTFGQGTKLEIK	85
CD19	huscFv4	QVQLQESGPGLVKPSETLSLTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYYQSSLKSRVTISKDNSKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYAMDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVMTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLIYHTSRLHSGIPARFSGSGSGTDYTLTISSLQPEDFAVYFCQQGNTLPYTFGQGTKLEIK	86
CD19	huscFv5	EIVMTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLIYHTSRLHSGIPARFSGSGSGTDYTLTISSLQPEDFAVYFCQQGNTLPYTFGQGTKLEIKGGGGSGGGGSGGGGSGGGGSQVQLQESGPGLVKPSETLSLTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYYSSSLKSRVTISKDNSKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYAMDYWGQGTLVTVSS	87
CD19	huscFv6	EIVMTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLIYHTSRLHSGIPARFSGSGSGTDYTLTISSLQPEDFAVYFCQQGNTLPYTFGQGTKLEIKGGGGSGGGGSGGGGSGGGGSQVQLQESGPGLVKPSETLSLTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYYQSSLKSRVTISKDNSKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYAMDYWGQGTLVTVSS	88
CD19	huscFv7	QVQLQESGPGLVKPSETLSLTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYYSSSLKSRVTISKDNSKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYAMDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVMTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLIYHTSRLHSGIPARFSGSGSGTDYTLTISSLQPEDFAVYFCQQGNTLPYTFGQGTKLEIK	89
CD19	huscFv8	QVQLQESGPGLVKPSETLSLTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYYQSSLKSRVTISKDNSKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYAMDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVMTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLIYHTSRLHS	90

		GIPARFSGSGSGTDYTLTISSLQPEDFAVYFCQQGNTLPYTFGQGTKLEIK	
CD19	huscFv9	EIVMTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLIYHTSRLHSGIPARFSGSGSGTDYTLTISSLQPEDFAVYFCQQGNTLPYTFGQGTKLEIKGGGGSGGGGSGGGGSGGGGSQVQLQESGPGLVKPSETLSLTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYYNSSLKSRVTISKDNSKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYAMDYWGQGTLVTVSS	91
CD19	Hu scFv10	QVQLQESGPGLVKPSETLSLTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYYNSSLKSRVTISKDNSKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYAMDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVMTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLIYHTSRLHSGIPARFSGSGSGTDYTLTISSLQPEDFAVYFCQQGNTLPYTFGQGTKLEIK	92
CD19	Hu scFv11	EIVMTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLIYHTSRLHSGIPARFSGSGSGTDYTLTISSLQPEDFAVYFCQQGNTLPYTFGQGTKLEIKGGGGSGGGGSGGGGSQVQLQESGPGLVKPSETLSLTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYYNSSLKSRVTISKDNSKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYAMDYWGQGTLVTVSS	93
CD19	Hu scFv12	QVQLQESGPGLVKPSETLSLTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYYNSSLKSRVTISKDNSKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYAMDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVMTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLIYHTSRLHSGIPARFSGSGSGTDYTLTISSLQPEDFAVYFCQQGNTLPYTFGQGTKLEIK	94

[00285] The sequences of the CDR sequences of the scFv domains of the CD19 antigen binding domains provided in Table 6 are shown in Table 7 for the heavy chain variable domains and in Table 8 for the light chain variable domains. "ID" stands for the respective SEQ ID NO for each CDR.

Table 7. Heavy Chain Variable Domain CDRs

Description	FW	HCDR1	SEQ ID NO:	HCDR2	SEQ ID NO:	HCDR3	SEQ ID NO:
murine_CART19		GVSLPDYGVS	255	VIWGSETTYYNSALKS	256	HYYYGGSYAMDY	260
humanized_CART19 a	VH4	GVSLPDYGVS	255	VIWGSETTYY***S***S***S***LKS	257	HYYYGGSYAMDY	260
humanized_CART19 b	VH4	GVSLPDYGVS	255	VIWGSETTYY***Q***S***S***LKS	258	HYYYGGSYAMDY	260
humanized_CART19 c	VH4	GVSLPDYGVS	255	VIWGSETTYYNS***S***LKS	259	HYYYGGSYAMDY	260

Table 8. Light Chain Variable Domain CDRs

Description	FW	LCDR1	SEQ ID	LCDR2	SEQ ID	LCDR3	SEQ ID

			NO:		NO:		NO:
murine_CART19		RASQDISKYLN	261	HTSRLHS	262	QQGNTLPYT	263
humanized_CART19 a	VK3	RASQDISKYLN	261	HTSRLHS	262	QQGNTLPYT	263
humanized_CART19 b	VK3	RASQDISKYLN	261	HTSRLHS	262	QQGNTLPYT	263
humanized_CART19 c	VK3	RASQDISKYLN	261	HTSRLHS	262	QQGNTLPYT	263

[00286] In an embodiment, the antigen binding domain comprises an anti-CD19 antibody, or fragment thereof, e.g., an scFv. For example, the antigen binding domain comprises a variable heavy chain and a variable light chain listed in Table 9. The linker sequence joining the variable heavy and variable light chains can be any of the linker sequences described herein, or alternatively, can be GSTSGSGKPGSGEGSTKG (SEQ ID NO: 81). The light chain variable region and heavy chain variable region of a scFv can be, e.g., in any of the following orientations: light chain variable region-linker-heavy chain variable region or heavy chain variable region-linker-light chain variable region.

Table 9. Additional Anti-CD19 antibody binding domains

Ab Name	VH Sequence	VL Sequence
SJ25-C1	QVQLLESGAELVRPGSSVKISCKASG YAFSSYWMNWVKQRPGQGLEWIGQIY PGDGDTNYNGKFKGQATLTADKSSST AYMQLSGLTSEDSAVYSCARKTISSV VDFYFDYWGQGTTVT (SEQ ID NO: 96)	ELVLTQSPKFMSTSVGDRVSVTCKASQNV GTNVAWYQQKPGQSPKPLIYSATYRNSGV PDRFTGSGSGTDFTLTITNVQSKDLADYF YFCQYNRYPYTSGGGTKLEIKRRS (SEQ ID NO: 97)
	ScFv Sequence	
SJ25-C1 scFv	QVQLLESGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIYPGDGD TNYNGKFKGQATLTADKSSSTAYMQLSGLTSEDSAVYSCARKTISSVVDFYFDYWGQ GTTVTGSTSGSGKPGSGEGSTKGELVLTQSPKFMSTSVGDRVSVTCKASQNVGTNVA WYQQKPGQSPKPLIYSATYRNSGVPDRFTGSGSGTDFTLTITNVQSKDLADYFYFCQ YNRYPYTSGGGTKLEIKRRS (SEQ ID NO: 112)	

[00287] In one embodiment, the CD19 binding domain comprises one or more (e.g., all three) light chain complementary determining region 1 (LC CDR1), light chain complementary determining region 2 (LC CDR2), and light chain complementary determining region 3 (LC CDR3) of a CD19 binding domain described herein, e.g., provided in Table 6 or 7, and/or one or more (e.g., all three) heavy chain complementary determining region 1 (HC CDR1), heavy chain complementary determining region 2 (HC CDR2), and heavy chain complementary

determining region 3 (HC CDR3) of a CD19 binding domain described herein, e.g., provided in Table 6 or 8. In one embodiment, the CD19 binding domain comprises one, two, or all of LC CDR1, LC CDR2, and LC CDR3 of any amino acid sequences as provided in Table 8, incorporated herein by reference; and one, two or all of HC CDR1, HC CDR2, and HC CDR3 of any amino acid sequences as provided in Table 7.

[00288] In one embodiment, the CD19 antigen binding domain comprises:

(i) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 261, a LC CDR2 amino acid sequence of SEQ ID NO: 262, and a LC CDR3 amino acid sequence of SEQ ID NO: 263; and
(b) a HC CDR1 amino acid sequence of SEQ ID NO: 255, a HC CDR2 amino acid sequence of SEQ ID NO: 256, and a HC CDR3 amino acid sequence of SEQ ID NO: 260

(ii) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 261, a LC CDR2 amino acid sequence of SEQ ID NO: 262, and a LC CDR3 amino acid sequence of SEQ ID NO: 263; and
(b) a HC CDR1 amino acid sequence of SEQ ID NO: 255, a HC CDR2 amino acid sequence of SEQ ID NO: 257, and a HC CDR3 amino acid sequence of SEQ ID NO: 260;

(iii) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 261, a LC CDR2 amino acid sequence of SEQ ID NO: 262, and a LC CDR3 amino acid sequence of SEQ ID NO: 263; and
(b) a HC CDR1 amino acid sequence of SEQ ID NO: 255, a HC CDR2 amino acid sequence of SEQ ID NO: 258, and a HC CDR3 amino acid sequence of SEQ ID NO: 260; or

(iv) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 261, a LC CDR2 amino acid sequence of SEQ ID NO: 262, and a LC CDR3 amino acid sequence of SEQ ID NO: 263; and
(b) a HC CDR1 amino acid sequence of SEQ ID NO: 255, a HC CDR2 amino acid sequence of SEQ ID NO: 259, and a HC CDR3 amino acid sequence of SEQ ID NO: 260.

[00289] In one embodiment, the CD19 binding domain comprises a light chain variable region described herein (e.g., in Table 6 or 9) and/or a heavy chain variable region described herein (e.g., in Table 6 or 9). In one embodiment, the CD19 binding domain is a scFv comprising a light chain and a heavy chain of an amino acid sequence listed in Table 6 or 9. In an embodiment, the CD19 binding domain (e.g., an scFv) comprises: a light chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence of a light chain variable region provided in Table 6 or 9, or a sequence with 95-99% identity with an amino acid sequence provided in Table 6 or 9; and/or a heavy chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence of a heavy chain variable region provided in Table 6 or 9, or a sequence with 95-99% identity to an amino acid sequence provided in Table 6 or 9.

[00290] In one embodiment, the CD19 binding domain comprises an amino acid sequence selected from a group consisting of SEQ ID NO: 83; SEQ ID NO: 84, SEQ ID NO: 85; SEQ ID NO: 86; SEQ ID NO: 87; SEQ ID NO: 88; SEQ ID NO: 89, SEQ ID NO: 90, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, and SEQ ID NO: 112; or an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) to any of the aforesaid sequences; or a sequence with 95-99% identity to any of the aforesaid sequences. In one embodiment, the CD19 binding domain is a scFv, and a light chain variable region comprising an amino acid sequence described herein, e.g., in Table 6 or 9, is attached to a heavy chain variable region comprising an amino acid sequence described herein, e.g., in Table 6 or 9, via a linker, e.g., a linker described herein. In one embodiment, the CD19 binding domain includes a (Gly4-Ser)n linker, wherein n is 1, 2, 3, 4, 5, or 6, preferably 4 (SEQ ID NO: 80). The light chain variable region and heavy chain variable region of a scFv can be, e.g., in any of the following orientations: light chain variable region-linker-heavy chain variable region or heavy chain variable region-linker-light chain variable region.

[00291] Any known CD19 CAR, e.g., the CD19 antigen binding domain of any known CD19 CAR, in the art can be used in accordance with the instant invention to construct a CAR. For example, CD19 CAR is described in the US Pat. No. 8,399,645; US Pat. No. 7,446,190; Xu et al., Leuk Lymphoma. 2013 54(2):255-260(2012); Cruz et al., Blood 122(17):2965-2973 (2013); Brentjens et al., Blood, 118(18):4817-4828 (2011); Kochenderfer et al., Blood 116(20):4099-102 (2010); Kochenderfer et al., Blood 122 (25):4129-39(2013); and 16th Annu Meet Am Soc Gen Cell Ther (ASGCT) (May 15-18, Salt Lake City) 2013, Abst 10, each of which is incorporated herein by referene in its entirety. In one embodiment, an antigen binding domain against CD19 is an antigen binding portion, e.g., CDRs, of a CAR, antibody or antigen-binding fragment thereof described in, e.g., PCT publication WO2012/079000; PCT publication WO2014/153270; Kochenderfer, J.N. et al., J. Immunother. 32 (7), 689-702 (2009); Kochenderfer, J.N., et al., Blood, 116 (20), 4099-4102 (2010); PCT publication WO2014/031687; Bejcek, Cancer Research, 55, 2346-2351, 1995; or U.S. Patent No. 7,446,190, each of which is incorporated herein by referene in its entirety.

[00292] In an embodiment, the antigen-binding domain of a CAR, e.g., the CAR expressed by a cell of the invention, binds to BCMA. BCMA is found preferentially expressed in mature B lymphocytes. In an embodiment, the antigen binding domain is a murine scFv domain that binds to human BCMA. In an embodiment, the antigen binding domain is a humanized antibody or antibody fragment, e.g., scFv domain, that binds human BCMA. In an embodiment, the antigen binding domain is a human antibody or antibody fragment that binds to human BCMA. Exemplary scFv domains (and their sequences, e.g., CDRs, VL and VH sequences) that bind to BCMA are provided in Table 12, Table 13, Table 14 and Table 15. The scFv domain sequences provided in Table 12 and Table 13 include a light chain variable region (VL) and a heavy chain variable region (VH). The VL and VH are attached by a linker, e.g., in the following orientation: VH-linker-VL.

Table 12. Antigen Binding domains that bind the B-Cell antigen BCMA

The amino acid sequences variable heavy chain and variable light chain sequences for each scFv is also provided.

Name/ Description	**SEQ ID NO:**	**Sequence**
139109		

139109- aa ScFv domain	349	EVQLVESGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEWVSG IVYSGSTYYAASVKGRFTISRDNSRNTLYLQMNSLRPEDTAIYYCSAHGG ESDVWGQGTTVTVSSASGGGGSGGRASGGGGSDIQLTQSPSSLSASVGDR VTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPYTFGQGTKVEIK
139109- nt ScFv domain	364	GAAGTGCAATTGGTGGAATCAGGGGGAGGACTTGTGCAGCCTGGAGGATC GCTGAGACTGTCATGTGCCGTGTCCGGCTTTGCCCTGTCCAACCACGGGA TGTCCTGGGTCCGCCGCGCGCCTGGAAAGGGCCTCGAATGGGTGTCGGGT ATTGTGTACAGCGGTAGCACCTACTATGCCGCATCCGTGAAGGGGAGATT CACCATCAGCCGGGACAACTCCAGGAACACTCTGTACCTCCAAATGAATT CGCTGAGGCCAGAGGACACTGCCATCTACTACTGCTCCGCGCATGGCGGA GAGTCCGACGTCTGGGGACAGGGGACCACCGTGACCGTGTCTAGCGCGTC CGGCGGAGGCGGCAGCGGGGGTCGGGCATCAGGGGGCGGCGGATCGGACA TCCAGCTCACCCAGTCCCCGAGCTCGCTGTCCGCCTCCGTGGGAGATCGG GTCACCATCACGTGCCGCGCCAGCCAGTCGATTTCCTCCTACCTGAACTG GTACCAACAGAAGCCCGGAAAAGCCCCGAAGCTTCTCATCTACGCCGCCT CGAGCCTGCAGTCAGGAGTGCCCTCACGGTTCTCCGGCTCCGGTTCCGGT ACTGATTTCACCCTGACCATTTCCTCCCTGCAACCGGAGGACTTCGCTAC TTACTACTGCCAGCAGTCGTACTCCACCCCCTACACTTTCGGACAAGGCA CCAAGGTCGAAATCAAG
139109- aa VH	379	EVQLVESGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEWVSG IVYSGSTYYAASVKGRFTISRDNSRNTLYLQMNSLRPEDTAIYYCSAHGG ESDVWGQGTTVTVSS
139109- aa VL	394	DIQLTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYA ASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPYTFGQ GTKVEIK
139103		
139103- aa ScFv domain	339	QVQLVESGGGLVQPGRSLRLSCAASGFTFSNYAMSWVRQAPGKGLGWVSG ISRSGENTYYADSVKGRFTISRDNSKNTLYLQMNSLRDEDTAVYYCARSP AHYYGGMDVWGQGTTVTVSSASGGGGSGGRASGGGGSDIVLTQSPGTLSL SPGERATLSCRASQSISSSFLAWYQQKPGQAPRLLIYGASRRATGIPDRF SGSGSGTDFTLTISRLEPEDSAVYYCQQYHSSPSWTFGQGTKLEIK
139103- nt ScFv domain	354	CAAGTGCAACTCGTGGAATCTGGTGGAGGACTCGTGCAACCCGGAAGATC GCTTAGACTGTCGTGTGCCGCCAGCGGGTTCACTTTCTCGAACTACGCGA TGTCCTGGGTCCGCCAGGCACCCGGAAAGGGACTCGGTTGGGTGTCCGGC ATTTCCCGGTCCGGCGAAAATACCTACTACGCCGACTCCGTGAAGGGCCG CTTCACCATCTCAAGGGACAACAGCAAAAACACCCTGTACTTGCAAATGA ACTCCCTGCGGGATGAAGATACAGCCGTGTACTATTGCGCCCGGTCGCCT GCCCATTACTACGGCGGAATGGACGTCTGGGGACAGGGAACCACTGTGAC TGTCAGCAGCGCGTCGGGTGGCGGCGGCTCAGGGGGTCGGGCCTCCGGGG GGGGAGGGTCCGACATCGTGCTGACCCAGTCCCCGGGAACCCTGAGCCTG AGCCCGGGAGAGCGCGCGACCCTGTCATGCCGGGCATCCCAGAGCATTAG CTCCTCCTTTCTCGCCTGGTATCAGCAGAAGCCCGGACAGGCCCCGAGGC TGCTGATCTACGGCGCTAGCAGAAGGGCTACCGGAATCCCAGACCGGTTC TCCGGCTCCGGTTCCGGGACCGATTTCACCCTTACTATCTCGCGCCTGGA ACCTGAGGACTCCGCCGTCTACTACTGCCAGCAGTACCACTCATCCCCGT CGTGGACGTTCGGACAGGGCACCAAGCTGGAGATTAAG
139103- aa VH	369	QVQLVESGGGLVQPGRSLRLSCAASGFTFSNYAMSWVRQAPGKGLGWVSG ISRSGENTYYADSVKGRFTISRDNSKNTLYLQMNSLRDEDTAVYYCARSP AHYYGGMDVWGQGTTVTVSS
139103- aa	384	DIVLTQSPGTLSLSPGERATLSCRASQSISSSFLAWYQQKPGQAPRLLIY

VL		GASRRATGIPDRFSGSGSGTDFTLTISRLEPEDSAVYYCQQYHSSPSWTF GQGTKLEIK
139105		
139105- aa ScFv domain	340	QVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSG ISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCSVHS FLAYWGQGTLVTVSSASGGGGSGGRASGGGGSDIVMTQTPLSLPVTPGEP ASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFS GSGSGTDFTLKISRVEAEDVGVYYCMQALQTPYTFGQGTKVEIK
139105- nt ScFv domain	355	CAAGTGCAACTCGTCGAATCCGGTGGAGGTCTGGTCCAACCTGGTAGAAG CCTGAGACTGTCGTGTGCGGCCAGCGGATTCACCTTTGATGACTATGCTA TGCACTGGGTGCGGCAGGCCCCAGGAAAGGGCCTGGAATGGGTGTCGGGA ATTAGCTGGAACTCCGGGTCCATTGGCTACGCCGACTCCGTGAAGGGCCG CTTCACCATCTCCCGCGACAACGCAAAGAACTCCCTGTACTTGCAAATGA ACTCGCTCAGGGCTGAGGATACCGCGCTGTACTACTGCTCCGTGCATTCC TTCCTGGCCTACTGGGGACAGGGAACTCTGGTCACCGTGTCGAGCGCCTC CGGCGGCGGGGGCTCGGGTGGACGGGCCTCGGGCGGAGGGGGGTCCGACA TCGTGATGACCCAGACCCCGCTGAGCTTGCCCGTGACTCCCGGAGAGCCT GCATCCATCTCCTGCCGGTCATCCCAGTCCCTTCTCCACTCCAACGGATA CAACTACCTCGACTGGTACCTCCAGAAGCCGGGACAGAGCCCTCAGCTTC TGATCTACCTGGGGTCAAATAGAGCCTCAGGAGTGCCGGATCGGTTCAGC GGATCTGGTTCGGGAACTGATTTCACTCTGAAGATTTCCCGCGTGGAAGC CGAGGACGTGGGCGTCTACTACTGTATGCAGGCGCTGCAGACCCCCTATA CCTTCGGCCAAGGGACGAAAGTGGAGATCAAG
139105- aa VH	370	QVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSG ISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCSVHS FLAYWGQGTLVTVSS
139105- aa VL	385	DIVMTQTPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQ LLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP YTFGQGTKVEIK
139111		
139111- aa ScFv domain	341	EVQLLESGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEWVSG IVYSGSTYYAASVKGRFTISRDNSRNTLYLQMNSLRPEDTAIYYCSAHGG ESDVWGQGTTVTVSSASGGGGSGGRASGGGGSDIVMTQTPLSLSVTPGQP ASISCKSSQSLLRNDGKTPLYWYLQKAGQPPQLLIYEVSNRFSGVPDRFS GSGSGTDFTLKISRVEAEDVGAYYCMQNIQFPSFGGGTKLEIK
139111- nt ScFv domain	356	GAAGTGCAATTGTTGGAATCTGGAGGAGGACTTGTGCAGCCTGGAGGATC ACTGAGACTTTCGTGTGCGGTGTCAGGCTTCGCCCTGAGCAACCACGGCA TGAGCTGGGTGCGGAGAGCCCCGGGGAAGGGTCTGGAATGGGTGTCCGGG ATCGTCTACTCCGGTTCAACTTACTACGCCGCAAGCGTGAAGGGTCGCTT CACCATTTCCCGCGATAACTCCCGGAACACCCTGTACCTCCAAATGAACT CCCTGCGGCCCGAGGACACCGCCATCTACTACTGTTCCGCGCATGGAGGA GAGTCCGATGTCTGGGGACAGGGCACTACCGTGACCGTGTCGAGCGCCTC GGGGGGAGGAGGCTCCGGCGGTCGCGCCTCCGGGGGGGGTGGCAGCGACA TTGTGATGACGCAGACTCCACTCTCGCTGTCCGTGACCCCGGGACAGCCC GCGTCCATCTCGTGCAAGAGCTCCCAGAGCCTGCTGAGGAACGACGGAAA GACTCCTCTGTATTGGTACCTCCAGAAGGCTGGACAGCCCCCGCAACTGC TCATCTACGAAGTGTCAAATCGCTTCTCCGGGGTGCCGGATCGGTTTTCC GGCTCGGGATCGGGCACCGACTTCACCCTGAAAATCTCCAGGGTCGAGGC CGAGGACGTGGGAGCCTACTACTGCATGCAAAACATCCAGTTCCCTTCCT TCGGCGGCGGCACAAAGCTGGAGATTAAG
139111- aa	371	EVQLLESGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEWVSG

VH		IVYSGSTYYAASVKGRFTISRDNSRNTLYLQMNSLRPEDTAIYYCSAHGG ESDVWGQGTTVTVSS
139111- aa VL	386	DIVMTQTPLSLSVTPGQPASISCKSSQSLLRNDGKTPLYWYLQKAGQPPQ LLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGAYYCMQNIQFP SFGGGTKLEIK
139100		
139100- aa ScFv domain	342	QVQLVQSGAEVRKTGASVKVSCKASGYIFDNFGINWVRQAPGQGLEWMGW INPKNNNTNYAQKFQGRVTITADESTNTAYMEVSSLRSEDTAVYYCARGP YYYQSYMDVWGQGTMVTVSSASGGGGSGGRASGGGGSDIVMTQTPLSLPV TPGEPASISCRSSQSLLHSNGYNYLNWYLQKPGQSPQLLIYLGSKRASGV PDRFSGSGSGTDFTLHITRVGAEDVGVYYCMQALQTPYTFGQGTKLEIK
139100- nt ScFv domain	357	CAAGTCCAACTCGTCCAGTCCGGCGCAGAAGTCAGAAAAACCGGTGCTAG CGTGAAAGTGTCCTGCAAGGCCTCCGGCTACATTTTCGATAACTTCGGAA TCAACTGGGTCAGACAGGCCCCGGGCCAGGGGCTGGAATGGATGGGATGG ATCAACCCCAAGAACAACAACACCAACTACGCACAGAAGTTCCAGGGCCG CGTGACTATCACCGCCGATGAATCGACCAATACCGCCTACATGGAGGTGT CCTCCCTGCGGTCGGAGGACACTGCCGTGTATTACTGCGCGAGGGGCCCA TACTACTACCAAAGCTACATGGACGTCTGGGGACAGGGAACCATGGTGAC CGTGTCATCCGCCTCCGGTGGTGGAGGCTCCGGGGGGCGGGCTTCAGGAG GCGGAGGAAGCGATATTGTGATGACCCAGACTCCGCTTAGCCTGCCCGTG ACTCCTGGAGAACCGGCCTCCATTTCCTGCCGGTCCTCGCAATCACTCCT GCATTCCAACGGTTACAACTACCTGAATTGGTACCTCCAGAAGCCTGGCC AGTCGCCCCAGTTGCTGATCTATCTGGGCTCGAAGCGCGCCTCCGGGGTG CCTGACCGGTTTAGCGGATCTGGGAGCGGCACGGACTTCACTCTCCACAT CACCCGCGTGGGAGCGGAGGACGTGGGAGTGTACTACTGTATGCAGGCGC TGCAGACTCCGTACACATTCGGACAGGGCACCAAGCTGGAGATCAAG
139100- aa VH	372	QVQLVQSGAEVRKTGASVKVSCKASGYIFDNFGINWVRQAPGQGLEWMGW INPKNNNTNYAQKFQGRVTITADESTNTAYMEVSSLRSEDTAVYYCARGP YYYQSYMDVWGQGTMVTVSS
139100- aa VL	387	DIVMTQTPLSLPVTPGEPASISCRSSQSLLHSNGYNYLNWYLQKPGQSPQ LLIYLGSKRASGVPDRFSGSGSGTDFTLHITRVGAEDVGVYYCMQALQTP YTFGQGTKLEIK
139101		
139101- aa ScFv domain	343	QVQLQESGGGLVQPGGSLRLSCAASGFTFSSDAMTWVRQAPGKGLEWVSV ISGSGGTTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLD SSGYYYARGPRYWGQGTLVTVSSASGGGGSGGRASGGGGSDIQLTQSPSS LSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYGASTLASGVPA RFSGSGSGTHFTLTINSLQSEDSATYYCQQSYKRASFGQGTKVEIK
139101- nt ScFv domain	358	CAAGTGCAACTTCAAGAATCAGGCGGAGGACTCGTGCAGCCCGGAGGATC ATTGCGGCTCTCGTGCGCCGCCTCGGGCTTCACCTTCTCGAGCGACGCCA TGACCTGGGTCCGCCAGGCCCCGGGGAAGGGGCTGGAATGGGTGTCTGTG ATTTCCGGCTCCGGGGGAACTACGTACTACGCCGATTCCGTGAAAGGTCG CTTCACTATCTCCCGGGACAACAGCAAGAACACCCTTTATCTGCAAATGA ATTCCCTCCGCGCCGAGGACACCGCCGTGTACTACTGCGCCAAGCTGGAC TCCTCGGGCTACTACTATGCCCGGGGTCCGAGATACTGGGGACAGGGAAC CCTCGTGACCGTGTCCTCCGCGTCCGGCGGAGGAGGGTCGGGAGGGCGGG CCTCCGGCGGCGGCGGTTCGGACATCCAGCTGACCCAGTCCCCATCCTCA CTGAGCGCAAGCGTGGGCGACAGAGTCACCATTACATGCAGGGCGTCCCA GAGCATCAGCTCCTACCTGAACTGGTACCAACAGAAGCCTGGAAAGGCTC CTAAGCTGTTGATCTACGGGGCTTCGACCCTGGCATCCGGGGTGCCCGCG AGGTTTAGCGGAAGCGGTAGCGGCACTCACTTCACTCTGACCATTAACAG

		CCTCCAGTCCGAGGATTCAGCCACTTACTACTGTCAGCAGTCCTACAAGC GGGCCAGCTTCGGACAGGGCACTAAGGTCGAGATCAAG
139101- aa VH	373	QVQLQESGGGLVQPGGSLRLSCAASGFTFSSDAMTWVRQAPGKGLEWVSV ISGSGGTTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLD SSGYYYARGPRYWGQGTLVTVSS
139101- aa VL	388	DIQLTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYG ASTLASGVPARFSGSGSGTHFTLTINSLQSEDSATYYCQQSYKRASFGQG TKVEIK
139102		
139102- aa ScFv domain	344	QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGW ISAYNGNTNYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARGP YYYYMDVWGKGTMVTVSSASGGGGSGGRASGGGGSEIVMTQSPLSLPVTP GEPASISCRSSQSLLYSNGYNYVDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFKLQISRVEAEDVGIYYCMQGRQFPYSFGQGTKVEIK
139102- nt ScFv domain	359	CAAGTCCAACTGGTCCAGAGCGGTGCAGAAGTGAAGAAGCCCGGAGCGAG CGTGAAAGTGTCCTGCAAGGCTTCCGGGTACACCTTCTCCAACTACGGCA TCACTTGGGTGCGCCAGGCCCCGGGACAGGGCCTGGAATGGATGGGGTGG ATTTCCGCGTACAACGGCAATACGAACTACGCTCAGAAGTTCCAGGGTAG AGTGACCATGACTAGGAACACCTCCATTTCCACCGCCTACATGGAACTGT CCTCCCTGCGGAGCGAGGACACCGCCGTGTACTATTGCGCCCGGGGACCA TACTACTACTACATGGATGTCTGGGGGAAGGGGACTATGGTCACCGTGTC ATCCGCCTCGGGAGGCGGCGGATCAGGAGGACGCGCCTCTGGTGGTGGAG GATCGGAGATCGTGATGACCCAGAGCCCTCTCTCCTTGCCCGTGACTCCT GGGGAGCCCGCATCCATTTCATGCCGGAGCTCCCAGTCACTTCTCTACTC CAACGGCTATAACTACGTGGATTGGTACCTCCAAAAGCCGGGCCAGAGCC CGCAGCTGCTGATCTACCTGGGCTCGAACAGGGCCAGCGGAGTGCCTGAC CGGTTCTCCGGGTCGGGAAGCGGGACCGACTTCAAGCTGCAAATCTCGAG AGTGGAGGCCGAGGACGTGGGAATCTACTACTGTATGCAGGGCCGCCAGT TTCCGTACTCGTTCGGACAGGGCACCAAAGTGGAAATCAAG
139102- aa VH	374	QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGW ISAYNGNTNYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARGP YYYYMDVWGKGTMVTVSS
139102- aa VL	389	EIVMTQSPLSLPVTPGEPASISCRSSQSLLYSNGYNYVDWYLQKPGQSPQ LLIYLGSNRASGVPDRFSGSGSGTDFKLQISRVEAEDVGIYYCMQGRQFP YSFGQGTKVEIK
139104		
139104- aa ScFv domain	345	EVQLLETGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEWVSG IVYSGSTYYAASVKGRFTISRDNSRNTLYLQMNSLRPEDTAIYYCSAHGG ESDVWGQGTTVTVSSASGGGGSGGRASGGGGSEIVLTQSPATLSVSPGES ATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRASGIPDRFSGSGSG TDFTLTISSLQAEDVAVYYCQQYGSSLTFGGGTKVEIK
139104- nt ScFv domain	360	GAAGTGCAATTGCTCGAAACTGGAGGAGGTCTGGTGCAACCTGGAGGATC ACTTCGCCTGTCCTGCGCCGTGTCGGGCTTTGCCCTGTCCAACCATGGAA TGAGCTGGGTCCGCCGCGCGCCGGGGAAGGGCCTCGAATGGGTGTCCGGC ATCGTCTACTCCGGCTCCACCTACTACGCCGCGTCCGTGAAGGGCCGGTT CACGATTTCACGGGACAACTCGCGGAACACCCTGTACCTCCAAATGAATT CCCTTCGGCCGGAGGATACTGCCATCTACTACTGCTCCGCCCACGGTGGC GAATCCGACGTCTGGGGCCAGGGAACCACCGTGACCGTGTCCAGCGCGTC CGGGGGAGGAGGAAGCGGGGGTAGAGCATCGGGTGGAGGCGGATCAGAGA TCGTGCTGACCCAGTCCCCCGCCACCTTGAGCGTGTCACCAGGAGAGTCC GCCACCCTGTCATGCCGCGCCAGCCAGTCCGTGTCCTCCAACCTGGCTTG

		GTACCAGCAGAAGCCGGGGCAGGCCCCTAGACTCCTGATCTATGGGGCGTCGACCCGGGCATCTGGAATTCCCGATAGGTTCAGCGGATCGGGCTCGGGCACTGACTTCACTCTGACCATCTCCTCGCTGCAAGCCGAGGACGTGGCTGTGTACTACTGTCAGCAGTACGGAAGCTCCCTGACTTTCGGTGGCGGGACCAAAGTCGAGATTAAG
139104- aa VH	375	EVQLLETGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEWVSGIVYSGSTYYAASVKGRFTISRDNSRNTLYLQMNSLRPEDTAIYYCSAHGGESDVWGQGTTVTVSS
139104- aa VL	390	EIVLTQSPATLSVSPGESATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRASGIPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYGSSLTFGGGTKVEIK
139106		
139106- aa ScFv domain	346	EVQLVETGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEWVSGIVYSGSTYYAASVKGRFTISRDNSRNTLYLQMNSLRPEDTAIYYCSAHGGESDVWGQGTTVTVSSASGGGGSGGRASGGGGSEIVMTQSPATLSVSPGERATLSCRASQSVSSKLAWYQQKPGQAPRLLMYGASIRATGIPDRFSGSGSGTEFTLTISSLEPEDFAVYYCQQYGSSSWTFGQGTKVEIK
139106- nt ScFv domain	361	GAAGTGCAATTGGTGGAAACTGGAGGAGGACTTGTGCAACCTGGAGGATCATTGAGACTGAGCTGCGCAGTGTCGGGATTCGCCCTGAGCAACCATGGAATGTCCTGGGTCAGAAGGGCCCCTGGAAAAGGCCTCGAATGGGTGTCAGGGATCGTGTACTCCGGTTCCACTTACTACGCCGCCTCCGTGAAGGGGCGCTTCACTATCTCACGGGATAACTCCCGCAATACCCTGTACCTCCAAATGAACAGCCTGCGGCCGGAGGATACCGCCATCTACTACTGTTCCGCCCACGGTGGAGAGTCTGACGTCTGGGGCCAGGGAACTACCGTGACCGTGTCCTCCGCGTCCGGCGGTGGAGGGAGCGGCGGCCGCGCCAGCGGCGGCGGAGGCTCCGAGATCGTGATGACCCAGAGCCCCGCTACTCTGTCGGTGTCGCCCGGAGAAAGGGCGACCCTGTCCTGCCGGGCGTCGCAGTCCGTGAGCAGCAAGCTGGCTTGGTACCAGCAGAAGCCGGGCCAGGCACCACGCCTGCTTATGTACGGTGCCTCCATTCGGGCCACCGGAATCCCGGACCGGTTCTCGGGGTCGGGGTCCGGTACCGAGTTCACACTGACCATTTCCTCGCTCGAGCCCGAGGACTTTGCCGTCTATTACTGCCAGCAGTACGGCTCCTCCTCATGGACGTTCGGCCAGGGGACCAAGGTCGAAATCAAG
139106- aa VH	376	EVQLVETGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEWVSGIVYSGSTYYAASVKGRFTISRDNSRNTLYLQMNSLRPEDTAIYYCSAHGGESDVWGQGTTVTVSS
139106- aa VL	391	EIVMTQSPATLSVSPGERATLSCRASQSVSSKLAWYQQKPGQAPRLLMYGASIRATGIPDRFSGSGSGTEFTLTISSLEPEDFAVYYCQQYGSSSWTFGQGTKVEIK
139107		
139107- aa ScFv domain	347	EVQLVETGGGVVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEWVSGIVYSGSTYYAASVKGRFTISRDNSRNTLYLQMNSLRPEDTAIYYCSAHGGESDVWGQGTTVTVSSASGGGGSGGRASGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVGSTNLAWYQQKPGQAPRLLIYDASNRATGIPDRFSGGGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPWTFGQGTKVEIK
139107- nt ScFv domain	362	GAAGTGCAATTGGTGGAGACTGGAGGAGGAGTGGTGCAACCTGGAGGAAGCCTGAGACTGTCATGCGCGGTGTCGGGCTTCGCCCTCTCCAACCACGGAATGTCCTGGGTCCGCCGGGCCCCTGGGAAAGGACTTGAATGGGTGTCCGGCATCGTGTACTCGGGTTCCACCTACTACGCGGCCTCAGTGAAGGGCCGGTTTACTATTAGCCGCGACAACTCCAGAAACACACTGTACCTCCAAATGAACTCGCTGCGGCCGGAAGATACCGCTATCTACTACTGCTCCGCCCATGGGGGAGAGTCGGACGTCTGGGGACAGGGCACCACTGTCACTGTGTCCAGCGCTTC

		CGGCGGTGGTGGAAGCGGGGGACGGGCCTCAGGAGGCGGTGGCAGCGAGA TTGTGCTGACCCAGTCCCCCGGGACCCTGAGCCTGTCCCCGGGAGAAAGG GCCACCCTCTCCTGTCGGGCATCCCAGTCCGTGGGGTCTACTAACCTTGC ATGGTACCAGCAGAAGCCCGGCCAGGCCCCTCGCCTGCTGATCTACGACG CGTCCAATAGAGCCACCGGCATCCCGGATCGCTTCAGCGGAGGCGGATCG GGCACCGACTTCACCCTCACCATTTCAAGGCTGGAACCGGAGGACTTCGC CGTGTACTACTGCCAGCAGTATGGTTCGTCCCCACCCTGGACGTTCGGCC AGGGGACTAAGGTCGAGATCAAG
139107- aa VH	377	EVQLVETGGGVVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEWVSG IVYSGSTYYAASVKGRFTISRDNSRNTLYLQMNSLRPEDTAIYYCSAHGG ESDVWGQGTTVTVSS
139107- aa VL	392	EIVLTQSPGTLSLSPGERATLSCRASQSVGSTNLAWYQQKPGQAPRLLIY DASNRATGIPDRFSGGGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPWTF GQGTKVEIK
139108		
139108- aa ScFv domain	348	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSY ISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARES GDGMDVWGQGTTVTVSSASGGGGSGGRASGGGGSDIQMTQSPSSLSASVG DRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYTLAFGQGTKVDIK
139108- nt ScFv domain	363	CAAGTGCAACTCGTGGAATCTGGTGGAGGACTCGTGAAACCTGGAGGATC ATTGAGACTGTCATGCGCGGCCTCGGGATTCACGTTCTCCGATTACTACA TGAGCTGGATTCGCCAGGCTCCGGGGAAGGGACTGGAATGGGTGTCCTAC ATTTCCTCATCCGGCTCCACCATCTACTACGCGGACTCCGTGAAGGGGAG ATTCACCATTAGCCGCGATAACGCCAAGAACAGCCTGTACCTTCAGATGA ACTCCCTGCGGGCTGAAGATACTGCCGTCTACTACTGCGCAAGGGAGAGC GGAGATGGGATGGACGTCTGGGGACAGGGTACCACTGTGACCGTGTCGTC GGCCTCCGGCGGAGGGGGTTCGGGTGGAAGGGCCAGCGGCGGCGGAGGCA GCGACATCCAGATGACCCAGTCCCCCTCATCGCTGTCCGCCTCCGTGGGC GACCGCGTCACCATCACATGCCGGGCCTCACAGTCGATCTCCTCCTACCT CAATTGGTATCAGCAGAAGCCCGGAAAGGCCCCTAAGCTTCTGATCTACG CAGCGTCCTCCCTGCAATCCGGGGTCCCATCTCGGTTCTCCGGCTCGGGC AGCGGTACCGACTTCACTCTGACCATCTCGAGCCTGCAGCCGGAGGACTT CGCCACTTACTACTGTCAGCAAAGCTACACCCTCGCGTTTGGCCAGGGCA CCAAAGTGGACATCAAG
139108- aa VH	378	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSY ISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARES GDGMDVWGQGTTVTVSS
139108- aa VL	393	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYA ASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYTLAFGQGT KVDIK
139110		
139110- aa ScFv domain	350	QVQLVQSGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSY ISSSGNTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARST MVREDYWGQGTLVTVSSASGGGGSGGRASGGGGSDIVLTQSPLSLPVTLG QPASISCKSSESLVHNSGKTYLNWFHQRPGQSPRRLIYEVSNRDSGVPDR FTGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWPGTFGQGTKLEIK
139110- nt ScFv domain	365	CAAGTGCAACTGGTGCAAAGCGGAGGAGGATTGGTCAAACCCGGAGGAAG CCTGAGACTGTCATGCGCGGCCTCTGGATTCACCTTCTCCGATTACTACA TGTCATGGATCAGACAGGCCCCGGGGAAGGGCCTCGAATGGGTGTCCTAC ATCTCGTCCTCCGGGAACACCATCTACTACGCCGACAGCGTGAAGGGCCG

		CTTTACCATTTCCCGCGACAACGCAAAGAACTCGCTGTACCTTCAGATGA ATTCCCTGCGGGCTGAAGATACCGCGGTGTACTATTGCGCCCGGTCCACT ATGGTCCGGGAGGACTACTGGGGACAGGGCACACTCGTGACCGTGTCCAG CGCGAGCGGGGGTGGAGGCAGCGGTGGACGCGCCTCCGGCGGCGGCGGTT CAGACATCGTGCTGACTCAGTCGCCCCTGTCGCTGCCGGTCACCCTGGGC CAACCGGCCTCAATTAGCTGCAAGTCCTCGGAGAGCCTGGTGCACAACTC AGGAAAGACTTACCTGAACTGGTTCCATCAGCGGCCTGGACAGTCCCCAC GGAGGCTCATCTATGAAGTGTCCAACAGGGATTCGGGGGTGCCCGACCGC TTCACTGGCTCCGGGTCCGGCACCGACTTCACCTTGAAAATCTCCAGAGT GGAAGCCGAGGACGTGGGCGTGTACTACTGTATGCAGGGTACCCACTGGC CTGGAACCTTTGGACAAGGAACTAAGCTCGAGATTAAG
139110- aa VH	380	QVQLVQSGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSY ISSSGNTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARST MVREDYWGQGTLVTVSS
139110- aa VL	395	DIVLTQSPLSLPVTLGQPASISCKSSESLVHNSGKTYLNWFHQRPGQSPR RLIYEVSNRDSGVPDRFTGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWP GTFGQGTKLEIK
139112		
139112- aa ScFv domain	351	QVQLVESGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEWVSG IVYSGSTYYAASVKGRFTISRDNSRNTLYLQMNSLRPEDTAIYYCSAHGG ESDVWGQGTTVTVSSASGGGGSGGRASGGGGSDIRLTQSPSPLSASVGDR VTITCQASEDINKFLNWYHQTPGKAPKLLIYDASTLQTGVPSRFSGSGSG TDFTLTINSLQPEDIGTYYCQQYESLPLTFGGGTKVEIK
139112- nt ScFv domain	366	CAAGTGCAACTCGTGGAATCTGGTGGAGGACTCGTGCAACCCGGTGGAAG CCTTAGGCTGTCGTGCGCCGTCAGCGGGTTTGCTCTGAGCAACCATGGAA TGTCCTGGGTCCGCCGGGCACCGGGAAAGGGCTGGAATGGGTGTCCGGC ATCGTGTACAGCGGGTCAACCTATTACGCCGCGTCCGTGAAGGGCAGATT CACTATCTCAAGAGACAACAGCCGGAACACCCTGTACTTGCAAATGAATT CCCTGCGCCCCGAGGACACCGCCATCTACTACTGCTCCGCCCACGGAGGA GAGTCGGACGTGTGGGGCCAGGGAACGACTGTGACTGTGTCCAGCGCATC AGGAGGGGGTGGTTCGGGCGGCCGGGCCTCGGGGGGAGGAGGTTCCGACA TTCGGCTGACCCAGTCCCCGTCCCCACTGTCGGCCTCCGTCGGCGACCGC GTGACCATCACTTGTCAGGCGTCCGAGGACATTAACAAGTTCCTGAACTG GTACCACCAGACCCCTGGAAAGGCCCCCAAGCTGCTGATCTACGATGCCT CGACCCTTCAAACTGGAGTGCCTAGCCGGTTCTCCGGGTCCGGCTCCGGC ACTGATTTCACTCTGACCATCAACTCATTGCAGCCGGAAGATATCGGGAC CTACTATTGCCAGCAGTACGAATCCCTCCCGCTCACATTCGGCGGGGGAA CCAAGGTCGAGATTAAG
139112- aa VH	381	QVQLVESGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEWVSG IVYSGSTYYAASVKGRFTISRDNSRNTLYLQMNSLRPEDTAIYYCSAHGG ESDVWGQGTTVTVSS
139112- aa VL	396	DIRLTQSPSPLSASVGDRVTITCQASEDINKFLNWYHQTPGKAPKLLIYD ASTLQTGVPSRFSGSGSGTDFTLTINSLQPEDIGTYYCQQYESLPLTFGG GTKVEIK
139113		
139113- aa ScFv domain	352	EVQLVETGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEWVSG IVYSGSTYYAASVKGRFTISRDNSRNTLYLQMNSLRPEDTAIYYCSAHGG ESDVWGQGTTVTVSSASGGGGSGGRASGGGGSETTLTQSPATLSVSPGER ATLSCRASQSVGSNLAWYQQKPGQGPRLLIYGASTRATGIPARFSGSGSG TEFTLTISSLQPEDFAVYYCQQYNDWLPVTFGQGTKVEIK
139113- nt	367	GAAGTGCAATTGGTGGAAACTGGAGGAGGACTTGTGCAACCTGGAGGATC

ScFv domain		ATTGCGGCTCTCATGCGCTGTCTCCGGCTTCGCCCTGTCAAATCACGGGA TGTCGTGGGTCAGACGGGCCCCGGGAAAGGGTCTGGAATGGGTGTCGGGG ATTGTGTACAGCGGCTCCACCTACTACGCCGCTTCGGTCAAGGGCCGCTT CACTATTTCACGGGACAACAGCCGCAACACCCTCTATCTGCAAATGAACT CTCTCCGCCCGGAGGATACCGCCATCTACTACTGCTCCGCACACGGCGGC GAATCCGACGTGTGGGGACAGGGAACCACTGTCACCGTGTCGTCCGCATC CGGTGGCGGAGGATCGGGTGGCCGGGCCTCCGGGGGCGGCGGCAGCGAGA CTACCCTGACCCAGTCCCCTGCCACTCTGTCCGTGAGCCCGGGAGAGAGA GCCACCCTTAGCTGCCGGGCCAGCCAGAGCGTGGGCTCCAACCTGGCCTG GTACCAGCAGAAGCCAGGACAGGGTCCCAGGCTGCTGATCTACGGAGCCT CCACTCGCGCGACCGGCATCCCCGCGAGGTTCTCCGGGTCGGGTTCCGGG ACCGAGTTCACCCTGACCATCTCCTCCCTCCAACCGGAGGACTTCGCGGT GTACTACTGTCAGCAGTACAACGATTGGCTGCCCGTGACATTTGGACAGG GGACGAAGGTGGAAATCAAA
139113- aa VH	382	EVQLVETGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEWVSG IVYSGSTYYAASVKGRFTISRDNSRNTLYLQMNSLRPEDTAIYYCSAHGG ESDVWGQGTTVTVSS
139113- aa VL	397	ETTLTQSPATLSVSPGERATLSCRASQSVGSNLAWYQQKPGQGPRLLIYG ASTRATGIPARFSGSGSGTEFTLTISSLQPEDFAVYYCQQYNDWLPVTFG QGTKVEIK
139114		
139114- aa ScFv domain	353	EVQLVESGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEWVSG IVYSGSTYYAASVKGRFTISRDNSRNTLYLQMNSLRPEDTAIYYCSAHGG ESDVWGQGTTVTVSSASGGGGSGGRASGGGGSEIVLTQSPGTLSLSPGER ATLSCRASQSIGSSSLAWYQQKPGQAPRLLMYGASSRASGIPDRFSGSGS GTDFTLTISRLEPEDFAVYYCQQYAGSPPFTFGQGTKVEIK
139114- nt ScFv domain	368	GAAGTGCAATTGGTGGAATCTGGTGGAGGACTTGTGCAACCTGGAGGATC ACTGAGACTGTCATGCGCGGTGTCCGGTTTTGCCCTGAGCAATCATGGGA TGTCGTGGGTCCGGCGCGCCCCCGGAAAGGGTCTGGAATGGGTGTCGGGT ATCGTCTACTCCGGGAGCACTTACTACGCCGCGAGCGTGAAGGGCCGCTT CACCATTTCCCGCGATAACTCCCGCAACACCCTGTACTTGCAAATGAACT CGCTCCGGCCTGAGGACACTGCCATCTACTACTGCTCCGCACACGGAGGA GAATCCGACGTGTGGGGCCAGGGAACTACCGTGACCGTCAGCAGCGCCTC CGGCGGCGGGGGCTCAGGCGGACGGGCTAGCGGCGGCGGTGGCTCCGAGA TCGTGCTGACCCAGTCGCCTGGCACTCTCTCGCTGAGCCCCGGGGAAAGG GCAACCCTGTCCTGTCGGGCCAGCCAGTCCATTGGATCATCCTCCCTCGC CTGGTATCAGCAGAAACCGGGACAGGCTCCGCGGCTGCTTATGTATGGGG CCAGCTCAAGAGCCTCCGGCATTCCCGACCGGTTCTCCGGGTCCGGTTCC GGCACCGATTTCACCCTGACTATCTCGAGGCTGGAGCCAGAGGACTTCGC CGTGTACTACTGCCAGCAGTACGCGGGGTCCCCGCCGTTCACGTTCGGAC AGGGAACCAAGGTCGAGATCAAG
139114- aa VH	383	EVQLVESGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEWVSG IVYSGSTYYAASVKGRFTISRDNSRNTLYLQMNSLRPEDTAIYYCSAHGG ESDVWGQGTTVTVSS
139114- aa VL	398	EIVLTQSPGTLSLSPGERATLSCRASQSIGSSSLAWYQQKPGQAPRLLMY GASSRASGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYAGSPPFTF GQGTKVEIK
149362		
149362-aa ScFv domain	429	QVQLQESGPGLVKPSETLSLTCTVSGGSISSSYYYWGWIRQPPGKGLEWI GSIYYSGSAYYNPSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARH WQEWPDAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSETTLTQSPAFMSAT

		PGDKVIISCKASQDIDDAMNWYQQKPGEAPLFIIQSATSPVPGIPPRFSG SGFGTDFSLTINNIESEDAAYYFCLQHDNFPLTFGQGTKLEIK
149362-nt ScFv domain	450	CAAGTGCAGCTTCAGGAAAGCGGACCGGGCCTGGTCAAGCCATCCGAAAC TCTCTCCCTGACTTGCACTGTGTCTGGCGGTTCCATCTCATCGTCGTACT ACTACTGGGGCTGGATTAGGCAGCCGCCCGGAAAGGGACTGGAGTGGATC GGAAGCATCTACTATTCCGGCTCGGCGTACTACAACCCTAGCCTCAAGTC GAGAGTGACCATCTCCGTGGATACCTCCAAGAACCAGTTTTCCCTGCGCC TGAGCTCCGTGACCGCCGCTGACACCGCCGTGTACTACTGTGCTCGGCAT TGGCAGGAATGGCCCGATGCCTTCGACATTTGGGGCCAGGGCACTATGGT CACTGTGTCATCCGGGGGTGGAGGCAGCGGGGGAGGAGGGTCCGGGGGGG GAGGTTCAGAGACAACCTTGACCCAGTCACCCGCATTCATGTCCGCCACT CCGGGAGACAAGGTCATCATCTCGTGCAAAGCGTCCCAGGATATCGACGA TGCCATGAATTGGTACCAGCAGAAGCCTGGCGAAGCGCCGCTGTTCATTA TCCAATCCGCAACCTCGCCCGTGCCTGGAATCCCACCGCGGTTCAGCGGC AGCGGTTTCGGAACCGACTTTTCCCTGACCATTAACAACATTGAGTCCGA GGACGCCGCCTACTACTTCTGCCTGCAACACGACAACTTCCCTCTCACGT TCGGCCAGGGAACCAAGCTGGAAATCAAG
149362-aa VH	471	QVQLQESGPGLVKPSETLSLTCTVSGGSISSSYYYWGWIRQPPGKGLEWI GSIYYSGSAYYNPSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARH WQEWPDAFDIWGQGTMVTVSS
149362-aa VL	492	ETTLTQSPAFMSATPGDKVIISCKASQDIDDAMNWYQQKPGEAPLFIIQS ATSPVPGIPPRFSGSGFGTDFSLTINNIESEDAAYYFCLQHDNFPLTFGQ GTKLEIK
149363		
149363-aa ScFv domain	430	QVNLRESGPALVKPTQTLTLTCTFSGFSLRTSGMCVSWIRQPPGKALEWL ARIDWDEDKFYSTSLKTRLTISKDTSDNQVVLRMTNMDPADTATYYCARS GAGGTSATAFDIWGPGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLS ASVGDRVTITCRASQDIYNNLAWFQLKPGSAPRSLMYAANKSQSGVPSRF SGSASGTDFTLTISSLQPEDFATYYCQHYYRFPYSFGQGTKLEIK
149363-nt ScFv domain	451	CAAGTCAATCTGCGCGAATCCGGCCCCGCCTTGGTCAAGCCTACCCAGAC CCTCACTCTGACCTGTACTTTCTCCGGCTTCTCCCTGCGGACTTCCGGGA TGTGCGTGTCCTGGATCAGACAGCCTCCGGGAAAGGCCCTGGAGTGGCTC GCTCGCATTGACTGGGATGAGGACAAGTTCTACTCCACCTCACTCAAGAC CAGGCTGACCATCAGCAAAGATACCTCTGACAACCAAGTGGTGCTCCGCA TGACCAACATGGACCCAGCCGACACTGCCACTTACTACTGCGCGAGGAGC GGAGCGGGCGGAACCTCCGCCACCGCCTTCGATATTTGGGGCCCGGGTAC CATGGTCACCGTGTCAAGCGGAGGAGGGGGGTCCGGGGGCGGCGGTTCCG GGGGAGGCGGATCGGACATTCAGATGACTCAGTCACCATCGTCCCTGAGC GCTAGCGTGGGCGACAGAGTGACAATCACTTGCCGGGCATCCCAGGACAT CTATAACAACCTTGCGTGGTTCCAGCTGAAGCCTGGTTCCGCACCGCGGT CACTTATGTACGCCGCCAACAAGAGCCAGTCGGGAGTGCCGTCCCGGTTT TCCGGTTCGGCCTCGGGAACTGACTTCACCCTGACGATCTCCAGCCTGCA ACCCGAGGATTTCGCCACCTACTACTGCCAGCACTACTACCGCTTTCCCT ACTCGTTCGGACAGGGAACCAAGCTGGAAATCAAG
149363-aa VH	472	QVNLRESGPALVKPTQTLTLTCTFSGFSLRTSGMCVSWIRQPPGKALEWL ARIDWDEDKFYSTSLKTRLTISKDTSDNQVVLRMTNMDPADTATYYCARS GAGGTSATAFDIWGPGTMVTVSS
149363-aa VL	493	DIQMTQSPSSLSASVGDRVTITCRASQDIYNNLAWFQLKPGSAPRSLMYA ANKSQSGVPSRFSGSASGTDFTLTISSLQPEDFATYYCQHYYRFPYSFGQ GTKLEIK
149364		

149364-aa ScFv domain	431	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAKTIAAVYAFDIWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPLSLPVTPEEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPYTFGQGTKLEIK
149364-nt ScFv domain	452	GAAGTGCAGCTTGTCGAATCCGGGGGGGGACTGGTCAAGCCGGGCGGATCACTGAGACTGTCCTGCGCCGCGAGCGGCTTCACGTTCTCCTCCTACTCCATGAACTGGGTCCGCCAAGCCCCCGGGAAGGGACTGGAATGGGTGTCCTCTATCTCCTCGTCGTCGTCCTACATCTACTACGCCGACTCCGTGAAGGGAAGATTCACCATTTCCCGCGACAACGCAAAGAACTCACTGTACTTGCAAATGAACTCACTCCGGGCCGAAGATACTGCTGTGTACTATTGCGCCAAGACTATTGCCGCCGTCTACGCTTTCGACATCTGGGGCCAGGGAACCACCGTGACTGTGTCGTCCGGTGGTGGTGGCTCGGGCGGAGGAGGAAGCGGCGGCGGGGGGTCCGAGATTGTGCTGACCCAGTCGCCACTGAGCCTCCCTGTGACCCCCGAGGAACCCGCCAGCATCAGCTGCCGGTCCAGCCAGTCCCTGCTCCACTCCAACGGATACAATTACCTCGATTGGTACCTTCAGAAGCCTGGACAAAGCCCGCAGCTGCTCATCTACTTGGGATCAAACCGCGCGTCAGGAGTGCCTGACCGGTTCTCCGGCTCGGGCAGCGGTACCGATTTCACCCTGAAAATCTCCAGGGTGGAGGCAGAGGACGTGGGAGTGTATTACTGTATGCAGGCGCTGCAGACTCCGTACACATTTGGGCAGGGCACCAAGCTGGAGATCAAG
149364-aa VH	473	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAKTIAAVYAFDIWGQGTTVTVSS
149364-aa VL	494	EIVLTQSPLSLPVTPEEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPYTFGQGTKLEIK
149365		
149365-aa ScFv domain	432	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLRGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSSYVLTQSPSVSAAPGYTATISCGGNNIGTKSVHWYQQKPGQAPLLVIRDDSVRPSKIPGRFSGSNSGNMATLTISGVQAGDEADFYCQVWDSDSEHVVFGGGTKLTVL
149365-nt ScFv domain	453	GAAGTCCAGCTCGTGGAGTCCGGCGGAGGCCTTGTGAAGCCTGGAGGTTCGCTGAGACTGTCCTGCGCCGCCTCCGGCTTCACCTTCTCCGACTACTACATGTCCTGGATCAGACAGGCCCCGGGAAAGGGCCTGGAATGGGTGTCCTACATCTCGTCATCGGGCAGCACTATCTACTACGCGGACTCAGTGAAGGGGCGGTTCACCATTTCCCGGGATAACGCGAAGAACTCGCTGTATCTGCAAATGAACTCACTGAGGGCCGAGGACACCGCCGTGTACTACTGCGCCCGCGATCTCCGCGGGGCATTTGACATCTGGGGACAGGGAACCATGGTCACAGTGTCCAGCGGAGGGGGAGGATCGGGTGGCGGAGGTTCCGGGGGTGGAGGCTCCTCCTACGTGCTGACTCAGAGCCCAAGCGTCAGCGCTGCGCCCGGTTACACGGCAACCATCTCCTGTGGCGGAAACAACATTGGGACCAAGTCTGTGCACTGGTATCAGCAGAAGCCGGGCCAAGCTCCCCTGTTGGTGATCCGCGATGACTCCGTGCGGCCTAGCAAAATTCCGGGACGGTTCTCCGGCTCCAACAGCGGCAATATGGCCACTCTCACCATCTCGGGAGTGCAGGCCGGAGATGAAGCCGACTTCTACTGCCAAGTCTGGGACTCAGACTCCGAGCATGTGGTGTTCGGGGGCGGAACCAAGCTGACTGTGCTC
149365-aa VH	474	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLRGAFDIWGQGTMVTVSS
149365-aa VL	495	SYVLTQSPSVSAAPGYTATISCGGNNIGTKSVHWYQQKPGQAPLLVIRDDSVRPSKIPGRFSGSNSGNMATLTISGVQAGDEADFYCQVWDSDSEHVVFG

		GGTKLTVL
149366		
149366-aa ScFv domain	433	QVQLVQSGAEVKKPGASVKVSCKPSGYTVTSHYIHWVRRAPGQGLEWMGM INPSGGVTAYSQTLQGRVTMTSDTSSSTVYMELSSLRSEDTAMYYCAREG SGSGWYFDFWGRGTLVTVSSGGGGSGGGGSGGGGSSYVLTQPPSVSVSPG QTASITCSGDGLSKKYVSWYQQKAGQSPVVLISRDKERPSGIPDRFSGSN SADTATLTISGTQAMDEADYYCQAWDDTTVVFGGGTKLTVL
149366-nt ScFv domain	454	CAAGTGCAGCTGGTGCAGAGCGGGGCCGAAGTCAAGAAGCCGGGAGCCTC CGTGAAAGTGTCCTGCAAGCCTTCGGGATACACCGTGACCTCCCACTACA TTCATTGGGTCCGCCGCGCCCCCGGCCAAGGACTCGAGTGGATGGGCATG ATCAACCCTAGCGGCGGAGTGACCGCGTACAGCCAGACGCTGCAGGGACG CGTGACTATGACCTCGGATACCTCCTCCTCCACCGTCTATATGGAACTGT CCAGCCTGCGGTCCGAGGATACCGCCATGTACTACTGCGCCCGGGAAGGA TCAGGCTCCGGGTGGTATTTCGACTTCTGGGGAAGAGGCACCCTCGTGAC TGTGTCATCTGGGGGAGGGGGTTCCGGTGGTGGCGGATCGGGAGGAGGCG GTTCATCCTACGTGCTGACCCAGCCACCCTCCGTGTCCGTGAGCCCCGGC CAGACTGCATCGATTACATGTAGCGGCGACGGCCTCTCCAAGAAATACGT GTCGTGGTACCAGCAGAAGGCCGGACAGAGCCCGGTGGTGCTGATCTCAA GAGATAAGGAGCGGCCTAGCGGAATCCCGGACAGGTTCTCGGGTTCCAAC TCCGCGGACACTGCTACTCTGACCATCTCGGGGACCCAGGCTATGGACGA AGCCGATTACTACTGCCAAGCCTGGGACGACACTACTGTCGTGTTTGGAG GGGGCACCAAGTTGACCGTCCTT
149366-aa VH	475	QVQLVQSGAEVKKPGASVKVSCKPSGYTVTSHYIHWVRRAPGQGLEWMGM INPSGGVTAYSQTLQGRVTMTSDTSSSTVYMELSSLRSEDTAMYYCAREG SGSGWYFDFWGRGTLVTVSS
149366-aa VL	496	SYVLTQPPSVSVSPGQTASITCSGDGLSKKYVSWYQQKAGQSPVVLISRD KERPSGIPDRFSGSNSADTATLTISGTQAMDEADYYCQAWDDTTVVFGGG TKLTVL
149367		
149367-aa ScFv domain	434	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWI GYIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARA GIAARLRGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIVMTQSPSSVS ASVGDRVIITCRASQGIRNWLAWYQQKPGKAPNLLIYAASNLQSGVPSRF SGSGSGADFTLTISSLQPEDVATYYCQKYNSAPFTFGPGTKVDIK
149367-nt ScFv domain	455	CAAGTGCAGCTTCAGGAGAGCGGCCCGGGACTCGTGAAGCCGTCCCAGAC CCTGTCCCTGACTTGCACCGTGTCGGGAGGAAGCATCTCGAGCGGAGGCT ACTATTGGTCGTGGATTCGGCAGCACCCTGGAAAGGGCCTGGAATGGATC GGCTACATCTACTACTCCGGCTCGACCTACTACAACCCATCGCTGAAGTC CAGAGTGACAATCTCAGTGGACACGTCCAAGAATCAGTTCAGCCTGAAGC TCTCTTCCGTGACTGCGGCCGACACCGCCGTGTACTACTGCGCACGCGCT GGAATTGCCGCCCGGCTGAGGGGTGCCTTCGACATTTGGGGACAGGGCAC CATGGTCACCGTGTCCTCCGGCGGCGGAGGTTCCGGGGGTGGAGGCTCAG GAGGAGGGGGGTCCGACATCGTCATGACTCAGTCGCCCTCAAGCGTCAGC GCGTCCGTCGGGGACAGAGTGATCATCACCTGTCGGGCGTCCCAGGGAAT TCGCAACTGGCTGGCCTGGTATCAGCAGAAGCCCGGAAAGGCCCCCAACC TGTTGATCTACGCCGCCTCAAACCTCCAATCCGGGGTGCCGAGCCGCTTC AGCGGCTCCGGTTCGGGTGCCGATTTCACTCTGACCATCTCCTCCCTGCA ACCTGAAGATGTGGCTACCTACTACTGCCAAAAGTACAACTCCGCACCTT TTACTTTCGGACCGGGGACCAAAGTGGACATTAAG
149367-aa VH	476	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWI GYIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARA

		GIAARLRGAFDIWGQGTMVTVSS
149367-aa VL	497	DIVMTQSPSSVSASVGDRVIITCRASQGIRNWLAWYQQKPGKAPNLLIYA ASNLQSGVPSRFSGSGSGADFTLTISSLQPEDVATYYCQKYNSAPFTFGP GTKVDIK
149368		
149368-aa ScFv domain	435	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGG IIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARRG GYQLLRWDVGLLRSAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSSYVLTQ PPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVLYGKNNRPSG VPDRFSGSRSGTTASLTITGAQAEDEADYYCSSRDSSGDHLRVFGTGTKV TVL
149368-nt ScFv domain	456	CAAGTGCAGCTGGTCCAGTCGGGCGCCGAGGTCAAGAAGCCCGGGAGCTC TGTGAAAGTGTCCTGCAAGGCCTCCGGGGGCACCTTTAGCTCCTACGCCA TCTCCTGGGTCCGCCAAGCACCGGGTCAAGGCCTGGAGTGGATGGGGGGA ATTATCCCTATCTTCGGCACTGCCAACTACGCCCAGAAGTTCCAGGGACG CGTGACCATTACCGCGGACGAATCCACCTCCACCGCTTATATGGAGCTGT CCAGCTTGCGCTCGGAAGATACCGCCGTGTACTACTGCGCCCGGAGGGGT GGATACCAGCTGCTGAGATGGGACGTGGGCCTCCTGCGGTCGGCGTTCGA CATCTGGGGCCAGGGCACTATGGTCACTGTGTCCAGCGGAGGAGGCGGAT CGGGAGGCGGCGGATCAGGGGGAGGCGGTTCCAGCTACGTGCTTACTCAA CCCCCTTCGGTGTCCGTGGCCCCGGGACAGACCGCCAGAATCACTTGCGG AGGAAACAACATTGGGTCCAAGAGCGTGCATTGGTACCAGCAGAAGCCAG GACAGGCCCCTGTGCTGGTGCTCTACGGGAAGAACAATCGGCCCAGCGGA GTGCCGGACAGGTTCTCGGGTTCACGCTCCGGTACAACCGCTTCACTGAC TATCACCGGGGCCCAGGCAGAGGATGAAGCGGACTACTACTGTTCCTCCC GGGATTCATCCGGCGACCACCTCCGGGTGTTCGGAACCGGAACGAAGGTC ACCGTGCTG
149368-aa VH	477	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGG IIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARRG GYQLLRWDVGLLRSAFDIWGQGTMVTVSS
149368-aa VL	498	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVLYGK NNRPSGVPDRFSGSRSGTTASLTITGAQAEDEADYYCSSRDSSGDHLRVF GTGTKVTVL
149369		
149369-aa ScFv domain	436	EVQLQQSGPGLVKPSQTLSLTCAISGDSVSSNSAAWNWIRQSPSRGLEWL GRTYYRSKWYSFYAISLKSRIIINPDTSKNQFSLQLKSVTPEDTAVYYCA RSSPEGLFLYWFDPWGQGTLVTVSSGGDGSGGGGSGGGGSSSELTQDPAV SVALGQTIRITCQGDSLGNYYATWYQQKPGQAPVLVIYGTNNRPSGIPDR FSASSSGNTASLTITGAQAEDEADYYCNSRDSSGHHLLFGTGTKVTVL
149369-nt ScFv domain	457	GAAGTGCAGCTCCAACAGTCAGGACCGGGGCTCGTGAAGCCATCCCAGAC CCTGTCCCTGACTTGTGCCATCTCGGGAGATAGCGTGTCATCGAACTCCG CCGCCTGGAACTGGATTCGGCAGAGCCCGTCCCGCGGACTGGAGTGGCTT GGAAGGACCTACTACCGGTCCAAGTGGTACTCTTTCTACGCGATCTCGCT GAAGTCCCGCATTATCATTAACCCTGATACCTCCAAGAATCAGTTCTCCC TCCAACTGAAATCCGTCACCCCCGAGGACACAGCAGTGTATTACTGCGCA CGGAGCAGCCCCGAAGGACTGTTCCTGTATTGGTTTGACCCCTGGGGCCA GGGGACTCTTGTGACCGTGTCGAGCGGCGGAGATGGGTCCGGTGGCGGTG GTTCGGGGGGCGGCGGATCATCATCCGAACTGACCCAGGACCCGGCTGTG TCCGTGGCGCTGGGACAAACCATCCGCATTACGTGCCAGGGAGACTCCCT GGGCAACTACTACGCCACTTGGTACCAGCAGAAGCCGGGCCAAGCCCCTG TGTTGGTCATCTACGGGACCAACAACAGACCTTCCGGCATCCCCGACCGG

		TTCAGCGCTTCGTCCTCCGGCAACACTGCCAGCCTGACCATCACTGGAGC GCAGGCCGAAGATGAGGCCGACTACTACTGCAACAGCAGAGACTCCTCGG GTCATCACCTCTTGTTCGGAACTGGAACCAAGGTCACCGTGCTG
149369-aa VH	478	EVQLQQSGPGLVKPSQTLSLTCAISGDSVSSNSAAWNWIRQSPSRGLEWL GRTYYRSKWYSFYAISLKSRIIINPDTSKNQFSLQLKSVTPEDTAVYYCA RSSPEGLFLYWFDPWGQGTLVTVSS
149369-aa VL	499	SSELTQDPAVSVALGQTIRITCQGDSLGNYYATWYQQKPGQAPVLVIYGT NNRPSGIPDRFSASSSGNTASLTITGAQAEDEADYYCNSRDSSGHHLLFG TGTKVTVL
BCMA_EBB-C1978-A4		
BCMA_EBB-C1978-A4 - aa ScFv domain	437	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSA ISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKVE GSGSLDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVMTQSPGTLSLSPGE RATLSCRASQSVSSAYLAWYQQKPGQPPRLLISGASTRATGIPDRFGGSG SGTDFTLTISRLEPEDFAVYYCQHYGSSFNGSSLFTFGQGTRLEIK
BCMA_EBB-C1978-A4 - nt ScFv domain	458	GAAGTGCAGCTCGTGGAGTCAGGAGGCGGCCTGGTCCAGCCGGGAGGGTC CCTTAGACTGTCATGCGCCGCAAGCGGATTCACTTTCTCCTCCTATGCCA TGAGCTGGGTCCGCCAAGCCCCCGGAAAGGGACTGGAATGGGTGTCCGCC ATCTCGGGGTCTGGAGGCTCAACTTACTACGCTGACTCCGTGAAGGGACG GTTCACCATTAGCCGCGACAACTCCAAGAACACCCTCTACCTCCAAATGA ACTCCCTGCGGGCCGAGGATACCGCCGTCTACTACTGCGCCAAAGTGGAA GGTTCAGGATCGCTGGACTACTGGGGACAGGGTACTCTCGTGACCGTGTC ATCGGGCGGAGGAGGTTCCGGCGGTGGCGGCTCCGGCGGCGGAGGGTCGG AGATCGTGATGACCCAGAGCCCTGGTACTCTGAGCCTTTCGCCGGGAGAA AGGGCCACCCTGTCCTGCCGCGCTTCCCAATCCGTGTCCTCCGCGTACTT GGCGTGGTACCAGCAGAAGCCGGGACAGCCCCCTCGGCTGCTGATCAGCG GGGCCAGCACCCGGGCAACCGGAATCCCAGACAGATTCGGGGGTTCCGGC AGCGGCACAGATTTCACCCTGACTATTTCGAGGTTGGAGCCCGAGGACTT TGCGGTGTATTACTGTCAGCACTACGGGTCGTCCTTTAATGGCTCCAGCC TGTTCACGTTCGGACAGGGGACCCGCCTGGAAATCAAG
BCMA_EBB-C1978-A4 - aa VH	479	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSA ISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKVE GSGSLDYWGQGTLVTVSS
BCMA_EBB-C1978-A4 - aa VL	500	EIVMTQSPGTLSLSPGERATLSCRASQSVSSAYLAWYQQKPGQPPRLLIS GASTRATGIPDRFGGSGSGTDFTLTISRLEPEDFAVYYCQHYGSSFNGSS LFTFGQGTRLEIK
BCMA_EBB-C1978-G1		
BCMA_EBB-C1978-G1 - aa ScFv domain	438	EVQLVETGGGLVQPGGSLRLSCAASGITFSRYPMSWVRQAPGKGLEWVSG ISDSGVSTYYADSAKGRFTISRDNSKNTLFLQMSSLRDEDTAVYYCVTRA GSEASDIWGQGTMVTVSSGGGGSGGGGSGGGGSEIVLTQSPATLSLSPGE RATLSCRASQSVSNSLAWYQQKPGQAPRLLIYDASSRATGIPDRFSGSGS GTDFTLTISRLEPEDFAIYYCQQFGTSSGLTFGGGTKLEIK
BCMA_EBB-C1978-G1 - nt ScFv domain	459	GAAGTGCAACTGGTGGAAACCGGTGGCGGCCTGGTGCAGCCTGGAGGATC ATTGAGGCTGTCATGCGCGGCCAGCGGTATTACCTTCTCCCGGTACCCCA TGTCCTGGGTCAGACAGGCCCCGGGGAAAGGGCTTGAATGGGTGTCCGGG ATCTCGGACTCCGGTGTCAGCACTTACTACGCCGACTCCGCCAAGGGACG CTTCACCATTTCCCGGGACAACTCGAAGAACACCCTGTTCCTCCAAATGA GCTCCCTCCGGGACGAGGATACTGCAGTGTACTACTGCGTGACCCGCGCC GGGTCCGAGGCGTCTGACATTTGGGGACAGGGCACTATGGTCACCGTGTC

		GTCCGGCGGAGGGGGCTCGGGAGGCGGTGGCAGCGGAGGAGGAGGGTCCGAGATCGTGCTGACCCAATCCCCGGCCACCCTCTCGCTGAGCCCTGGAGAAAGGGCAACCTTGTCCTGTCGCGCGAGCCAGTCCGTGAGCAACTCCCTGGCCTGGTACCAGCAGAAGCCCGGACAGGCTCCGAGACTTCTGATCTACGACGCTTCGAGCCGGGCCACTGGAATCCCCGACCGCTTTTCGGGGTCCGGCTCAGGAACCGATTTCACCCTGACAATCTCACGGCTGGAGCCAGAGGATTTCGCCATCTATTACTGCCAGCAGTTCGGTACTTCCTCCGGCCTGACTTTCGGAGGCGGCACGAAGCTCGAAATCAAG
BCMA_EBB-C1978-G1 - aa VH	480	EVQLVETGGGLVQPGGSLRLSCAASGITFSRYPMSWVRQAPGKGLEWVSGISDSGVSTYYADSAKGRFTISRDNSKNTLFLQMSSLRDEDTAVYYCVTRAGSEASDIWGQGTMVTVSS
BCMA_EBB-C1978-G1 - aa VL	501	EIVLTQSPATLSLSPGERATLSCRASQSVSNSLAWYQQKPGQAPRLLIYDASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAIYYCQQFGTSSGLTFGGGTKLEIK
BCMA_EBB-C1979-C1		
BCMA_EBB-C1979-C1 - aa ScFv domain	439	QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAIYYCARATYKRELRYYYGMDVWGQGTMVTVSSGGGGSGGGGSGGGGSEIVMTQSPGTVSLSPGERATLSCRASQSVSSSFLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDSAVYYCQQYHSSPSWTFGQGTRLEIK
BCMA_EBB-C1979-C1 - nt ScFv domain	460	CAAGTGCAGCTCGTGGAATCGGGTGGCGGACTGGTGCAGCCGGGGGGCTCACTTAGACTGTCCTGCGCGGCCAGCGGATTCACTTTCTCCTCCTACGCCATGTCCTGGGTCAGACAGGCCCCTGGAAAGGGCCTGGAATGGGTGTCCGCAATCAGCGGCAGCGGCGGCTCGACCTATTACGCGGATTCAGTGAAGGGCAGATTCACCATTTCCCGGGACAACGCCAAGAACTCCTTGTACCTTCAAATGAACTCCCTCCGCGCGGAAGATACCGCAATCTACTACTGCGCTCGGGCCACTTACAAGAGGGAACTGCGCTACTACTACGGGATGGACGTCTGGGGCCAGGGAACCATGGTCACCGTGTCCAGCGGAGGAGGAGGATCGGGAGGAGGCGGTAGCGGGGGTGGAGGGTCGGAGATCGTGATGACCCAGTCCCCCGGCACTGTGTCGCTGTCCCCCGGCGAACGGGCCACCCTGTCATGTCGGGCCAGCCAGTCAGTGTCGTCAAGCTTCCTCGCCTGGTACCAGCAGAAACCGGGACAAGCTCCCCGCCTGCTGATCTACGGAGCCAGCAGCCGGGCCACCGGTATTCCTGACCGGTTCTCCGGTTCGGGGTCCGGGACCGACTTTACTCTGACTATCTCTCGCCTCGAGCCAGAGGACTCCGCCGTGTATTACTGCCAGCAGTACCACTCCTCCCCGTCCTGGACGTTCGGACAGGGCACAAGGCTGGAGATTAAG
BCMA_EBB-C1979-C1 - aa VH	481	QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAIYYCARATYKRELRYYYGMDVWGQGTMVTVSS
BCMA_EBB-C1979-C1 - aa VL	502	EIVMTQSPGTVSLSPGERATLSCRASQSVSSSFLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDSAVYYCQQYHSSPSWTFGQGTRLEIK
BCMA_EBB-C1978-C7		
BCMA_EBB-C1978-C7 - aa ScFv domain	440	EVQLVETGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNTLKAEDTAVYYCARATYKRELRYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPSTLSLSPGESATLSCRASQSVSTTFLAWYQQKPGQAPRLLIYGSSNRATGIPDRFSGSGSGTDFTLTIRRLEPEDFAVYYCQQYHSSPSWTFGQGTKVEIK

BCMA_EBB-C1978-C7 - nt ScFv domain	461	GAGGTGCAGCTTGTGGAAACCGGTGGCGGACTGGTGCAGCCCGGAGGAAGCCTCAGGCTGTCCTGCGCCGCGTCCGGCTTCACCTTCTCCTCGTACGCCATGTCCTGGGTCCGCCAGGCCCCCGGAAAGGGCCTGGAATGGGTGTCCGCCATCTCTGGAAGCGGAGGTTCCACGTACTACGCGGACAGCGTCAAGGGAAGGTTCACAATCTCCCGCGATAATTCGAAGAACACTCTGTACCTTCAAATGAACACCCTGAAGGCCGAGGACACTGCTGTGTACTACTGCGCACGGGCCACCTACAAGAGAGAGCTCCGGTACTACTACGGAATGGACGTCTGGGGCCAGGGAACTACTGTGACCGTGTCCTCGGGAGGGGGTGGCTCCGGGGGGGGCGGCTCCGGCGGAGGCGGTTCCGAGATTGTGCTGACCCAGTCACCTTCAACTCTGTCGCTGTCCCCGGGAGAGAGCGCTACTCTGAGCTGCCGGGCCAGCCAGTCCGTGTCCACCACCTTCCTCGCCTGGTATCAGCAGAAGCCGGGGCAGGCACCACGGCTCTTGATCTACGGGTCAAGCAACAGAGCGACCGGAATTCCTGACCGCTTCTCGGGGAGCGGTTCAGGCACCGACTTCACCCTGACTATCCGGCGCCTGGAACCCGAAGATTTCGCCGTGTATTACTGTCAACAGTACCACTCCTCGCCGTCCTGGACCTTTGGCCAAGGAACCAAAGTGGAAATCAAG
BCMA_EBB-C1978-C7 - aa VH	482	EVQLVETGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNTLKAEDTAVYYCARATYKRELRYYYGMDVWGQGTTVTVSS
BCMA_EBB-C1978-C7 - aa VL	503	EIVLTQSPSTLSLSPGESATLSCRASQSVSTTFLAWYQQKPGQAPRLLIYGSSNRATGIPDRFSGSGSGTDFTLTIRRLEPEDFAVYYCQQYHSSPSWTFGQGTKVEIK
BCMA_EBB-C1978-D10		
BCMA_EBB-C1978-D10 - aa ScFv domain	441	EVQLVETGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCARVGKAVPDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIVMTQTPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPYSFGQGTRLEIK
BCMA_EBB-C1978-D10- nt ScFv domain	462	GAAGTGCAGCTCGTGGAAACTGGAGGTGGACTCGTGCAGCCTGGACGGTCGCTGCGGCTGAGCTGCGCTGCATCCGGCTTCACCTTCGACGATTATGCCATGCACTGGGTCAGACAGGCGCCAGGGAAGGGACTTGAGTGGGTGTCCGGTATCAGCTGGAATAGCGGCTCAATCGGATACGCGGACTCCGTGAAGGGAAGGTTCACCATTTCCCGCGACAACGCCAAGAACTCCCTGTACTTGCAAATGAACAGCCTCCGGGATGAGGACACTGCCGTGTACTACTGCGCCCGCGTCGGAAAAGCTGTGCCCGACGTCTGGGGCCAGGGAACCACTGTGACCGTGTCCAGCGGCGGGGGTGGATCGGGCGGTGGAGGGTCCGGTGGAGGGGGCTCAGATATTGTGATGACCCAGACCCCCTCGTCCCTGTCCGCCTCGGTCGGCGACCGCGTGACTATCACATGTAGAGCCTCGCAGAGCATCTCCAGCTACCTGAACTGGTATCAGCAGAAGCCGGGGAAGGCCCCGAAGCTCCTGATCTACGCGGCATCATCACTGCAATCGGGAGTGCCGAGCCGGTTTTCCGGGTCCGGCTCCGGCACCGACTTCACGCTGACCATTTCTTCCCTGCAACCCGAGGACTTCGCCACTTACTACTGCCAGCAGTCCTACTCCACCCCTTACTCCTTCGGCCAAGGAACCAGGCTGGAAATCAAG
BCMA_EBB-C1978-D10 - aa VH	483	EVQLVETGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCARVGKAVPDVWGQGTTVTVSS
BCMA_EBB-C1978-D10- aa	504	DIVMTQTPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPYSFGQGTRLEIK

VL		
BCMA_EBB-C1979-C12		
BCMA_EBB-C1979-C12-aa ScFv domain	442	EVQLVESGGGLVQPGRSLRLSCTASGFTFDDYAMHWVRQRPGKGLEWVASINWKGNSLAYGDSVKGRFAISRDNAKNTVFLQMNSLRTEDTAVYYCASHQGVAYYNYAMDVWGRGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRATQSIGSSFLAWYQQRPGQAPRLLIYGASQRATGIPDRFSGRGSGTDFTLTISRVEPEDSAVYYCQHYESSPSWTFGQGTKVEIK
BCMA_EBB-C1979-C12 - nt ScFv domain	463	GAAGTGCAGCTCGTGGAGAGCGGGGGAGGATTGGTGCAGCCCGGAAGGTCCCTGCGGCTCTCCTGCACTGCGTCTGGCTTCACCTTCGACGACTACGCGATGCACTGGGTCAGACAGCGCCCGGGAAAGGGCCTGGAATGGGTCGCCTCAATCAACTGGAAGGGAAACTCCCTGGCCTATGGCGACAGCGTGAAGGGCCGCTTCGCCATTTCGCGCGACAACGCCAAGAACACCGTGTTTCTGCAAATGAATTCCCTGCGGACCGAGGATACCGCTGTGTACTACTGCGCCAGCCACCAGGGCGTGGCATACTATAACTACGCCATGGACGTGTGGGGAAGAGGGACGCTCGTCACCGTGTCCTCCGGGGGCGGTGGATCGGGTGGAGGAGGAAGCGGTGGCGGGGGCAGCGAAATCGTGCTGACTCAGAGCCCGGGAACTCTTTCACTGTCCCCGGGAGAACGGGCCACTCTCTCGTGCCGGGCCACCCAGTCCATCGGCTCCTCCTTCCTTGCCTGGTACCAGCAGAGGCCAGGACAGGCGCCCCGCCTGCTGATCTACGGTGCTTCCCAACGCGCCACTGGCATTCCTGACCGGTTCAGCGGCAGAGGGTCGGGAACCGATTTCACACTGACCATTTCCCGGGTGGAGCCCGAAGATTCGGCAGTCTACTACTGTCAGCATTACGAGTCCTCCCCTTCATGGACCTTCGGTCAAGGGACCAAAGTGGAGATCAAG
BCMA_EBB-C1979-C12 - aa VH	484	EVQLVESGGGLVQPGRSLRLSCTASGFTFDDYAMHWVRQRPGKGLEWVASINWKGNSLAYGDSVKGRFAISRDNAKNTVFLQMNSLRTEDTAVYYCASHQGVAYYNYAMDVWGRGTLVTVSS
BCMA_EBB-C1979-C12 - aa VL	505	EIVLTQSPGTLSLSPGERATLSCRATQSIGSSFLAWYQQRPGQAPRLLIYGASQRATGIPDRFSGRGSGTDFTLTISRVEPEDSAVYYCQHYESSPSWTFGQGTKVEIK
BCMA_EBB-C1980-G4		
BCMA_EBB-C1980-G4- aa ScFv domain	443	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKVVRDGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGNGSGTDFTLTISRLEPEDFAVYYCQQYGSPPRFTFGPGTKVDIK
BCMA_EBB-C1980-G4- nt ScFv domain	464	GAGGTGCAGTTGGTCGAAAGCGGGGGCGGGCTTGTGCAGCCTGGCGGATCACTGCGGCTGTCCTGCGCGGCATCAGGCTTCACGTTTTCTTCCTACGCCATGTCCTGGGTGCGCCAGGCCCCTGGAAAGGGACTGGAATGGGTGTCCGCGATTTCGGGGTCCGGCGGGAGCACCTACTACGCCGATTCCGTGAAGGGCCGCTTCACTATCTCGCGGGACAACTCCAAGAACACCCTCTACCTCCAAATGAATAGCCTGCGGGCCGAGGATACCGCCGTCTACTATTGCGCTAAGGTCGTGCGCGACGGAATGGACGTGTGGGGACAGGGTACCACCGTGACAGTGTCCTCGGGGGGAGGCGGTAGCGGCGGAGGAGGAAGCGGTGGTGGAGGTTCCGAGATTGTGCTGACTCAATCACCCGCGACCCTGAGCCTGTCCCCCGGCGAAAGGGCCACTCTGTCCTGTCGGGCCAGCCAATCAGTCTCCTCCTCGTACCTGGCCTGGTACCAGCAGAAGCCAGGACAGGCTCCGAGACTCCTTATCTATGGCGCATCCTCCCGCGCCACCGGAATCCCGGATAGGTTCTCGGGAAACGGATCGGGGACCGACTTCACTCTCACCATCTCCCGGCTGGAACCGGAGGACTTCGCCGTGTACTACTGCCAGCAGTACGGCAGCCCGCCTAGATTCACTTTCGGCCCCGGCACCAAAGTGGACATCAAG

BCMA_EBB-C1980-G4- aa VH	485	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKVVRDGMDVWGQGTTVTVSS
BCMA_EBB-C1980-G4- aa VL	506	EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGNGSGTDFTLTISRLEPEDFAVYYCQQYGSPPRFTFGPGTKVDIK
BCMA_EBB-C1980-D2		
BCMA_EBB-C1980-D2- aa ScFv domain	444	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKIPQTGTFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQHYGSSPSWTFGQGTRLEIK
BCMA_EBB-C1980-D2- nt ScFv domain	465	GAAGTGCAGCTGCTGGAGTCCGGCGGTGGATTGGTGCAACCGGGGGGATCGCTCAGACTGTCCTGTGCGGCGTCAGGCTTCACCTTCTCGAGCTACGCCATGTCATGGGTCAGACAGGCCCCTGGAAAGGGTCTGGAATGGGTGTCCGCCATTTCCGGGAGCGGGGGATCTACATACTACGCCGATAGCGTGAAGGGCCGCTTCACCATTTCCCGGGACAACTCCAAGAACACTCTCTATCTGCAAATGAACTCCCTCCGCGCTGAGGACACTGCCGTGTACTACTGCGCCAAAATCCCTCAGACCGGCACCTTCGACTACTGGGGACAGGGGACTCTGGTCACCGTCAGCAGCGGTGGCGGAGGTTCGGGGGGAGGAGGAAGCGGCGGCGGAGGGTCCGAGATTGTGCTGACCCAGTCACCCGGCACTTTGTCCCTGTCGCCTGGAGAAAGGGCCACCCTTTCCTGCCGGGCATCCCAATCCGTGTCCTCCTCGTACCTGGCCTGGTACCAGCAGAGGCCCGGACAGGCCCCACGGCTTCTGATCTACGGAGCAAGCAGCCGCGCGACCGGTATCCCGGACCGGTTTTCGGGCTCGGGCTCAGGAACTGACTTCACCCTCACCATCTCCCGCCTGGAACCCGAAGATTTCGCTGTGTATTACTGCCAGCACTACGGCAGCTCCCCGTCCTGGACGTTCGGCCAGGGAACTCGGCTGGAGATCAAG
BCMA_EBB-C1980-D2- aa VH	486	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKIPQTGTFDYWGQGTLVTVSS
BCMA_EBB-C1980-D2- aa VL	507	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQHYGSSPSWTFGQGTRLEIK
BCMA_EBB-C1978-A10		
BCMA_EBB-C1978-A10- aa ScFv domain	445	EVQLVETGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTMSRENDKNSVFLQMNSLRVEDTGVYYCARANYKRELRYYYGMDVWGQGTMVTVSSGGGGSGGGGSGGGGSEIVMTQSPGTLSLSPGESATLSCRASQRVASNYLAWYQHKPGQAPSLLISGASSRATGVPDRFSGSGSGTDFTLAISRLEPEDSAVYYCQHYDSSPSWTFGQGTKVEIK
BCMA_EBB-C1978-A10- nt ScFv domain	466	GAAGTGCAACTGGTGGAAACCGGTGGAGGACTCGTGCAGCCTGGCGGCAGCCTCCGGCTGAGCTGCGCCGCTTCGGGATTCACCTTTTCCTCCTACGCGATGTCTTGGGTCAGACAGGCCCCCGGAAAGGGGCTGGAATGGGTGTCAGCCATCTCCGGCTCCGGCGGATCAACGTACTACGCCGACTCCGTGAAAGGCCGGTTCACCATGTCGCGCGAGAATGACAAGAACTCCGTGTTCCTGCAAATGAACTCCCTGAGGGTGGAGGACACCGGAGTGTACTATTGTGCGCGCGCCAACTACAAGAGAGAGCTGCGGTACTACTACGGAATGGACGTCTGGGGACAGGGAACTATGGTGACCGTGTCATCCGGTGGAGGGGGAAGCGGCGGTGGAGGCAGCGGGGGCGGGGGTTCAGAAATTGTCATGACCCAGTCCCCGGGAACTCTTTCCCTCTCCCCCGGGGAATCCGCGACTTTGTCCTGCCGGGCCAGCCAGCGCGTGGCCTCGAACTACCTCGCATGGTACCAGCATAAGCCAGGCCAAGCCCCTTCCCTGCTGATTTCCGGGGCTAGCAGCCGCGCCACTGGCGTGCCGGAT

		AGGTTCTCGGGAAGCGGCTCGGGTACCGATTTCACCCTGGCAATCTCGCG GCTGGAACCGGAGGATTCGGCCGTGTACTACTGCCAGCACTATGACTCAT CCCCCTCCTGGACATTCGGACAGGGCACCAAGGTCGAGATCAAG
BCMA_EBB-C1978-A10-aa VH	487	EVQLVETGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSA ISGSGGSTYYADSVKGRFTMSRENDKNSVFLQMNSLRVEDTGVYYCARAN YKRELRYYYGMDVWGQGTMVTVSS
BCMA_EBB-C1978-A10-aa VL	508	EIVMTQSPGTLSLSPGESATLSCRASQRVASNYLAWYQHKPGQAPSLLIS GASSRATGVPDRFSGSGSGTDFTLAISRLEPEDSAVYYCQHYDSSPSWTF GQGTKVEIK
BCMA_EBB-C1978-D4		
BCMA_EBB-C1978-D4- aa ScFv domain	446	EVQLLETGGGLVQPGGSLRLSCAASGFSFSSYAMSWVRQAPGKGLEWVSA ISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKAL VGATGAFDIWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSP GERATLSCRASQSLSSNFLAWYQQKPGQAPGLLIYGASNWATGTPDRFSG SGSGTDFTLTITRLEPEDFAVYYCQYYGTSPMYTFGQGTKVEIK
BCMA_EBB-C1978-D4- nt ScFv domain	467	GAAGTGCAGCTGCTCGAAACCGGTGGAGGGCTGGTGCAGCCAGGGGGCTC CCTGAGGCTTTCATGCGCCGCTAGCGGATTCTCCTTCTCCTCTTACGCCA TGTCGTGGGTCCGCCAAGCCCCTGGAAAAGGCCTGGAATGGGTGTCCGCG ATTTCCGGGAGCGGAGGTTCGACCTATTACGCCGACTCCGTGAAGGGCCG CTTTACCATCTCCCGGGATAACTCCAAGAACACTCTGTACCTCCAAATGA ACTCGCTGAGAGCCGAGGACACCGCCGTGTATTACTGCGCGAAGGCGCTG GTCGGCGCGACTGGGGCATTCGACATCTGGGGACAGGGAACTCTTGTGAC CGTGTCGAGCGGAGGCGGCGGCTCCGGCGGAGGAGGGAGCGGGGGCGGTG GTTCCGAAATCGTGTTGACTCAGTCCCCGGGAACCCTGAGCTTGTCACCC GGGGAGCGGGCCACTCTCTCCTGTCGCGCCTCCCAATCGCTCTCATCCAA TTTCCTGGCCTGGTACCAGCAGAAGCCCGGACAGGCCCCGGGCCTGCTCA TCTACGGCGCTTCAAACTGGGCAACGGGAACCCCTGATCGGTTCAGCGGA AGCGGATCGGGTACTGACTTTACCCTGACCATCACCAGACTGGAACCGGA GGACTTCGCCGTGTACTACTGCCAGTACTACGGCACCTCCCCCATGTACA CATTCGGACAGGGTACCAAGGTCGAGATTAAG
BCMA_EBB-C1978-D4- aa VH	488	EVQLLETGGGLVQPGGSLRLSCAASGFSFSSYAMSWVRQAPGKGLEWVSA ISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKAL VGATGAFDIWGQGTLVTVSS
BCMA_EBB-C1978-D4- aa VL	509	EIVLTQSPGTLSLSPGERATLSCRASQSLSSNFLAWYQQKPGQAPGLLIY GASNWATGTPDRFSGSGSGTDFTLTITRLEPEDFAVYYCQYYGTSPMYTF GQGTKVEIK
BCMA_EBB-C1980-A2		
BCMA_EBB-C1980-A2- aa ScFv domain	447	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSA ISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVLWF GEGFDPWGQGTLVTVSSGGGGSGGGGSGGGGSDIVLTQSPLSLPVTPGEP ASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFS GSGSGTDFTLKISRVEAEDVGVYYCMQALQTPLTFGGGTKVDIK
BCMA_EBB-C1980-A2- nt ScFv domain	468	GAAGTGCAGCTGCTTGAGAGCGGTGGAGGTCTGGTGCAGCCCGGGGGATC ACTGCGCCTGTCCTGTGCCGCGTCCGGTTTCACTTTCTCCTCGTACGCCA TGTCGTGGGTCAGACAGGCACCGGGAAAGGGACTGGAATGGGTGTCAGCC ATTTCGGGTTCGGGGGGCAGCACCTACTACGCTGACTCCGTGAAGGGCCG GTTCACCATTTCCCGCGACAACTCCAAGAACACCTTGTACCTCCAAATGA ACTCCCTGCGGGCCGAAGATACCGCCGTGTATTACTGCGTGCTGTGGTTC GGAGAGGGATTCGACCCGTGGGGACAAGGAACACTCGTGACTGTGTCATC

		CGGCGGAGGCGGCAGCGGTGGCGGCGGTTCCGGCGGCGGCGGATCTGACA TCGTGTTGACCCAGTCCCCTCTGAGCCTGCCGGTCACTCCTGGCGAACCA GCCAGCATCTCCTGCCGGTCGAGCCAGTCCCTCCTGCACTCCAATGGGTA CAACTACCTCGATTGGTATCTGCAAAAGCCGGGCCAGAGCCCCCAGCTGC TGATCTACCTTGGGTCAAACCGCGCTTCCGGGGTGCCTGATAGATTCTCC GGGTCCGGGAGCGGAACCGACTTTACCCTGAAAATCTCGAGGGTGGAGGC CGAGGACGTCGGAGTGTACTACTGCATGCAGGCGCTCCAGACTCCCCTGA CCTTCGGAGGAGGAACGAAGGTCGACATCAAGA
BCMA_EBB-C1980-A2- aa VH	489	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSA ISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVLWF GEGFDPWGQGTLVTVSS
BCMA_EBB-C1980-A2- aa VL	510	DIVLTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQ LLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP LTFGGGTKVDIK
BCMA_EBB-C1981-C3		
BCMA_EBB-C1981-C3- aa ScFv domain	448	QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSA ISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKVG YDSSGYYRDYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPG TLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGI SDRFSGSGSGTDFTLTISRLEPEDFAVYYCQHYGNSPPKFTFGPGTKLEI K
BCMA_EBB-C1981-C3- nt ScFv domain	469	CAAGTGCAGCTCGTGGAGTCAGGCGGAGGACTGGTGCAGCCCGGGGGCTC CCTGAGACTTTCCTGCGCGGCATCGGGTTTTACCTTCTCCTCCTATGCTA TGTCCTGGGTGCGCCAGGCCCCGGGAAAGGGACTGGAATGGGTGTCCGCA ATCAGCGGTAGCGGGGGCTCAACATACTACGCCGACTCCGTCAAGGGTCG CTTCACTATTTCCCGGGACAACTCCAAGAATACCCTGTACCTCCAAATGA ACAGCCTCAGGGCCGAGGATACTGCCGTGTACTACTGCGCCAAAGTCGGA TACGATAGCTCCGGTTACTACCGGGACTACTACGGAATGGACGTGTGGGG ACAGGGCACCACCGTGACCGTGTCAAGCGGCGGAGGCGGTTCAGGAGGGG GAGGCTCCGGCGGTGGAGGGTCCGAAATCGTCCTGACTCAGTCGCCTGGC ACTCTGTCGTTGTCCCCGGGGGAGCGCGCTACCCTGTCGTGTCGGGCGTC GCAGTCCGTGTCGAGCTCCTACCTCGCGTGGTACCAGCAGAAGCCCGGAC AGGCCCCTAGACTTCTGATCTACGGCACTTCTTCACGCGCCACCGGGATC AGCGACAGGTTCAGCGGCTCCGGCTCCGGGACCGACTTCACCCTGACCAT TAGCCGGCTGGAGCCTGAAGATTTCGCCGTGTATTACTGCCAACACTACG GAAACTCGCCGCCAAAGTTCACGTTCGGACCCGGAACCAAGCTGGAAATC AAG
BCMA_EBB-C1981-C3- aa VH	490	QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSA ISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKVG YDSSGYYRDYYGMDVWGQGTTVTVSS
BCMA_EBB-C1981-C3- aa VL	511	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIY GTSSRATGISDRFSGSGSGTDFTLTISRLEPEDFAVYYCQHYGNSPPKFT FGPGTKLEIK
BCMA_EBB-C1978-G4		
BCMA_EBB-C1978-G4- aa ScFv domain	449	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSA ISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKMG WSSGYLGAFDIWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSL SPGERATLSCRASQSVASSFLAWYQQKPGQAPRLLIYGASGRATGIPDRF SGSGSGTDFTLTISRLEPEDFAVYYCQHYGGSPRLTFGGGTKVDIK
BCMA_EBB-C1978-G4- nt	470	GAAGTCCAACTGGTGGAGTCCGGGGGAGGGCTCGTGCAGCCCGGAGGCAG CCTTCGGCTGTCGTGCGCCGCCTCCGGGTTCACGTTCTCATCCTACGCGA

ScFv domain		TGTCGTGGGTCAGACAGGCACCAGGAAAGGGACTGGAATGGGTGTCCGCC ATTAGCGGCTCCGGCGGTAGCACCTACTATGCCGACTCAGTGAAGGGAAG GTTCACTATCTCCCGCGACAACAGCAAGAACACCCTGTACCTCCAAATGA ACTCTCTGCGGGCCGAGGATACCGCGGTGTACTATTGCGCCAAGATGGGT TGGTCCAGCGGATACTTGGGAGCCTTCGACATTTGGGGACAGGGCACTAC TGTGACCGTGTCCTCCGGGGGTGGCGGATCGGGAGGCGGCGGCTCGGGTG GAGGGGGTTCCGAAATCGTGTTGACCCAGTCACCGGGAACCCTCTCGCTG TCCCCGGGAGAACGGGCTACACTGTCATGTAGAGCGTCCCAGTCCGTGGC TTCCTCGTTCCTGGCCTGGTACCAGCAGAAGCCGGGACAGGCACCCCGCC TGCTCATCTACGGAGCCAGCGGCCGGGCGACCGGCATCCCTGACCGCTTC TCCGGTTCCGGCTCGGGCACCGACTTTACTCTGACCATTAGCAGGCTTGA GCCCGAGGATTTTGCCGTGTACTACTGCCAACACTACGGGGGGAGCCCTC GCCTGACCTTCGGAGGCGGAACTAAGGTCGATATCAAAA
BCMA_EBB-C1978-G4- aa VH	491	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSA ISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKMG WSSGYLGAFDIWGQGTTVTVSS
BCMA_EBB-C1978-G4- aa VL	512	EIVLTQSPGTLSLSPGERATLSCRASQSVASSFLAWYQQKPGQAPRLLIY GASGRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQHYGGSPRLTF GGGTKVDIK

[00293] In embodiments, additional exemplary BCMA CAR constructs are generated using the VH and VL sequences from PCT Publication WO2012/0163805 (the contents of which are hereby incorporated by reference in its entirety). In embodiments, additional exemplary BCMA CAR constructs are generated using the VH and VL sequences from PCT Publication WO2016/014565 (the contents of which are hereby incorporated by reference in its entirety). In embodiments, additional exemplary BCMA CAR constructs are generated using the VH and VL sequences from PCT Publication WO2014/122144 (the contents of which are hereby incorporated by reference in its entirety). In embodiments, additional exemplary BCMA CAR constructs are generated using the CAR molecules, and/or the VH and VL sequences from PCT Publication WO2016/014789 (the contents of which are hereby incorporated by reference in its entirety). In embodiments, additional exemplary BCMA CAR constructs are generated using the CAR molecules, and/or the VH and VL sequences from PCT Publication WO2014/089335 (the contents of which are hereby incorporated by reference in its entirety). In embodiments, additional exemplary BCMA CAR constructs are generated using the CAR molecules, and/or the VH and VL sequences from PCT Publication WO2014/140248 (the contents of which are hereby incorporated by reference in its entirety).

[00294] In embodiments, additional exemplary BCMA CAR constructs can also be generated using the VH and VL sequences found in Table 13. The amino acid sequences of

exemplary scFv domains comprising the VH and VL domains and a linker sequence, and full-length CARs are also found in Table 13.

Table 13. Additional exemplary BCMA binding domain sequences

Name	Sequence	SEQ ID NO:
A7D12.2 VH	QIQLVQSGPDLKKPGETVKLSCKASGYTFTNFGMNWVKQAPGKGFKWMAWINTYTGESYFADDFKGRFAFSVETSATTAYLQINNLKTEDTATYFCARGEIYYGYDGGFAYWGQGTLVTVSA	555
A7D12.2 VL	DVVMTQSHRFMSTSVGDRVSITCRASQDVNTAVSWYQQKPGQSPKLLIFSASYRYTGVPDRFTGSGSGADFTLTISSVQAEDLAVYYCQQHYSTPWTFGGGTKLDIK	559
A7D12.2 scFv domain	QIQLVQSGPDLKKPGETVKLSCKASGYTFTNFGMNWVKQAPGKGFKWMAWINTYTGESYFADDFKGRFAFSVETSATTAYLQINNLKTEDTATYFCARGEIYYGYDGGFAYWGQGTLVTVSAGGGGSGGGGSGGGGSDVVMTQSHRFMSTSVGDRVSITCRASQDVNTAVSWYQQKPGQSPKLLIFSASYRYTGVPDRFTGSGSGADFTLTISSVQAEDLAVYYCQQHYSTPWTFGGGTKLDIK	563
C11D5.3 VH	QIQLVQSGPELKKPGETVKISCKASGYTFTDYSINWVKRAPGKGLKWMGWINTETREPAYAYDFRGRFAFSLETSASTAYLQINNLKYEDTATYFCALDYSYAMDYWGQGTSVTVSS	556
C11D5.3 VL	DIVLTQSPASLAMSLGKRATISCRASESVSVIGAHLIHWYQQKPGQPPKLLIYLASNLETGVPARFSGSGSGTDFTLTIDPVEEDDVAIYSCLQSRIFPRTFGGGTKLEIK	560
C11D5.3 scFv domain	QIQLVQSGPELKKPGETVKISCKASGYTFTDYSINWVKRAPGKGLKWMGWINTETREPAYAYDFRGRFAFSLETSASTAYLQINNLKYEDTATYFCALDYSYAMDYWGQGTSVTVSSGGGGSGGGGSGGGGSQIQLVQSGPELKKPGETVKISCKASGYTFTDYSINWVKRAPGKGLKWMGWINTETREPAYAYDFRGRFAFSLETSASTAYLQINNLKYEDTATYFCALDYSYAMDYWGQGTSVTVSS	564
C12A3.2 VH	QIQLVQSGPELKKPGETVKISCKASGYTFRHYSMNWVKQAPGKGLKWMGRINTESGVPIYADDFKGRFAFSVETSASTAYLVINNLKDEDTASYFCSNDYLYSLDFWGQGTALTVSS	557
C12A3.2 VL	DIVLTQSPPSLAMSLGKRATISCRASESVTILGSHLIYWYQQKPGQPPTLLIQLASNVQTGVPARFSGSGSRTDFTLTIDPVEEDDVAVYYCLQSRTIPRTFGGGTKLEIK	561
C12A3.2 scFv domain	QIQLVQSGPELKKPGETVKISCKASGYTFRHYSMNWVKQAPGKGLKWMGRINTESGVPIYADDFKGRFAFSVETSASTAYLVINNLKDEDTASYFCSNDYLYSLDFWGQGTALTVSSGGGGSGGGGSGGGGSDIVLTQSPPSLAMSLGKRATISCRASESVTILGSHLIYWYQQKPGQPPTLLIQLASNVQTGVPARFSGSGSRTDFTLTIDPVEEDDVAVYYCLQSRTIPRTFGGGTKLEIK	565
C13F12.1 VH	QIQLVQSGPELKKPGETVKISCKASGYTFTHYSMNWVKQAPGKGLKWMGRINTETGEPLYADDFKGRFAFSLETSASTAYLVINNLKNEDTATFFCSNDYLYSCDYWGQGTTLTVSS	558
C13F12.1 VL	DIVLTQSPPSLAMSLGKRATISCRASESVTILGSHLIYWYQQKPGQPPTLLIQLASNVQTGVPARFSGSGSRTDFTLTIDPVEEDDVAVYYCLQSRTIPRTFGGGTKLEIK	562
C13F12.1 scFv	QIQLVQSGPELKKPGETVKISCKASGYTFTHYSMNWVKQAPGKGLKWMGRINTETGEPLYADDFKGRFAFSLETSASTAYLVINNLKNEDTATFFCSNDYLYSCDYWGQGTTLTVSSGGGGSGGGGSGGGGSDIVLTQSPPSLAMSLGKRATISCRASESVTILGSHLIYWYQQKPGQPPTLL	566

domain	IQLASNVQTGVPARFSGSGSRTDFTLTIDPVEEDDVAVYYCLQSRTIPRTFGGGTKLEIK	

[00295] The sequences of human CDR sequences of the scFv domains are shown in Table 14 for the heavy chain variable domains and in Table 15 for the light chain variable domains. "ID" stands for the respective SEQ ID NO for each CDR. The CDRs are shown according to the Kabat definition, however, the CDRs under other convention, for example, Chothia or the combined Kabat/Chothia definitions may be readily deduced based on the VH and VL sequences above.

Table 14: Heavy Chain Variable Domain CDRs according to the Kabat numbering scheme (Kabat et al. (1991), "Sequences of Proteins of Immunological Interest," 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD)

Candidate	HCDR1	SEQ ID NO:	HCDR2	SEQ ID NO:	HCDR3	SEQ ID NO:
139109	NHGMS	694	GIVYSGSTYYAAS VKG	734	HGGESDV	774
139103	NYAMS	684	GISRSGENTYYAD SVKG	724	SPAHYYGGMDV	764
139105	DYAMH	685	GISWNSGSIGYAD SVKG	725	HSFLAY	765
139111	NHGMS	686	GIVYSGSTYYAAS VKG	726	HGGESDV	766
139100	NFGIN	687	WINPKNNNTNYA QKFQG	727	GPYYYQSYMDV	767
139101	SDAMT	688	VISGSGGTTYYAD SVKG	728	LDSSGYYYARGPRY	768
139102	NYGIT	689	WISAYNGNTNYA QKFQG	729	GPYYYYMDV	769
139104	NHGMS	690	GIVYSGSTYYAAS VKG	730	HGGESDV	770
139106	NHGMS	691	GIVYSGSTYYAAS VKG	731	HGGESDV	771
139107	NHGMS	692	GIVYSGSTYYAAS VKG	732	HGGESDV	772
139108	DYYMS	693	YISSSGSTIYYADS VKG	733	ESGDGMDV	773
139110	DYYMS	695	YISSSGNTIYYADS VKG	735	STMVREDY	775
139112	NHGMS	696	GIVYSGSTYYAAS VKG	736	HGGESDV	776
139113	NHGMS	697	GIVYSGSTYYAAS VKG	737	HGGESDV	777
139114	NHGMS	698	GIVYSGSTYYAAS VKG	738	HGGESDV	778
149362	SSYYYWG	699	SIYYSGSAYYNPS LKS	739	HWQEWPDAFDI	779
149363	TSGMCVS	700	RIDWDEDKFYSTS	740	SGAGGTSATAFDI	780

			LKT			
149364	SYSMN	701	SISSSSSYIYYADS VKG	741	TIAAVYAFDI	781
149365	DYYMS	702	YISSSGSTIYYADS VKG	742	DLRGAFDI	782
149366	SHYIH	703	MINPSGGVTAYSQ TLQG	743	EGSGSGWYFDF	783
149367	SGGYYWS	704	YIYYSGSTYYNPS LKS	744	AGIAARLRGAFDI	784
149368	SYAIS	705	GIIPIFGTANYAQK FQG	745	RGGYQLLRWDVGLL RSAFDI	785
149369	SNSAAWN	706	RTYYRSKWYSFY AISLKS	746	SSPEGLFLYWFDP	786
BCMA_EBB-C1978-A4	SYAMS	707	AISGSGGSTYYAD SVKG	747	VEGSGSLDY	787
BCMA_EBB-C1978-G1	RYPMS	708	GISDSGVSTYYAD SAKG	748	RAGSEASDI	788
BCMA_EBB-C1979-C1	SYAMS	709	AISGSGGSTYYAD SVKG	749	ATYKRELRYYYGM DV	789
BCMA_EBB-C1978-C7	SYAMS	710	AISGSGGSTYYAD SVKG	750	ATYKRELRYYYGM DV	790
BCMA_EBB-C1978-D10	DYAMH	711	GISWNSGSIGYAD SVKG	751	VGKAVPDV	791
BCMA_EBB-C1979-C12	DYAMH	712	SINWKGNSLAYG DSVKG	752	HQGVAYYNYAMDV	792
BCMA_EBB-C1980-G4	SYAMS	713	AISGSGGSTYYAD SVKG	753	VVRDGMDV	793
BCMA_EBB-C1980-D2	SYAMS	714	AISGSGGSTYYAD SVKG	754	IPQTGTFDY	794
BCMA_EBB-C1978-A10	SYAMS	715	AISGSGGSTYYAD SVKG	755	ANYKRELRYYYGM DV	795
BCMA_EBB-C1978-D4	SYAMS	716	AISGSGGSTYYAD SVKG	756	ALVGATGAFDI	796
BCMA_EBB-C1980-A2	SYAMS	717	AISGSGGSTYYAD SVKG	757	WFGEGFDP	797
BCMA_EBB-C1981-C3	SYAMS	718	AISGSGGSTYYAD SVKG	758	VGYDSSGYYRDYYG MDV	798
BCMA_EBB-C1978-G4	SYAMS	719	AISGSGGSTYYAD SVKG	759	MGWSSGYLGAFDI	799
A7D12.2	NFGMN	720	WINTYTGESYFAD DFKG	760	GEIYYGYDGGFAY	800
C11D5.3	DYSIN	721	WINTETREPAYAY DFRG	761	DYSYAMDY	801
C12A3.2	HYSMN	722	RINTESGVPIYAD DFKG	762	DYLYSLDF	802
C13F12.1	HYSMN	723	RINTETGEPLYAD DFKG	763	DYLYSCDY	803

Table 15: Light Chain Variable Domain CDRs according to the Kabat numbering scheme (Kabat et al. (1991), "Sequences of Proteins of Immunological Interest," 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD)

Candidate	LCDR1	SE	LCDR2	SEQ	LCDR3	SE

		Q ID NO:		ID NO:		Q ID NO:
139109	RASQSISSYLN	814	AASSLQS	854	QQSYSTPYT	894
139103	RASQSISSSFLA	804	GASRRAT	844	QQYHSSPSWT	884
139105	RSSQSLLHSNGYNYLD	805	LGSNRAS	845	MQALQTPYT	885
139111	KSSQSLLRNDGKTPLY	806	EVSNRFS	846	MQNIQFPS	886
139100	RSSQSLLHSNGYNYLN	807	LGSKRAS	847	MQALQTPYT	887
139101	RASQSISSYLN	808	GASTLAS	848	QQSYKRAS	888
139102	RSSQSLLYSNGYNYVD	809	LGSNRAS	849	MQGRQFPYS	889
139104	RASQSVSSNLA	810	GASTRAS	850	QQYGSSLT	890
139106	RASQSVSSKLA	811	GASIRAT	851	QQYGSSSWT	891
139107	RASQSVGSTNLA	812	DASNRAT	852	QQYGSSPPWT	892
139108	RASQSISSYLN	813	AASSLQS	853	QQSYTLA	893
139110	KSSESLVHNSGKTYLN	815	EVSNRDS	855	MQGTHWPGT	895
139112	QASEDINKFLN	816	DASTLQT	856	QQYESLPLT	896
139113	RASQSVGSNLA	817	GASTRAT	857	QQYNDWLPVT	897
139114	RASQSIGSSSLA	818	GASSRAS	858	QQYAGSPPFT	898
149362	KASQDIDDAMN	819	SATSPVP	859	LQHDNFPLT	899
149363	RASQDIYNNLA	820	AANKSQS	860	QHYYRFPYS	900
149364	RSSQSLLHSNGYNYLD	821	LGSNRAS	861	MQALQTPYT	901
149365	GGNNIGTKSVH	822	DDSVRPS	862	QVWDSDSEHV V	902
149366	SGDGLSKKYVS	823	RDKERPS	863	QAWDDTTVV	903
149367	RASQGIRNWLA	824	AASNLQS	864	QKYNSAPFT	904
149368	GGNNIGSKSVH	825	GKNNRPS	865	SSRDSSGDHLR V	905
149369	QGDSLGNYYAT	826	GTNNRPS	866	NSRDSSGHHLL	906
BCMA_EBB-C1978-A4	RASQSVSSAYLA	827	GASTRAT	867	QHYGSSFNGSS LFT	907
BCMA_EBB-C1978-G1	RASQSVSNSLA	828	DASSRAT	868	QQFGTSSGLT	908
BCMA_EBB-C1979-C1	RASQSVSSSFLA	829	GASSRAT	869	QQYHSSPSWT	909
BCMA_EBB-C1978-C7	RASQSVSTTFLA	830	GSSNRAT	870	QQYHSSPSWT	910
BCMA_EBB-C1978-D10	RASQSISSYLN	831	AASSLQS	871	QQSYSTPYS	911
BCMA_EBB-C1979-C12	RATQSIGSSFLA	832	GASQRAT	872	QHYESSPSWT	912
BCMA_EBB-C1980-G4	RASQSVSSSYLA	833	GASSRAT	873	QQYGSPPRFT	913
BCMA_EBB-C1980-D2	RASQSVSSSYLA	834	GASSRAT	874	QHYGSSPSWT	914
BCMA_EBB-C1978-A10	RASQRVASNYLA	835	GASSRAT	875	QHYDSSPSWT	915
BCMA_EBB-C1978-D4	RASQSLSSNFLA	836	GASNWAT	876	QYYGTSPMYT	916

BCMA_EBB-C1980-A2	RSSQSLLHSNGYNYLD	837	LGSNRAS	877	MQALQTPLT	917
BCMA_EBB-C1981-C3	RASQSVSSSYLA	838	GTSSRAT	878	QHYGNSPPKFT	918
BCMA_EBB-C1978-G4	RASQSVASSFLA	839	GASGRAT	879	QHYGGSPRLT	919
A7D12.2	RASQDVNTAVS	840	SASYRYT	880	QQHYSTPWT	920
C11D5.3	RASESVSVIGAHLIH	841	LASNLET	881	LQSRIFPRT	921
C12A3.2	RASESVTILGSHLIY	842	LASNVQT	882	LQSRTIPRT	922
C13F12.1	RASESVTILGSHLIY	843	LASNVQT	883	LQSRTIPRT	923

[00296] In one embodiment, the BCMA binding domain comprises one or more (e.g., all three) light chain complementary determining region 1 (LC CDR1), light chain complementary determining region 2 (LC CDR2), and light chain complementary determining region 3 (LC CDR3) of a BCMA binding domain described herein, e.g., provided in Table 12, 13 or 15, and/or one or more (e.g., all three) heavy chain complementary determining region 1 (HC CDR1), heavy chain complementary determining region 2 (HC CDR2), and heavy chain complementary determining region 3 (HC CDR3) of a BCMA binding domain described herein, e.g., provided in Table 12, 13 or 14. In one embodiment, the BCMA binding domain comprises one, two, or all of LC CDR1, LC CDR2, and LC CDR3 of any amino acid sequences as provided in Table 12, incorporated herein by reference; and one, two or all of HC CDR1, HC CDR2, and HC CDR3 of any amino acid sequences as provided in Table 12.

[00297] In one embodiment, the BCMA antigen binding domain comprises:

(v) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 814, a LC CDR2 amino acid sequence of SEQ ID NO: 854, and a LC CDR3 amino acid sequence of SEQ ID NO: 894; and
(b) a HC CDR1 amino acid sequence of SEQ ID NO: 694, a HC CDR2 amino acid sequence of SEQ ID NO: 734, and a HC CDR3 amino acid sequence of SEQ ID NO: 774

(vi) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 804, a LC CDR2 amino acid sequence of SEQ ID NO: 844, and a LC CDR3 amino acid sequence of SEQ ID NO: 884; and
(b) a HC CDR1 amino acid sequence of SEQ ID NO: 684, a HC CDR2 amino acid sequence of SEQ ID NO: 724, and a HC CDR3 amino acid sequence of SEQ ID NO: 764

(vii) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 805, a LC CDR2 amino acid sequence of SEQ ID NO: 845, and a LC CDR3 amino acid sequence of SEQ ID NO: 885; and
(b) a HC CDR1 amino acid sequence of SEQ ID NO: 685, a HC CDR2 amino acid sequence of SEQ ID NO: 725, and a HC CDR3 amino acid sequence of SEQ ID NO: 765

(viii) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 806, a LC CDR2 amino acid sequence of SEQ ID NO: 846, and a LC CDR3 amino acid sequence of SEQ ID NO: 886; and
(b) a HC CDR1 amino acid sequence of SEQ ID NO: 686, a HC CDR2 amino acid sequence of SEQ ID NO: 726, and a HC CDR3 amino acid sequence of SEQ ID NO: 766

(ix) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 807, a LC CDR2 amino acid sequence of SEQ ID NO: 847, and a LC CDR3 amino acid sequence of SEQ ID NO: 887; and
(b) a HC CDR1 amino acid sequence of SEQ ID NO: 687, a HC CDR2 amino acid sequence of SEQ ID NO: 727, and a HC CDR3 amino acid sequence of SEQ ID NO: 767

(x) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 808, a LC CDR2 amino acid sequence of SEQ ID NO: 848, and a LC CDR3 amino acid sequence of SEQ ID NO: 888; and
(b) a HC CDR1 amino acid sequence of SEQ ID NO: 688, a HC CDR2 amino acid sequence of SEQ ID NO: 728, and a HC CDR3 amino acid sequence of SEQ ID NO: 768

(xi) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 809, a LC CDR2 amino acid sequence of SEQ ID NO: 849, and a LC CDR3 amino acid sequence of SEQ ID NO: 889; and
(b) a HC CDR1 amino acid sequence of SEQ ID NO: 689, a HC CDR2 amino acid sequence of SEQ ID NO: 729, and a HC CDR3 amino acid sequence of SEQ ID NO: 769

(xii) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 810, a LC CDR2 amino acid sequence of SEQ ID NO: 850, and a LC CDR3 amino acid sequence of SEQ ID NO: 890; and
(b) a HC CDR1 amino acid sequence of SEQ ID NO: 690, a HC CDR2 amino acid sequence of SEQ ID NO: 730, and a HC CDR3 amino acid sequence of SEQ ID NO: 770

(xiii) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 811, a LC CDR2 amino acid sequence of SEQ ID NO: 851, and a LC CDR3 amino acid sequence of SEQ ID NO: 891; and
(b) a HC CDR1 amino acid sequence of SEQ ID NO: 691, a HC CDR2 amino acid sequence of SEQ ID NO: 731, and a HC CDR3 amino acid sequence of SEQ ID NO: 771

(xiv) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 812, a LC CDR2 amino acid sequence of SEQ ID NO: 852, and a LC CDR3 amino acid sequence of SEQ ID NO: 892; and
(b) a HC CDR1 amino acid sequence of SEQ ID NO: 692, a HC CDR2 amino acid sequence of SEQ ID NO: 732, and a HC CDR3 amino acid sequence of SEQ ID NO: 772

(xv) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 813, a LC CDR2 amino acid sequence of SEQ ID NO: 853, and a LC CDR3 amino acid sequence of SEQ ID NO: 893; and
(b) a HC CDR1 amino acid sequence of SEQ ID NO: 693, a HC CDR2 amino acid sequence of SEQ ID NO: 733, and a HC CDR3 amino acid sequence of SEQ ID NO: 773

(xvi) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 815, a LC CDR2 amino acid sequence of SEQ ID NO: 855, and a LC CDR3 amino acid sequence of SEQ ID NO: 895; and
(b) a HC CDR1 amino acid sequence of SEQ ID NO: 695, a HC CDR2 amino acid sequence of SEQ ID NO: 735, and a HC CDR3 amino acid sequence of SEQ ID NO: 775

(xvii) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 816, a LC CDR2 amino acid sequence of SEQ ID NO: 856, and a LC CDR3 amino acid sequence of SEQ ID NO: 896; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 696, a HC CDR2 amino acid sequence of SEQ ID NO: 736, and a HC CDR3 amino acid sequence of SEQ ID NO: 776

(xviii) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 817, a LC CDR2 amino acid sequence of SEQ ID NO: 857, and a LC CDR3 amino acid sequence of SEQ ID NO: 897; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 697, a HC CDR2 amino acid sequence of SEQ ID NO: 737, and a HC CDR3 amino acid sequence of SEQ ID NO: 777

(xix) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 818, a LC CDR2 amino acid sequence of SEQ ID NO: 858, and a LC CDR3 amino acid sequence of SEQ ID NO: 898; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 698, a HC CDR2 amino acid sequence of SEQ ID NO: 738, and a HC CDR3 amino acid sequence of SEQ ID NO: 778

(xx) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 819, a LC CDR2 amino acid sequence of SEQ ID NO: 859, and a LC CDR3 amino acid sequence of SEQ ID NO: 899; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 699, a HC CDR2 amino acid sequence of SEQ ID NO: 739, and a HC CDR3 amino acid sequence of SEQ ID NO: 779

(xxi) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 820, a LC CDR2 amino acid sequence of SEQ ID NO: 860, and a LC CDR3 amino acid sequence of SEQ ID NO: 900; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 700, a HC CDR2 amino acid sequence of SEQ ID NO: 740, and a HC CDR3 amino acid sequence of SEQ ID NO: 780

(xxii) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 821, a LC CDR2 amino acid sequence of SEQ ID NO: 861, and a LC CDR3 amino acid sequence of SEQ ID NO: 901; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 701, a HC CDR2 amino acid sequence of SEQ ID NO: 741, and a HC CDR3 amino acid sequence of SEQ ID NO: 781

(xxiii) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 822, a LC CDR2 amino acid sequence of SEQ ID NO: 862, and a LC CDR3 amino acid sequence of SEQ ID NO: 902; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 702, a HC CDR2 amino acid sequence of SEQ ID NO: 742, and a HC CDR3 amino acid sequence of SEQ ID NO: 782

(xxiv) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 823, a LC CDR2 amino acid sequence of SEQ ID NO: 863, and a LC CDR3 amino acid sequence of SEQ ID NO: 903; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 703, a HC CDR2 amino acid sequence of SEQ ID NO: 743, and a HC CDR3 amino acid sequence of SEQ ID NO: 783

(xxv) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 824, a LC CDR2 amino acid sequence of SEQ ID NO: 864, and a LC CDR3 amino acid sequence of SEQ ID NO: 904; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 704, a HC CDR2 amino acid sequence of SEQ ID NO: 744, and a HC CDR3 amino acid sequence of SEQ ID NO: 784

(xxvi) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 825, a LC CDR2 amino acid sequence of SEQ ID NO: 865, and a LC CDR3 amino acid sequence of SEQ ID NO: 905; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 705, a HC CDR2 amino acid sequence of SEQ ID NO: 745, and a HC CDR3 amino acid sequence of SEQ ID NO: 785 or

(xxvii) (a) a LC CDR1 amino acid sequence of SEQ ID NO: 826, a LC CDR2 amino acid sequence of SEQ ID NO: 866, and a LC CDR3 amino acid sequence of SEQ ID NO: 906; and

(b) a HC CDR1 amino acid sequence of SEQ ID NO: 706, a HC CDR2 amino acid sequence of SEQ ID NO: 746, and a HC CDR3 amino acid sequence of SEQ ID NO: 786.

[00298] In one embodiment, the BCMA binding domain comprises a light chain variable region described herein (e.g., in Table 12 or 13) and/or a heavy chain variable region described herein (e.g., in Table 12 or 13). In one embodiment, the BCMA binding domain is a scFv comprising a light chain and a heavy chain of an amino acid sequence listed in Table 12 or 13. In an embodiment, the BCMA binding domain (e.g., an scFv) comprises: a light chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence of a light chain variable region provided in Table 12 or 13, or a sequence with 95-99% identity with an amino acid sequence provided in Table 12 or 13; and/or a heavy chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence of a heavy chain variable region provided in Table 12 or 13, or a sequence with 95-99% identity to an amino acid sequence provided in Table 12 or 13.

[00299] In one embodiment, the BCMA binding domain comprises an amino acid sequence selected from a group consisting of SEQ ID NO: 349; SEQ ID NO: 339, SEQ ID NO: 340; SEQ ID NO: 341; SEQ ID NO: 342; SEQ ID NO: 343; SEQ ID NO: 344, SEQ ID NO: 345, SEQ ID NO: 346, SEQ ID NO: 347, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 351, SEQ ID NO: 352, SEQ ID NO: 353, SEQ ID NO: 429, SEQ ID NO: 430, SEQ ID NO: 431, SEQ ID NO: 432, SEQ ID NO: 433, SEQ ID NO: 434, SEQ ID NO: 435, SEQ ID NO: 436, SEQ ID NO: 437, SEQ ID NO: 438, SEQ ID NO: 439, SEQ ID NO: 440, SEQ ID NO: 441, SEQ ID NO: 442, SEQ ID NO: 443, SEQ ID NO: 444, SEQ ID NO: 445, SEQ ID NO: 446, SEQ ID NO: 447, SEQ ID NO: 448, SEQ ID NO: 449, SEQ ID NO: 563, SEQ ID NO: 564, SEQ ID NO: 565 and SEQ ID NO: 566; or an amino acid sequence having at least one, two or

three modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions, e.g., conservative substitutions) to any of the aforesaid sequences; or a sequence with 95-99% identity to any of the aforesaid sequences. In one embodiment, the BCMA binding domain is a scFv, and a light chain variable region comprising an amino acid sequence described herein, e.g., in Table 12 or 13, is attached to a heavy chain variable region comprising an amino acid sequence described herein, e.g., in Table 12 or 13, via a linker, e.g., a linker described herein. In one embodiment, the BCMA binding domain includes a (Gly4-Ser)n linker, wherein n is 1, 2, 3, 4, 5, or 6, preferably 4 (SEQ ID NO: 80). The light chain variable region and heavy chain variable region of a scFv can be, e.g., in any of the following orientations: light chain variable region-linker-heavy chain variable region or heavy chain variable region-linker-light chain variable region.

[00300] Any known BCMA CAR, e.g., the BMCA antigen binding domain of any known BCMA CAR, in the art can be used in accordance with the instant invention to construct a CAR. For example, those described herein.

[00301] In one embodiment, an antigen binding domain against ROR1 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Hudecek et al., Clin Cancer Res 19(12):3153-3164 (2013); WO 2011159847; and US20130101607.

[00302] In one embodiment, an antigen binding domain against CD22 is an antigen binding portion, e.g., CDRs, of an antibody described in, e.g., Haso et al., Blood, 121(7): 1165-1174 (2013); Wayne et al., Clin Cancer Res 16(6): 1894-1903 (2010); Kato et al., Leuk Res 37(1):83-88 (2013); Creative BioMart (creativebiomart.net): MOM-18047-S(P).

[00303] In one embodiment, an antigen binding domain against CD20 is an antigen binding portion, e.g., CDRs, of the antibody Rituximab, Ofatumumab, Ocrelizumab, Veltuzumab, or GA101, or derivatives thereof.

[00304] In one embodiment, the antigen binding domain comprises one, two three (e.g., all three) heavy chain CDRs, HC CDR1, HC CDR2 and HC CDR3, from an antibody listed above, and/or one, two, three (e.g., all three) light chain CDRs, LC CDR1, LC CDR2 and LC CDR3, from an antibody that binds a tumor antigen or a B cell antigen listed above. In one embodiment, the antigen binding domain comprises a heavy chain variable region and/or a

variable light chain region of an antibody that binds a tumor antigen or a B cell antigen listed above.

[00305] A humanized antibody can be produced using a variety of techniques known in the art, including but not limited to, CDR-grafting (see, e.g., European Patent No. EP 239,400; International Publication No. WO 91/09967; and U.S. Pat. Nos. 5,225,539, 5,530,101, and 5,585,089, each of which is incorporated herein in its entirety by reference), veneering or resurfacing (see, e.g., European Patent Nos. EP 592,106 and EP 519,596; Padlan, 1991, Molecular Immunology, 28(4/5):489-498; Studnicka et al., 1994, Protein Engineering, 7(6):805-814; and Roguska et al., 1994, PNAS, 91:969-973, each of which is incorporated herein by its entirety by reference), chain shuffling (see, e.g., U.S. Pat. No. 5,565,332, which is incorporated herein in its entirety by reference), and techniques disclosed in, e.g., U.S. Patent Application Publication No. US2005/0042664, U.S. Patent Application Publication No. US2005/0048617, U.S. Pat. No. 6,407,213, U.S. Pat. No. 5,766,886, International Publication No. WO 9317105, Tan et al., J. Immunol., 169:1119-25 (2002), Caldas et al., Protein Eng., 13(5):353-60 (2000), Morea et al., Methods, 20(3):267-79 (2000), Baca et al., J. Biol. Chem., 272(16):10678-84 (1997), Roguska et al., Protein Eng., 9(10):895-904 (1996), Couto et al., Cancer Res., 55 (23 Supp):5973s-5977s (1995), Couto et al., Cancer Res., 55(8):1717-22 (1995), Sandhu J S, Gene, 150(2):409-10 (1994), and Pedersen et al., J. Mol. Biol., 235(3):959-73 (1994), each of which is incorporated herein in its entirety by reference. Often, framework residues in the framework regions will be substituted with the corresponding residue from the CDR donor antibody to alter, for example improve, antigen binding. These framework substitutions are identified by methods well-known in the art, e.g., by modeling of the interactions of the CDR and framework residues to identify framework residues important for antigen binding and sequence comparison to identify unusual framework residues at particular positions. (See, e.g., Queen et al., U.S. Pat. No. 5,585,089; and Riechmann et al., 1988, Nature, 332:323, which are incorporated herein by reference in their entireties.)

[00306] Examples of solid tumor associated antigens (i.e., solid tumor antigens) include, without limitation: EGFRvIII, mesothelin, GD2, Tn antigen, sTn antigen, Tn-O-Glycopeptides, sTn-O-Glycopeptides, PSMA, CD97, TAG72, CD44v6, CEA, EPCAM, KIT, IL-13Ra2, leguman, GD3, CD171, IL-11Ra, PSCA, MAD-CT-1, MAD-CT-2, VEGFR2, LewisY, CD24, PDGFR-beta, SSEA-4, folate receptor alpha, ERBBs (e.g., ERBB2), Her2/neu, MUC1, EGFR,

NCAM, Ephrin B2, CAIX, LMP2, sLe, HMWMAA, o-acetyl-GD2, folate receptor beta, TEM1/CD248, TEM7R, FAP, Legumain, HPV E6 or E7, ML-IAP, CLDN6, TSHR, GPRC5D, ALK, Polysialic acid, Fos-related antigen, neutrophil elastase, TRP-2, CYP1B1, sperm protein 17, beta human chorionic gonadotropin, AFP, thyroglobulin, PLAC1, globoH, RAGE1, MN-CA IX, human telomerase reverse transcriptase, intestinal carboxyl esterase, mut hsp 70-2, NA-17, NY-BR-1, UPK2, HAVCR1, ADRB3, PANX3, NY-ESO-1, GPR20, Ly6k, OR51E2, TARP, GFRα4, and a peptide of any of these antigens presented on MHC.

[00307] In one aspect, the CAR comprises an antigen binding domain that binds to a B cell antigen. In one embodiment, the CAR comprises a CD19 antigen binding domain (e.g., a murine, human or humanized antibody or antibody fragment that specifically binds to CD19), a transmembrane domain, and an intracellular signaling domain (e.g., an intracellular signaling domain comprising a costimulatory domain and/or a primary signaling domain).

[00308] Exemplary CAR molecules described herein are provided in Table 10. The CAR molecules in Table 10 comprise a CD19 antigen binding domain, e.g., an amino acid sequence of any CD19 antigen binding domain provided in Table 6.

Table 10. Exemplary CD19 CAR molecules

B cell antigen	**Name**	**Amino Acid Sequence**	**SEQ ID NO:**
CD19	CTL019	MALPVTALLLPLALLLHAARPDIQMTQTTSSLSASLGDRVTISCRASQDISKYL NWYQQKPDGTVKLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYF CQQGNTLPYTFGGGTKLEITGGGGSGGGGSGGGGSEVKLQESGPGLVAPSQSLS VTCTVSGVSLPDYGVSWIRQPPRKGLEWLGVIWGSETTYYNSALKSRLTIIKDN SKSQVFLKMNSLQTDDTAIYYCAKHYYYGGSYAMDYWGQGTSVTVSSTTTPAPR PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLL SLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKF SRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGL YNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	**281**
CD19	CAR 1	MALPVTALLLPLALLLHAARPEIVMTQSPATLSLSPGERATLSCRASQDISKYL NWYQQKPGQAPRLLIYHTSRLHSGIPARFSGSGSGTDYTLTISSLQPEDFAVYF CQQGNTLPYTFGQGTKLEIKGGGGSGGGGSGGGGSQVQLQESGPGLVKPSETLS LTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYYSSSLKSRVTISKDN SKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYAMDYWGQGTLVTVSSTTTPAPR PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLL SLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKF SRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGL YNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	**269**
CD19	CAR 2	MALPVTALLLPLALLLHAARPEIVMTQSPATLSLSPGERATLSCRASQDISKYL NWYQQKPGQAPRLLIYHTSRLHSGIPARFSGSGSGTDYTLTISSLQPEDFAVYF CQQGNTLPYTFGQGTKLEIKGGGGSGGGGSGGGGSQVQLQESGPGLVKPSETLS LTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYYQSSLKSRVTISKDN SKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYAMDYWGQGTLVTVSSTTTPAPR	**270**

		PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLL SLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKF SRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGL YNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	
CD19	CAR 3	MALPVTALLLPLALLLHAARPQVQLQESGPGLVKPSETLSLTCTVSGVSLPDYG VSWIRQPPGKGLEWIGVIWGSETTYYSSSLKSRVTISKDNSKNQVSLKLSSVTA ADTAVYYCAKHYYYGGSYAMDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVMTQ SPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLIYHTSRLHSGIPA RFSGSGSGTDYTLTISSLQPEDFAVYFCQQGNTLPYTFGQGTKLEIKTTTPAPR PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLL SLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKF SRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGL YNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	**271**
CD19	CAR 4	MALPVTALLLPLALLLHAARPQVQLQESGPGLVKPSETLSLTCTVSGVSLPDYG VSWIRQPPGKGLEWIGVIWGSETTYYQSSLKSRVTISKDNSKNQVSLKLSSVTA ADTAVYYCAKHYYYGGSYAMDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVMTQ SPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLIYHTSRLHSGIPA RFSGSGSGTDYTLTISSLQPEDFAVYFCQQGNTLPYTFGQGTKLEIKTTTPAPR PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLL SLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKF SRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGL YNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	**272**
CD19	CAR 5	MALPVTALLLPLALLLHAARPEIVMTQSPATLSLSPGERATLSCRASQDISKYL NWYQQKPGQAPRLLIYHTSRLHSGIPARFSGSGSGTDYTLTISSLQPEDFAVYF CQQGNTLPYTFGQGTKLEIKGGGGSGGGGSGGGGSGGGGSQVQLQESGPGLVKP SETLSLTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYYSSSLKSRVT ISKDNSKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYAMDYWGQGTLVTVSSTT TPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTC GVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKN PQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQ ALPPR	**273**
CD19	CAR 6	MALPVTALLLPLALLLHAARPEIVMTQSPATLSLSPGERATLSCRASQDISKYL NWYQQKPGQAPRLLIYHTSRLHSGIPARFSGSGSGTDYTLTISSLQPEDFAVYF CQQGNTLPYTFGQGTKLEIKGGGGSGGGGSGGGGSGGGGSQVQLQESGPGLVKP SETLSLTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYYQSSLKSRVT ISKDNSKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYAMDYWGQGTLVTVSSTT TPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTC GVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKN PQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQ ALPPR	**274**
CD19	CAR 7	MALPVTALLLPLALLLHAARPQVQLQESGPGLVKPSETLSLTCTVSGVSLPDYG VSWIRQPPGKGLEWIGVIWGSETTYYSSSLKSRVTISKDNSKNQVSLKLSSVTA ADTAVYYCAKHYYYGGSYAMDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSE IVMTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLIYHTSRLH SGIPARFSGSGSGTDYTLTISSLQPEDFAVYFCQQGNTLPYTFGQGTKLEIKTT TPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTC GVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKN PQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQ ALPPR	**275**
CD19	CAR 8	MALPVTALLLPLALLLHAARPQVQLQESGPGLVKPSETLSLTCTVSGVSLPDYG VSWIRQPPGKGLEWIGVIWGSETTYYQSSLKSRVTISKDNSKNQVSLKLSSVTA ADTAVYYCAKHYYYGGSYAMDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSE IVMTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLIYHTSRLH SGIPARFSGSGSGTDYTLTISSLQPEDFAVYFCQQGNTLPYTFGQGTKLEIKTT	**276**

		TPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTC GVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKN PQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQ ALPPR	
CD19	CAR 9	MALPVTALLLPLALLLHAARPEIVMTQSPATLSLSPGERATLSCRASQDISKYL NWYQQKPGQAPRLLIYHTSRLHSGIPARFSGSGSGTDYTLTISSLQPEDFAVYF CQQGNTLPYTFGQGTKLEIKGGGGSGGGGSGGGGSGGGGSQVQLQESGPGLVKP SETLSLTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYYNSSLKSRVT ISKDNSKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYAMDYWGQGTLVTVSSTT TPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTC GVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKN PQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQ ALPPR	**277**
CD19	CAR 10	MALPVTALLLPLALLLHAARPEIVMTQSPATLSLSPGERATLSCRASQDISKYL NWYQQKPGQAPRLLIYHTSRLHSGIPARFSGSGSGTDYTLTISSLQPEDFAVYF CQQGNTLPYTFGQGTKLEIKGGGGSGGGGSGGGGSGGGGSQVQLQESGPGLVKP SETLSLTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYYNSSLKSRVT ISKDNSKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYAMDYWGQGTLVTVSSTT TPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTC GVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKN PQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQ ALPPR	**278**
CD19	CAR 11	MALPVTALLLPLALLLHAARPQVQLQESGPGLVKPSETLSLTCTVSGVSLPDYG VSWIRQPPGKGLEWIGVIWGSETTYYNSSLKSRVTISKDNSKNQVSLKLSSVTA ADTAVYYCAKHYYYGGSYAMDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSE IVMTQSPATLSLSPGERATLSCRASQDISKYLNWYQQKPGQAPRLLIYHTSRLH SGIPARFSGSGSGTDYTLTISSLQPEDFAVYFCQQGNTLPYTFGQGTKLEIKTT TPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTC GVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKN PQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQ ALPPR	**279**
CD19	CAR 12	MALPVTALLLPLALLLHAARPEIVMTQSPATLSLSPGERATLSCRASQDISKYL NWYQQKPGQAPRLLIYHTSRLHSGIPARFSGSGSGTDYTLTISSLQPEDFAVYF CQQGNTLPYTFGQGTKLEIKGGGGSGGGGSGGGGSQVQLQESGPGLVKPSETLS LTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYYNSSLKSRVTISKDN SKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYAMDYWGQGTLVTVSSTTTPAPR PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLL SLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKF SRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGL YNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	**280**

[00309] In one embodiment, the CAR molecule comprises (e.g., consists of) an amino acid sequence as provided in Table 10, or in Table 3 of International Publication No. WO2014/153270, filed March 15, 2014; incorporated herein by reference. In one embodiment, the CAR molecule (e.g., consists of) an amino acid sequence of SEQ ID NO: 269, SEQ ID NO: 270, SEQ ID NO: 271, SEQ ID NO: 272, SEQ ID NO: 273, SEQ ID NO: 274, SEQ ID NO: 275, SEQ ID NO: 276, SEQ ID NO: 277, SEQ ID NO: 278, SEQ ID NO: 279, SEQ ID NO:

280, or SEQ ID NO: 281; or an amino acid sequence having at least one, two, three, four, five, 10, 15, 20 or 30 modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 60, 50, or 40 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence of SEQ ID NO: 269, SEQ ID NO: 270, SEQ ID NO: 271, SEQ ID NO: 272, SEQ ID NO: 273, SEQ ID NO: 274, SEQ ID NO: 275, SEQ ID NO: 276, SEQ ID NO: 277, SEQ ID NO: 278, SEQ ID NO: 279, SEQ ID NO: 280, or SEQ ID NO: 281; or an amino acid sequence having 85%, 90%, 95%, 96%, 97%, 98%, 99% identity to an amino acid sequence of SEQ ID NO: 269, SEQ ID NO: 270, SEQ ID NO: 271, SEQ ID NO: 272, SEQ ID NO: 273, SEQ ID NO: 274, SEQ ID NO: 275, SEQ ID NO: 276, SEQ ID NO: 277, SEQ ID NO: 278, SEQ ID NO: 279, SEQ ID NO: 280, or SEQ ID NO: 281.

[00310] In one aspect, the CAR comprises an antigen binding domain that binds to a B cell antigen. In one embodiment, CAR comprises a BCMA antigen binding domain (e.g., a murine, human or humanized antibody or antibody fragment that specifically binds to BCMA, e.g., human BCMA), a transmembrane domain, and an intracellular signaling domain (e.g., an intracellular signaling domain comprising a costimulatory domain and/or a primary signaling domain).

[00311] Exemplary CAR molecules described herein are provided in Table 29, or Table 1 of WO2016/014565, or as otherwise described herein. The CAR molecules in Table 29 comprise a BCMA antigen binding domain, e.g., an amino acid sequence of any BCMA antigen binding domain provided in Table 12 or 13.

Table 29. Exemplary BCMA CAR molecules. Sequences are provided with a leader sequence.

Name/ Description	**SEQ ID NO:**	**Sequence**
139109		
139109- aa Full CAR	959	MALPVTALLLPLALLLHAARPEVQLVESGGGLVQPGGSLRLSCAVSGFALS NHGMSWVRRAPGKGLEWVSGIVYSGSTYYAASVKGRFTISRDNSRNTLYLQ MNSLRPEDTAIYYCSAHGGESDVWGQGTTVTVSSASGGGGSGGRASGGGGS DIQLTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAA SSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPYTFGQGT KVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDI YIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDG LYQGLSTATKDTYDALHMQALPPR
139109- nt Full CAR	974	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCGAAGTGCAATTGGTGGAATCAGGGGGAGGACTTGTGCAG

		CCTGGAGGATCGCTGAGACTGTCATGTGCCGTGTCCGGCTTTGCCCTGTCC AACCACGGGATGTCCTGGGTCCGCCGCGCGCCTGGAAAGGGCCTCGAATGG GTGTCGGGTATTGTGTACAGCGGTAGCACCTACTATGCCGCATCCGTGAAG GGGAGATTCACCATCAGCCGGGACAACTCCAGGAACACTCTGTACCTCCAA ATGAATTCGCTGAGGCCAGAGGACACTGCCATCTACTACTGCTCCGCGCAT GGCGGAGAGTCCGACGTCTGGGGACAGGGGACCACCGTGACCGTGTCTAGC GCGTCCGGCGGAGGCGGCAGCGGGGGTCGGGCATCAGGGGGCGGCGGATCG GACATCCAGCTCACCCAGTCCCCGAGCTCGCTGTCCGCCTCCGTGGGAGAT CGGGTCACCATCACGTGCCGCGCCAGCCAGTCGATTTCCTCCTACCTGAAC TGGTACCAACAGAAGCCCGGAAAAGCCCCGAAGCTTCTCATCTACGCCGCC TCGAGCCTGCAGTCAGGAGTGCCCTCACGGTTCTCCGGCTCCGGTTCCGGT ACTGATTTCACCCTGACCATTTCCTCCCTGCAACCGGAGGACTTCGCTACT TACTACTGCCAGCAGTCGTACTCCACCCCCTACACTTTCGGACAAGGCACC AAGGTCGAAATCAAGACCACTACCCCAGCACCGAGGCCACCCACCCCGGCT CCTACCATCGCCTCCCAGCCTCTGTCCCTGCGTCCGGAGGCATGTAGACCC GCAGCTGGTGGGGCCGTGCATACCCGGGGTCTTGACTTCGCCTGCGATATC TACATTTGGGCCCCTCTGGCTGGTACTTGCGGGGTCCTGCTGCTTTCACTC GTGATCACTCTTTACTGTAAGCGCGGTCGGAAGAAGCTGCTGTACATCTTT AAGCAACCCTTCATGAGGCCTGTGCAGACTACTCAAGAGGAGGACGGCTGT TCATGCCGGTTCCCAGAGGAGGAGGAAGGCGGCTGCGAACTGCGCGTGAAA TTCAGCCGCAGCGCAGATGCTCCAGCCTACAAGCAGGGGCAGAACCAGCTC TACAACGAACTCAATCTTGGTCGGAGAGAGGAGTACGACGTGCTGGACAAG CGGAGAGGACGGGACCCAGAAATGGGCGGGAAGCCGCGCAGAAAGAATCCC CAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAAGATGGCAGAAGCCTAT AGCGAGATTGGTATGAAAGGGGAACGCAGAAGAGGCAAAGGCCACGACGGA CTGTACCAGGGACTCAGCACCGCCACCAAGGACACCTATGACGCTCTTCAC ATGCAGGCCCTGCCGCCTCGG
139103		
139103- aa Full CAR	949	MALPVTALLLPLALLLHAARPQVQLVESGGGLVQPGRSLRLSCAASGFTFS NYAMSWVRQAPGKGLGWVSGISRSGENTYYADSVKGRFTISRDNSKNTLYL QMNSLRDEDTAVYYCARSPAHYYGGMDVWGQGTTVTVSSASGGGGSGGRAS GGGGSDIVLTQSPGTLSLSPGERATLSCRASQSISSSFLAWYQQKPGQAPR LLIYGASRRATGIPDRFSGSGSGTDFTLTISRLEPEDSAVYYCQQYHSSPS WTFGQGTKLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRG LDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQT TQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERR RGKGHDGLYQGLSTATKDTYDALHMQALPPR
139103- nt Full CAR	964	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCCAAGTGCAACTCGTGGAATCTGGTGGAGGACTCGTGCAA CCCGGAAGATCGCTTAGACTGTCGTGTGCCGCCAGCGGGTTCACTTTCTCG AACTACGCGATGTCCTGGGTCCGCCAGGCACCCGGAAAGGGACTCGGTTGG GTGTCCGGCATTTCCCGGTCCGGCGAAAATACCTACTACGCCGACTCCGTG AAGGGCCGCTTCACCATCTCAAGGGACAACAGCAAAAACACCCTGTACTTG CAAATGAACTCCCTGCGGGATGAAGATACAGCCGTGTACTATTGCGCCCGG TCGCCTGCCCATTACTACGGCGGAATGGACGTCTGGGGACAGGGAACCACT GTGACTGTCAGCAGCGCGTCGGGTGGCGGCGGCTCAGGGGGTCGGGCCTCC GGGGGGGGAGGGTCCGACATCGTGCTGACCCAGTCCCCGGGAACCCTGAGC CTGAGCCCGGGAGAGCGCGCGACCCTGTCATGCCGGGCATCCCAGAGCATT AGCTCCTCCTTTCTCGCCTGGTATCAGCAGAAGCCCGGACAGGCCCCGAGG CTGCTGATCTACGGCGCTAGCAGAAGGGCTACCGGAATCCCAGACCGGTTC

		TCCGGCTCCGGTTCCGGGACCGATTTCACCCTTACTATCTCGCGCCTGGAA CCTGAGGACTCCGCCGTCTACTACTGCCAGCAGTACCACTCATCCCCGTCG TGGACGTTCGGACAGGGCACCAAGCTGGAGATTAAGACCACTACCCCAGCA CCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTG CGTCCGGAGGCATGTAGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGT CTTGACTTCGCCTGCGATATCTACATTTGGGCCCCTCTGGCTGGTACTTGC GGGGTCCTGCTGCTTTCACTCGTGATCACTCTTTACTGTAAGCGCGGTCGG AAGAAGCTGCTGTACATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACT ACTCAAGAGGAGGACGGCTGTTCATGCCGGTTCCCAGAGGAGGAGGAAGGC GGCTGCGAACTGCGCGTGAAATTCAGCCGCAGCGCAGATGCTCCAGCCTAC AAGCAGGGGCAGAACCAGCTCTACAACGAACTCAATCTTGGTCGGAGAGAG GAGTACGACGTGCTGGACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGG AAGCCGCGCAGAAAGAATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAG GATAAGATGGCAGAAGCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGA AGAGGCAAAGGCCACGACGGACTGTACCAGGGACTCAGCACCGCCACCAAG GACACCTATGACGCTCTTCACATGCAGGCCCTGCCGCCTCGG
139105		
139105- aa Full CAR	950	MALPVTALLLPLALLLHAARPQVQLVESGGGLVQPGRSLRLSCAASGFTFD DYAMHWVRQAPGKGLEWVSGISWNSGSIGYADSVKGRFTISRDNAKNSLYL QMNSLRAEDTALYYCSVHSFLAYWGQGTLVTVSSASGGGGSGGRASGGGGS DIVMTQTPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPYT FGQGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLD FACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQ EEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRG KGHDGLYQGLSTATKDTYDALHMQALPPR
139105- nt Full CAR	965	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCCAAGTGCAACTCGTCGAATCCGGTGGAGGTCTGGTCCAA CCTGGTAGAAGCCTGAGACTGTCGTGTGCGGCCAGCGGATTCACCTTTGAT GACTATGCTATGCACTGGGTGCGGCAGGCCCCAGGAAAGGGCCTGGAATGG GTGTCGGGAATTAGCTGGAACTCCGGGTCCATTGGCTACGCCGACTCCGTG AAGGGCCGCTTCACCATCTCCCGCGACAACGCAAAGAACTCCCTGTACTTG CAAATGAACTCGCTCAGGGCTGAGGATACCGCGCTGTACTACTGCTCCGTG CATTCCTTCCTGGCCTACTGGGGACAGGGAACTCTGGTCACCGTGTCGAGC GCCTCCGGCGGCGGGGGCTCGGGTGGACGGGCCTCGGGCGGAGGGGGGTCC GACATCGTGATGACCCAGACCCCGCTGAGCTTGCCCGTGACTCCCGGAGAG CCTGCATCCATCTCCTGCCGGTCATCCCAGTCCCTTCTCCACTCCAACGGA TACAACTACCTCGACTGGTACCTCCAGAAGCCGGGACAGAGCCCTCAGCTT CTGATCTACCTGGGGTCAAATAGAGCCTCAGGAGTGCCGGATCGGTTCAGC GGATCTGGTTCGGGAACTGATTTCACTCTGAAGATTTCCCGCGTGGAAGCC GAGGACGTGGGCGTCTACTACTGTATGCAGGCGCTGCAGACCCCCTATACC TTCGGCCAAGGGACGAAAGTGGAGATCAAGACCACTACCCCAGCACCGAGG CCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTGCGTCCG GAGGCATGTAGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGTCTTGAC TTCGCCTGCGATATCTACATTTGGGCCCCTCTGGCTGGTACTTGCGGGGTC CTGCTGCTTTCACTCGTGATCACTCTTTACTGTAAGCGCGGTCGGAAGAAG CTGCTGTACATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACTACTCAA GAGGAGGACGGCTGTTCATGCCGGTTCCCAGAGGAGGAGGAAGGCGGCTGC GAACTGCGCGTGAAATTCAGCCGCAGCGCAGATGCTCCAGCCTACAAGCAG GGGCAGAACCAGCTCTACAACGAACTCAATCTTGGTCGGAGAGAGGAGTAC GACGTGCTGGACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGGAAGCCG

		CGCAGAAAGAATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAAG ATGGCAGAAGCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGAAGAGGC AAAGGCCACGACGGACTGTACCAGGGACTCAGCACCGCCACCAAGGACACC TATGACGCTCTTCACATGCAGGCCCTGCCGCCTCGG
139111		
139111- aa Full CAR	951	MALPVTALLLPLALLLHAARPEVQLLESGGGLVQPGGSLRLSCAVSGFALS NHGMSWVRRAPGKGLEWVSGIVYSGSTYYAASVKGRFTISRDNSRNTLYLQ MNSLRPEDTAIYYCSAHGGESDVWGQGTTVTVSSASGGGGSGGRASGGGGS DIVMTQTPLSLSVTPGQPASISCKSSQSLLRNDGKTPLYWYLQKAGQPPQL LIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGAYYCMQNIQFPSF GGGTKLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDF ACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQE EDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
139111- nt Full CAR	966	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCGAAGTGCAATTGTTGGAATCTGGAGGAGGACTTGTGCAG CCTGGAGGATCACTGAGACTTTCGTGTGCGGTGTCAGGCTTCGCCCTGAGC AACCACGGCATGAGCTGGGTGCGGAGAGCCCCGGGGAAGGGTCTGGAATGG GTGTCCGGGATCGTCTACTCCGGTTCAACTTACTACGCCGCAAGCGTGAAG GGTCGCTTCACCATTTCCCGCGATAACTCCCGGAACACCCTGTACCTCCAA ATGAACTCCCTGCGGCCCGAGGACACCGCCATCTACTACTGTTCCGCGCAT GGAGGAGAGTCCGATGTCTGGGGACAGGGCACTACCGTGACCGTGTCGAGC GCCTCGGGGGGAGGAGGCTCCGGCGGTCGCGCCTCCGGGGGGGGTGGCAGC GACATTGTGATGACGCAGACTCCACTCTCGCTGTCCGTGACCCCGGGACAG CCCGCGTCCATCTCGTGCAAGAGCTCCCAGAGCCTGCTGAGGAACGACGGA AAGACTCCTCTGTATTGGTACCTCCAGAAGGCTGGACAGCCCCCGCAACTG CTCATCTACGAAGTGTCAAATCGCTTCTCCGGGGTGCCGGATCGGTTTTCC GGCTCGGGATCGGGCACCGACTTCACCCTGAAAATCTCCAGGGTCGAGGCC GAGGACGTGGGAGCCTACTACTGCATGCAAAACATCCAGTTCCCTTCCTTC GGCGGCGGCACAAAGCTGGAGATTAAGACCACTACCCCAGCACCGAGGCCA CCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTGCGTCCGGAG GCATGTAGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGTCTTGACTTC GCCTGCGATATCTACATTTGGGCCCCTCTGGCTGGTACTTGCGGGGTCCTG CTGCTTTCACTCGTGATCACTCTTTACTGTAAGCGCGGTCGGAAGAAGCTG CTGTACATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACTACTCAAGAG GAGGACGGCTGTTCATGCCGGTTCCCAGAGGAGGAGGAAGGCGGCTGCGAA CTGCGCGTGAAATTCAGCCGCAGCGCAGATGCTCCAGCCTACAAGCAGGGG CAGAACCAGCTCTACAACGAACTCAATCTTGGTCGGAGAGAGGAGTACGAC GTGCTGGACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGGAAGCCGCGC AGAAAGAATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAAGATG GCAGAAGCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGAAGAGGCAAA GGCCACGACGGACTGTACCAGGGACTCAGCACCGCCACCAAGGACACCTAT GACGCTCTTCACATGCAGGCCCTGCCGCCTCGG
139100		
139100- aa Full CAR	952	MALPVTALLLPLALLLHAARPQVQLVQSGAEVRKTGASVKVSCKASGYIFD NFGINWVRQAPGQGLEWMGWINPKNNNTNYAQKFQGRVTITADESTNTAYM EVSSLRSEDTAVYYCARGPYYYQSYMDVWGQGTMVTVSSASGGGGSGGRAS GGGGSDIVMTQTPLSLPVTPGEPASISCRSSQSLLHSNGYNYLNWYLQKPG QSPQLLIYLGSKRASGVPDRFSGSGSGTDFTLHITRVGAEDVGVYYCMQAL QTPYTFGQGTKLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVH TRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRP

		VQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLG RREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKG ERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
139100- nt Full CAR	967	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCCAAGTCCAACTCGTCCAGTCCGGCGCAGAAGTCAGAAAA ACCGGTGCTAGCGTGAAAGTGTCCTGCAAGGCCTCCGGCTACATTTTCGAT AACTTCGGAATCAACTGGGTCAGACAGGCCCCGGGCCAGGGGCTGGAATGG ATGGGATGGATCAACCCCAAGAACAACAACACCAACTACGCACAGAAGTTC CAGGGCCGCGTGACTATCACCGCCGATGAATCGACCAATACCGCCTACATG GAGGTGTCCTCCCTGCGGTCGGAGGACACTGCCGTGTATTACTGCGCGAGG GGCCCATACTACTACCAAAGCTACATGGACGTCTGGGGACAGGGAACCATG GTGACCGTGTCATCCGCCTCCGGTGGTGGAGGCTCCGGGGGGCGGGCTTCA GGAGGCGGAGGAAGCGATATTGTGATGACCCAGACTCCGCTTAGCCTGCCC GTGACTCCTGGAGAACCGGCCTCCATTTCCTGCCGGTCCTCGCAATCACTC CTGCATTCCAACGGTTACAACTACCTGAATTGGTACCTCCAGAAGCCTGGC CAGTCGCCCCAGTTGCTGATCTATCTGGGCTCGAAGCGCGCCTCCGGGGTG CCTGACCGGTTTAGCGGATCTGGGAGCGGCACGGACTTCACTCTCCACATC ACCCGCGTGGGAGCGGAGGACGTGGGAGTGTACTACTGTATGCAGGCGCTG CAGACTCCGTACACATTCGGACAGGGCACCAAGCTGGAGATCAAGACCACT ACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCT CTGTCCCTGCGTCCGGAGGCATGTAGACCCGCAGCTGGTGGGGCCGTGCAT ACCCGGGGTCTTGACTTCGCCTGCGATATCTACATTTGGGCCCCTCTGGCT GGTACTTGCGGGGTCCTGCTGCTTTCACTCGTGATCACTCTTTACTGTAAG CGCGGTCGGAAGAAGCTGCTGTACATCTTTAAGCAACCCTTCATGAGGCCT GTGCAGACTACTCAAGAGGAGGACGGCTGTTCATGCCGGTTCCCAGAGGAG GAGGAAGGCGGCTGCGAACTGCGCGTGAAATTCAGCCGCAGCGCAGATGCT CCAGCCTACAAGCAGGGGCAGAACCAGCTCTACAACGAACTCAATCTTGGT CGGAGAGAGGAGTACGACGTGCTGGACAAGCGGAGAGGACGGGACCCAGAA ATGGGCGGGAAGCCGCGCAGAAAGAATCCCCAAGAGGGCCTGTACAACGAG CTCCAAAAGGATAAGATGGCAGAAGCCTATAGCGAGATTGGTATGAAAGGG GAACGCAGAAGAGGCAAAGGCCACGACGGACTGTACCAGGGACTCAGCACC GCCACCAAGGACACCTATGACGCTCTTCACATGCAGGCCCTGCCGCCTCGG
139101		
139101- aa Full CAR	953	MALPVTALLLPLALLLHAARPQVQLQESGGGLVQPGGSLRLSCAASGFTFS SDAMTWVRQAPGKGLEWVSVISGSGGTTYYADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCAKLDSSGYYYARGPRYWGQGTLVTVSSASGGGGSGG RASGGGGSDIQLTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKA PKLLIYGASTLASGVPARFSGSGSGTHFTLTINSLQSEDSATYYCQQSYKR ASFGQGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRG LDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQT TQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERR RGKGHDGLYQGLSTATKDTYDALHMQALPPR
139101- nt Full CAR	968	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCCAAGTGCAACTTCAAGAATCAGGCGGAGGACTCGTGCAG CCCGGAGGATCATTGCGGCTCTCGTGCGCCGCCTCGGGCTTCACCTTCTCG AGCGACGCCATGACCTGGGTCCGCCAGGCCCCGGGGAAGGGGCTGGAATGG GTGTCTGTGATTTCCGGCTCCGGGGGAACTACGTACTACGCCGATTCCGTG AAAGGTCGCTTCACTATCTCCCGGGACAACAGCAAGAACACCCTTTATCTG CAAATGAATTCCCTCCGCGCCGAGGACACCGCCGTGTACTACTGCGCCAAG CTGGACTCCTCGGGCTACTACTATGCCCGGGGTCCGAGATACTGGGGACAG GGAACCCTCGTGACCGTGTCCTCCGCGTCCGGCGGAGGAGGGTCGGGAGGG

		CGGGCCTCCGGCGGCGGCGGTTCGGACATCCAGCTGACCCAGTCCCCATCC TCACTGAGCGCAAGCGTGGGCGACAGAGTCACCATTACATGCAGGGCGTCC CAGAGCATCAGCTCCTACCTGAACTGGTACCAACAGAAGCCTGGAAAGGCT CCTAAGCTGTTGATCTACGGGGCTTCGACCCTGGCATCCGGGGTGCCCGCG AGGTTTAGCGGAAGCGGTAGCGGCACTCACTTCACTCTGACCATTAACAGC CTCCAGTCCGAGGATTCAGCCACTTACTACTGTCAGCAGTCCTACAAGCGG GCCAGCTTCGGACAGGGCACTAAGGTCGAGATCAAGACCACTACCCCAGCA CCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTG CGTCCGGAGGCATGTAGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGT CTTGACTTCGCCTGCGATATCTACATTTGGGCCCCTCTGGCTGGTACTTGC GGGGTCCTGCTGCTTTCACTCGTGATCACTCTTTACTGTAAGCGCGGTCGG AAGAAGCTGCTGTACATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACT ACTCAAGAGGAGGACGGCTGTTCATGCCGGTTCCCAGAGGAGGAGGAAGGC GGCTGCGAACTGCGCGTGAAATTCAGCCGCAGCGCAGATGCTCCAGCCTAC AAGCAGGGGCAGAACCAGCTCTACAACGAACTCAATCTTGGTCGGAGAGAG GAGTACGACGTGCTGGACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGG AAGCCGCGCAGAAAGAATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAG GATAAGATGGCAGAAGCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGA AGAGGCAAAGGCCACGACGGACTGTACCAGGGACTCAGCACCGCCACCAAG GACACCTATGACGCTCTTCACATGCAGGCCCTGCCGCCTCGG
139102		
139102- aa Full CAR	954	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFS NYGITWVRQAPGQGLEWMGWISAYNGNTNYAQKFQGRVTMTRNTSISTAYM ELSSLRSEDTAVYYCARGPYYYYMDVWGKGTMVTVSSASGGGGSGGRASGG GGSEIVMTQSPLSLPVTPGEPASISCRSSQSLLYSNGYNYVDWYLQKPGQS PQLLIYLGSNRASGVPDRFSGSGSGTDFKLQISRVEAEDVGIYYCMQGRQF PYSFGQGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTR GLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQ TTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGER RRGKGHDGLYQGLSTATKDTYDALHMQALPPR
139102- nt Full CAR	969	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCCAAGTCCAACTGGTCCAGAGCGGTGCAGAAGTGAAGAAG CCCGGAGCGAGCGTGAAAGTGTCCTGCAAGGCTTCCGGGTACACCTTCTCC AACTACGGCATCACTTGGGTGCGCCAGGCCCCGGGACAGGGCCTGGAATGG ATGGGGTGGATTTCCGCGTACAACGGCAATACGAACTACGCTCAGAAGTTC CAGGGTAGAGTGACCATGACTAGGAACACCTCCATTTCCACCGCCTACATG GAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTATTGCGCCCGG GGACCATACTACTACTACATGGATGTCTGGGGGAAGGGGACTATGGTCACC GTGTCATCCGCCTCGGGAGGCGGCGGATCAGGAGGACGCGCCTCTGGTGGT GGAGGATCGGAGATCGTGATGACCCAGAGCCCTCTCTCCTTGCCCGTGACT CCTGGGGAGCCCGCATCCATTTCATGCCGGAGCTCCCAGTCACTTCTCTAC TCCAACGGCTATAACTACGTGGATTGGTACCTCCAAAAGCCGGGCCAGAGC CCGCAGCTGCTGATCTACCTGGGCTCGAACAGGGCCAGCGGAGTGCCTGAC CGGTTCTCCGGGTCGGGAAGCGGGACCGACTTCAAGCTGCAAATCTCGAGA GTGGAGGCCGAGGACGTGGGAATCTACTACTGTATGCAGGGCCGCCAGTTT CCGTACTCGTTCGGACAGGGCACCAAAGTGGAAATCAAGACCACTACCCCA GCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCC CTGCGTCCGGAGGCATGTAGACCCGCAGCTGGTGGGGCCGTGCATACCCGG GGTCTTGACTTCGCCTGCGATATCTACATTTGGGCCCCTCTGGCTGGTACT TGCGGGGTCCTGCTGCTTTCACTCGTGATCACTCTTTACTGTAAGCGCGGT CGGAAGAAGCTGCTGTACATCTTTAAGCAACCCTTCATGAGGCCTGTGCAG

		ACTACTCAAGAGGAGGACGGCTGTTCATGCCGGTTCCCAGAGGAGGAGGAA GGCGGCTGCGAACTGCGCGTGAAATTCAGCCGCAGCGCAGATGCTCCAGCC TACAAGCAGGGGCAGAACCAGCTCTACAACGAACTCAATCTTGGTCGGAGA GAGGAGTACGACGTGCTGGACAAGCGGAGAGGACGGGACCCAGAAATGGGC GGGAAGCCGCGCAGAAAGAATCCCCAAGAGGGCCTGTACAACGAGCTCCAA AAGGATAAGATGGCAGAAGCCTATAGCGAGATTGGTATGAAAGGGGAACGC AGAAGAGGCAAAGGCCACGACGGACTGTACCAGGGACTCAGCACCGCCACC AAGGACACCTATGACGCTCTTCACATGCAGGCCCTGCCGCCTCGG
139104		
139104- aa Full CAR	955	MALPVTALLLPLALLLHAARPEVQLLETGGGLVQPGGSLRLSCAVSGFALS NHGMSWVRRAPGKGLEWVSGIVYSGSTYYAASVKGRFTISRDNSRNTLYLQ MNSLRPEDTAIYYCSAHGGESDVWGQGTTVTVSSASGGGGSGGRASGGGGS EIVLTQSPATLSVSPGESATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGA STRASGIPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYGSSLTFGGGTK VEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIY IWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCS CRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGL YQGLSTATKDTYDALHMQALPPR
139104- nt Full CAR	970	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCGAAGTGCAATTGCTCGAAACTGGAGGAGGTCTGGTGCAA CCTGGAGGATCACTTCGCCTGTCCTGCGCCGTGTCGGGCTTTGCCCTGTCC AACCATGGAATGAGCTGGGTCCGCCGCGCGCCGGGGAAGGGCCTCGAATGG GTGTCCGGCATCGTCTACTCCGGCTCCACCTACTACGCCGCGTCCGTGAAG GGCCGGTTCACGATTTCACGGGACAACTCGCGGAACACCCTGTACCTCCAA ATGAATTCCCTTCGGCCGGAGGATACTGCCATCTACTACTGCTCCGCCCAC GGTGGCGAATCCGACGTCTGGGGCCAGGGAACCACCGTGACCGTGTCCAGC GCGTCCGGGGGAGGAGGAAGCGGGGGTAGAGCATCGGGTGGAGGCGGATCA GAGATCGTGCTGACCCAGTCCCCCGCCACCTTGAGCGTGTCACCAGGAGAG TCCGCCACCCTGTCATGCCGCGCCAGCCAGTCCGTGTCCTCCAACCTGGCT TGGTACCAGCAGAAGCCGGGGCAGGCCCCTAGACTCCTGATCTATGGGGCG TCGACCCGGGCATCTGGAATTCCCGATAGGTTCAGCGGATCGGGCTCGGGC ACTGACTTCACTCTGACCATCTCCTCGCTGCAAGCCGAGGACGTGGCTGTG TACTACTGTCAGCAGTACGGAAGCTCCCTGACTTTCGGTGGCGGGACCAAA GTCGAGATTAAGACCACTACCCCAGCACCGAGGCCACCCACCCCGGCTCCT ACCATCGCCTCCCAGCCTCTGTCCCTGCGTCCGGAGGCATGTAGACCCGCA GCTGGTGGGGCCGTGCATACCCGGGGTCTTGACTTCGCCTGCGATATCTAC ATTTGGGCCCCTCTGGCTGGTACTTGCGGGGTCCTGCTGCTTTCACTCGTG ATCACTCTTTACTGTAAGCGCGGTCGGAAGAAGCTGCTGTACATCTTTAAG CAACCCTTCATGAGGCCTGTGCAGACTACTCAAGAGGAGGACGGCTGTTCA TGCCGGTTCCCAGAGGAGGAGGAAGGCGGCTGCGAACTGCGCGTGAAATTC AGCCGCAGCGCAGATGCTCCAGCCTACAAGCAGGGGCAGAACCAGCTCTAC AACGAACTCAATCTTGGTCGGAGAGAGGAGTACGACGTGCTGGACAAGCGG AGAGGACGGGACCCAGAAATGGGCGGGAAGCCGCGCAGAAAGAATCCCCAA GAGGGCCTGTACAACGAGCTCCAAAAGGATAAGATGGCAGAAGCCTATAGC GAGATTGGTATGAAAGGGGAACGCAGAAGAGGCAAAGGCCACGACGGACTG TACCAGGGACTCAGCACCGCCACCAAGGACACCTATGACGCTCTTCACATG CAGGCCCTGCCGCCTCGG
139106		
139106- aa Full CAR	956	MALPVTALLLPLALLLHAARPEVQLVETGGGLVQPGGSLRLSCAVSGFALS NHGMSWVRRAPGKGLEWVSGIVYSGSTYYAASVKGRFTISRDNSRNTLYLQ MNSLRPEDTAIYYCSAHGGESDVWGQGTTVTVSSASGGGGSGGRASGGGGS

		EIVMTQSPATLSVSPGERATLSCRASQSVSSKLAWYQQKPGQAPRLLMYGA SIRATGIPDRFSGSGSGTEFTLTISSLEPEDFAVYYCQQYGSSSWTFGQGT KVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDI YIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDG LYQGLSTATKDTYDALHMQALPPR
139106- nt Full CAR	971	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCGAAGTGCAATTGGTGGAAACTGGAGGAGGACTTGTGCAA CCTGGAGGATCATTGAGACTGAGCTGCGCAGTGTCGGGATTCGCCCTGAGC AACCATGGAATGTCCTGGGTCAGAAGGGCCCCTGGAAAAGGCCTCGAATGG GTGTCAGGGATCGTGTACTCCGGTTCCACTTACTACGCCGCCTCCGTGAAG GGGCGCTTCACTATCTCACGGGATAACTCCCGCAATACCCTGTACCTCCAA ATGAACAGCCTGCGGCCGGAGGATACCGCCATCTACTACTGTTCCGCCCAC GGTGGAGAGTCTGACGTCTGGGGCCAGGGAACTACCGTGACCGTGTCCTCC GCGTCCGGCGGTGGAGGGAGCGGCGGCCGCGCCAGCGGCGGCGGAGGCTCC GAGATCGTGATGACCCAGAGCCCCGCTACTCTGTCGGTGTCGCCCGGAGAA AGGGCGACCCTGTCCTGCCGGGCGTCGCAGTCCGTGAGCAGCAAGCTGGCT TGGTACCAGCAGAAGCCGGGCCAGGCACCACGCCTGCTTATGTACGGTGCC TCCATTCGGGCCACCGGAATCCCGGACCGGTTCTCGGGGTCGGGGTCCGGT ACCGAGTTCACACTGACCATTTCCTCGCTCGAGCCCGAGGACTTTGCCGTC TATTACTGCCAGCAGTACGGCTCCTCCTCATGGACGTTCGGCCAGGGGACC AAGGTCGAAATCAAGACCACTACCCCAGCACCGAGGCCACCCACCCCGGCT CCTACCATCGCCTCCCAGCCTCTGTCCCTGCGTCCGGAGGCATGTAGACCC GCAGCTGGTGGGGCCGTGCATACCCGGGGTCTTGACTTCGCCTGCGATATC TACATTTGGGCCCCTCTGGCTGGTACTTGCGGGGTCCTGCTGCTTTCACTC GTGATCACTCTTTACTGTAAGCGCGGTCGGAAGAAGCTGCTGTACATCTTT AAGCAACCCTTCATGAGGCCTGTGCAGACTACTCAAGAGGAGGACGGCTGT TCATGCCGGTTCCCAGAGGAGGAGGAAGGCGGCTGCGAACTGCGCGTGAAA TTCAGCCGCAGCGCAGATGCTCCAGCCTACAAGCAGGGGCAGAACCAGCTC TACAACGAACTCAATCTTGGTCGGAGAGAGGAGTACGACGTGCTGGACAAG CGGAGAGGACGGGACCCAGAAATGGGCGGGAAGCCGCGCAGAAAGAATCCC CAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAAGATGGCAGAAGCCTAT AGCGAGATTGGTATGAAAGGGGAACGCAGAAGAGGCAAAGGCCACGACGGA CTGTACCAGGGACTCAGCACCGCCACCAAGGACACCTATGACGCTCTTCAC ATGCAGGCCCTGCCGCCTCGG
139107		
139107- aa Full CAR	957	MALPVTALLLPLALLLHAARPEVQLVETGGGVVQPGGSLRLSCAVSGFALS NHGMSWVRRAPGKGLEWVSGIVYSGSTYYAASVKGRFTISRDNSRNTLYLQ MNSLRPEDTAIYYCSAHGGESDVWGQGTTVTVSSASGGGGSGGRASGGGGS EIVLTQSPGTLSLSPGERATLSCRASQSVGSTNLAWYQQKPGQAPRLLIYD ASNRATGIPDRFSGGGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPWTFGQ GTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFAC DIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEED GCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGH DGLYQGLSTATKDTYDALHMQALPPR
139107- nt Full CAR	972	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCGAAGTGCAATTGGTGGAGACTGGAGGAGGAGTGGTGCAA CCTGGAGGAAGCCTGAGACTGTCATGCGCGGTGTCGGGCTTCGCCCTCTCC AACCACGGAATGTCCTGGGTCCGCCGGGCCCCTGGGAAAGGACTTGAATGG GTGTCCGGCATCGTGTACTCGGGTTCCACCTACTACGCGGCCTCAGTGAAG

		GGCCGGTTTACTATTAGCCGCGACAACTCCAGAAACACACTGTACCTCCAA ATGAACTCGCTGCGGCCGGAAGATACCGCTATCTACTACTGCTCCGCCCAT GGGGGAGAGTCGGACGTCTGGGGACAGGGCACCACTGTCACTGTGTCCAGC GCTTCCGGCGGTGGTGGAAGCGGGGGACGGGCCTCAGGAGGCGGTGGCAGC GAGATTGTGCTGACCCAGTCCCCCGGGACCCTGAGCCTGTCCCCGGGAGAA AGGGCCACCCTCTCCTGTCGGGCATCCCAGTCCGTGGGGTCTACTAACCTT GCATGGTACCAGCAGAAGCCCGGCCAGGCCCCTCGCCTGCTGATCTACGAC GCGTCCAATAGAGCCACCGGCATCCCGGATCGCTTCAGCGGAGGCGGATCG GGCACCGACTTCACCCTCACCATTTCAAGGCTGGAACCGGAGGACTTCGCC GTGTACTACTGCCAGCAGTATGGTTCGTCCCCACCCTGGACGTTCGGCCAG GGGACTAAGGTCGAGATCAAGACCACTACCCCAGCACCGAGGCCACCCACC CCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTGCGTCCGGAGGCATGT AGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGTCTTGACTTCGCCTGC GATATCTACATTTGGGCCCCTCTGGCTGGTACTTGCGGGGTCCTGCTGCTT TCACTCGTGATCACTCTTTACTGTAAGCGCGGTCGGAAGAAGCTGCTGTAC ATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACTACTCAAGAGGAGGAC GGCTGTTCATGCCGGTTCCCAGAGGAGGAGGAAGGCGGCTGCGAACTGCGC GTGAAATTCAGCCGCAGCGCAGATGCTCCAGCCTACAAGCAGGGGCAGAAC CAGCTCTACAACGAACTCAATCTTGGTCGGAGAGAGGAGTACGACGTGCTG GACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGGAAGCCGCGCAGAAAG AATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAAGATGGCAGAA GCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGAAGAGGCAAAGGCCAC GACGGACTGTACCAGGGACTCAGCACCGCCACCAAGGACACCTATGACGCT CTTCACATGCAGGCCCTGCCGCCTCGG
139108		
139108- aa Full CAR	958	MALPVTALLLPLALLLHAARPQVQLVESGGGLVKPGGSLRLSCAASGFTFS DYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYL QMNSLRAEDTAVYYCARESGDGMDVWGQGTTVTVSSASGGGGSGGRASGGG GSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIY AASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYTLAFGQGT KVDIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDI YIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDG LYQGLSTATKDTYDALHMQALPPR
139108- nt Full CAR	973	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCCAAGTGCAACTCGTGGAATCTGGTGGAGGACTCGTGAAA CCTGGAGGATCATTGAGACTGTCATGCGCGGCCTCGGGATTCACGTTCTCC GATTACTACATGAGCTGGATTCGCCAGGCTCCGGGGAAGGGACTGGAATGG GTGTCCTACATTTCCTCATCCGGCTCCACCATCTACTACGCGGACTCCGTG AAGGGGAGATTCACCATTAGCCGCGATAACGCCAAGAACAGCCTGTACCTT CAGATGAACTCCCTGCGGGCTGAAGATACTGCCGTCTACTACTGCGCAAGG GAGAGCGGAGATGGGATGGACGTCTGGGGACAGGGTACCACTGTGACCGTG TCGTCGGCCTCCGGCGGAGGGGGTTCGGGTGGAAGGGCCAGCGGCGGCGGA GGCAGCGACATCCAGATGACCCAGTCCCCCTCATCGCTGTCCGCCTCCGTG GGCGACCGCGTCACCATCACATGCCGGGCCTCACAGTCGATCTCCTCCTAC CTCAATTGGTATCAGCAGAAGCCCGGAAAGGCCCCTAAGCTTCTGATCTAC GCAGCGTCCTCCCTGCAATCCGGGGTCCCATCTCGGTTCTCCGGCTCGGGC AGCGGTACCGACTTCACTCTGACCATCTCGAGCCTGCAGCCGGAGGACTTC GCCACTTACTACTGTCAGCAAAGCTACACCCTCGCGTTTGGCCAGGGCACC AAAGTGGACATCAAGACCACTACCCCAGCACCGAGGCCACCCACCCCGGCT CCTACCATCGCCTCCCAGCCTCTGTCCCTGCGTCCGGAGGCATGTAGACCC

		GCAGCTGGTGGGGCCGTGCATACCCGGGGTCTTGACTTCGCCTGCGATATC TACATTTGGGCCCCTCTGGCTGGTACTTGCGGGGTCCTGCTGCTTTCACTC GTGATCACTCTTTACTGTAAGCGCGGTCGGAAGAAGCTGCTGTACATCTTT AAGCAACCCTTCATGAGGCCTGTGCAGACTACTCAAGAGGAGGACGGCTGT TCATGCCGGTTCCCAGAGGAGGAGGAAGGCGGCTGCGAACTGCGCGTGAAA TTCAGCCGCAGCGCAGATGCTCCAGCCTACAAGCAGGGGCAGAACCAGCTC TACAACGAACTCAATCTTGGTCGGAGAGAGGAGTACGACGTGCTGGACAAG CGGAGAGGACGGGACCCAGAAATGGGCGGGAAGCCGCGCAGAAAGAATCCC CAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAAGATGGCAGAAGCCTAT AGCGAGATTGGTATGAAAGGGGAACGCAGAAGAGGCAAAGGCCACGACGGA CTGTACCAGGGACTCAGCACCGCCACCAAGGACACCTATGACGCTCTTCAC ATGCAGGCCCTGCCGCCTCGG
139110		
139110- aa Full CAR	960	MALPVTALLLPLALLLHAARPQVQLVQSGGGLVKPGGSLRLSCAASGFTFS DYYMSWIRQAPGKGLEWVSYISSSGNTIYYADSVKGRFTISRDNAKNSLYL QMNSLRAEDTAVYYCARSTMVREDYWGQGTLVTVSSASGGGGSGGRASGGG GSDIVLTQSPLSLPVTLGQPASISCKSSESLVHNSGKTYLNWFHQRPGQSP RRLIYEVSNRDSGVPDRFTGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWP GTFGQGTKLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRG LDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQT TQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERR RGKGHDGLYQGLSTATKDTYDALHMQALPPR
139110- nt Full CAR	975	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCCAAGTGCAACTGGTGCAAAGCGGAGGAGGATTGGTCAAA CCCGGAGGAAGCCTGAGACTGTCATGCGCGGCCTCTGGATTCACCTTCTCC GATTACTACATGTCATGGATCAGACAGGCCCCGGGGAAGGGCCTCGAATGG GTGTCCTACATCTCGTCCTCCGGGAACACCATCTACTACGCCGACAGCGTG AAGGGCCGCTTTACCATTTCCCGCGACAACGCAAAGAACTCGCTGTACCTT CAGATGAATTCCCTGCGGGCTGAAGATACCGCGGTGTACTATTGCGCCCGG TCCACTATGGTCCGGGAGGACTACTGGGGACAGGGCACACTCGTGACCGTG TCCAGCGCGAGCGGGGGTGGAGGCAGCGGTGGACGCGCCTCCGGCGGCGGC GGTTCAGACATCGTGCTGACTCAGTCGCCCCTGTCGCTGCCGGTCACCCTG GGCCAACCGGCCTCAATTAGCTGCAAGTCCTCGGAGAGCCTGGTGCACAAC TCAGGAAAGACTTACCTGAACTGGTTCCATCAGCGGCCTGGACAGTCCCCA CGGAGGCTCATCTATGAAGTGTCCAACAGGGATTCGGGGGTGCCCGACCGC TTCACTGGCTCCGGGTCCGGCACCGACTTCACCTTGAAAATCTCCAGAGTG GAAGCCGAGGACGTGGGCGTGTACTACTGTATGCAGGGTACCCACTGGCCT GGAACCTTTGGACAAGGAACTAAGCTCGAGATTAAGACCACTACCCCAGCA CCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTG CGTCCGGAGGCATGTAGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGT CTTGACTTCGCCTGCGATATCTACATTTGGGCCCCTCTGGCTGGTACTTGC GGGGTCCTGCTGCTTTCACTCGTGATCACTCTTTACTGTAAGCGCGGTCGG AAGAAGCTGCTGTACATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACT ACTCAAGAGGAGGACGGCTGTTCATGCCGGTTCCCAGAGGAGGAGGAAGGC GGCTGCGAACTGCGCGTGAAATTCAGCCGCAGCGCAGATGCTCCAGCCTAC AAGCAGGGGCAGAACCAGCTCTACAACGAACTCAATCTTGGTCGGAGAGAG GAGTACGACGTGCTGGACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGG AAGCCGCGCAGAAAGAATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAG GATAAGATGGCAGAAGCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGA AGAGGCAAAGGCCACGACGGACTGTACCAGGGACTCAGCACCGCCACCAAG GACACCTATGACGCTCTTCACATGCAGGCCCTGCCGCCTCGG

139112		
139112- aa Full CAR	961	MALPVTALLLPLALLLHAARPQVQLVESGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEWVSGIVYSGSTYYAASVKGRFTISRDNSRNTLYLQMNSLRPEDTAIYYCSAHGGESDVWGQGTTVTVSSASGGGGSGGRASGGGGSDIRLTQSPSPLSASVGDRVTITCQASEDINKFLNWYHQTPGKAPKLLIYDASTLQTGVPSRFSGSGSGTDFTLTINSLQPEDIGTYYCQQYESLPLTFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
139112- nt Full CAR	976	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGCCCCAAGTGCAACTCGTGGAATCTGGTGGAGGACTCGTGCAACCCGGTGGAAGCCTTAGGCTGTCGTGCGCCGTCAGCGGGTTTGCTCTGAGCAACCATGGAATGTCCTGGGTCCGCCGGGCACCGGGAAAAGGGCTGGAATGGGTGTCCGGCATCGTGTACAGCGGGTCAACCTATTACGCCGCGTCCGTGAAGGGCAGATTCACTATCTCAAGAGACAACAGCCGGAACACCCTGTACTTGCAAATGAATTCCCTGCGCCCCGAGGACACCGCCATCTACTACTGCTCCGCCCACGGAGGAGAGTCGGACGTGTGGGGCCAGGGAACGACTGTGACTGTGTCCAGCGCATCAGGAGGGGGTGGTTCGGGCGGCCGGGCCTCGGGGGGAGGAGGTTCCGACATTCGGCTGACCCAGTCCCCGTCCCCACTGTCGGCCTCCGTCGGCGACCGCGTGACCATCACTTGTCAGGCGTCCGAGGACATTAACAAGTTCCTGAACTGGTACCACCAGACCCCTGGAAAGGCCCCCAAGCTGCTGATCTACGATGCCTCGACCCTTCAAACTGGAGTGCCTAGCCGGTTCTCCGGGTCCGGCTCCGGCACTGATTTCACTCTGACCATCAACTCATTGCAGCCGGAAGATATCGGGACCTACTATTGCCAGCAGTACGAATCCCTCCCGCTCACATTCGGCGGGGGAACCAAGGTCGAGATTAAGACCACTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTGCGTCCGGAGGCATGTAGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGTCTTGACTTCGCCTGCGATATCTACATTTGGGCCCCTCTGGCTGGTACTTGCGGGGTCCTGCTGCTTTCACTCGTGATCACTCTTTACTGTAAGCGCGGTCGGAAGAAGCTGCTGTACATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACTACTCAAGAGGAGGACGGCTGTTCATGCCGGTTCCCAGAGGAGGAGGAAGGCGGCTGCGAACTGCGCGTGAAATTCAGCCGCAGCGCAGATGCTCCAGCCTACAAGCAGGGGCAGAACCAGCTCTACAACGAACTCAATCTTGGTCGGAGAGAGGAGTACGACGTGCTGGACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGGAAGCCGCGCAGAAAGAATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAAGATGGCAGAAGCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGAAGAGGCAAAGGCCACGACGGACTGTACCAGGGACTCAGCACCGCCACCAAGGACACCTATGACGCTCTTCACATGCAGGCCCTGCCGCCTCGG
139113		
139113- aa Full CAR	962	MALPVTALLLPLALLLHAARPEVQLVETGGGLVQPGGSLRLSCAVSGFALSNHGMSWVRRAPGKGLEWVSGIVYSGSTYYAASVKGRFTISRDNSRNTLYLQMNSLRPEDTAIYYCSAHGGESDVWGQGTTVTVSSASGGGGSGGRASGGGGSETTLTQSPATLSVSPGERATLSCRASQSVGSNLAWYQQKPGQGPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQPEDFAVYYCQQYNDWLPVTFGQGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
139113- nt	977	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC

Full CAR		GCCGCTCGGCCCGAAGTGCAATTGGTGGAAACTGGAGGAGGACTTGTGCAA CCTGGAGGATCATTGCGGCTCTCATGCGCTGTCTCCGGCTTCGCCCTGTCA AATCACGGGATGTCGTGGGTCAGACGGGCCCCGGGAAAGGGTCTGGAATGG GTGTCGGGGATTGTGTACAGCGGCTCCACCTACTACGCCGCTTCGGTCAAG GGCCGCTTCACTATTTCACGGGACAACAGCCGCAACACCCTCTATCTGCAA ATGAACTCTCTCCGCCCGGAGGATACCGCCATCTACTACTGCTCCGCACAC GGCGGCGAATCCGACGTGTGGGGACAGGGAACCACTGTCACCGTGTCGTCC GCATCCGGTGGCGGAGGATCGGGTGGCCGGGCCTCCGGGGGCGGCGGCAGC GAGACTACCCTGACCCAGTCCCCTGCCACTCTGTCCGTGAGCCCGGGAGAG AGAGCCACCCTTAGCTGCCGGGCCAGCCAGAGCGTGGGCTCCAACCTGGCC TGGTACCAGCAGAAGCCAGGACAGGGTCCCAGGCTGCTGATCTACGGAGCC TCCACTCGCGCGACCGGCATCCCCGCGAGGTTCTCCGGGTCGGGTTCCGGG ACCGAGTTCACCCTGACCATCTCCTCCCTCCAACCGGAGGACTTCGCGGTG TACTACTGTCAGCAGTACAACGATTGGCTGCCCGTGACATTTGGACAGGGG ACGAAGGTGGAAATCAAAACCACTACCCCAGCACCGAGGCCACCCACCCCG GCTCCTACCATCGCCTCCCAGCCTCTGTCCCTGCGTCCGGAGGCATGTAGA CCCGCAGCTGGTGGGGCCGTGCATACCCGGGGTCTTGACTTCGCCTGCGAT ATCTACATTTGGGCCCCTCTGGCTGGTACTTGCGGGGTCCTGCTGCTTTCA CTCGTGATCACTCTTTACTGTAAGCGCGGTCGGAAGAAGCTGCTGTACATC TTTAAGCAACCCTTCATGAGGCCTGTGCAGACTACTCAAGAGGAGGACGGC TGTTCATGCCGGTTCCCAGAGGAGGAGGAAGGCGGCTGCGAACTGCGCGTG AAATTCAGCCGCAGCGCAGATGCTCCAGCCTACAAGCAGGGGCAGAACCAG CTCTACAACGAACTCAATCTTGGTCGGAGAGAGGAGTACGACGTGCTGGAC AAGCGGAGAGGACGGGACCCAGAAATGGGCGGGAAGCCGCGCAGAAAGAAT CCCCAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAAGATGGCAGAAGCC TATAGCGAGATTGGTATGAAAGGGGAACGCAGAAGAGGCAAAGGCCACGAC GGACTGTACCAGGGACTCAGCACCGCCACCAAGGACACCTATGACGCTCTT CACATGCAGGCCCTGCCGCCTCGG
139114		
139114- aa Full CAR	963	MALPVTALLLPLALLLHAARPEVQLVESGGGLVQPGGSLRLSCAVSGFALS NHGMSWVRRAPGKGLEWVSGIVYSGSTYYAASVKGRFTISRDNSRNTLYLQ MNSLRPEDTAIYYCSAHGGESDVWGQGTTVTVSSASGGGGSGGRASGGGGS EIVLTQSPGTLSLSPGERATLSCRASQSIGSSSLAWYQQKPGQAPRLLMYG ASSRASGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYAGSPPFTFGQ GTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFAC DIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEED GCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGH DGLYQGLSTATKDTYDALHMQALPPR
139114- nt Full CAR	978	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCGAAGTGCAATTGGTGGAATCTGGTGGAGGACTTGTGCAA CCTGGAGGATCACTGAGACTGTCATGCGCGGTGTCCGGTTTTGCCCTGAGC AATCATGGGATGTCGTGGGTCCGGCGCGCCCCCGGAAAGGGTCTGGAATGG GTGTCGGGTATCGTCTACTCCGGGAGCACTTACTACGCCGCGAGCGTGAAG GGCCGCTTCACCATTTCCCGCGATAACTCCCGCAACACCCTGTACTTGCAA ATGAACTCGCTCCGGCCTGAGGACACTGCCATCTACTACTGCTCCGCACAC GGAGGAGAATCCGACGTGTGGGGCCAGGGAACTACCGTGACCGTCAGCAGC GCCTCCGGCGGCGGGGGCTCAGGCGGACGGGCTAGCGGCGGCGGTGGCTCC GAGATCGTGCTGACCCAGTCGCCTGGCACTCTCTCGCTGAGCCCCGGGGAA AGGGCAACCCTGTCCTGTCGGGCCAGCCAGTCCATTGGATCATCCTCCCTC GCCTGGTATCAGCAGAAACCGGGACAGGCTCCGCGGCTGCTTATGTATGGG GCCAGCTCAAGAGCCTCCGGCATTCCCGACCGGTTCTCCGGGTCCGGTTCC

		GGCACCGATTTCACCCTGACTATCTCGAGGCTGGAGCCAGAGGACTTCGCC GTGTACTACTGCCAGCAGTACGCGGGGTCCCCGCCGTTCACGTTCGGACAG GGAACCAAGGTCGAGATCAAGACCACTACCCCAGCACCGAGGCCACCCACC CCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTGCGTCCGGAGGCATGT AGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGTCTTGACTTCGCCTGC GATATCTACATTTGGGCCCCTCTGGCTGGTACTTGCGGGGTCCTGCTGCTT TCACTCGTGATCACTCTTTACTGTAAGCGCGGTCGGAAGAAGCTGCTGTAC ATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACTACTCAAGAGGAGGAC GGCTGTTCATGCCGGTTCCCAGAGGAGGAGGAAGGCGGCTGCGAACTGCGC GTGAAATTCAGCCGCAGCGCAGATGCTCCAGCCTACAAGCAGGGGCAGAAC CAGCTCTACAACGAACTCAATCTTGGTCGGAGAGAGGAGTACGACGTGCTG GACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGGAAGCCGCGCAGAAAG AATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAAGATGGCAGAA GCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGAAGAGGCAAAGGCCAC GACGGACTGTACCAGGGACTCAGCACCGCCACCAAGGACACCTATGACGCT CTTCACATGCAGGCCCTGCCGCCTCGG
149362		
149362-aa Full CAR	979	MALPVTALLLPLALLLHAARPQVQLQESGPGLVKPSETLSLTCTVSGGSIS SSYYYWGWIRQPPGKGLEWIGSIYYSGSAYYNPSLKSRVTISVDTSKNQFS LRLSSVTAADTAVYYCARHWQEWPDAFDIWGQGTMVTVSSGGGGSGGGGSG GGGSETTLTQSPAFMSATPGDKVIISCKASQDIDDAMNWYQQKPGEAPLFI IQSATSPVPGIPPRFSGSGFGTDFSLTINNIESEDAAYYFCLQHDNFPLTF GQGTKLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDF ACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQE EDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
149362-nt Full CAR	1001	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCCAAGTGCAGCTTCAGGAAAGCGGACCGGGCCTGGTCAAG CCATCCGAAACTCTCTCCCTGACTTGCACTGTGTCTGGCGGTTCCATCTCA TCGTCGTACTACTACTGGGGCTGGATTAGGCAGCCGCCCGGAAAGGGACTG GAGTGGATCGGAAGCATCTACTATTCCGGCTCGGCGTACTACAACCCTAGC CTCAAGTCGAGAGTGACCATCTCCGTGGATACCTCCAAGAACCAGTTTTCC CTGCGCCTGAGCTCCGTGACCGCCGCTGACACCGCCGTGTACTACTGTGCT CGGCATTGGCAGGAATGGCCCGATGCCTTCGACATTTGGGGCCAGGGCACT ATGGTCACTGTGTCATCCGGGGGTGGAGGCAGCGGGGGAGGAGGGTCCGGG GGGGGAGGTTCAGAGACAACCTTGACCCAGTCACCCGCATTCATGTCCGCC ACTCCGGGAGACAAGGTCATCATCTCGTGCAAAGCGTCCCAGGATATCGAC GATGCCATGAATTGGTACCAGCAGAAGCCTGGCGAAGCGCCGCTGTTCATT ATCCAATCCGCAACCTCGCCCGTGCCTGGAATCCCACCGCGGTTCAGCGGC AGCGGTTTCGGAACCGACTTTTCCCTGACCATTAACAACATTGAGTCCGAG GACGCCGCCTACTACTTCTGCCTGCAACACGACAACTTCCCTCTCACGTTC GGCCAGGGAACCAAGCTGGAAATCAAGACCACTACCCCAGCACCGAGGCCA CCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTGCGTCCGGAG GCATGTAGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGTCTTGACTTC GCCTGCGATATCTACATTTGGGCCCCTCTGGCTGGTACTTGCGGGGTCCTG CTGCTTTCACTCGTGATCACTCTTTACTGTAAGCGCGGTCGGAAGAAGCTG CTGTACATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACTACTCAAGAG GAGGACGGCTGTTCATGCCGGTTCCCAGAGGAGGAGGAAGGCGGCTGCGAA CTGCGCGTGAAATTCAGCCGCAGCGCAGATGCTCCAGCCTACAAGCAGGGG CAGAACCAGCTCTACAACGAACTCAATCTTGGTCGGAGAGAGGAGTACGAC GTGCTGGACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGGAAGCCGCGC

		AGAAAGAATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAAGATG GCAGAAGCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGAAGAGGCAAA GGCCACGACGGACTGTACCAGGGACTCAGCACCGCCACCAAGGACACCTAT GACGCTCTTCACATGCAGGCCCTGCCGCCTCGG
149363		
149363-aa Full CAR	980	MALPVTALLLPLALLLHAARPQVNLRESGPALVKPTQTLTLTCTFSGFSLR TSGMCVSWIRQPPGKALEWLARIDWDEDKFYSTSLKTRLTISKDTSDNQVV LRMTNMDPADTATYYCARSGAGGTSATAFDIWGPGTMVTVSSGGGGSGGGG SGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDIYNNLAWFQLKPGSAPR SLMYAANKSQSGVPSRFSGSASGTDFTLTISSLQPEDFATYYCQHYYRFPY SFGQGTKLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGL DFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTT QEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRR GKGHDGLYQGLSTATKDTYDALHMQALPPR
149363-nt Full CAR	1002	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCCAAGTCAATCTGCGCGAATCCGGCCCCGCCTTGGTCAAG CCTACCCAGACCCTCACTCTGACCTGTACTTTCTCCGGCTTCTCCCTGCGG ACTTCCGGGATGTGCGTGTCCTGGATCAGACAGCCTCCGGGAAAGGCCCTG GAGTGGCTCGCTCGCATTGACTGGGATGAGGACAAGTTCTACTCCACCTCA CTCAAGACCAGGCTGACCATCAGCAAAGATACCTCTGACAACCAAGTGGTG CTCCGCATGACCAACATGGACCCAGCCGACACTGCCACTTACTACTGCGCG AGGAGCGGAGCGGGCGGAACCTCCGCCACCGCCTTCGATATTTGGGGCCCG GGTACCATGGTCACCGTGTCAAGCGGAGGAGGGGGGTCCGGGGGCGGCGGT TCCGGGGGAGGCGGATCGGACATTCAGATGACTCAGTCACCATCGTCCCTG AGCGCTAGCGTGGGCGACAGAGTGACAATCACTTGCCGGGCATCCCAGGAC ATCTATAACAACCTTGCGTGGTTCCAGCTGAAGCCTGGTTCCGCACCGCGG TCACTTATGTACGCCGCCAACAAGAGCCAGTCGGGAGTGCCGTCCCGGTTT TCCGGTTCGGCCTCGGGAACTGACTTCACCCTGACGATCTCCAGCCTGCAA CCCGAGGATTTCGCCACCTACTACTGCCAGCACTACTACCGCTTTCCCTAC TCGTTCGGACAGGGAACCAAGCTGGAAATCAAGACCACTACCCCAGCACCG AGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTGCGT CCGGAGGCATGTAGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGTCTT GACTTCGCCTGCGATATCTACATTTGGGCCCCTCTGGCTGGTACTTGCGGG GTCCTGCTGCTTTCACTCGTGATCACTCTTTACTGTAAGCGCGGTCGGAAG AAGCTGCTGTACATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACTACT CAAGAGGAGGACGGCTGTTCATGCCGGTTCCCAGAGGAGGAGGAAGGCGGC TGCGAACTGCGCGTGAAATTCAGCCGCAGCGCAGATGCTCCAGCCTACAAG CAGGGGCAGAACCAGCTCTACAACGAACTCAATCTTGGTCGGAGAGAGGAG TACGACGTGCTGGACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGGAAG CCGCGCAGAAAGAATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAGGAT AAGATGGCAGAAGCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGAAGA GGCAAAGGCCACGACGGACTGTACCAGGGACTCAGCACCGCCACCAAGGAC ACCTATGACGCTCTTCACATGCAGGCCCTGCCGCCTCGG
149364		
149364-aa Full CAR	981	MALPVTALLLPLALLLHAARPEVQLVESGGGLVKPGGSLRLSCAASGFTFS SYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVKGRFTISRDNAKNSLYL QMNSLRAEDTAVYYCAKTIAAVYAFDIWGQGTTVTVSSGGGGSGGGGSGGG GSEIVLTQSPLSLPVTPEEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSP QLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP YTFGQGTKLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRG LDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQT

		TQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERR RGKGHDGLYQGLSTATKDTYDALHMQALPPR
149364-nt Full CAR	1003	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCGAAGTGCAGCTTGTCGAATCCGGGGGGGGACTGGTCAAG CCGGGCGGATCACTGAGACTGTCCTGCGCCGCGAGCGGCTTCACGTTCTCC TCCTACTCCATGAACTGGGTCCGCCAAGCCCCCGGGAAGGGACTGGAATGG GTGTCCTCTATCTCCTCGTCGTCGTCCTACATCTACTACGCCGACTCCGTG AAGGGAAGATTCACCATTTCCCGCGACAACGCAAAGAACTCACTGTACTTG CAAATGAACTCACTCCGGGCCGAAGATACTGCTGTGTACTATTGCGCCAAG ACTATTGCCGCCGTCTACGCTTTCGACATCTGGGGCCAGGGAACCACCGTG ACTGTGTCGTCCGGTGGTGGTGGCTCGGGCGGAGGAGGAAGCGGCGGCGGG GGGTCCGAGATTGTGCTGACCCAGTCGCCACTGAGCCTCCCTGTGACCCCC GAGGAACCCGCCAGCATCAGCTGCCGGTCCAGCCAGTCCCTGCTCCACTCC AACGGATACAATTACCTCGATTGGTACCTTCAGAAGCCTGGACAAAGCCCG CAGCTGCTCATCTACTTGGGATCAAACCGCGCGTCAGGAGTGCCTGACCGG TTCTCCGGCTCGGGCAGCGGTACCGATTTCACCCTGAAAATCTCCAGGGTG GAGGCAGAGGACGTGGGAGTGTATTACTGTATGCAGGCGCTGCAGACTCCG TACACATTTGGGCAGGGCACCAAGCTGGAGATCAAGACCACTACCCCAGCA CCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTG CGTCCGGAGGCATGTAGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGT CTTGACTTCGCCTGCGATATCTACATTTGGGCCCCTCTGGCTGGTACTTGC GGGGTCCTGCTGCTTTCACTCGTGATCACTCTTTACTGTAAGCGCGGTCGG AAGAAGCTGCTGTACATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACT ACTCAAGAGGAGGACGGCTGTTCATGCCGGTTCCCAGAGGAGGAGGAAGGC GGCTGCGAACTGCGCGTGAAATTCAGCCGCAGCGCAGATGCTCCAGCCTAC AAGCAGGGGCAGAACCAGCTCTACAACGAACTCAATCTTGGTCGGAGAGAG GAGTACGACGTGCTGGACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGG AAGCCGCGCAGAAAGAATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAG GATAAGATGGCAGAAGCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGA AGAGGCAAAGGCCACGACGGACTGTACCAGGGACTCAGCACCGCCACCAAG GACACCTATGACGCTCTTCACATGCAGGCCCTGCCGCCTCGG
149365		
149365-aa Full CAR	982	MALPVTALLLPLALLLHAARPEVQLVESGGGLVKPGGSLRLSCAASGFTFS DYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYL QMNSLRAEDTAVYYCARDLRGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGS SYVLTQSPSVSAAPGYTATISCGGNNIGTKSVHWYQQKPGQAPLLVIRDDS VRPSKIPGRFSGSNSGNMATLTISGVQAGDEADFYCQVWDSDSEHVVFGGG TKLTVLTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACD IYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDG CSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLD KRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHD GLYQGLSTATKDTYDALHMQALPPR
149365-nt Full CAR	1004	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCGAAGTCCAGCTCGTGGAGTCCGGCGGAGGCCTTGTGAAG CCTGGAGGTTCGCTGAGACTGTCCTGCGCCGCCTCCGGCTTCACCTTCTCC GACTACTACATGTCCTGGATCAGACAGGCCCCGGGAAAGGGCCTGGAATGG GTGTCCTACATCTCGTCATCGGGCAGCACTATCTACTACGCGGACTCAGTG AAGGGGCGGTTCACCATTTCCCGGGATAACGCGAAGAACTCGCTGTATCTG CAAATGAACTCACTGAGGGCCGAGGACACCGCCGTGTACTACTGCGCCCGC GATCTCCGCGGGGCATTTGACATCTGGGGACAGGGAACCATGGTCACAGTG TCCAGCGGAGGGGGAGGATCGGGTGGCGGAGGTTCCGGGGGTGGAGGCTCC

		TCCTACGTGCTGACTCAGAGCCCAAGCGTCAGCGCTGCGCCCGGTTACACG GCAACCATCTCCTGTGGCGGAAACAACATTGGGACCAAGTCTGTGCACTGG TATCAGCAGAAGCCGGGCCAAGCTCCCCTGTTGGTGATCCGCGATGACTCC GTGCGGCCTAGCAAAATTCCGGGACGGTTCTCCGGCTCCAACAGCGGCAAT ATGGCCACTCTCACCATCTCGGGAGTGCAGGCCGGAGATGAAGCCGACTTC TACTGCCAAGTCTGGGACTCAGACTCCGAGCATGTGGTGTTCGGGGGCGGA ACCAAGCTGACTGTGCTCACCACTACCCCAGCACCGAGGCCACCCACCCCG GCTCCTACCATCGCCTCCCAGCCTCTGTCCCTGCGTCCGGAGGCATGTAGA CCCGCAGCTGGTGGGGCCGTGCATACCCGGGGTCTTGACTTCGCCTGCGAT ATCTACATTTGGGCCCCTCTGGCTGGTACTTGCGGGGTCCTGCTGCTTTCA CTCGTGATCACTCTTTACTGTAAGCGCGGTCGGAAGAAGCTGCTGTACATC TTTAAGCAACCCTTCATGAGGCCTGTGCAGACTACTCAAGAGGAGGACGGC TGTTCATGCCGGTTCCCAGAGGAGGAGGAAGGCGGCTGCGAACTGCGCGTG AAATTCAGCCGCAGCGCAGATGCTCCAGCCTACAAGCAGGGGCAGAACCAG CTCTACAACGAACTCAATCTTGGTCGGAGAGAGGAGTACGACGTGCTGGAC AAGCGGAGAGGACGGGACCCAGAAATGGGCGGGAAGCCGCGCAGAAAGAAT CCCCAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAAGATGGCAGAAGCC TATAGCGAGATTGGTATGAAAGGGGAACGCAGAAGAGGCAAAGGCCACGAC GGACTGTACCAGGGACTCAGCACCGCCACCAAGGACACCTATGACGCTCTT CACATGCAGGCCCTGCCGCCTCGG
149366		
149366-aa Full CAR	983	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKPSGYTVT SHYIHWVRRAPGQGLEWMGMINPSGGVTAYSQTLQGRVTMTSDTSSSTVYM ELSSLRSEDTAMYYCAREGSGSGWYFDFWGRGTLVTVSSGGGGSGGGGSGG GGSSYVLTQPPSVSVSPGQTASITCSGDGLSKKYVSWYQQKAGQSPVVLIS RDKERPSGIPDRFSGSNSADTATLTISGTQAMDEADYYCQAWDDTTVVFGG GTKLTVLTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFAC DIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEED GCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGH DGLYQGLSTATKDTYDALHMQALPPR
149366-nt Full CAR	1005	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCCAAGTGCAGCTGGTGCAGAGCGGGGCCGAAGTCAAGAAG CCGGGAGCCTCCGTGAAAGTGTCCTGCAAGCCTTCGGGATACACCGTGACC TCCCACTACATTCATTGGGTCCGCCGCGCCCCCGGCCAAGGACTCGAGTGG ATGGGCATGATCAACCCTAGCGGCGGAGTGACCGCGTACAGCCAGACGCTG CAGGGACGCGTGACTATGACCTCGGATACCTCCTCCTCCACCGTCTATATG GAACTGTCCAGCCTGCGGTCCGAGGATACCGCCATGTACTACTGCGCCCGG GAAGGATCAGGCTCCGGGTGGTATTTCGACTTCTGGGGAAGAGGCACCCTC GTGACTGTGTCATCTGGGGGAGGGGGTTCCGGTGGTGGCGGATCGGGAGGA GGCGGTTCATCCTACGTGCTGACCCAGCCACCCTCCGTGTCCGTGAGCCCC GGCCAGACTGCATCGATTACATGTAGCGGCGACGGCCTCTCCAAGAAATAC GTGTCGTGGTACCAGCAGAAGGCCGGACAGAGCCCGGTGGTGCTGATCTCA AGAGATAAGGAGCGGCCTAGCGGAATCCCGGACAGGTTCTCGGGTTCCAAC TCCGCGGACACTGCTACTCTGACCATCTCGGGGACCCAGGCTATGGACGAA GCCGATTACTACTGCCAAGCCTGGGACGACACTACTGTCGTGTTTGGAGGG GGCACCAAGTTGACCGTCCTTACCACTACCCCAGCACCGAGGCCACCCACC CCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTGCGTCCGGAGGCATGT AGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGTCTTGACTTCGCCTGC GATATCTACATTTGGGCCCCTCTGGCTGGTACTTGCGGGGTCCTGCTGCTT TCACTCGTGATCACTCTTTACTGTAAGCGCGGTCGGAAGAAGCTGCTGTAC ATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACTACTCAAGAGGAGGAC

		GGCTGTTCATGCCGGTTCCCAGAGGAGGAGGAAGGCGGCTGCGAACTGCGC GTGAAATTCAGCCGCAGCGCAGATGCTCCAGCCTACAAGCAGGGGCAGAAC CAGCTCTACAACGAACTCAATCTTGGTCGGAGAGAGGAGTACGACGTGCTG GACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGGAAGCCGCGCAGAAAG AATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAAGATGGCAGAA GCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGAAGAGGCAAAGGCCAC GACGGACTGTACCAGGGACTCAGCACCGCCACCAAGGACACCTATGACGCT CTTCACATGCAGGCCCTGCCGCCTCGG
149367		
149367-aa Full CAR	984	MALPVTALLLPLALLLHAARPQVQLQESGPGLVKPSQTLSLTCTVSGGSIS SGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRVTISVDTSKNQFS LKLSSVTAADTAVYYCARAGIAARLRGAFDIWGQGTMVTVSSGGGGSGGGG SGGGGSDIVMTQSPSSVSASVGDRVIITCRASQGIRNWLAWYQQKPGKAPN LLIYAASNLQSGVPSRFSGSGSGADFTLTISSLQPEDVATYYCQKYNSAPF TFGPGTKVDIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGL DFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTT QEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRR GKGHDGLYQGLSTATKDTYDALHMQALPPR
149367-nt Full CAR	1006	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCCAAGTGCAGCTTCAGGAGAGCGGCCCGGGACTCGTGAAG CCGTCCCAGACCCTGTCCCTGACTTGCACCGTGTCGGGAGGAAGCATCTCG AGCGGAGGCTACTATTGGTCGTGGATTCGGCAGCACCCTGGAAAGGGCCTG GAATGGATCGGCTACATCTACTACTCCGGCTCGACCTACTACAACCCATCG CTGAAGTCCAGAGTGACAATCTCAGTGGACACGTCCAAGAATCAGTTCAGC CTGAAGCTCTCTTCCGTGACTGCGGCCGACACCGCCGTGTACTACTGCGCA CGCGCTGGAATTGCCGCCCGGCTGAGGGGTGCCTTCGACATTTGGGGACAG GGCACCATGGTCACCGTGTCCTCCGGCGGCGGAGGTTCCGGGGGTGGAGGC TCAGGAGGAGGGGGGTCCGACATCGTCATGACTCAGTCGCCCTCAAGCGTC AGCGCGTCCGTCGGGGACAGAGTGATCATCACCTGTCGGGCGTCCCAGGGA ATTCGCAACTGGCTGGCCTGGTATCAGCAGAAGCCCGGAAAGGCCCCCAAC CTGTTGATCTACGCCGCCTCAAACCTCCAATCCGGGGTGCCGAGCCGCTTC AGCGGCTCCGGTTCGGGTGCCGATTTCACTCTGACCATCTCCTCCCTGCAA CCTGAAGATGTGGCTACCTACTACTGCCAAAAGTACAACTCCGCACCTTTT ACTTTCGGACCGGGGACCAAAGTGGACATTAAGACCACTACCCCAGCACCG AGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTGCGT CCGGAGGCATGTAGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGTCTT GACTTCGCCTGCGATATCTACATTTGGGCCCCTCTGGCTGGTACTTGCGGG GTCCTGCTGCTTTCACTCGTGATCACTCTTTACTGTAAGCGCGGTCGGAAG AAGCTGCTGTACATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACTACT CAAGAGGAGGACGGCTGTTCATGCCGGTTCCCAGAGGAGGAGGAAGGCGGC TGCGAACTGCGCGTGAAATTCAGCCGCAGCGCAGATGCTCCAGCCTACAAG CAGGGGCAGAACCAGCTCTACAACGAACTCAATCTTGGTCGGAGAGAGGAG TACGACGTGCTGGACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGGAAG CCGCGCAGAAAGAATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAGGAT AAGATGGCAGAAGCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGAAGA GGCAAAGGCCACGACGGACTGTACCAGGGACTCAGCACCGCCACCAAGGAC ACCTATGACGCTCTTCACATGCAGGCCCTGCCGCCTCGG
149368		
149368-aa Full CAR	985	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGSSVKVSCKASGGTFS SYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYM ELSSLRSEDTAVYYCARRGGYQLLRWDVGLLRSAFDIWGQGTMVTVSSGGG

		GSGGGGSGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKP GQAPVLVLYGKNNRPSGVPDRFSGSRSGTTASLTITGAQAEDEADYYCSSR DSSGDHLRVFGTGTKVTVLTTTPAPRPPTPAPTIASQPLSLRPEACRPAAG GAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNE LNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
149368-nt Full CAR	1007	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCCAAGTGCAGCTGGTCCAGTCGGGCGCCGAGGTCAAGAAG CCCGGGAGCTCTGTGAAAGTGTCCTGCAAGGCCTCCGGGGGCACCTTTAGC TCCTACGCCATCTCCTGGGTCCGCCAAGCACCGGGTCAAGGCCTGGAGTGG ATGGGGGGAATTATCCCTATCTTCGGCACTGCCAACTACGCCCAGAAGTTC CAGGGACGCGTGACCATTACCGCGGACGAATCCACCTCCACCGCTTATATG GAGCTGTCCAGCTTGCGCTCGGAAGATACCGCCGTGTACTACTGCGCCCGG AGGGGTGGATACCAGCTGCTGAGATGGGACGTGGGCCTCCTGCGGTCGGCG TTCGACATCTGGGGCCAGGGCACTATGGTCACTGTGTCCAGCGGAGGAGGC GGATCGGGAGGCGGCGGATCAGGGGGAGGCGGTTCCAGCTACGTGCTTACT CAACCCCCTTCGGTGTCCGTGGCCCCGGGACAGACCGCCAGAATCACTTGC GGAGGAAACAACATTGGGTCCAAGAGCGTGCATTGGTACCAGCAGAAGCCA GGACAGGCCCCTGTGCTGGTGCTCTACGGGAAGAACAATCGGCCCAGCGGA GTGCCGGACAGGTTCTCGGGTTCACGCTCCGGTACAACCGCTTCACTGACT ATCACCGGGGCCCAGGCAGAGGATGAAGCGGACTACTACTGTTCCTCCCGG GATTCATCCGGCGACCACCTCCGGGTGTTCGGAACCGGAACGAAGGTCACC GTGCTGACCACTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATC GCCTCCCAGCCTCTGTCCCTGCGTCCGGAGGCATGTAGACCCGCAGCTGGT GGGGCCGTGCATACCCGGGGTCTTGACTTCGCCTGCGATATCTACATTTGG GCCCCTCTGGCTGGTACTTGCGGGGTCCTGCTGCTTTCACTCGTGATCACT CTTTACTGTAAGCGCGGTCGGAAGAAGCTGCTGTACATCTTTAAGCAACCC TTCATGAGGCCTGTGCAGACTACTCAAGAGGAGGACGGCTGTTCATGCCGG TTCCCAGAGGAGGAGGAAGGCGGCTGCGAACTGCGCGTGAAATTCAGCCGC AGCGCAGATGCTCCAGCCTACAAGCAGGGGCAGAACCAGCTCTACAACGAA CTCAATCTTGGTCGGAGAGAGGAGTACGACGTGCTGGACAAGCGGAGAGGA CGGGACCCAGAAATGGGCGGGAAGCCGCGCAGAAAGAATCCCCAAGAGGGC CTGTACAACGAGCTCCAAAAGGATAAGATGGCAGAAGCCTATAGCGAGATT GGTATGAAAGGGGAACGCAGAAGAGGCAAAGGCCACGACGGACTGTACCAG GGACTCAGCACCGCCACCAAGGACACCTATGACGCTCTTCACATGCAGGCC CTGCCGCCTCGG
149369		
149369-aa Full CAR	986	MALPVTALLLPLALLLHAARPEVQLQQSGPGLVKPSQTLSLTCAISGDSVS SNSAAWNWIRQSPSRGLEWLGRTYYRSKWYSFYAISLKSRIIINPDTSKNQ FSLQLKSVTPEDTAVYYCARSSPEGLFLYWFDPWGQGTLVTVSSGGDGSGG GGSGGGGSSSELTQDPAVSVALGQTIRITCQGDSLGNYYATWYQQKPGQAP VLVIYGTNNRPSGIPDRFSASSSGNTASLTITGAQAEDEADYYCNSRDSSG HHLLFGTGTKVTVLTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGE RRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
149369-nt Full CAR	1008	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCGAAGTGCAGCTCCAACAGTCAGGACCGGGGCTCGTGAAG CCATCCCAGACCCTGTCCCTGACTTGTGCCATCTCGGGAGATAGCGTGTCA TCGAACTCCGCCGCCTGGAACTGGATTCGGCAGAGCCCGTCCCGCGGACTG

		GAGTGGCTTGGAAGGACCTACTACCGGTCCAAGTGGTACTCTTTCTACGCG ATCTCGCTGAAGTCCCGCATTATCATTAACCCTGATACCTCCAAGAATCAG TTCTCCCTCCAACTGAAATCCGTCACCCCCGAGGACACAGCAGTGTATTAC TGCGCACGGAGCAGCCCCGAAGGACTGTTCCTGTATTGGTTTGACCCCTGG GGCCAGGGGACTCTTGTGACCGTGTCGAGCGGCGGAGATGGGTCCGGTGGC GGTGGTTCGGGGGGCGGCGGATCATCATCCGAACTGACCCAGGACCCGGCT GTGTCCGTGGCGCTGGGACAAACCATCCGCATTACGTGCCAGGGAGACTCC CTGGGCAACTACTACGCCACTTGGTACCAGCAGAAGCCGGGCCAAGCCCCT GTGTTGGTCATCTACGGGACCAACAACAGACCTTCCGGCATCCCCGACCGG TTCAGCGCTTCGTCCTCCGGCAACACTGCCAGCCTGACCATCACTGGAGCG CAGGCCGAAGATGAGGCCGACTACTACTGCAACAGCAGAGACTCCTCGGGT CATCACCTCTTGTTCGGAACTGGAACCAAGGTCACCGTGCTGACCACTACC CCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTG TCCCTGCGTCCGGAGGCATGTAGACCCGCAGCTGGTGGGGCCGTGCATACC CGGGGTCTTGACTTCGCCTGCGATATCTACATTTGGGCCCCTCTGGCTGGT ACTTGCGGGGTCCTGCTGCTTTCACTCGTGATCACTCTTTACTGTAAGCGC GGTCGGAAGAAGCTGCTGTACATCTTTAAGCAACCCTTCATGAGGCCTGTG CAGACTACTCAAGAGGAGGACGGCTGTTCATGCCGGTTCCCAGAGGAGGAG GAAGGCGGCTGCGAACTGCGCGTGAAATTCAGCCGCAGCGCAGATGCTCCA GCCTACAAGCAGGGGCAGAACCAGCTCTACAACGAACTCAATCTTGGTCGG AGAGAGGAGTACGACGTGCTGGACAAGCGGAGAGGACGGGACCCAGAAATG GGCGGGAAGCCGCGCAGAAAGAATCCCCAAGAGGGCCTGTACAACGAGCTC CAAAAGGATAAGATGGCAGAAGCCTATAGCGAGATTGGTATGAAAGGGGAA CGCAGAAGAGGCAAAGGCCACGACGGACTGTACCAGGGACTCAGCACCGCC ACCAAGGACACCTATGACGCTCTTCACATGCAGGCCCTGCCGCCTCGG
BCMA_EBB-C1978-A4		
BCMA_EBB-C1978-A4 – aa Full CART	987	MALPVTALLLPLALLLHAARPEVQLVESGGGLVQPGGSLRLSCAASGFTFS SYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCAKVEGSGSLDYWGQGTLVTVSSGGGGSGGGGSGGGG SEIVMTQSPGTLSLSPGERATLSCRASQSVSSAYLAWYQQKPGQPPRLLIS GASTRATGIPDRFGGSGSGTDFTLTISRLEPEDFAVYYCQHYGSSFNGSSL FTFGQGTRLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRG LDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQT TQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERR RGKGHDGLYQGLSTATKDTYDALHMQALPPR
BCMA_EBB-C1978-A4 – nt Full CART	1009	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCGAAGTGCAGCTCGTGGAGTCAGGAGGCGGCCTGGTCCAG CCGGGAGGGTCCCTTAGACTGTCATGCGCCGCAAGCGGATTCACTTTCTCC TCCTATGCCATGAGCTGGGTCCGCCAAGCCCCCGGAAAGGGACTGGAATGG GTGTCCGCCATCTCGGGGTCTGGAGGCTCAACTTACTACGCTGACTCCGTG AAGGGACGGTTCACCATTAGCCGCGACAACTCCAAGAACACCCTCTACCTC CAAATGAACTCCCTGCGGGCCGAGGATACCGCCGTCTACTACTGCGCCAAA GTGGAAGGTTCAGGATCGCTGGACTACTGGGGACAGGGTACTCTCGTGACC GTGTCATCGGGCGGAGGAGGTTCCGGCGGTGGCGGCTCCGGCGGCGGAGGG TCGGAGATCGTGATGACCCAGAGCCCTGGTACTCTGAGCCTTTCGCCGGGA GAAAGGGCCACCCTGTCCTGCCGCGCTTCCCAATCCGTGTCCTCCGCGTAC TTGGCGTGGTACCAGCAGAAGCCGGGACAGCCCCCTCGGCTGCTGATCAGC GGGGCCAGCACCCGGGCAACCGGAATCCCAGACAGATTCGGGGGTTCCGGC AGCGGCACAGATTTCACCCTGACTATTTCGAGGTTGGAGCCCGAGGACTTT GCGGTGTATTACTGTCAGCACTACGGGTCGTCCTTTAATGGCTCCAGCCTG TTCACGTTCGGACAGGGGACCCGCCTGGAAATCAAGACCACTACCCCAGCA

		CCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTG CGTCCGGAGGCATGTAGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGT CTTGACTTCGCCTGCGATATCTACATTTGGGCCCCTCTGGCTGGTACTTGC GGGGTCCTGCTGCTTTCACTCGTGATCACTCTTTACTGTAAGCGCGGTCGG AAGAAGCTGCTGTACATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACT ACTCAAGAGGAGGACGGCTGTTCATGCCGGTTCCCAGAGGAGGAGGAAGGC GGCTGCGAACTGCGCGTGAAATTCAGCCGCAGCGCAGATGCTCCAGCCTAC AAGCAGGGGCAGAACCAGCTCTACAACGAACTCAATCTTGGTCGGAGAGAG GAGTACGACGTGCTGGACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGG AAGCCGCGCAGAAAGAATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAG GATAAGATGGCAGAAGCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGA AGAGGCAAAGGCCACGACGGACTGTACCAGGGACTCAGCACCGCCACCAAG GACACCTATGACGCTCTTCACATGCAGGCCCTGCCGCCTCGG
BCMA_EBB-C1978-G1		
BCMA_EBB-C1978-G1 – aa Full CART	988	MALPVTALLLPLALLLHAARPEVQLVETGGGLVQPGGSLRLSCAASGITFS RYPMSWVRQAPGKGLEWVSGISDSGVSTYYADSAKGRFTISRDNSKNTLFL QMSSLRDEDTAVYYCVTRAGSEASDIWGQGTMVTVSSGGGGSGGGGSGGGG SEIVLTQSPATLSLSPGERATLSCRASQSVSNSLAWYQQKPGQAPRLLIYD ASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAIYYCQQFGTSSGLTFGG GTKLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFAC DIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEED GCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGH DGLYQGLSTATKDTYDALHMQALPPR
BCMA_EBB-C1978-G1 – nt Full CART	1010	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCGAAGTGCAACTGGTGGAAACCGGTGGCGGCCTGGTGCAG CCTGGAGGATCATTGAGGCTGTCATGCGCGGCCAGCGGTATTACCTTCTCC CGGTACCCCATGTCCTGGGTCAGACAGGCCCCGGGGAAAGGGCTTGAATGG GTGTCCGGGATCTCGGACTCCGGTGTCAGCACTTACTACGCCGACTCCGCC AAGGGACGCTTCACCATTTCCCGGGACAACTCGAAGAACACCCTGTTCCTC CAAATGAGCTCCCTCCGGGACGAGGATACTGCAGTGTACTACTGCGTGACC CGCGCCGGGTCCGAGGCGTCTGACATTTGGGGACAGGGCACTATGGTCACC GTGTCGTCCGGCGGAGGGGGCTCGGGAGGCGGTGGCAGCGGAGGAGGAGGG TCCGAGATCGTGCTGACCCAATCCCCGGCCACCCTCTCGCTGAGCCCTGGA GAAAGGGCAACCTTGTCCTGTCGCGCGAGCCAGTCCGTGAGCAACTCCCTG GCCTGGTACCAGCAGAAGCCCGGACAGGCTCCGAGACTTCTGATCTACGAC GCTTCGAGCCGGGCCACTGGAATCCCCGACCGCTTTTCGGGGTCCGGCTCA GGAACCGATTTCACCCTGACAATCTCACGGCTGGAGCCAGAGGATTTCGCC ATCTATTACTGCCAGCAGTTCGGTACTTCCTCCGGCCTGACTTTCGGAGGC GGCACGAAGCTCGAAATCAAGACCACTACCCCAGCACCGAGGCCACCCACC CCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTGCGTCCGGAGGCATGT AGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGTCTTGACTTCGCCTGC GATATCTACATTTGGGCCCCTCTGGCTGGTACTTGCGGGGTCCTGCTGCTT TCACTCGTGATCACTCTTTACTGTAAGCGCGGTCGGAAGAAGCTGCTGTAC ATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACTACTCAAGAGGAGGAC GGCTGTTCATGCCGGTTCCCAGAGGAGGAGGAAGGCGGCTGCGAACTGCGC GTGAAATTCAGCCGCAGCGCAGATGCTCCAGCCTACAAGCAGGGGCAGAAC CAGCTCTACAACGAACTCAATCTTGGTCGGAGAGAGGAGTACGACGTGCTG GACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGGAAGCCGCGCAGAAAG AATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAAGATGGCAGAA GCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGAAGAGGCAAAGGCCAC GACGGACTGTACCAGGGACTCAGCACCGCCACCAAGGACACCTATGACGCT

		CTTCACATGCAGGCCCTGCCGCCTCGG
BCMA_EBB-C1979-C1		
BCMA_EBB-C1979-C1 - aa Full CART	989	MALPVTALLLPLALLLHAARPQVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAIYYCARATYKRELRYYYGMDVWGQGTMVTVSSGGGGSGGGGSGGGGSEIVMTQSPGTVSLSPGERATLSCRASQSVSSSFLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDSAVYYCQQYHSSPSWTFGQGTRLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
BCMA_EBB-C1979-C1 - nt Full CART	1011	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGCCCCAAGTGCAGCTCGTGGAATCGGGTGGCGGACTGGTGCAGCCGGGGGGCTCACTTAGACTGTCCTGCGCGGCCAGCGGATTCACTTTCTCCTCCTACGCCATGTCCTGGGTCAGACAGGCCCCTGGAAAGGGCCTGGAATGGGTGTCCGCAATCAGCGGCAGCGGCGGCTCGACCTATTACGCGGATTCAGTGAAGGGCAGATTCACCATTTCCCGGGACAACGCCAAGAACTCCTTGTACCTTCAAATGAACTCCCTCCGCGCGGAAGATACCGCAATCTACTACTGCGCTCGGGCCACTTACAAGAGGGAACTGCGCTACTACTACGGGATGGACGTCTGGGGCCAGGGAACCATGGTCACCGTGTCCAGCGGAGGAGGAGGATCGGGAGGAGGCGGTAGCGGGGGTGGAGGGTCGGAGATCGTGATGACCCAGTCCCCCGGCACTGTGTCGCTGTCCCCCGGCGAACGGGCCACCCTGTCATGTCGGGCCAGCCAGTCAGTGTCGTCAAGCTTCCTCGCCTGGTACCAGCAGAAACCGGGACAAGCTCCCCGCCTGCTGATCTACGGAGCCAGCAGCCGGGCCACCGGTATTCCTGACCGGTTCTCCGGTTCGGGGTCCGGGACCGACTTTACTCTGACTATCTCTCGCCTCGAGCCAGAGGACTCCGCCGTGTATTACTGCCAGCAGTACCACTCCTCCCCGTCCTGGACGTTCGGACAGGGCACAAGGCTGGAGATTAAGACCACTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTGCGTCCGGAGGCATGTAGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGTCTTGACTTCGCCTGCGATATCTACATTTGGGCCCCTCTGGCTGGTACTTGCGGGGTCCTGCTGCTTTCACTCGTGATCACTCTTTACTGTAAGCGCGGTCGGAAGAAGCTGCTGTACATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACTACTCAAGAGGAGGACGGCTGTTCATGCCGGTTCCCAGAGGAGGAGGAAGGCGGCTGCGAACTGCGCGTGAAATTCAGCCGCAGCGCAGATGCTCCAGCCTACAAGCAGGGGCAGAACCAGCTCTACAACGAACTCAATCTTGGTCGGAGAGAGGAGTACGACGTGCTGGACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGGAAGCCGCGCAGAAAGAATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAAGATGGCAGAAGCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGAAGAGGCAAAGGCCACGACGGACTGTACCAGGGACTCAGCACCGCCACCAAGGACACCTATGACGCTCTTCACATGCAGGCCCTGCCGCCTCGG
BCMA_EBB-C1978-C7		
BCMA_EBB-C1978-C7 - aa Full CART	990	MALPVTALLLPLALLLHAARPEVQLVETGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNTLKAEDTAVYYCARATYKRELRYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPSTLSLSPGESATLSCRASQSVSTTFLAWYQQKPGQAPRLLIYGSSNRATGIPDRFSGSGSGTDFTLTIRRLEPEDFAVYYCQQYHSSPSWTFGQGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

BCMA_EBB-C1978-C7 - nt Full CART	1012	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGCCCGAGGTGCAGCTTGTGGAAACCGGTGGCGGACTGGTGCAGCCCGGAGGAAGCCTCAGGCTGTCCTGCGCCGCGTCCGGCTTCACCTTCTCCTCGTACGCCATGTCCTGGGTCCGCCAGGCCCCCGGAAAGGGCCTGGAATGGGTGTCCGCCATCTCTGGAAGCGGAGGTTCCACGTACTACGCGGACAGCGTCAAGGGAAGGTTCACAATCTCCCGCGATAATTCGAAGAACACTCTGTACCTTCAAATGAACACCCTGAAGGCCGAGGACACTGCTGTGTACTACTGCGCACGGGCCACCTACAAGAGAGAGCTCCGGTACTACTACGGAATGGACGTCTGGGGCCAGGGAACTACTGTGACCGTGTCCTCGGGAGGGGGTGGCTCCGGGGGGGGCGGCTCCGGCGGAGGCGGTTCCGAGATTGTGCTGACCCAGTCACCTTCAACTCTGTCGCTGTCCCCGGGAGAGAGCGCTACTCTGAGCTGCCGGGCCAGCCAGTCCGTGTCCACCACCTTCCTCGCCTGGTATCAGCAGAAGCCGGGGCAGGCACCACGGCTCTTGATCTACGGGTCAAGCAACAGAGCGACCGGAATTCCTGACCGCTTCTCGGGGAGCGGTTCAGGCACCGACTTCACCCTGACTATCCGGCGCCTGGAACCCGAAGATTTCGCCGTGTATTACTGTCAACAGTACCACTCCTCGCCGTCCTGGACCTTTGGCCAAGGAACCAAAGTGGAAATCAAGACCACTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTGCGTCCGGAGGCATGTAGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGTCTTGACTTCGCCTGCGATATCTACATTTGGGCCCCTCTGGCTGGTACTTGCGGGGTCCTGCTGCTTTCACTCGTGATCACTCTTTACTGTAAGCGCGGTCGGAAGAAGCTGCTGTACATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACTACTCAAGAGGAGGACGGCTGTTCATGCCGGTTCCCAGAGGAGGAGGAAGGCGGCTGCGAACTGCGCGTGAAATTCAGCCGCAGCGCAGATGCTCCAGCCTACAAGCAGGGGCAGAACCAGCTCTACAACGAACTCAATCTTGGTCGGAGAGAGGAGTACGACGTGCTGGACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGGAAGCCGCGCAGAAAGAATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAAGATGGCAGAAGCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGAAGAGGCAAAGGCCACGACGGACTGTACCAGGGACTCAGCACCGCCACCAAGGACACCTATGACGCTCTTCACATGCAGGCCCTGCCGCCTCGG
BCMA_EBB-C1978-D10		
BCMA_EBB-C1978-D10 - aa Full CART	991	MALPVTALLLPLALLLHAARPEVQLVETGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCARVGKAVPDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIVMTQTPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPYSFGQGTRLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
BCMA_EBB-C1978-D10 - nt Full CART	1013	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCACGCCGCTCGGCCCGAAGTGCAGCTCGTGGAAACTGGAGGTGGACTCGTGCAGCCTGGACGGTCGCTGCGGCTGAGCTGCGCTGCATCCGGCTTCACCTTCGACGATTATGCCATGCACTGGGTCAGACAGGCGCCAGGGAAGGGACTTGAGTGGGTGTCCGGTATCAGCTGGAATAGCGGCTCAATCGGATACGCGGACTCCGTGAAGGGAAGGTTCACCATTTCCCGCGACAACGCCAAGAACTCCCTGTACTTGCAAATGAACAGCCTCCGGGATGAGGACACTGCCGTGTACTACTGCGCCCGCGTCGGAAAAGCTGTGCCCGACGTCTGGGGCCAGGGAACCACTGTGACCGTGTCCAGCGGCGGGGGTGGATCGGGCGGTGGAGGGTCCGGTGGAGGGGGCTCAGATATTGTGATGACCCAGACCCCCTCGTCCCTGTCCGCCTCGGTCGGCGACCGCGTGACTATCACATGTAGAGCCTCGCAGAGCATCTCCAGCTACCTGAACTGGTATCAGCAGAAGCCGGGGAAGGCCCCGAAGCTCCTGATCTACGCGGCA

		TCATCACTGCAATCGGGAGTGCCGAGCCGGTTTTCCGGGTCCGGCTCCGGC ACCGACTTCACGCTGACCATTTCTTCCCTGCAACCCGAGGACTTCGCCACT TACTACTGCCAGCAGTCCTACTCCACCCCTTACTCCTTCGGCCAAGGAACC AGGCTGGAAATCAAGACCACTACCCCAGCACCGAGGCCACCCACCCCGGCT CCTACCATCGCCTCCCAGCCTCTGTCCCTGCGTCCGGAGGCATGTAGACCC GCAGCTGGTGGGGCCGTGCATACCCGGGGTCTTGACTTCGCCTGCGATATC TACATTTGGGCCCCTCTGGCTGGTACTTGCGGGGTCCTGCTGCTTTCACTC GTGATCACTCTTTACTGTAAGCGCGGTCGGAAGAAGCTGCTGTACATCTTT AAGCAACCCTTCATGAGGCCTGTGCAGACTACTCAAGAGGAGGACGGCTGT TCATGCCGGTTCCCAGAGGAGGAGGAAGGCGGCTGCGAACTGCGCGTGAAA TTCAGCCGCAGCGCAGATGCTCCAGCCTACAAGCAGGGGCAGAACCAGCTC TACAACGAACTCAATCTTGGTCGGAGAGAGGAGTACGACGTGCTGGACAAG CGGAGAGGACGGGACCCAGAAATGGGCGGGAAGCCGCGCAGAAAGAATCCC CAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAAGATGGCAGAAGCCTAT AGCGAGATTGGTATGAAAGGGGAACGCAGAAGAGGCAAAGGCCACGACGGA CTGTACCAGGGACTCAGCACCGCCACCAAGGACACCTATGACGCTCTTCAC ATGCAGGCCCTGCCGCCTCGG
BCMA_EBB-C1979-C12		
BCMA_EBB-C1979-C12 - aa Full CART	992	MALPVTALLLPLALLLHAARPEVQLVESGGGLVQPGRSLRLSCTASGFTFD DYAMHWVRQRPGKGLEWVASINWKGNSLAYGDSVKGRFAISRDNAKNTVFL QMNSLRTEDTAVYYCASHQGVAYYNYAMDVWGRGTLVTVSSGGGGSGGGGS GGGGSEIVLTQSPGTLSLSPGERATLSCRATQSIGSSFLAWYQQRPGQAPR LLIYGASQRATGIPDRFSGRGSGTDFTLTISRVEPEDSAVYYCQHYESSPS WTFGQGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRG LDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQT TQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERR RGKGHDGLYQGLSTATKDTYDALHMQALPPR
BCMA_EBB-C1979-C12 - nt Full CART	1014	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCGAAGTGCAGCTCGTGGAGAGCGGGGGAGGATTGGTGCAG CCCGGAAGGTCCCTGCGGCTCTCCTGCACTGCGTCTGGCTTCACCTTCGAC GACTACGCGATGCACTGGGTCAGACAGCGCCCGGGAAAGGGCCTGGAATGG GTCGCCTCAATCAACTGGAAGGGAAACTCCCTGGCCTATGGCGACAGCGTG AAGGGCCGCTTCGCCATTTCGCGCGACAACGCCAAGAACACCGTGTTTCTG CAAATGAATTCCCTGCGGACCGAGGATACCGCTGTGTACTACTGCGCCAGC CACCAGGGCGTGGCATACTATAACTACGCCATGGACGTGTGGGGAAGAGGG ACGCTCGTCACCGTGTCCTCCGGGGGCGGTGGATCGGGTGGAGGAGGAAGC GGTGGCGGGGGCAGCGAAATCGTGCTGACTCAGAGCCCGGGAACTCTTTCA CTGTCCCCGGGAGAACGGGCCACTCTCTCGTGCCGGGCCACCCAGTCCATC GGCTCCTCCTTCCTTGCCTGGTACCAGCAGAGGCCAGGACAGGCGCCCCGC CTGCTGATCTACGGTGCTTCCCAACGCGCCACTGGCATTCCTGACCGGTTC AGCGGCAGAGGGTCGGGAACCGATTTCACACTGACCATTTCCCGGGTGGAG CCCGAAGATTCGGCAGTCTACTACTGTCAGCATTACGAGTCCTCCCCTTCA TGGACCTTCGGTCAAGGGACCAAAGTGGAGATCAAGACCACTACCCCAGCA CCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTG CGTCCGGAGGCATGTAGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGT CTTGACTTCGCCTGCGATATCTACATTTGGGCCCCTCTGGCTGGTACTTGC GGGGTCCTGCTGCTTTCACTCGTGATCACTCTTTACTGTAAGCGCGGTCGG AAGAAGCTGCTGTACATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACT ACTCAAGAGGAGGACGGCTGTTCATGCCGGTTCCCAGAGGAGGAGGAAGGC GGCTGCGAACTGCGCGTGAAATTCAGCCGCAGCGCAGATGCTCCAGCCTAC AAGCAGGGGCAGAACCAGCTCTACAACGAACTCAATCTTGGTCGGAGAGAG

		GAGTACGACGTGCTGGACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGG AAGCCGCGCAGAAAGAATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAG GATAAGATGGCAGAAGCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGA AGAGGCAAAGGCCACGACGGACTGTACCAGGGACTCAGCACCGCCACCAAG GACACCTATGACGCTCTTCACATGCAGGCCCTGCCGCCTCGG
BCMA_EBB-C1980-G4		
BCMA_EBB-C1980-G4-aa Full CART	993	MALPVTALLLPLALLLHAARPEVQLVESGGGLVQPGGSLRLSCAASGFTFS SYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCAKVVRDGMDVWGQGTTVTVSSGGGGSGGGGSGGGGS EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYG ASSRATGIPDRFSGNGSGTDFTLTISRLEPEDFAVYYCQQYGSPPRFTFGP GTKVDIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFAC DIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEED GCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGH DGLYQGLSTATKDTYDALHMQALPPR
BCMA_EBB-C1980-G4-nt Full CART	1015	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCGAGGTGCAGTTGGTCGAAAGCGGGGGCGGGCTTGTGCAG CCTGGCGGATCACTGCGGCTGTCCTGCGCGGCATCAGGCTTCACGTTTTCT TCCTACGCCATGTCCTGGGTGCGCCAGGCCCCTGGAAAGGGACTGGAATGG GTGTCCGCGATTTCGGGGTCCGGCGGGAGCACCTACTACGCCGATTCCGTG AAGGGCCGCTTCACTATCTCGCGGGACAACTCCAAGAACACCCTCTACCTC CAAATGAATAGCCTGCGGGCCGAGGATACCGCCGTCTACTATTGCGCTAAG GTCGTGCGCGACGGAATGGACGTGTGGGGACAGGGTACCACCGTGACAGTG TCCTCGGGGGGAGGCGGTAGCGGCGGAGGAGGAAGCGGTGGTGGAGGTTCC GAGATTGTGCTGACTCAATCACCCGCGACCCTGAGCCTGTCCCCCGGCGAA AGGGCCACTCTGTCCTGTCGGGCCAGCCAATCAGTCTCCTCCTCGTACCTG GCCTGGTACCAGCAGAAGCCAGGACAGGCTCCGAGACTCCTTATCTATGGC GCATCCTCCCGCGCCACCGGAATCCCGGATAGGTTCTCGGGAAACGGATCG GGGACCGACTTCACTCTCACCATCTCCCGGCTGGAACCGGAGGACTTCGCC GTGTACTACTGCCAGCAGTACGGCAGCCCGCCTAGATTCACTTTCGGCCCC GGCACCAAAGTGGACATCAAGACCACTACCCCAGCACCGAGGCCACCCACC CCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTGCGTCCGGAGGCATGT AGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGTCTTGACTTCGCCTGC GATATCTACATTTGGGCCCCTCTGGCTGGTACTTGCGGGGTCCTGCTGCTT TCACTCGTGATCACTCTTTACTGTAAGCGCGGTCGGAAGAAGCTGCTGTAC ATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACTACTCAAGAGGAGGAC GGCTGTTCATGCCGGTTCCCAGAGGAGGAGGAAGGCGGCTGCGAACTGCGC GTGAAATTCAGCCGCAGCGCAGATGCTCCAGCCTACAAGCAGGGGCAGAAC CAGCTCTACAACGAACTCAATCTTGGTCGGAGAGAGGAGTACGACGTGCTG GACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGGAAGCCGCGCAGAAAG AATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAAGATGGCAGAA GCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGAAGAGGCAAAGGCCAC GACGGACTGTACCAGGGACTCAGCACCGCCACCAAGGACACCTATGACGCT CTTCACATGCAGGCCCTGCCGCCTCGG
BCMA_EBB-C1980-D2		
BCMA_EBB-C1980-D2-aa Full CART	994	MALPVTALLLPLALLLHAARPEVQLLESGGGLVQPGGSLRLSCAASGFTFS SYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCAKIPQTGTFDYWGQGTLVTVSSGGGGSGGGGSGGGG SEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIY GASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQHYGSSPSWTFG QGTRLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFA

		CDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEE DGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKG HDGLYQGLSTATKDTYDALHMQALPPR
BCMA_EBB-C1980-D2-nt Full CART	1016	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCGAAGTGCAGCTGCTGGAGTCCGGCGGTGGATTGGTGCAA CCGGGGGGATCGCTCAGACTGTCCTGTGCGGCGTCAGGCTTCACCTTCTCG AGCTACGCCATGTCATGGGTCAGACAGGCCCCTGGAAAGGGTCTGGAATGG GTGTCCGCCATTTCCGGGAGCGGGGGATCTACATACTACGCCGATAGCGTG AAGGGCCGCTTCACCATTTCCCGGGACAACTCCAAGAACACTCTCTATCTG CAAATGAACTCCCTCCGCGCTGAGGACACTGCCGTGTACTACTGCGCCAAA ATCCCTCAGACCGGCACCTTCGACTACTGGGGACAGGGGACTCTGGTCACC GTCAGCAGCGGTGGCGGAGGTTCGGGGGGAGGAGGAAGCGGCGGCGGAGGG TCCGAGATTGTGCTGACCCAGTCACCCGGCACTTTGTCCCTGTCGCCTGGA GAAAGGGCCACCCTTTCCTGCCGGGCATCCCAATCCGTGTCCTCCTCGTAC CTGGCCTGGTACCAGCAGAGGCCCGGACAGGCCCCACGGCTTCTGATCTAC GGAGCAAGCAGCCGCGCGACCGGTATCCCGGACCGGTTTTCGGGCTCGGGC TCAGGAACTGACTTCACCCTCACCATCTCCCGCCTGGAACCCGAAGATTTC GCTGTGTATTACTGCCAGCACTACGGCAGCTCCCCGTCCTGGACGTTCGGC CAGGGAACTCGGCTGGAGATCAAGACCACTACCCCAGCACCGAGGCCACCC ACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTGCGTCCGGAGGCA TGTAGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGTCTTGACTTCGCC TGCGATATCTACATTTGGGCCCCTCTGGCTGGTACTTGCGGGGTCCTGCTG CTTTCACTCGTGATCACTCTTTACTGTAAGCGCGGTCGGAAGAAGCTGCTG TACATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACTACTCAAGAGGAG GACGGCTGTTCATGCCGGTTCCCAGAGGAGGAGGAAGGCGGCTGCGAACTG CGCGTGAAATTCAGCCGCAGCGCAGATGCTCCAGCCTACAAGCAGGGGCAG AACCAGCTCTACAACGAACTCAATCTTGGTCGGAGAGAGGAGTACGACGTG CTGGACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGGAAGCCGCGCAGA AAGAATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAAGATGGCA GAAGCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGAAGAGGCAAAGGC CACGACGGACTGTACCAGGGACTCAGCACCGCCACCAAGGACACCTATGAC GCTCTTCACATGCAGGCCCTGCCGCCTCGG
BCMA_EBB-C1978-A10		
BCMA_EBB-C1978-A10-aa Full CART	995	MALPVTALLLPLALLLHAARPEVQLVETGGGLVQPGGSLRLSCAASGFTFS SYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTMSRENDKNSVFL QMNSLRVEDTGVYYCARANYKRELRYYYGMDVWGQGTMVTVSSGGGGSGGG GSGGGGSEIVMTQSPGTLSLSPGESATLSCRASQRVASNYLAWYQHKPGQA PSLLISGASSRATGVPDRFSGSGSGTDFTLAISRLEPEDSAVYYCQHYDSS PSWTFGQGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGE RRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
BCMA_EBB-C1978-A10-nt Full CART	1017	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCGAAGTGCAACTGGTGGAAACCGGTGGAGGACTCGTGCAG CCTGGCGGCAGCCTCCGGCTGAGCTGCGCCGCTTCGGGATTCACCTTTTCC TCCTACGCGATGTCTTGGGTCAGACAGGCCCCCGGAAAGGGGCTGGAATGG GTGTCAGCCATCTCCGGCTCCGGCGGATCAACGTACTACGCCGACTCCGTG AAAGGCCGGTTCACCATGTCGCGCGAGAATGACAAGAACTCCGTGTTCCTG CAAATGAACTCCCTGAGGGTGGAGGACACCGGAGTGTACTATTGTGCGCGC GCCAACTACAAGAGAGAGCTGCGGTACTACTACGGAATGGACGTCTGGGGA

		CAGGGAACTATGGTGACCGTGTCATCCGGTGGAGGGGGAAGCGGCGGTGGA GGCAGCGGGGGCGGGGGTTCAGAAATTGTCATGACCCAGTCCCCGGGAACT CTTTCCCTCTCCCCCGGGGAATCCGCGACTTTGTCCTGCCGGGCCAGCCAG CGCGTGGCCTCGAACTACCTCGCATGGTACCAGCATAAGCCAGGCCAAGCC CCTTCCCTGCTGATTTCCGGGGCTAGCAGCCGCGCCACTGGCGTGCCGGAT AGGTTCTCGGGAAGCGGCTCGGGTACCGATTTCACCCTGGCAATCTCGCGG CTGGAACCGGAGGATTCGGCCGTGTACTACTGCCAGCACTATGACTCATCC CCCTCCTGGACATTCGGACAGGGCACCAAGGTCGAGATCAAGACCACTACC CCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTG TCCCTGCGTCCGGAGGCATGTAGACCCGCAGCTGGTGGGGCCGTGCATACC CGGGGTCTTGACTTCGCCTGCGATATCTACATTTGGGCCCCTCTGGCTGGT ACTTGCGGGGTCCTGCTGCTTTCACTCGTGATCACTCTTTACTGTAAGCGC GGTCGGAAGAAGCTGCTGTACATCTTTAAGCAACCCTTCATGAGGCCTGTG CAGACTACTCAAGAGGAGGACGGCTGTTCATGCCGGTTCCCAGAGGAGGAG GAAGGCGGCTGCGAACTGCGCGTGAAATTCAGCCGCAGCGCAGATGCTCCA GCCTACAAGCAGGGGCAGAACCAGCTCTACAACGAACTCAATCTTGGTCGG AGAGAGGAGTACGACGTGCTGGACAAGCGGAGAGGACGGGACCCAGAAATG GGCGGGAAGCCGCGCAGAAAGAATCCCCAAGAGGGCCTGTACAACGAGCTC CAAAAGGATAAGATGGCAGAAGCCTATAGCGAGATTGGTATGAAAGGGGAA CGCAGAAGAGGCAAAGGCCACGACGGACTGTACCAGGGACTCAGCACCGCC ACCAAGGACACCTATGACGCTCTTCACATGCAGGCCCTGCCGCCTCGG
BCMA_EBB-C1978-D4		
BCMA_EBB-C1978-D4-aa Full CART	996	MALPVTALLLPLALLLHAARPEVQLLETGGGLVQPGGSLRLSCAASGFSFS SYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCAKALVGATGAFDIWGQGTLVTVSSGGGGSGGGGSGG GGSEIVLTQSPGTLSLSPGERATLSCRASQSLSSNFLAWYQQKPGQAPGLL IYGASNWATGTPDRFSGSGSGTDFTLTITRLEPEDFAVYYCQYYGTSPMYT FGQGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLD FACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQ EEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRG KGHDGLYQGLSTATKDTYDALHMQALPPR
BCMA_EBB-C1978-D4-nt Full CART	1018	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCGAAGTGCAGCTGCTCGAAACCGGTGGAGGGCTGGTGCAG CCAGGGGGCTCCCTGAGGCTTTCATGCGCCGCTAGCGGATTCTCCTTCTCC TCTTACGCCATGTCGTGGGTCCGCCAAGCCCCTGGAAAAGGCCTGGAATGG GTGTCCGCGATTTCCGGGAGCGGAGGTTCGACCTATTACGCCGACTCCGTG AAGGGCCGCTTTACCATCTCCCGGGATAACTCCAAGAACACTCTGTACCTC CAAATGAACTCGCTGAGAGCCGAGGACACCGCCGTGTATTACTGCGCGAAG GCGCTGGTCGGCGCGACTGGGGCATTCGACATCTGGGGACAGGGAACTCTT GTGACCGTGTCGAGCGGAGGCGGCGGCTCCGGCGGAGGAGGGAGCGGGGGC GGTGGTTCCGAAATCGTGTTGACTCAGTCCCCGGGAACCCTGAGCTTGTCA CCCGGGGAGCGGGCCACTCTCTCCTGTCGCGCCTCCCAATCGCTCTCATCC AATTTCCTGGCCTGGTACCAGCAGAAGCCCGGACAGGCCCCGGGCCTGCTC ATCTACGGCGCTTCAAACTGGGCAACGGGAACCCCTGATCGGTTCAGCGGA AGCGGATCGGGTACTGACTTTACCCTGACCATCACCAGACTGGAACCGGAG GACTTCGCCGTGTACTACTGCCAGTACTACGGCACCTCCCCCATGTACACA TTCGGACAGGGTACCAAGGTCGAGATTAAGACCACTACCCCAGCACCGAGG CCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTGCGTCCG GAGGCATGTAGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGTCTTGAC TTCGCCTGCGATATCTACATTTGGGCCCCTCTGGCTGGTACTTGCGGGGTC CTGCTGCTTTCACTCGTGATCACTCTTTACTGTAAGCGCGGTCGGAAGAAG

		CTGCTGTACATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACTACTCAA GAGGAGGACGGCTGTTCATGCCGGTTCCCAGAGGAGGAGGAAGGCGGCTGC GAACTGCGCGTGAAATTCAGCCGCAGCGCAGATGCTCCAGCCTACAAGCAG GGGCAGAACCAGCTCTACAACGAACTCAATCTTGGTCGGAGAGAGGAGTAC GACGTGCTGGACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGGAAGCCG CGCAGAAAGAATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAAG ATGGCAGAAGCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGAAGAGGC AAAGGCCACGACGGACTGTACCAGGGACTCAGCACCGCCACCAAGGACACC TATGACGCTCTTCACATGCAGGCCCTGCCGCCTCGG
BCMA_EBB-C1980-A2		
BCMA_EBB-C1980-A2-aa Full CART	997	MALPVTALLLPLALLLHAARPEVQLLESGGGLVQPGGSLRLSCAASGFTFS SYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCVLWFGEGFDPWGQGTLVTVSSGGGGSGGGGSGGGGS DIVLTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPLT FGGGTKVDIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLD FACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQ EEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRG KGHDGLYQGLSTATKDTYDALHMQALPPR
BCMA_EBB-C1980-A2-nt Full CART	1019	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCGAAGTGCAGCTGCTTGAGAGCGGTGGAGGTCTGGTGCAG CCCGGGGGATCACTGCGCCTGTCCTGTGCCGCGTCCGGTTTCACTTTCTCC TCGTACGCCATGTCGTGGGTCAGACAGGCACCGGGAAAGGGACTGGAATGG GTGTCAGCCATTTCGGGTTCGGGGGGCAGCACCTACTACGCTGACTCCGTG AAGGGCCGGTTCACCATTTCCCGCGACAACTCCAAGAACACCTTGTACCTC CAAATGAACTCCCTGCGGGCCGAAGATACCGCCGTGTATTACTGCGTGCTG TGGTTCGGAGAGGGATTCGACCCGTGGGGACAAGGAACACTCGTGACTGTG TCATCCGGCGGAGGCGGCAGCGGTGGCGGCGGTTCCGGCGGCGGCGGATCT GACATCGTGTTGACCCAGTCCCCTCTGAGCCTGCCGGTCACTCCTGGCGAA CCAGCCAGCATCTCCTGCCGGTCGAGCCAGTCCCTCCTGCACTCCAATGGG TACAACTACCTCGATTGGTATCTGCAAAAGCCGGGCCAGAGCCCCCAGCTG CTGATCTACCTTGGGTCAAACCGCGCTTCCGGGGTGCCTGATAGATTCTCC GGGTCCGGGAGCGGAACCGACTTTACCCTGAAAATCTCGAGGGTGGAGGCC GAGGACGTCGGAGTGTACTACTGCATGCAGGCGCTCCAGACTCCCCTGACC TTCGGAGGAGGAACGAAGGTCGACATCAAGACCACTACCCCAGCACCGAGG CCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTGCGTCCG GAGGCATGTAGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGTCTTGAC TTCGCCTGCGATATCTACATTTGGGCCCCTCTGGCTGGTACTTGCGGGGTC CTGCTGCTTTCACTCGTGATCACTCTTTACTGTAAGCGCGGTCGGAAGAAG CTGCTGTACATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACTACTCAA GAGGAGGACGGCTGTTCATGCCGGTTCCCAGAGGAGGAGGAAGGCGGCTGC GAACTGCGCGTGAAATTCAGCCGCAGCGCAGATGCTCCAGCCTACAAGCAG GGGCAGAACCAGCTCTACAACGAACTCAATCTTGGTCGGAGAGAGGAGTAC GACGTGCTGGACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGGAAGCCG CGCAGAAAGAATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAGGATAAG ATGGCAGAAGCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGAAGAGGC AAAGGCCACGACGGACTGTACCAGGGACTCAGCACCGCCACCAAGGACACC TATGACGCTCTTCACATGCAGGCCCTGCCGCCTCGG
BCMA_EBB-C1981-C3		
BCMA_EBB-C1981-C3-	998	MALPVTALLLPLALLLHAARPQVQLVESGGGLVQPGGSLRLSCAASGFTFS SYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYL

aa **Full CART**		QMNSLRAEDTAVYYCAKVGYDSSGYYRDYYGMDVWGQGTTVTVSSGGGGSG GGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPG QAPRLLIYGTSSRATGISDRFSGSGSGTDFTLTISRLEPEDFAVYYCQHYG NSPPKFTFGPGTKLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGA VHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFM RPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELN LGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGM KGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
BCMA_EBB-C1981-C3-nt **Full CART**	1020	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCCAAGTGCAGCTCGTGGAGTCAGGCGGAGGACTGGTGCAG CCCGGGGGCTCCCTGAGACTTTCCTGCGCGGCATCGGGTTTTACCTTCTCC TCCTATGCTATGTCCTGGGTGCGCCAGGCCCCGGGAAAGGGACTGGAATGG GTGTCCGCAATCAGCGGTAGCGGGGGCTCAACATACTACGCCGACTCCGTC AAGGGTCGCTTCACTATTTCCCGGGACAACTCCAAGAATACCCTGTACCTC CAAATGAACAGCCTCAGGGCCGAGGATACTGCCGTGTACTACTGCGCCAAA GTCGGATACGATAGCTCCGGTTACTACCGGGACTACTACGGAATGGACGTG TGGGGACAGGGCACCACCGTGACCGTGTCAAGCGGCGGAGGCGGTTCAGGA GGGGGAGGCTCCGGCGGTGGAGGGTCCGAAATCGTCCTGACTCAGTCGCCT GGCACTCTGTCGTTGTCCCCGGGGGAGCGCGCTACCCTGTCGTGTCGGGCG TCGCAGTCCGTGTCGAGCTCCTACCTCGCGTGGTACCAGCAGAAGCCCGGA CAGGCCCCTAGACTTCTGATCTACGGCACTTCTTCACGCGCCACCGGGATC AGCGACAGGTTCAGCGGCTCCGGCTCCGGGACCGACTTCACCCTGACCATT AGCCGGCTGGAGCCTGAAGATTTCGCCGTGTATTACTGCCAACACTACGGA AACTCGCCGCCAAAGTTCACGTTCGGACCCGGAACCAAGCTGGAAATCAAG ACCACTACCCCAGCACCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCC CAGCCTCTGTCCCTGCGTCCGGAGGCATGTAGACCCGCAGCTGGTGGGGCC GTGCATACCCGGGGTCTTGACTTCGCCTGCGATATCTACATTTGGGCCCCT CTGGCTGGTACTTGCGGGGTCCTGCTGCTTTCACTCGTGATCACTCTTTAC TGTAAGCGCGGTCGGAAGAAGCTGCTGTACATCTTTAAGCAACCCTTCATG AGGCCTGTGCAGACTACTCAAGAGGAGGACGGCTGTTCATGCCGGTTCCCA GAGGAGGAGGAAGGCGGCTGCGAACTGCGCGTGAAATTCAGCCGCAGCGCA GATGCTCCAGCCTACAAGCAGGGGCAGAACCAGCTCTACAACGAACTCAAT CTTGGTCGGAGAGAGGAGTACGACGTGCTGGACAAGCGGAGAGGACGGGAC CCAGAAATGGGCGGGAAGCCGCGCAGAAAGAATCCCCAAGAGGGCCTGTAC AACGAGCTCCAAAAGGATAAGATGGCAGAAGCCTATAGCGAGATTGGTATG AAAGGGGAACGCAGAAGAGGCAAAGGCCACGACGGACTGTACCAGGGACTC AGCACCGCCACCAAGGACACCTATGACGCTCTTCACATGCAGGCCCTGCCG CCTCGG
BCMA_EBB-C1978-G4		
BCMA_EBB-C1978-G4-aa **Full CART**	999	MALPVTALLLPLALLLHAARPEVQLVESGGGLVQPGGSLRLSCAASGFTFS SYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCAKMGWSSGYLGAFDIWGQGTTVTVSSGGGGSGGGGS GGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVASSFLAWYQQKPGQAPR LLIYGASGRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQHYGGSPR LTFGGGTKVDIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRG LDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQT TQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERR RGKGHDGLYQGLSTATKDTYDALHMQALPPR
BCMA_EBB-C1978-G4-nt	1021	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTTCTGCTCCAC GCCGCTCGGCCCGAAGTCCAACTGGTGGAGTCCGGGGGAGGGCTCGTGCAG CCCGGAGGCAGCCTTCGGCTGTCGTGCGCCGCCTCCGGGTTCACGTTCTCA

Full CART		TCCTACGCGATGTCGTGGGTCAGACAGGCACCAGGAAAGGGACTGGAATGG GTGTCCGCCATTAGCGGCTCCGGCGGTAGCACCTACTATGCCGACTCAGTG AAGGGAAGGTTCACTATCTCCCGCGACAACAGCAAGAACACCCTGTACCTC CAAATGAACTCTCTGCGGGCCGAGGATACCGCGGTGTACTATTGCGCCAAG ATGGGTTGGTCCAGCGGATACTTGGGAGCCTTCGACATTTGGGGACAGGGC ACTACTGTGACCGTGTCCTCCGGGGGTGGCGGATCGGGAGGCGGCGGCTCG GGTGGAGGGGGTTCCGAAATCGTGTTGACCCAGTCACCGGGAACCCTCTCG CTGTCCCCGGGAGAACGGGCTACACTGTCATGTAGAGCGTCCCAGTCCGTG GCTTCCTCGTTCCTGGCCTGGTACCAGCAGAAGCCGGGACAGGCACCCCGC CTGCTCATCTACGGAGCCAGCGGCCGGGCGACCGGCATCCCTGACCGCTTC TCCGGTTCCGGCTCGGGCACCGACTTTACTCTGACCATTAGCAGGCTTGAG CCCGAGGATTTTGCCGTGTACTACTGCCAACACTACGGGGGGAGCCCTCGC CTGACCTTCGGAGGCGGAACTAAGGTCGATATCAAAACCACTACCCCAGCA CCGAGGCCACCCACCCCGGCTCCTACCATCGCCTCCCAGCCTCTGTCCCTG CGTCCGGAGGCATGTAGACCCGCAGCTGGTGGGGCCGTGCATACCCGGGGT CTTGACTTCGCCTGCGATATCTACATTTGGGCCCCTCTGGCTGGTACTTGC GGGGTCCTGCTGCTTTCACTCGTGATCACTCTTTACTGTAAGCGCGGTCGG AAGAAGCTGCTGTACATCTTTAAGCAACCCTTCATGAGGCCTGTGCAGACT ACTCAAGAGGAGGACGGCTGTTCATGCCGGTTCCCAGAGGAGGAGGAAGGC GGCTGCGAACTGCGCGTGAAATTCAGCCGCAGCGCAGATGCTCCAGCCTAC AAGCAGGGGCAGAACCAGCTCTACAACGAACTCAATCTTGGTCGGAGAGAG GAGTACGACGTGCTGGACAAGCGGAGAGGACGGGACCCAGAAATGGGCGGG AAGCCGCGCAGAAAGAATCCCCAAGAGGGCCTGTACAACGAGCTCCAAAAG GATAAGATGGCAGAAGCCTATAGCGAGATTGGTATGAAAGGGGAACGCAGA AGAGGCAAAGGCCACGACGGACTGTACCAGGGACTCAGCACCGCCACCAAG GACACCTATGACGCTCTTCACATGCAGGCCCTGCCGCCTCGG

[00312] In one embodiment, the CAR molecule comprises (e.g., consists of) an amino acid sequence provided in Table 29, or Table 1 of WO2016/014565, or as otherwise described herein. In one embodiment, the CAR molecule comprises (e.g., consists of) an amino acid sequence of SEQ ID NO: 949, SEQ ID NO: 950, SEQ ID NO: 951, SEQ ID NO: 952, SEQ ID NO: 953, SEQ ID NO: 954, SEQ ID NO: 955, SEQ ID NO: 956, SEQ ID NO: 957, SEQ ID NO: 958, SEQ ID NO: 959, SEQ ID NO: 960, SEQ ID NO: 961, SEQ ID NO: 962, SEQ ID NO: 963, SEQ ID NO: 979, SEQ ID NO: 980, SEQ ID NO: 981, SEQ ID NO: 982, SEQ ID NO: 983, SEQ ID NO: 984, SEQ ID NO: 985, SEQ ID NO: 986, SEQ ID NO: 987, SEQ ID NO: 988, SEQ ID NO: 989, SEQ ID NO: 990, SEQ ID NO: 991, SEQ ID NO: 992, SEQ ID NO: 993, SEQ ID NO: 994, SEQ ID NO: 995, SEQ ID NO: 996, SEQ ID NO: 997, SEQ ID NO: 998, or SEQ ID NO: 999; or an amino acid sequence having at least one, two, three, four, five, 10, 15, 20 or 30 modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 60, 50, or 40 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence of SEQ ID NO: 949, SEQ ID NO: 950, SEQ ID NO: 951, SEQ ID NO: 952, SEQ ID NO: 953, SEQ ID NO: 954, SEQ ID NO: 955, SEQ ID NO: 956, SEQ ID NO:

957, SEQ ID NO: 958, SEQ ID NO: 959, SEQ ID NO: 960, SEQ ID NO: 961, SEQ ID NO: 962, SEQ ID NO: 963, SEQ ID NO: 979, SEQ ID NO: 980, SEQ ID NO: 981, SEQ ID NO: 982, SEQ ID NO: 983, SEQ ID NO: 984, SEQ ID NO: 985, SEQ ID NO: 986, SEQ ID NO: 987, SEQ ID NO: 988, SEQ ID NO: 989, SEQ ID NO: 990, SEQ ID NO: 991, SEQ ID NO: 992, SEQ ID NO: 993, SEQ ID NO: 994, SEQ ID NO: 995, SEQ ID NO: 996, SEQ ID NO: 997, SEQ ID NO: 998, or SEQ ID NO: 999; or an amino acid sequence having 85%, 90%, 95%, 96%, 97%, 98%, 99% identity to an amino acid sequence of SEQ ID NO: 949, SEQ ID NO: 950, SEQ ID NO: 951, SEQ ID NO: 952, SEQ ID NO: 953, SEQ ID NO: 954, SEQ ID NO: 955, SEQ ID NO: 956, SEQ ID NO: 957, SEQ ID NO: 958, SEQ ID NO: 959, SEQ ID NO: 960, SEQ ID NO: 961, SEQ ID NO: 962, SEQ ID NO: 963, SEQ ID NO: 979, SEQ ID NO: 980, SEQ ID NO: 981, SEQ ID NO: 982, SEQ ID NO: 983, SEQ ID NO: 984, SEQ ID NO: 985, SEQ ID NO: 986, SEQ ID NO: 987, SEQ ID NO: 988, SEQ ID NO: 989, SEQ ID NO: 990, SEQ ID NO: 991, SEQ ID NO: 992, SEQ ID NO: 993, SEQ ID NO: 994, SEQ ID NO: 995, SEQ ID NO: 996, SEQ ID NO: 997, SEQ ID NO: 998, or SEQ ID NO: 999.

[00313] Exemplary CAR molecules that target mesothelin are described herein, and are provided in Table 11. The CAR molecules in Table 11 comprise a mesothelin antigen binding domain, e.g., an amino acid sequence of any mesothelin antigen binding domain provided in Table 2. The leader sequence is in bold and underlined, CDRs are underlined, and the linker sequence between the heavy and light chain of the antigen binding region is shaded in grey.

Table 11. Exemplary mesothelin CAR molecules

Name	Amino Acid Sequence	SEQ ID NO:
M5 CAR	**MALPVTALLLPLALLLHAARP**QVQLVQSGAEVEKPGASVKVSCKASGYTFTDYYMHWVRQ APGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCASG WDFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIVMTQSPSSLSASVGDRVTITCR ASQSIRYYLSWYQQKPGKAPKLLIYTASILQNGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCLQTYTTPDFGPGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTR GLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCS CRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQ ALPPR	**286**
M11 CAR	**MALPVTALLLPLALLLHAARP**QVQLQQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQ APGQGLEWMGWINPNSGGTNYAQNFQGRVTMTRDTSISTAYMELRRLRSDDTAVYYCASG WDFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIRMTQSPSSLSASVGDRVTITCR ASQSIRYYLSWYQQKPGKAPKLLIYTASILQNGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCLQTYTTPDFGPGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTR GLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCS CRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG	**292**

	KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	
SS1 CAR	**MALPVTALLLPLALLLHAARP**QVQLQQSGPELEKPGASVKISCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSYNQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSGGGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEITTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPA	**306**
M1 CAR	**MALPVTALLLPLALLLHAARP**QVQLQQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGRINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGRYYGMDVWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPATLSLSPGERATISCRASQSVSSNFAWYQQRPGQAPRLLIYDASNRATGIPPRFSGSGSGTDFTLTISSLEPEDFAAYYCHQRSNWLYTFGQGTKVDIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	**282**
M2 CAR	**MALPVTALLLPLALLLHAARP**QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARDLRRTVVTPRAYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSTLSASVGDRVTITCQASQDISNSLNWYQQKAGKAPKLLIYDASTLETGVPSRFSGSGSGTDFSFTISSLQPEDIATYYCQQHDNLPLTFGQGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	**283**
M3 CAR	**MALPVTALLLPLALLLHAARP**QVQLVQSGAEVKKPGAPVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGEWDGSYYYDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIVLTQTPSSLSASVGDRVTITCRASQSINTYLNWYQHKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSFSPLTFGGGTKLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	**284**
M4 CAR	**MALPVTALLLPLALLLHAARP**QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMHWVRQVPGKGLVWVSRINTDGSTTTYADSVEGRFTISRDNAKNTLYLQMNSLRDDDTAVYYCVGGHWAVWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISDRLAWYQQKPGKAPKLLIYKASSLESGVPSRFSGSGSGTEFTLTISSLQPDDFAVYYCQQYGHLPMYTFGQGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	**285**
M6 CAR	**MALPVTALLLPLALLLHAARP**QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGSTSYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARYRLIAVAGDYYYYGMDVWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRVTITCRASQGVGRWLAWYQQKPGTAPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTINNLQPEDFATYYCQQANSFPLTFGGGTRLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	**287**
M7	**MALPVTALLLPLALLLHAARP**QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARW	**288**

CAR	KVSSSSPAFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPATLSLSPGER AILSCRASQSVYTKYLGWYQQKPGQAPRLLIYDASTRATGIPDRFSGSGSGTDFTLTINR LEPEDFAVYYCQHYGGSPLITFGQGTRLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRP AAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQ TTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR	
M8 CAR	**MALPVTALLLPLALLLHAARP**QVQLQQSGAEVKKPGASVKVSCKTSGYPFTGYSLHWVRQ APGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARD HYGGNSLFYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSSISASVGDTVS ITCRASQDSGTWLAWYQQKPGKAPNLLMYDASTLEDGVPSRFSGSASGTEFTLTVNRLQP EDSATYYCQQYNSYPLTFGGGTKVDIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGG AVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQE EDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRD PEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR	**289**
M9 CAR	**MALPVTALLLPLALLLHAARP**QVQLVQSGAEVKKPGASVEVSCKASGYTFTSYYMHWVRQ APGQGLEWMGIINPSGGSTGYAQKFQGRVTMTRDTSTSTVHMELSSLRSEDTAVYYCARG GYSSSSDAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPPSLSASVGDR VTITCRASQDISSALAWYQQKPGTPPKLLIYDASSLESGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQFSSYPLTFGGGTRLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTT QEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR	**290**
M10 CAR	**MALPVTALLLPLALLLHAARP**QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQ APGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARV AGGIYYYYGMDVWGQGTTITVSSGGGGSGGGGSGGGGSGGGGSDIVMTQTPDSLAVSLGE RATISCKSSHSVLYNRNNKNYLAWYQQKPGQPPKLLFYWASTRKSGVPDRFSGSGSGTDF TLTISSLQPEDFATYFCQQTQTFPLTFGQGTRLEINTTTPAPRPPTPAPTIASQPLSLRP EACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPF MRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGL STATKDTYDALHMQALPPR	**291**
M12 CAR	**MALPVTALLLPLALLLHAARP**QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQ APGQGLEWMGRINPNSGGTNYAQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCART TTSYAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSTLSASVGDRVTI TCRASQSISTWLAWYQQKPGKAPNLLIYKASTLESGVPSRFSGSGSGTEFTLTISSLQPD DFATYYCQQYNTYSPYTFGQGTKLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGG AVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQE EDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRD PEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR	**293**
M13 CAR	**MALPVTALLLPLALLLHAARP**QVQLVQSGGGLVKPGGSLRLSCEASGFIFSDYYMGWIRQ APGKGLEWVSYIGRSGSSMYYADSVKGRFTFSRDNAKNSLYLQMNSLRAEDTAVYYCAAS PVVAATEDFQHWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIVMTQTPATLSLSPGER ATLSCRASQSVTSNYLAWYQQKPGQAPRLLLFGASTRATGIPDRFSGSGSGTDFTLTINR LEPEDFAMYYCQQYGSAPVTFGQGTKLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPA AGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQT TQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRR GRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR	**294**
M14 CAR	**MALPVTALLLPLALLLHAARP**QVQLVQSGAEVRAPGASVKISCKASGFTFRGYYIHWVRQ APGQGLEWMGIINPSGGSRAYAQKFQGRVTMTRDTSTSTVYMELSSLRSDDTAMYYCART ASCGGDCYYLDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPPTLSASVGD RVTITCRASENVNIWLAWYQQKPGKAPKLLIYKSSSLASGVPSRFSGSGSGAEFTLTISS LQPDDFATYYCQQYQSYPLTFGGGTKVDIKTTTPAPRPPTPAPTIASQPLSLRPEACRPA	**295**

	AGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	
M15 CAR	**MALPVTALLLPLALLLHAARP**QVQLVQSGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAKDGSSSWSWGYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSSSELTQDPAVSVALGQTVRTTCQGDALRSYYASWYQQKPGQAPMLVIYGKNNRPSGIPDRFSGSDSGDTASLTITGAQAEDEADYYCNSRDSSGYPVFGTGTKVTVLTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	**296**
M16 CAR	**MALPVTALLLPLALLLHAARP**EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSTGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAKDSSSWYGGGSAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSSSELTQEPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIFGRSRRPSGIPDRFSGSSSGNTASLIITGAQAEDEADYYCNSRDNTANHYVFGTGTKLTVLTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	**297**
M17 CAR	**MALPVTALLLPLALLLHAARP**EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSTGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAKDSSSWYGGGSAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSSSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRGSSGNHYVFGTGTKVTVLTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	**298**
M18 CAR	**MALPVTALLLPLALLLHAARP**QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYWMHWVRQAPGKGLVWVSRINSDGSSTSYADSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCVRTGWVGSYYYYMDVWGKGTTVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSNYLAWYQQKPGQPPRLLIYDVSTRATGIPARFSGGGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPWTFGQGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	**299**
M19 CAR	**MALPVTALLLPLALLLHAARP**QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGYSRYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSEIVMTQSPATLSLSPGERAILSCRASQSVYTKYLGWYQQKPGQAPRLLIYDASTRATGIPDRFSGSGSGTDFTLTINRLEPEDFAVYYCQHYGGSPLITFGQGTKVDIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	**300**
M20 CAR	**MALPVTALLLPLALLLHAARP**QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKREAAAGHDWYFDLWGRGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIRVTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSIPLTFGQGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD	**301**

	TYDALHMQALPPR	
M21 CAR	**MALPVTALLLPLALLLHAARP**QVQLVQSWAEVKKPGASVKVSCKASGYTFTSYYMHWVRQ APGQGLEWMGIINPSGGSTSYAQKFQGRVTMTRDTSTSTVYMELSNLRSEDTAVYYCARS PRVTTGYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSTLSASVGDRV TITCRASQSISSWLAWYQQKPGKAPKLLIYKASSLESGVPSRFSGSGSGTEFTLTISSLQ PDDFATYYCQQYSSYPLTFGGGTRLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAG GAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQ EEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTY DALHMQALPPR	**302**
M22 CAR	**MALPVTALLLPLALLLHAARP**QVQLVQSGAEVRRPGASVKISCRASGDTSTRHYIHWLRQ APGQGPEWMGVINPTTGPATGSPAYAQMLQGRVTMTRDTSTRTVYMELRSLRFEDTAVYY CARSVVGRSAPYYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCRASQGISDYSAWYQQKPGKAPKLLIYAASTLQSGVPSRFSGSGSGTDFTL TISYLQSEDFATYYCQQYYSYPLTFGGGTKVDIKTTTPAPRPPTPAPTIASQPLSLRPEA CRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMR PVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLST ATKDTYDALHMQALPPR	**303**
M23 CAR	**MALPVTALLLPLALLLHAARP**QVQLQQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQ APGQGLEWMGIINPSGGYTTYAQKFQGRLTMTRDTSTSTVYMELSSLRSEDTAVYYCARI RSCGGDCYYFDNWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSTLSASVGD RVTITCRASENVNIWLAWYQQKPGKAPKLLIYKSSSLASGVPSRFSGSGSGAEFTLTISS LQPDDFATYYCQQYQSYPLTFGGGTKVDIKTTTPAPRPPTPAPTIASQPLSLRPEACRPA AGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQT TQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRR GRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR	**304**
M24 CAR	**MALPVTALLLPLALLLHAARP**QITLKESGPALVKPTQTLTLTCTFSGFSLSTAGVHVGWI RQPPGKALEWLALISWADDKRYRPSLRSRLDITRVTSKDQVVLSMTNMQPEDTATYYCAL QGFDGYEANWGPGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIVMTQSPSSLSASAGDRVT ITCRASRGISSALAWYQQKPGKPPKLLIYDASSLESGVPSRFSGSGSGTDFTLTIDSLEP EDFATYYCQQSYSTPWTFGQGTKVDIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGG AVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQE EDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRD PEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR	**305**

[00314] In one embodiment, the cell of the invention comprises a CAR molecule that binds mesothelin, and comprises (e.g., consists of) an amino acid sequence as provided in Table 11 and Table 2 of International Publication No. WO2015/090230, filed December 19, 2014; incorporated herein by reference. In one embodiment, the CAR molecule comprises (e.g., consists of) an amino acid sequence of SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, or SEQ ID NO: 306; or an amino acid sequence having at least one, two,

three, four, five, 10, 15, 20 or 30 modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 60, 50, or 40 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence of SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, or SEQ ID NO: 306; or an amino acid sequence having 85%, 90%, 95%, 96%, 97%, 98%, 99% identity to an amino acid sequence of SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, or SEQ ID NO: 306.

[00315] In one aspect, the cell of the invention comprises a CAR molecule comprising an antigen binding domain that binds to a tumor antigen. In one embodiment, the CAR comprises a EGFRvIII antigen binding domain (e.g., a murine, human or humanized antibody or antibody fragment that specifically binds to mesothelin), a transmembrane domain, and an intracellular signaling domain (e.g., an intracellular signaling domain comprising a costimulatory domain and/or a primary signaling domain).

[00316] Exemplary CAR molecules that target EGFRvIII are described herein, and are provided in Table 30, or in Table 2 of WO/2014/130657 or as described in WO2016/014789.

Table 30. Humanized EGFRvIII CAR Constructs. Sequences are provided with a leader, and the CDRs are underlined. Nt stands for nucleic acid and aa stands for amino acid

Name	SEQ ID NO:	Sequence
CAR 1		
CAR 1 – Full – nt	1042	atggccctccctgtcaccgccctgctgcttccgctggctcttctgctccacgccgctcggcccgagatcc agctggtgcagtcgggagctgaagtcaaaaagcctggcgcaaccgtcaagatctcgtgcaaaggatc agggttcaacatcgaggactactacatccattgggtgcaacaggcacccggaaaaggcctggagtgg atggggaggattgacccagaaaatgacgaaaccaagtacggaccgatcttccaaggacgggtgacca

		tcacggctgacacttccactaacaccgtctacatggaactctcgagccttcgctcggaagataccgcgg tgtactactgcgcctttagaggtggagtctactggggacaagggactaccgtcaccgtgtcgtcaggtg gcggaggatcaggcggaggcggctccggtggaggaggaagcggaggaggtggctccgacgtggt gatgacgcagtcaccggactccttggcggtgagcctgggtgaacgcgccactatcaactgcaagagct cccagagcttgctggactccgatggaaagacttatctcaattggctgcaacagaagcctggccagccg ccaaagagactcatctcactggtgagcaagctggatagcggagtgccagatcggttttcgggatcggg ctcaggcaccgacttcaccctgactatttcctccctccaagccgaggatgtggccgtctactactgttggc aggggactcacttcccggggaccttcggtggaggcactaaggtggagatcaaaaccactaccccagc accgaggccacccaccccggctcctaccatcgcctcccagcctctgtccctgcgtccggaggcatgta gacccgcagctggtggggccgtgcatacccggggtcttgacttcgcctgcgatatctacatttgggccc ctctggctggtacttgcggggtcctgctgctttcactcgtgatcactctttactgtaagcgcggtcggaag aagctgctgtacatctttaagcaacccttcatgaggcctgtgcagactactcaagaggaggacggctgtt catgccggttcccagaggaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcag atgctccagcctacaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagagga gtacgacgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaag aatccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgagattg gtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcagcaccgcc accaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
CAR 1 – Full - aa	1043	malpvtalllplalllhaarpeiqlvqsgaevkkpgatvkisckgsgfnie**<u>dyyih</u>**wvqqapgkgle wmg**<u>ridpendetkygpifqg</u>**rvtitadtstntvymelsslrsedtavyycaf**<u>rggv</u>**ywgqgttvt vssggggsggggsggggsggggsdvvmtqspdslavslgeratinc**<u>kssqslldsdgktyln</u>**wlq qkpgqppkrlis**<u>lvsklds</u>**gvpdrfsgsgsgtdftltisslqaedvavyyc**<u>wqgthfpgt</u>**fgggtkv eiktttpaprpptpaptiasqplslrpeacrpaaggavhtrgldfacdiyiwaplagtcgvlllslvitlyc krgrkkllyifkqpfmrpvqttqeedgcscrfpeeeeggcelrvkfsrsadapaykqgqnqlyneln lgrreeydvldkrrgrdpemggkprrknpqeglynelqkdkmaeayseigmkgerrrgkghdgl yqglstatkdtydalhmqalppr
CAR 2		
CAR 2 - Full - nt	1048	atggccctccctgtcaccgccctgctgcttccgctggctcttctgctccacgccgctcggcccgacgtg gtcatgactcaaagcccagattccttggctgtctcccttggagaaagagcaacgatcaattgcaaaagct cgcagtccctgttggactccgatggaaaaacctacctcaactggctgcagcagaagccgggacaacc accaaagcggctgatttccctcgtgtccaagctggacagcggcgtgccggatcgcttctcgggcagcg gctcgggaaccgattttactctcactatttcgtcactgcaagcggaggacgtggcggtgtattactgctgg cagggcactcacttcccgggtacttttggtggaggtaccaaagtcgaaatcaagggtggaggcggga gcggaggaggcgggtcgggaggaggaggatcgggtggcggaggctcagaaatccagctggtgca

		gtcaggtgccgaagtgaagaagcctggggccacggtgaagatctcgtgcaaggggagcggattcaa catcgaggattactacatccattgggtgcaacaggcccctggcaaagggctggaatggatgggaagg atcgaccccgagaatgacgagactaagtacggcccgatcttccaaggacgggtgaccatcactgcag acacttcaaccaacaccgtctacatggaactctcctcgctgcgctccgaggacaccgccgtgtactact gtgctttcagaggaggagtctactggggacagggaacgaccgtgaccgtcagctcaaccactacccc agcaccgaggccacccaccccggctcctaccatcgcctcccagcctctgtccctgcgtccggaggcat gtagacccgcagctggtggggccgtgcatacccggggtcttgacttcgcctgcgatatctacatttggg cccctctggctggtacttgcggggtcctgctgctttcactcgtgatcactctttactgtaagcgcggtcgg aagaagctgctgtacatctttaagcaacccttcatgaggcctgtgcagactactcaagaggaggacggc tgttcatgccggttcccagaggaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcg cagatgctccagcctacaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagaga ggagtacgacgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcaga aagaatccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgag attggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcagcacc gccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
CAR 2 - Full - aa	1049	malpvtalllplalllhaarpdvvmtqspdslavslgeratinc**<u>kssqslldsdgktyln</u>**wlqqkpgq ppkrlis**<u>lvsklds</u>**gvpdrfsgsgsgtdftltisslqaedvavyyc**<u>wqgthfpgt</u>**fgggtkveikggg gsggggsggggsggggseiqlvqsgaevkkpgatvkisckgsgfnie**<u>dyyih</u>**wvqqapgkgle wmg**<u>ridpendetkygpifqg</u>**rvtitadtstntvymelsslrsedtavyyca**<u>frggvy</u>**wgqgttvt vssttpaprpptpaptiasqplslrpeacrpaaggavhtrgldfacdiyiwaplagtcgvlllslvitlyc krgrkkllyifkqpfmrpvqttqeedgcscrfpeeeeggcelrvkfsrsadapaykqgqnqlyneln lgrreeydvldkrrgrdpemggkprrknpqeglynelqkdkmaeayseigmkgerrrgkghdgl yqglstatkdtydalhmqalppr
CAR 3		
CAR 3 – Full - nt	1054	atggccctccctgtcaccgccctgctgcttccgctggctcttctgctccacgccgctcggcccgaaatcc agctggtgcaaagcggagccgaggtgaagaagcccggagaatccctgcgcatctcgtgtaagggttc cggctttaacatcgaggattactacatccactgggtgagacagatgccgggcaaaggtctggaatggat gggccgcatcgacccggagaacgacgaaaccaaatacggaccaatcttccaaggacatgtgactattt ccgcggatacctccatcaacactgtctacttgcagtggagctcgctcaaggcgtcggataccgccatgt actactgcgcattcagaggaggtgtgtactggggccagggcactacggtcaccgtgtcctcgggaggt ggagggtcaggaggcggaggctcgggcggtggaggatcaggcggaggaggaagcgatgtggtca tgactcaatccccactgtcactgcctgtcactctggggcaaccggcttccatctcatgcaagtcaagcca atcgctgctcgactccgacggaaaaacctacctcaattggcttcagcagcgcccaggccagtcgcctc ggaggctgatctcactcgtgtcgaagcttgactccggggtgccggatcggtttagcggaagcggatcg

		gggaccgacttcacgttgaagattagccgggtggaagccgaggacgtgggagtctattactgctggca ggggacccacttcccggggactttcggaggaggcaccaaagtcgagattaagaccactaccccagca ccgaggccacccaccccggctcctaccatcgcctcccagcctctgtccctgcgtccggaggcatgtag acccgcagctggtggggccgtgcatacccggggtcttgacttcgcctgcgatatctacatttgggcccc tctggctggtacttgcggggtcctgctgctttcactcgtgatcactctttactgtaagcgcggtcggaaga agctgctgtacatctttaagcaacccttcatgaggcctgtgcagactactcaagaggaggacggctgttc atgccggttcccagaggaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcaga tgctccagcctacaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggag tacgacgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaaga atccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgagattgg tatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcagcaccgcca ccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
CAR 3 – Full - aa	1055	malpvtalllplalllhaarpeiqlvqsgaevkkpgeslrisckgsgfnie**dyyih**wvrqmpgkgle wmg**ridpendetkygpifqg**hvtisadtsintvylqwsslkasdtamyycaf**rggvy**wgqgttv tvssggggsggggsggggsggggsdvvmtqsplslpvtlgqpasisc**kssqslldsdgktyln**wl qqrpgqsprrlis**lvsklds**gvpdrfsgsgsgtdftlkisrveaedvgvyyc**wqgthfpgt**fgggtk veikttpaprpptpaptiasqplslrpeacrpaaggavhtrgldfacdiyiwaplagtcgvlllslvitly ckrgrkkllyifkqpfmrpvqttqeedgcscrfpeeeeggcelrvkfsrsadapaykqgqnqlynel nlgrreeydvldkrrgrdpemggkprrknpqeglynelqkdkmaeayseigmkgerrrgkghdg lyqglstatkdtydalhmqalppr
CAR 4		
CAR 4 – Full - nt	1060	atggccctccctgtcaccgccctgctgcttccgctggctcttctgctccacgccgctcggcccgacgtcg tcatgacccaatcccctctctccctgccggtcaccctgggtcagccggcgtcgatctcatgcaaaagctc acagtccctgctggattcggacggaaaaacctacttgaactggctccaacagaggccgggtcagtccc ctcgcagactgatctcgctggtgagcaagctcgactcgggtgtgccggatcggttctccgggtcaggat cgggcaccgactttacgctcaagatttcgagagtggaggccgaggatgtgggagtgtactattgctggc agggcacgcatttccccgggacctttggaggcgggactaaggtggaaatcaagggaggtggcggat caggcggaggaggcagcggcggaggtggatcaggaggcggagggtcagagatccagctggtcca aagcggagcagaggtgaagaagccaggcgagtcccttcgcatttcgtgcaaagggagcggcttcaac attgaagattactacatccactgggtgcggcaaatgccaggaaagggtctggaatggatgggacggat cgacccagaaaatgatgaaactaagtacggaccgatcttccaaggacacgtcactatctccgcggaca cttcgatcaacaccgtgtacctccagtggagcagcttgaaagcctccgacaccgctatgtactactgtgc cttccgcggaggagtctactggggacaggggactactgtgaccgtgtcgtccaccactaccccagcac cgaggccacccaccccggctcctaccatcgcctcccagcctctgtccctgcgtccggaggcatgtaga

		cccgcagctggtggggccgtgcatacccggggtcttgacttcgcctgcgatatctacatttgggcccct ctggctggtacttgcggggtcctgctgctttcactcgtgatcactctttactgtaagcgcggtcggaagaa gctgctgtacatctttaagcaacccttcatgaggcctgtgcagactactcaagaggaggacggctgttca tgccggttcccagaggaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagat gctccagcctacaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagt acgacgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaa tccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgagattggt atgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcagcaccgccac caaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
CAR 4 – Full - aa	1061	malpvtalllplalllhaarpdvvmtqsplslpvtlgqpasisc**<u>kssqslldsdgktyln</u>**wlqqrpgq sprrlis**<u>lvsklds</u>**gvpdrfsgsgsgtdftlkisrveaedvgvyyyc**<u>wqgthfpgt</u>**fgggtkveikgg ggsggggsggggsggggseiqlvqsgaevkkpgeslrisckgsgfnie**dyyih**wvrqmpgkgle wmg**<u>ridpendetkygpifqg</u>**hvtisadtsintvylqwsslkasdtamyycaf**<u>rggyy</u>**wgqgttv tvssttpaprpptpaptiasqplslrpeacrpaaggavhtrgldfacdiyiwaplagtcgvlllslvitly ckrgrkkllyifkqpfmrpvqttqeedgcscrfpeeeeggcelrvkfsrsadapaykqgqnqlynel nlgrreeydvldkrrgrdpemggkprrknpqeglynelqkdkmaeayseigmkgerrrgkghdg lyqglstatkdtydalhmqalppr
CAR 5		
CAR 5 – Full - nt	1066	atggccctccctgtcaccgccctgctgcttccgctggctcttctgctccacgccgctcggcccgaaatcc agctcgtgcagagcggagccgaggtcaagaaaccgggtgctaccgtgaagatttcatgcaagggatc gggcttcaacatcgaggattactacatccactgggtgcagcaggcaccaggaaaaggacttgaatgga tgggccggatcgacccggaaaatgacgagactaagtacggccctatcttccaaggacgggtgacgat caccgcagacactagcaccaacaccgtctatatggaactctcgtccctgaggtccgaagatactgccgt gtactactgtgcgtttcgcggaggtgtgtactggggacagggtaccaccgtcaccgtgtcatcgggcg gtggaggctccggtggaggagggtcaggaggcggtggaagcggaggaggcggcagcgacgtggt catgactcaatcgccgctgtcgctgcccgtcactctgggacaacccgcgtccatcagctgcaaatcctc gcagtcactgcttgactccgatggaaagacctacctcaactggctgcagcaacgcccaggccaatccc caagacgcctgatctcgttggtgtcaaagctggactcaggggtgccggaccggttctccgggagcgg gtcgggcacggatttcactctcaagatctccagagtggaagccgaggatgtgggagtctactactgctg gcagggaacccatttccctggaacttttggcggaggaactaaggtcgagattaaaaccactaccccag caccgaggccacccaccccggctcctaccatcgcctcccagcctctgtccctgcgtccggaggcatgt agacccgcagctggtggggccgtgcatacccggggtcttgacttcgcctgcgatatctacatttgggcc cctctggctggtacttgcggggtcctgctgctttcactcgtgatcactctttactgtaagcgcggtcggaa gaagctgctgtacatctttaagcaacccttcatgaggcctgtgcagactactcaagaggaggacggctg

		ttcatgccggttcccagaggaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcctacaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacgacgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaatccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgagattggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcagcaccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
CAR 5 – Full - aa	1067	malpvtalllplalllhaarpeiqlvqsgaevkkpgatvkisckgsgfnie**<u>dyyih</u>**wvqqapgkglewmg**<u>ridpendetkygpifqg</u>**rvtitadtstntvymelsslrsedtavyycaf**<u>rggvy</u>**wgqgttvtvssggggsggggsggggsggggsdvvmtqsplslpvtlgqpasisc**<u>kssqslldsdgktyln</u>**wlqqrpgqsprrlis**<u>lvsklds</u>**gvpdrfsgsgsgtdftlkisrveaedvgvyyc**<u>wqgthfpgt</u>**fgggtkveikttpaprpptpaptiasqplslrpeacrpaaggavhtrgldfacdiyiwaplagtcgvlllslvitlyckrgrkkllyifkqpfmrpvqttqeedgcscrfpeeeeggcelrvkfsrsadapaykqgqnqlynelnlgrreeydvldkrrgrdpemggkprrknpqeglynelqkdkmaeayseigmkgerrrgkghdglyqglstatkdtydalhmqalppr
CAR 6		
CAR6 – Full - nt	1072	atggccctccctgtcaccgccctgctgcttccgctggctcttctgctccacgccgctcggcccgagattcagctcgtgcaatcgggagcggaagtcaagaagccaggagagtccttgcggatctcatgcaagggtagcggctttaacatcgaggattactacatccactgggtgaggcagatgccggggaagggactcgaatggatgggacggatcgacccagaaaacgacgaaactaagtacggtccgatcttccaaggccatgtgactattagcgccgatacttcaatcaataccgtgtatctgcaatggtcctcattgaaagcctcagataccgcgatgtactactgtgctttcagaggaggggtctactggggacagggaactaccgtgactgtctcgtccggcggaggcgggtcaggaggtggcggcagcggaggaggagggtccggcggaggtgggtccgacgtcgtgatgacccagagccctgacagcctggcagtgagcctgggcgaaagagctaccattaactgcaaatcgtcgcagagcctgctggactcggacggaaaaacgtacctcaattggctgcagcaaaagcctggccagccaccgaagcgccttatctcactggtgtcgaagctggattcgggagtgcccgatcgcttctccggctcgggatcgggtactgacttcaccctcactatctcctcgcttcaagcagaggacgtggccgtctactactgctggcagggaacccactttccgggaaccttcggcggagggacgaaagtggagatcaagaccactaccccagcaccgaggccacccaccccggctcctaccatcgcctcccagcctctgtccctgcgtccggaggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttcgcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcactcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacccttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagaggaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcctacaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacgacgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaag

		aatccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgagattg gtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcagcaccgcc accaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
CAR6 – Full – aa	1073	malpvtalllplalllhaarpeiqlvqsgaevkkpgeslrisckgsgfnie**dyyih**wvrqmpgkgle wmg**ridpendetkygpifqg**hvtisadtsintvylqwsslkasdtamyycaf**rggvy**wgqgttv tvssggggsggggsggggsggggsdvvmtqspdslavslgeratinc**kssqsllds dgktyln**wl qqkpgqppkrlis**lvsklds**gvpdrfsgsgsgtdftltisslqaedvavyyc**wqgthfpgt**fgggtk veiktttpaprpptpaptiasqplslrpeacrpaaggavhtrgldfacdiyiwaplagtcgvlllslvitly ckrgrkkllyifkqpfmrpvqttqeedgcscrfpeeeeggcelrvkfsrsadapaykqgqnqlynel nlgrreeydvldkrrgrdpemggkprrknpqeglynelqkdkmaeayseigmkgerrrgkghdg lyqglstatkdtydalhmqalppr
CAR 7		
CAR 7 Full - nt	1078	atggccctccctgtcaccgccctgctgcttccgctggctcttctgctccacgccgctcggcccgacgtg gtgatgactcagtcgcctgactcgctggctgtgtcccttggagagcgggccactatcaattgcaagtcat cccagtcgctgctggattccgacgggaaaacctacctcaattggctgcagcaaaaaccgggacagcct ccaaagcggctcatcagcctggtgtccaagttggacagcggcgtgccagaccgcttctccggttcggg aagcggtactgatttcacgctgaccatctcatccctccaagcggaggatgtggcagtctactactgttgg cagggcacgcattttccgggcacttttggaggagggaccaaggtcgaaatcaagggaggaggtggct cgggcggaggaggctcgggaggaggaggatcaggaggcggtggaagcgagattcaactggtcca gagcggcgcagaagtcaagaagccgggtgaatcgctcagaatctcgtgcaaaggatcgggattcaac atcgaggactactacattcactgggtcagacaaatgccgggcaaagggctggaatggatggggagga tcgaccccgaaaacgatgaaaccaagtacggaccaatcttccaagggcacgtgaccatttcggcgga cacctcaatcaacactgtgtacctccagtggagctcacttaaggccagcgataccgccatgtactattgc gctttccgcggaggggtgtactggggacagggcactactgtgaccgtgtcatccaccactaccccagc accgaggccacccaccccggctcctaccatcgcctcccagcctctgtccctgcgtccggaggcatgta gacccgcagctggtggggccgtgcatacccggggtcttgacttcgcctgcgatatctacatttgggccc ctctggctggtacttgcggggtcctgctgctttcactcgtgatcactctttactgtaagcgcggtcggaag aagctgctgtacatctttaagcaacccttcatgaggcctgtgcagactactcaagaggaggacggctgtt catgccggttcccagaggaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcag atgctccagcctacaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagagga gtacgacgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaag aatccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgagattg gtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcagcaccgcc accaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg

CAR 7 Full - aa	1079	malpvtalllplalllhaarpdvvmtqspdslavslgeratinc**kssqslldsdgktyln**wlqqkpgqppkrlis**lvsklds**gvpdrfsgsgsgtdftltisslqaedvavyyc**wqgthfpgt**fgggtkveikggggsggggsggggsggggseiqlvqsgaevkkpgeslrisckgsgfnie**dyyih**wvrqmpgkglewmg**ridpendetkygpifqg**hvtisadtsintvylqwsslkasdtamyycaf**rggvy**wgqgttvtvssttpaprpptpaptiasqplslrpeacrpaaggavhtrgldfacdiyiwaplagtcgvlllslvitlyckrgrkkllyifkqpfmrpvqttqeedgcscrfpeeeeggcelrvkfsrsadapaykqgqnqlynelnlgrreeydvldkrrgrdpemggkprrknpqeglynelqkdkmaeayseigmkgerrrgkghdglyqglstatkdtydalhmqalppr
CAR 8		
CAR 8 – Full - nt	1084	atggccctccctgtcaccgccctgctgcttccgctggctcttctgctccacgccgctcggcccgatgtggtcatgacgcagtcaccactgtccctccccgtgacccttggacagccagcgtcgattagctgcaagtcatcccaatccctgctcgattcggatggaaagacctatctcaactggctgcagcaaagacccggtcagagccctaggagactcatctcgttggtgtcaaagctggacagcggagtgccggaccggttttccggttcgggatcggggacggacttcactctgaagatttcacgggtggaagctgaggatgtgggagtgtactactgctggcagggaacccatttccctggcacttttggcggaggaactaaggtcgaaatcaagggaggaggtggctcgggaggaggcggatcgggcggaggcgggagcggcggaggagggtccgaaatccaacttgtccagtcaggagccgaagtgaagaaaccgggagccaccgtcaaaatcagctgtaagggatcgggattcaatatcgaggactactacatccactgggtgcagcaagctccgggcaaaggactggagtggatggggcgcatcgacccagagaacgacgaaaccaaatacggcccgatcttccaagggcgggtgaccatcaccgcggacacctcaactaacactgtgtacatggagctgagctccctgcgctccgaagatactgcagtctactactgcgccttccgcggtggtgtgtactggggacagggcaccactgtgactgtcagctcgaccactaccccagcaccgaggccacccaccccggctcctaccatcgcctcccagcctctgtccctgcgtccggaggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttcgcctgcgatatctacatttgggccccctctggctggtacttgcggggtcctgctgctttcactcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacccttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagaggaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcctacaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacgacgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaatccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgagattggtatgaaaggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcagcaccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
CAR 8 – Full - aa	1085	malpvtalllplalllhaarpdvvmtqsplslpvtlgqpasisc**kssqslldsdgktyln**wlqqrpgqsprrlis**lvsklds**gvpdrfsgsgsgtdftlkisrveaedvgvyyc**wqgthfpgt**fgggtkveikggggsggggsggggsggggseiqlvqsgaevkkpgatvkisckgsgfnie**dyyih**wvqqapgkgle

		wmg**ridpendetkygpifqg**rvtitadtstntvymelsslrsedtavyycaf**rggvy**wgqgttvtvssttpaprpptpaptiasqplslrpeacrpaaggavhtrgldfacdiyiwaplagtcgvlllslvitlyckrgrkkllyifkqpfmrpvqttqeedgcscrfpeeeeggcelrvkfsrsadapaykqgqnqlynelnlgrreeydvldkrrgrdpemggkprrknpqeglynelqkdkmaeayseigmkgerrrgkghdglyqglstatkdtydalhmqalppr
CAR 9		Mouse anti-EGFRvIII clone 3C10
CAR 9 – Full - nt	1089	atggccctccctgtcaccgccctgctgcttccgctggctcttctgctccacgccgctcggcccgagatccagctccaacagagcggagccgaactggtcaaaccgggagcgtcggtgaagttgtcatgcactggatcgggcttcaacatcgaggattactacatccactgggtcaagcaacgcaccgagcaggggctggaatggatcggacggatcgaccccgaaaacgatgaaaccaagtacgggcctatcttccaaggacgggccaccattacggctgacacgtcaagcaataccgtctacctccagctttccagcctgacctccgaggacactgccgtgtactactgcgccttcagaggaggcgtgtactggggaccaggaaccactttgaccgtgtccagcggaggcggtggatcaggaggaggaggctcaggcggtggcggctcgcacatggacgtggtcatgactcagtccccgctgaccctgtcggtggcaattggacagagcgcatccatctcgtgcaagagctcacagtcgctgctggattccgacggaaagacttatctgaactggctgctccaaagaccagggcaatcaccgaaacgccttatctccctggtgtcgaaactcgactcgggtgtgccggatcggtttaccggtagcgggtccggcacggacttcactctccgcatttcgagggtggaagcggaggatctcgggatctactactgttggcagggaacccacttccctgggacttttggaggcggaactaagctggaaatcaagaccactaccccagcaccgaggccacccaccccggctcctaccatcgcctcccagcctctgtccctgcgtccggaggcatgtagacccgcagctggtggggccgtgcatacccggggtcttgacttcgcctgcgatatctacatttgggcccctctggctggtacttgcggggtcctgctgctttcactcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaagcaacccttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagaggaggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcctacaagcaggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacgacgtgctggacaagcggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaatccccaagagggcctgtacaacgagctccaaaaggataagatggcagaagcctatagcgagattggtatgaaagggggaacgcagaagaggcaaaggccacgacggactgtaccagggactcagcaccgccaccaaggacacctatgacgctcttcacatgcaggccctgccgcctcgg
CAR 9 – Full - aa	1090	malpvtalllplalllhaarpeiqlqqsgaelvkpgasvklsctgsgfnie**dyyih**wvkqrteqglewig**ridpendetkygpifqg**ratitadtssntvylqlssltsedtavyyca**frggvy**wgpgttltvssggggsggggsggggshmdvvmtqspltlsvaigqsasisc**kssqslldsdgktyln**wllqrpgqspkrlis**lvsklds**gvpdrftgsgsgtdftlrisrveaedlgiyyc**wqgthfpgt**fgggtkleikttpaprpptpaptiasqplslrpeacrpaaggavhtrgldfacdiyiwaplagtcgvlllslvitlyckrgrkkllyifkqpfmrpvqttqeedgcscrfpeeeeggcelrvkfsrsadapaykqgqnqlynelnlgrreeydvld

		krrgrdpemggkprrknpqeglynelqkdkmaeayseigmkgerrrgkghdglyqglstatkdt ydalhmqalppr
CAR10		Anti-EGFRvIII clone 139
CAR 10 Full - nt	1095	atggccctccctgtcaccgccctgctgcttccgctggctcttctgctccacgccgctcggcccgatatcc aaatgactcagagcccttcatccctgagcgccagcgtcggagacagggtgaccatcacgtgccgggc atcccaaggcattagaaataacttggcgtggtatcagcaaaaaccaggaaaggccccgaagcgcctg atctacgcggcctccaaccttcagtcaggagtgccctcgcgcttcaccgggagcggtagcggaactga gtttacccttatcgtgtcgtccctgcagccagaggacttcgcgacctactactgcctccagcatcactcgt acccgttgacttcgggaggcggaaccaaggtcgaaatcaaacgcactggctcgacgtcagggtccgg taaaccgggatcgggagaaggatcggaagtccaagtgctggagagcggaggcggactcgtgcaac ctggcgggtcgctgcggctcagctgtgccgcgtcgggttttactttcagctcgtacgctatgtcatgggt gcggcaggctccgggaaaggggctggaatgggtgtccgctatttccggctcgggtggaagcaccaat tacgccgactccgtgaagggacgcttcaccatctcacgggataactccaagaatactctgtacctccag atgaactcgctgagagccgaggacaccgcagtgtactactgcgcagggtcaagcggctggtccgaat actggggacagggcaccctcgtcactgtcagctccaccactaccccagcaccgaggccacccacccc ggctcctaccatcgcctcccagcctctgtccctgcgtccggaggcatgtagacccgcagctggtgggg ccgtgcatacccggggtcttgacttcgcctgcgatatctacatttgggcccctctggctggtacttgcggg gtcctgctgctttcactcgtgatcactctttactgtaagcgcggtcggaagaagctgctgtacatctttaag caacccttcatgaggcctgtgcagactactcaagaggaggacggctgttcatgccggttcccagagga ggaggaaggcggctgcgaactgcgcgtgaaattcagccgcagcgcagatgctccagcctacaagca ggggcagaaccagctctacaacgaactcaatcttggtcggagagaggagtacgacgtgctggacaag cggagaggacgggacccagaaatgggcgggaagccgcgcagaaagaatccccaagagggcctgt acaacgagctccaaaaggataagatggcagaagcctatagcgagattggtatgaaaggggaacgca gaagaggcaaaggccacgacggactgtaccagggactcagcaccgccaccaaggacacctatgac gctcttcacatgcaggccctgccgcctcgg
CAR 10 Full - aa	1096	malpvtalllplalllhaarpdiqmtqspsslsasvgdrvtitcrasqgirnnlawyqqkpgkapkrli yaasnlqsgvpsrftgsgsgteftlivsslqpedfatyyclqhhsypltsgggtkveikrtgstsgsgkp gsgegsevqvlesggglvqpggslrlscaasgftfssyamswvrqapgkglewvsaisgsggstny adsvkgrftisrdnskntlylqmnslraedtavyycagssgwseywgqgtlvtvsstttpaprpptpa ptiasqplslrpeacrpaaggavhtrgldfacdiyiwaplagtcgvlllslvitlyckrgrkkllyifkqpf mrpvqttqeedgcscrfpeeeeggcelrvkfsrsadapaykqgqnqlynelnlgrreeydvldkrrg rdpemggkprrknpqeglynelqkdkmaeayseigmkgerrrgkghdglyqglstatkdtydal hmqalppr

[00317] In one embodiment, the cell of the invention comprises a CAR molecule that binds EGFRvIII that comprises (e.g., consists of) an amino acid sequence as provided in Table 30. In one embodiment, the CAR that binds EGFRvIII comprises (e.g., consists of) an amino acid sequence of SEQ ID NO: 1043, SEQ ID NO: 1049, SEQ ID NO: 1055, SEQ ID NO: 1061, SEQ ID NO: 1067, SEQ ID NO: 1073, SEQ ID NO: 1079, SEQ ID NO: 1085, SEQ ID NO: 1090, or SEQ ID NO: 1096; or an amino acid sequence having at least one, two, three, four, five, 10, 15, 20 or 30 modifications (e.g., substitutions, e.g., conservative substitutions) but not more than 60, 50, or 40 modifications (e.g., substitutions, e.g., conservative substitutions) of an amino acid sequence of SEQ ID NO: 1043, SEQ ID NO: 1049, SEQ ID NO: 1055, SEQ ID NO: 1061, SEQ ID NO: 1067, SEQ ID NO: 1073, SEQ ID NO: 1079, SEQ ID NO: 1085, SEQ ID NO: 1090, or SEQ ID NO: 1096; or an amino acid sequence having 85%, 90%, 95%, 96%, 97%, 98%, 99% identity to an amino acid sequence of SEQ ID NO: 1043, SEQ ID NO: 1049, SEQ ID NO: 1055, SEQ ID NO: 1061, SEQ ID NO: 1067, SEQ ID NO: 1073, SEQ ID NO: 1079, SEQ ID NO: 1085, SEQ ID NO: 1090, or SEQ ID NO: 1096.

[00318] In one aspect, the cell of the invention comprises a CAR molecule comprising an antigen binding domain that binds to a tumor antigen. In one embodiment, the CAR comprises a CAR molecule comprising a CD123 antigen binding domain (e.g., a murine, human or humanized antibody or antibody fragment that specifically binds to mesothelin), a transmembrane domain, and an intracellular signaling domain (e.g., an intracellular signaling domain comprising a costimulatory domain and/or a primary signaling domain).

[00319] Exemplary CAR molecules that target CD123 are described herein (e.g., Table 26 or Table 27), and are provided in Tables 2, 6 and 9 of WO2016/028896. Other exemplary CAR molecules that target CD123 are described in WO/2014/130635 (e.g., Table 1 of WO/2014/130635). Other exemplary CAR molecules that target CD123 are described in WO/2014/144622.

[00320] In one aspect, the cell of the invention comprises a CAR molecule comprising an antigen binding domain that binds to a tumor antigen. In one embodiment, the CAR comprises CD33 antigen binding domain (e.g., a murine, human or humanized antibody or antibody fragment that specifically binds to CD33), a transmembrane domain, and an intracellular signaling domain (e.g., an intracellular signaling domain comprising a costimulatory domain

and/or a primary signaling domain). Exemplary CAR molecules that target CD33 are described herein, and are provided in WO2016/014576, e.g., in Table 2 of WO2016/014576.

[00321] In one aspect, the cell of the invention comprises a CAR molecule comprising an antigen binding domain that binds to a tumor antigen. In one embodiment, the CAR comprises CLL-1 antigen binding domain (e.g., a murine, human or humanized antibody or antibody fragment that specifically binds to CLL-1), a transmembrane domain, and an intracellular signaling domain (e.g., an intracellular signaling domain comprising a costimulatory domain and/or a primary signaling domain). Exemplary CAR molecules that target CLL-1 are described herein, and are provided in WO/2016/014535, e.g., in Table 2 of WO2016/014535.

[00322] In one embodiment, the antigen binding domain of a CAR described herein is a scFv antibody fragment. In one aspect, such antibody fragments are functional in that they retain the equivalent binding affinity, e.g., they bind the same antigen with comparable efficacy, as the IgG antibody from which it is derived. In other embodiments, the antibody fragment has a lower binding affinity, e.g., it binds the same antigen with a lower binding affinity than the antibody from which it is derived, but is functional in that it provides a biological response described herein. In one embodiment, the CAR molecule comprises an antibody fragment that has a binding affinity K_D of 10^{-4} M to 10^{-8} M, e.g., 10^{-5} M to 10^{-7} M, e.g., 10^{-6} M or 10^{-7} M, for the target antigen. In one embodiment, the antibody fragment has a binding affinity that is at least five-fold, 10-fold, 20-fold, 30-fold, 50-fold, 100-fold or 1,000-fold less than a reference antibody, e.g., an antibody described herein.

[00323] In one embodiment, the antigen binding domain comprises a non-human antibody or antibody fragment, e.g., a mouse antibody or antibody fragment.

[00324] In another embodiment, the antigen binding domain comprises a humanized antibody or an antibody fragment. In some aspects, a non-human antibody is humanized, where specific sequences or regions of the antibody are modified to increase similarity to an antibody naturally produced in a human or fragment thereof. In one aspect, the antigen binding domain is humanized compared to the murine sequence of the antibody or antibody fragment, e.g., scFv, from which it is derived.

[00325] A humanized antibody can be produced using a variety of techniques known in the art, including but not limited to, CDR-grafting (see, e.g., European Patent No. EP 239,400;

International Publication No. WO 91/09967; and U.S. Pat. Nos. 5,225,539, 5,530,101, and 5,585,089, each of which is incorporated herein in its entirety by reference), veneering or resurfacing (see, e.g., European Patent Nos. EP 592,106 and EP 519,596; Padlan, 1991, Molecular Immunology, 28(4/5):489-498; Studnicka et al., 1994, Protein Engineering, 7(6):805-814; and Roguska et al., 1994, PNAS, 91:969-973, each of which is incorporated herein by its entirety by reference), chain shuffling (see, e.g., U.S. Pat. No. 5,565,332, which is incorporated herein in its entirety by reference), and techniques disclosed in, e.g., U.S. Patent Application Publication No. US2005/0042664, U.S. Patent Application Publication No. US2005/0048617, U.S. Pat. No. 6,407,213, U.S. Pat. No. 5,766,886, International Publication No. WO 9317105, Tan et al., J. Immunol., 169:1119-25 (2002), Caldas et al., Protein Eng., 13(5):353-60 (2000), Morea et al., Methods, 20(3):267-79 (2000), Baca et al., J. Biol. Chem., 272(16):10678-84 (1997), Roguska et al., Protein Eng., 9(10):895-904 (1996), Couto et al., Cancer Res., 55 (23 Supp):5973s-5977s (1995), Couto et al., Cancer Res., 55(8):1717-22 (1995), Sandhu J S, Gene, 150(2):409-10 (1994), and Pedersen et al., J. Mol. Biol., 235(3):959-73 (1994), each of which is incorporated herein in its entirety by reference. Often, framework residues in the framework regions will be substituted with the corresponding residue from the CDR donor antibody to alter, for example improve, antigen binding. These framework substitutions are identified by methods well-known in the art, e.g., by modeling of the interactions of the CDR and framework residues to identify framework residues important for antigen binding and sequence comparison to identify unusual framework residues at particular positions. (See, e.g., Queen et al., U.S. Pat. No. 5,585,089; and Riechmann et al., 1988, Nature, 332:323, which are incorporated herein by reference in their entireties.)

[00326] A humanized antibody or antibody fragment has one or more amino acid residues remaining in it from a source which is nonhuman. These nonhuman amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. As provided herein, humanized antibodies or antibody fragments comprise one or more CDRs from nonhuman immunoglobulin molecules and framework regions wherein the amino acid residues comprising the framework are derived completely or mostly from human germline. Multiple techniques for humanization of antibodies or antibody fragments are well-known in the art and can essentially be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327

(1988); Verhoeyen et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody, i.e., CDR-grafting (EP 239,400; PCT Publication No. WO 91/09967; and U.S. Pat. Nos. 4,816,567; 6,331,415; 5,225,539; 5,530,101; 5,585,089; 6,548,640, the contents of which are incorporated herein by reference herein in their entirety). In such humanized antibodies and antibody fragments, substantially less than an intact human variable domain has been substituted by the corresponding sequence from a nonhuman species. Humanized antibodies are often human antibodies in which some CDR residues and possibly some framework (FR) residues are substituted by residues from analogous sites in rodent antibodies. Humanization of antibodies and antibody fragments can also be achieved by veneering or resurfacing (EP 592,106; EP 519,596; Padlan, 1991, Molecular Immunology, 28(4/5):489-498; Studnicka et al., Protein Engineering, 7(6):805-814 (1994); and Roguska et al., PNAS, 91:969-973 (1994)) or chain shuffling (U.S. Pat. No. 5,565,332), the contents of which are incorporated herein by reference herein in their entirety.

[00327] The choice of human variable domains, both light and heavy, to be used in making the humanized antibodies is to reduce antigenicity. According to the so-called “best-fit” method, the sequence of the variable domain of a rodent antibody is screened against the entire library of known human variable-domain sequences. The human sequence which is closest to that of the rodent is then accepted as the human framework (FR) for the humanized antibody (Sims et al., J. Immunol., 151:2296 (1993); Chothia et al., J. Mol. Biol., 196:901 (1987), the contents of which are incorporated herein by reference herein in their entirety). Another method uses a particular framework derived from the consensus sequence of all human antibodies of a particular subgroup of light or heavy chains. The same framework may be used for several different humanized antibodies (see, e.g., Nicholson et al. Mol. Immun. 34 (16-17): 1157-1165 (1997); Carter et al., Proc. Natl. Acad. Sci. USA, 89:4285 (1992); Presta et al., J. Immunol., 151:2623 (1993), the contents of which are incorporated herein by reference herein in their entirety). In some embodiments, the framework region, e.g., all four framework regions, of the heavy chain variable region are derived from a VH4_4-59 germline sequence. In one embodiment, the framework region can comprise, one, two, three, four or five modifications, e.g., substitutions, e.g., from the amino acid at the corresponding murine sequence. In one embodiment, the framework region, e.g., all four framework regions of the light chain variable

region are derived from a VK3_1.25 germline sequence. In one embodiment, the framework region can comprise, one, two, three, four or five modifications, e.g., substitutions, e.g., from the amino acid at the corresponding murine sequence.

[00328] In some aspects, the portion of a CAR of the invention that comprises an antibody fragment is humanized with retention of high affinity for the target antigen and other favorable biological properties. According to one aspect of the invention, humanized antibodies and antibody fragments are prepared by a process of analysis of the parental sequences and various conceptual humanized products using three-dimensional models of the parental and humanized sequences. Three-dimensional immunoglobulin models are commonly available and are familiar to those skilled in the art. Computer programs are available which illustrate and display probable three-dimensional conformational structures of selected candidate immunoglobulin sequences. Inspection of these displays permits analysis of the likely role of the residues in the functioning of the candidate immunoglobulin sequence, e.g., the analysis of residues that influence the ability of the candidate immunoglobulin to bind the target antigen. In this way, FR residues can be selected and combined from the recipient and import sequences so that the desired antibody or antibody fragment characteristic, such as increased affinity for the target antigen, is achieved. In general, the CDR residues are directly and most substantially involved in influencing antigen binding.

[00329] A humanized antibody or antibody fragment may retain a similar antigenic specificity as the original antibody, e.g., in the present disclosure, the ability to bind human a tumor antigen as described herein. In some embodiments, a humanized antibody or antibody fragment may have improved affinity and/or specificity of binding to a tumor antigen as described herein or a B cell antigen as described herein. In some embodiments, a humanized antibody or antibody fragment may have lower affinity and/or specificity of a tumor antigen as described herein or a B cell antigen as described herein.

[00330] In one aspect, the antigen binding domain of the invention is characterized by particular functional features or properties of an antibody or antibody fragment. For example, in one aspect, the portion of a CAR of the invention that comprises an antigen binding domain specifically binds a tumor antigen as described herein.

[00331] In one aspect, the antigen binding domain is a fragment, e.g., a single chain variable fragment (scFv). In one aspect, the anti- tumor antigen as described herein binding domain is a Fv, a Fab, a (Fab')2, or a bi-functional (e.g. bi-specific) hybrid antibody (e.g., Lanzavecchia et al., Eur. J. Immunol. 17, 105 (1987)). In one aspect, the antibodies and fragments thereof of the invention binds a tumor antigen as described herein protein with wild-type or enhanced affinity.

[00332] In some instances, scFvs can be prepared according to method known in the art (see, for example, Bird et al., (1988) Science 242:423-426 and Huston et al., (1988) Proc. Natl. Acad. Sci. USA 85:5879-5883). ScFv molecules can be produced by linking VH and VL regions together using flexible polypeptide linkers. The scFv molecules comprise a linker (e.g., a Ser-Gly linker) with an optimized length and/or amino acid composition. The linker length can greatly affect how the variable regions of a scFv fold and interact. In fact, if a short polypeptide linker is employed (e.g., between 5-10 amino acids) intrachain folding is prevented. Interchain folding is also required to bring the two variable regions together to form a functional epitope binding site. For examples of linker orientation and size see, e.g., Hollinger et al. 1993 Proc Natl Acad. Sci. U.S.A. 90:6444-6448, U.S. Patent Application Publication Nos. 2005/0100543, 2005/0175606, 2007/0014794, and PCT publication Nos. WO2006/020258 and WO2007/024715, is incorporated herein by reference.

[00333] An scFv can comprise a linker of at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, or more amino acid residues between its VL and VH regions. The linker sequence may comprise any naturally occurring amino acid. In some embodiments, the linker sequence comprises amino acids glycine and serine. In another embodiment, the linker sequence comprises sets of glycine and serine repeats such as $(Gly_4Ser)n$, where n is a positive integer equal to or greater than 1 (SEQ ID NO:22). In one embodiment, the linker can be $(Gly_4Ser)_4$ (SEQ ID NO:29) or $(Gly_4Ser)_3$(SEQ ID NO:30). Variation in the linker length may retain or enhance activity, giving rise to superior efficacy in activity studies.

[00334] In another aspect, the antigen binding domain is a T cell receptor ("TCR"), an engineered TCR, or a fragment thereof, for example, a single chain TCR (scTCR). Methods to make such TCRs are known in the art. See, e.g., Willemsen RA et al, Gene Therapy 7: 1369–1377 (2000); Zhang T et al, Cancer Gene Ther 11: 487–496 (2004); Aggen et al, Gene Ther. 19(4):365-74 (2012) (references are incorporated herein by its entirety). For example, scTCR

can be engineered that contains the Vα and Vβ genes from a T cell clone linked by a linker (e.g., a flexible peptide). This approach is very useful to cancer associated target that itself is intracellular, however, a fragment of such antigen (peptide) is presented on the surface of the cancer cells by MHC.

[00335] In one aspect, the antigen binding domain of the CAR comprises an amino acid sequence that is homologous to an antigen binding domain amino acid sequence described herein, and the antigen binding domain retains the desired functional properties of the antigen binding domain described herein.

[00336] In one specific aspect, the CAR composition of the invention comprises an antibody fragment. In a further aspect, the antibody fragment comprises a scFv. In a further aspect, the antibody fragment comprises a variable heavy chain (VH) only.

[00337] In various aspects, the antigen binding domain of the CAR is engineered by modifying one or more amino acids within one or both variable regions (e.g., VH and/or VL), for example within one or more CDR regions and/or within one or more framework regions. In one specific aspect, the CAR composition of the invention comprises an antibody fragment. In a further aspect, the antibody fragment comprises an scFv.

[00338] It will be understood by one of ordinary skill in the art that the antibody or antibody fragment of the invention may further be modified such that they vary in amino acid sequence (e.g., from wild-type), but not in desired activity. For example, additional nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues may be made to the protein. For example, a nonessential amino acid residue in a molecule may be replaced with another amino acid residue from the same side chain family. In another embodiment, a string of amino acids can be replaced with a structurally similar string that differs in order and/or composition of side chain family members, e.g., a conservative substitution, in which an amino acid residue is replaced with an amino acid residue having a similar side chain, may be made.

[00339] Families of amino acid residues having similar side chains have been defined in the art, including basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine,

isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine).

[00340] Percent identity in the context of two or more nucleic acids or polypeptide sequences, refers to two or more sequences that are the same. Two sequences are "substantially identical" if two sequences have a specified percentage of amino acid residues or nucleotides that are the same (e.g., 60% identity, optionally 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identity over a specified region, or, when not specified, over the entire sequence), when compared and aligned for maximum correspondence over a comparison window, or designated region as measured using one of the following sequence comparison algorithms or by manual alignment and visual inspection. Optionally, the identity exists over a region that is at least about 50 nucleotides (or 10 amino acids) in length, or more preferably over a region that is 100 to 500 or 1000 or more nucleotides (or 20, 50, 200 or more amino acids) in length.

[00341] For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters. Methods of alignment of sequences for comparison are well known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman, (1970) Adv. Appl. Math. 2:482c, by the homology alignment algorithm of Needleman and Wunsch, (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman, (1988) Proc. Nat'l. Acad. Sci. USA 85:2444, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Brent et al., (2003) Current Protocols in Molecular Biology).

[00342] Two examples of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al., (1977) Nuc. Acids Res. 25:3389-3402; and Altschul et al., (1990) J. Mol. Biol. 215:403-410, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information.

[00343] The percent identity between two amino acid sequences can also be determined using the algorithm of E. Meyers and W. Miller, (1988) Comput. Appl. Biosci. 4:11-17) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4. In addition, the percent identity between two amino acid sequences can be determined using the Needleman and Wunsch (1970) J. Mol. Biol. 48:444-453) algorithm which has been incorporated into the GAP program in the GCG software package (available at www.gcg.com), using either a Blossom 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6.

[00344] In one aspect, the present disclosure contemplates modifications of the starting antibody or fragment (e.g., scFv) amino acid sequence that generate functionally equivalent molecules. For example, the VH or VL of an antigen binding domain to -a tumor antigen described herein, e.g., scFv, comprised in the CAR can be modified to retain at least about 70%, 71%. 72%. 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%,81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identity of the starting VH or VL framework region of the antigen binding domain to the tumor antigen described herein, e.g., scFv. The present disclosure contemplates modifications of the entire CAR construct, e.g., modifications in one or more amino acid sequences of the various domains of the CAR construct in order to generate functionally equivalent molecules. The CAR construct can be modified to retain at least about 70%, 71%. 72%. 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identity of the starting CAR construct.

[00345] Bispecific CARs

[00346] In an embodiment a multispecific antibody molecule is a bispecific antibody molecule. A bispecific antibody has specificity for no more than two antigens. A bispecific

antibody molecule is characterized by a first immunoglobulin variable domain sequence which has binding specificity for a first epitope and a second immunoglobulin variable domain sequence that has binding specificity for a second epitope. In an embodiment the first and second epitopes are on the same antigen, e.g., the same protein (or subunit of a multimeric protein). In an embodiment the first and second epitopes overlap. In an embodiment the first and second epitopes do not overlap. In an embodiment the first and second epitopes are on different antigens, e.g., different proteins (or different subunits of a multimeric protein). In an embodiment a bispecific antibody molecule comprises a heavy chain variable domain sequence and a light chain variable domain sequence which have binding specificity for a first epitope and a heavy chain variable domain sequence and a light chain variable domain sequence which have binding specificity for a second epitope. In an embodiment a bispecific antibody molecule comprises a half antibody having binding specificity for a first epitope and a half antibody having binding specificity for a second epitope. In an embodiment a bispecific antibody molecule comprises a half antibody, or fragment thereof, having binding specificity for a first epitope and a half antibody, or fragment thereof, having binding specificity for a second epitope. In an embodiment a bispecific antibody molecule comprises a scFv, or fragment thereof, have binding specificity for a first epitope and a scFv, or fragment thereof, have binding specificity for a second epitope.

[00347] In certain embodiments, the antibody molecule is a multi-specific (*e.g.*, a bispecific or a trispecific) antibody molecule. Protocols for generating bispecific or heterodimeric antibody molecules are known in the art; including but not limited to, for example, the "knob in a hole" approach described in, *e.g.*, US 5731168; the electrostatic steering Fc pairing as described in, *e.g.*, WO 09/089004, WO 06/106905 and WO 2010/129304; Strand Exchange Engineered Domains (SEED) heterodimer formation as described in, *e.g.*, WO 07/110205; Fab arm exchange as described in, *e.g.*, WO 08/119353, WO 2011/131746, and WO 2013/060867; double antibody conjugate, *e.g.*, by antibody cross-linking to generate a bi-specific structure using a heterobifunctional reagent having an amine-reactive group and a sulfhydryl reactive group as described in, *e.g.*, US 4433059; bispecific antibody determinants generated by recombining half antibodies (heavy-light chain pairs or Fabs) from different antibodies through cycle of reduction and oxidation of disulfide bonds between the two heavy chains, as described in, *e.g.*, US 4444878; trifunctional antibodies, *e.g.*, three Fab' fragments cross-linked through

sulfhdryl reactive groups, as described in, *e.g.*, US5273743; biosynthetic binding proteins, *e.g.*, pair of scFvs cross-linked through C-terminal tails preferably through disulfide or amine-reactive chemical cross-linking, as described in, *e.g.*, US5534254; bifunctional antibodies, *e.g.*, Fab fragments with different binding specificities dimerized through leucine zippers (*e.g.*, c-fos and c-jun) that have replaced the constant domain, as described in, *e.g.*, US5582996; bispecific and oligospecific mono-and oligovalent receptors, *e.g.*, VH-CH1 regions of two antibodies (two Fab fragments) linked through a polypeptide spacer between the CH1 region of one antibody and the VH region of the other antibody typically with associated light chains, as described in, *e.g.*, US5591828; bispecific DNA-antibody conjugates, *e.g.*, crosslinking of antibodies or Fab fragments through a double stranded piece of DNA, as described in, *e.g.*, US5635602; bispecific fusion proteins, *e.g.*, an expression construct containing two scFvs with a hydrophilic helical peptide linker between them and a full constant region, as described in, *e.g.*, US5637481; multivalent and multispecific binding proteins, *e.g.*, dimer of polypeptides having first domain with binding region of Ig heavy chain variable region, and second domain with binding region of Ig light chain variable region, generally termed diabodies (higher order structures are also encompassed creating for bispecifc, trispecific, or tetraspecific molecules, as described in, *e.g.*, US5837242; minibody constructs with linked VL and VH chains further connected with peptide spacers to an antibody hinge region and CH3 region, which can be dimerized to form bispecific/multivalent molecules, as described in, *e.g.*, US5837821; VH and VL domains linked with a short peptide linker (*e.g.*, 5 or 10 amino acids) or no linker at all in either orientation, which can form dimers to form bispecific diabodies; trimers and tetramers, as described in, *e.g.*, US5844094; String of VH domains (or VL domains in family members) connected by peptide linkages with crosslinkable groups at the C-terminus futher associated with VL domains to form a series of FVs (or scFvs), as described in, *e.g.*, US5864019; and single chain binding polypeptides with both a VH and a VL domain linked through a peptide linker are combined into multivalent structures through non-covalent or chemical crosslinking to form, *e.g.*, homobivalent, heterobivalent, trivalent, and tetravalent structures using both scFV or diabody type format, as described in, *e.g.*, US5869620. Additional exemplary multispecific and bispecific molecules and methods of making the same are found, for example, in US5910573, US5932448, US5959083, US5989830, US6005079, US6239259, US6294353, US6333396, US6476198, US6511663, US6670453, US6743896, US6809185, US6833441,

US7129330, US7183076, US7521056, US7527787, US7534866, US7612181, US2002004587A1, US2002076406A1, US2002103345A1, US2003207346A1, US2003211078A1, US2004219643A1, US2004220388A1, US2004242847A1, US2005003403A1, US2005004352A1, US2005069552A1, US2005079170A1, US2005100543A1, US2005136049A1, US2005136051A1, US2005163782A1, US2005266425A1, US2006083747A1, US2006120960A1, US2006204493A1, US2006263367A1, US2007004909A1, US2007087381A1, US2007128150A1, US2007141049A1, US2007154901A1, US2007274985A1, US2008050370A1, US2008069820A1, US2008152645A1, US2008171855A1, US2008241884A1, US2008254512A1, US2008260738A1, US2009130106A1, US2009148905A1, US2009155275A1, US2009162359A1, US2009162360A1, US2009175851A1, US2009175867A1, US2009232811A1, US2009234105A1, US2009263392A1, US2009274649A1, EP346087A2, WO0006605A2, WO02072635A2, WO04081051A1, WO06020258A2, WO2007044887A2, WO2007095338A2, WO2007137760A2, WO2008119353A1, WO2009021754A2, WO2009068630A1, WO9103493A1, WO9323537A1, WO9409131A1, WO9412625A2, WO9509917A1, WO9637621A2, WO9964460A1. The contents of the above-referenced applications are incorporated herein by reference in their entireties.

[00348] Within each antibody or antibody fragment (e.g., scFv) of a bispecific antibody molecule, the VH can be upstream or downstream of the VL. In some embodiments, the upstream antibody or antibody fragment (e.g., scFv) is arranged with its VH (VH_1) upstream of its VL (VL_1) and the downstream antibody or antibody fragment (e.g., scFv) is arranged with its VL (VL_2) upstream of its VH (VH_2), such that the overall bispecific antibody molecule has the arrangement VH_1-VL_1-VL_2-VH_2. In other embodiments, the upstream antibody or antibody fragment (e.g., scFv) is arranged with its VL (VL_1) upstream of its VH (VH_1) and the downstream antibody or antibody fragment (e.g., scFv) is arranged with its VH (VH_2) upstream of its VL (VL_2), such that the overall bispecific antibody molecule has the arrangement VL_1-VH_1-VH_2-VL_2. Optionally, a linker is disposed between the two antibodies or antibody fragments (e.g., scFvs), e.g., between VL_1 and VL_2 if the construct is arranged as VH_1-VL_1-VL_2-VH_2, or between VH_1 and VH_2 if the construct is arranged as VL_1-VH_1-VH_2-VL_2. The linker may be a linker as described herein, e.g., a (Gly_4-Ser)n linker, wherein n is 1, 2, 3, 4, 5,

or 6, preferably 4 (SEQ ID NO: 80). In general, the linker between the two scFvs should be long enough to avoid mispairing between the domains of the two scFvs. Optionally, a linker is disposed between the VL and VH of the first scFv. Optionally, a linker is disposed between the VL and VH of the second scFv. In constructs that have multiple linkers, any two or more of the linkers can be the same or different. Accordingly, in some embodiments, a bispecific CAR comprises VLs, VHs, and optionally one or more linkers in an arrangement as described herein.

[00349] In one aspect, the invention provides a chimeric antigen receptor comprising a bispecific antigen binding domain, a transmembrane domain (e.g., as described herein), and an intracellular signaling domain (e.g., as described herein). In another aspect, the invention provides a cell (e.g., a population of cells), e.g., an immune effector cell, e.g., a T cell or NK cell, e.g., as described herein, which is engineered to express (e.g., comprises) a bispecific CAR as described herein. Without being bound by any theory, it is believed that cells expressing such bispecific CARs are useful in the methods and compositions described herein.

[00350] Chimeric TCR

[00351] In one aspect, the antigen binding domains described herein, e.g., the antibodies and antibody fragments, e.g., provided in the Tables herein, can be grafted to one or more constant domain of a T cell receptor ("TCR") chain, for example, a TCR alpha or TCR beta chain, to create an chimeric TCR that binds specifically to a tumor antigen, e.g., a solid tumor antigen or antigen expressed on a tumor associated with TAMs, described herein. Without being bound by theory, it is believed that chimeric TCRs will signal through the TCR complex upon antigen binding. For example, a mesothelin or CD19 scFv or a fragment there of, e.g., a VL domain, or VH domain, as disclosed herein, can be grafted to the constant domain, e.g., at least a portion of the extracellular constant domain, the transmembrane domain and the cytoplasmic domain, of a TCR chain, for example, the TCR alpha chain and/or the TCR beta chain. As another example, the CDRs of an antibody or antibody fragment, e.g., the CDRs of anyantibody or antibody fragment as described in Tables provided herein may be grafted into a TCR alpha and/or beta chain to create a chimeric TCR that binds specifically to a tumor antigen, e.g., a solid tumor antigen or antigen expressed on a tumor associated with TAMs, described herein. For example, the LCDRs disclosed herein may be grafted into the variable domain of a TCR alpha chain and the HCDRs disclosed herein may be grafted to the variable domain of a TCR beta chain, or vice versa. Such chimeric TCRs may be produced by methods known in

the art (For example, Willemsen RA et al, Gene Therapy 2000; 7: 1369–1377; Zhang T et al, Cancer Gene Ther 2004; 11: 487–496; Aggen et al, Gene Ther. 2012 Apr;19(4):365-74).

[00352] Transmembrane domain

[00353] With respect to the transmembrane domain, in various embodiments, a CAR can be designed to comprise a transmembrane domain that is attached to the extracellular domain of the CAR, e.g., the antigen binding domain. A transmembrane domain can include one or more additional amino acids adjacent to the transmembrane region, e.g., one or more amino acid associated with the extracellular region of the protein from which the transmembrane was derived (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 up to 15 amino acids of the extracellular region) and/or one or more additional amino acids associated with the intracellular region of the protein from which the transmembrane protein is derived (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 up to 15 amino acids of the intracellular region). In one aspect, the transmembrane domain is one that is associated with one of the other domains of the CAR, for example, the transmembrane domain is from the same protein as the intracellular signalling domain, e.g., the costimulatory domain. In some instances, the transmembrane domain can be selected or modified by amino acid substitution to avoid binding of such domains to the transmembrane domains of the same or different surface membrane proteins, e.g., to minimize interactions with other members of the receptor complex. In one aspect, the transmembrane domain is capable of homodimerization with another CAR on the cell surface of a CAR-expressing cell. In a different aspect, the amino acid sequence of the transmembrane domain may be modified or substituted so as to minimize interactions with the binding domains of the native binding partner present in the same CAR-expressing cell.

[00354] The transmembrane domain may be derived either from a natural or from a recombinant source. Where the source is natural, the domain may be derived from any membrane-bound or transmembrane protein. In one aspect the transmembrane domain is capable of signaling to the intracellular domain(s) whenever the CAR has bound to a target. A transmembrane domain of particular use in this invention may include at least the transmembrane region(s) of e.g., the alpha, beta or zeta chain of the T-cell receptor, CD28, CD27, CD3 epsilon, CD45, CD4, CD5, CD8, CD9, CD16, CD22, CD33, CD37, CD64, CD80, CD86, CD134, CD137, CD154. In some embodiments, a transmembrane domain may include at least the transmembrane region(s) of, e.g., KIRDS2, OX40, CD2, CD27, LFA-1 (CD11a,

CD18), ICOS (CD278), 4-1BB (CD137), GITR, CD40, BAFFR, HVEM (LIGHTR), SLAMF7, NKp80 (KLRF1), NKp44, NKp30, NKp46, CD160, CD19, IL2R beta, IL2R gamma, IL7R α, ITGA1, VLA1, CD49a, ITGA4, IA4, CD49D, ITGA6, VLA-6, CD49f, ITGAD, CD11d, ITGAE, CD103, ITGAL, CD11a, LFA-1, ITGAM, CD11b, ITGAX, CD11c, ITGB1, CD29, ITGB2, CD18, LFA-1, ITGB7, TNFR2, DNAM1 (CD226), SLAMF4 (CD244, 2B4), CD84, CD96 (Tactile), CEACAM1, CRTAM, Ly9 (CD229), CD160 (BY55), PSGL1, CD100 (SEMA4D), SLAMF6 (NTB-A, Ly108), SLAM (SLAMF1, CD150, IPO-3), BLAME (SLAMF8), SELPLG (CD162), LTBR, PAG/Cbp, NKG2D, NKG2C.

[00355] In some instances, the transmembrane domain can be attached to the extracellular region of the CAR, e.g., the antigen binding domain of the CAR, via a hinge, e.g., a hinge from a human protein. For example, in one embodiment, the hinge can be a human Ig (immunoglobulin) hinge, e.g., an IgG4 hinge, or a CD8a hinge. In one embodiment, the hinge or spacer comprises (e.g., consists of) the amino acid sequence of SEQ ID NO:4. In one aspect, the transmembrane domain comprises (e.g., consists of) a transmembrane domain of SEQ ID NO: 12.

[00356] In one aspect, the hinge or spacer comprises an IgG4 hinge. For example, in one embodiment, the hinge or spacer comprises a hinge of the amino acid sequence SEQ ID NO: 6. In some embodiments, the hinge or spacer comprises a hinge encoded by a nucleotide sequence of SEQ ID NO: 7. In one aspect, the hinge or spacer comprises an IgD hinge. For example, in one embodiment, the hinge or spacer comprises a hinge of the amino acid sequence SEQ ID NO: 8. In some embodiments, the hinge or spacer comprises a hinge encoded by a nucleotide sequence of SEQ ID NO: 9.

[00357] In one aspect, the transmembrane domain may be recombinant, in which case it will comprise predominantly hydrophobic residues such as leucine and valine. In one aspect a triplet of phenylalanine, tryptophan and valine can be found at each end of a recombinant transmembrane domain.

[00358] Optionally, a short oligo- or polypeptide linker, between 2 and 10 amino acids in length may form the linkage between the transmembrane domain and the cytoplasmic region of the CAR. A glycine-serine doublet provides a particularly suitable linker. For example, in one aspect, the linker comprises the amino acid sequence of GGGGSGGGGS (SEQ ID NO:10). In

some embodiments, the linker is encoded by a nucleotide sequence of GGTGGCGGAGGTTCTGGAGGTGGAGGTTCC (SEQ ID NO:11).

[00359] In one aspect, the hinge or spacer comprises a KIR2DS2 hinge.

[00360] Cytoplasmic domain

[00361] The cytoplasmic domain or region of the CAR includes an intracellular signaling domain. An intracellular signaling domain is generally responsible for activation of at least one of the normal effector functions of the immune cell in which the CAR has been introduced. The term “effector function” refers to a specialized function of a cell. Effector function of a T cell, for example, may be cytolytic activity or helper activity including the secretion of cytokines. Thus the term “intracellular signaling domain” refers to the portion of a protein which transduces the effector function signal and directs the cell to perform a specialized function. While usually the entire intracellular signaling domain can be employed, in many cases it is not necessary to use the entire chain. To the extent that a truncated portion of the intracellular signaling domain is used, such truncated portion may be used in place of the intact chain as long as it transduces the effector function signal. The term intracellular signaling domain is thus meant to include any truncated portion of the intracellular signaling domain sufficient to transduce the effector function signal.

[00362] Examples of intracellular signaling domains for use in the CAR of the invention include the cytoplasmic sequences of the T cell receptor (TCR) and co-receptors that act in concert to initiate signal transduction following antigen receptor engagement, as well as any derivative or variant of these sequences and any recombinant sequence that has the same functional capability.

[00363] It is known that signals generated through the TCR alone are insufficient for full activation of the T cell and that a secondary and/or costimulatory signal is also required. Thus, T cell activation can be said to be mediated by two distinct classes of cytoplasmic signaling sequences: those that initiate antigen-dependent primary activation through the TCR (primary intracellular signaling domains) and those that act in an antigen-independent manner to provide a secondary or costimulatory signal (secondary cytoplasmic domain, e.g., a costimulatory domain).

[00364] A primary signaling domain regulates primary activation of the TCR complex either in a stimulatory way, or in an inhibitory way. Primary intracellular signaling domains that act in a stimulatory manner may contain signaling motifs which are known as immunoreceptor tyrosine-based activation motifs or ITAMs.

[00365] Examples of ITAM containing primary intracellular signaling domains that are of particular use in the invention include those of TCR zeta, FcR gamma, FcR beta, CD3 gamma, CD3 delta , CD3 epsilon, CD5, CD22, CD79a, CD79b, CD278 (also known as "ICOS"), FcεRI, DAP10, DAP12,and CD66d. In one embodiment, a CAR of the invention comprises an intracellular signaling domain, e.g., a primary signaling domain of CD3-zeta, e.g., a CD3-zeta sequence described herein.

[00366] In one embodiment, a primary signaling domain comprises a modified ITAM domain, e.g., a mutated ITAM domain which has altered (e.g., increased or decreased) activity as compared to the native ITAM domain. In one embodiment, a primary signaling domain comprises a modified ITAM-containing primary intracellular signaling domain, e.g., an optimized and/or truncated ITAM-containing primary intracellular signaling domain. In an embodiment, a primary signaling domain comprises one, two, three, four or more ITAM motifs.

[00367] The intracellular signaling domain of the CAR can comprise the CD3-zeta signaling domain by itself or it can be combined with any other desired intracellular signaling domain(s) useful in the context of a CAR of the invention. For example, the intracellular signaling domain of the CAR can comprise a CD3 zeta chain portion and a costimulatory signaling domain. The costimulatory signaling domain refers to a portion of the CAR comprising the intracellular domain of a costimulatory molecule. A costimulatory molecule is a cell surface molecule other than an antigen receptor or its ligands that is required for an efficient response of lymphocytes to an antigen. Examples of such molecules include CD27, CD28, 4-1BB (CD137), OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, B7-H3, and a ligand that specifically binds with CD83, and the like. For example, CD27 costimulation has been demonstrated to enhance expansion, effector function, and survival of human CART cells in vitro and augments human T cell persistence and antitumor activity in vivo (Song et al. Blood. 2012; 119(3):696-706). Further examples of such costimulatory molecules include an MHC class I molecule, a TNF receptor protein, an

Immunoglobulin-like protein, a cytokine receptor, an integrin, a signaling lymphocytic activation molecule (SLAM protein), an activating NK cell receptor, BTLA, a Toll ligand receptor, OX40, CD2, CD7, CD27, CD28, CD30, CD40, CDS, ICAM-1, LFA-1 (CD11a/CD18), 4-1BB (CD137), B7-H3, CDS, ICAM-1, ICOS (CD278), GITR, BAFFR, LIGHT, HVEM (LIGHTR), KIRDS2, SLAMF7, NKp80 (KLRF1), NKp44, NKp30, NKp46, CD19, CD4, CD8alpha, CD8beta, IL2R beta, IL2R gamma, IL7R alpha, ITGA4, VLA1, CD49a, ITGA4, IA4, CD49D, ITGA6, VLA-6, CD49f, ITGAD, CD11d, ITGAE, CD103, ITGAL, CD11a, LFA-1, ITGAM, CD11b, ITGAX, CD11c, ITGB1, CD29, ITGB2, CD18, LFA-1, ITGB7, NKG2D, NKG2C, TNFR2, TRANCE/RANKL, DNAM1 (CD226), SLAMF4 (CD244, 2B4), CD84, CD96 (Tactile), CEACAM1, CRTAM, Ly9 (CD229), CD160 (BY55), PSGL1, CD100 (SEMA4D), CD69, SLAMF6 (NTB-A, Ly108), SLAM (SLAMF1, CD150, IPO-3), BLAME (SLAMF8), SELPLG (CD162), LTBR, LAT, GADS, SLP-76, PAG/Cbp, CD19a, and a ligand that specifically binds with CD83.

[00368] The intracellular signaling sequences within the cytoplasmic portion of the CAR of the invention may be linked to each other in a random or specified order. Optionally, a short oligo- or polypeptide linker, for example, between 2 and 10 amino acids (e.g., 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids) in length may form the linkage between intracellular signaling sequence. In one embodiment, a glycine-serine doublet can be used as a suitable linker. In one embodiment, a single amino acid, e.g., an alanine, a glycine, can be used as a suitable linker.

[00369] In one aspect, the intracellular signaling domain is designed to comprise two or more, e.g., 2, 3, 4, 5, or more, costimulatory signaling domains. In an embodiment, the two or more, e.g., 2, 3, 4, 5, or more, costimulatory signaling domains, are separated by a linker molecule, e.g., a linker molecule described herein. In one embodiment, the intracellular signaling domain comprises two costimulatory signaling domains. In some embodiments, the linker molecule is a glycine residue. In some embodiments, the linker is an alanine residue.

[00370] In one aspect, the intracellular signaling domain is designed to comprise the signaling domain of CD3-zeta and the signaling domain of CD28. In one aspect, the intracellular signaling domain is designed to comprise the signaling domain of CD3-zeta and the signaling domain of 4-1BB. In one aspect, the signaling domain of 4-1BB is a signaling domain of SEQ ID NO: 14. In one aspect, the signaling domain of CD3-zeta is a signaling domain of SEQ ID NO: 18.

[00371] In one aspect, the intracellular signaling domain is designed to comprise the signaling domain of CD3-zeta and the signaling domain of CD27. In one aspect, the signaling domain of CD27 comprises an amino acid sequence of SEQ ID NO:16. In one aspect, the signalling domain of CD27 is encoded by a nucleic acid sequence of SEQ ID NO:17.

[00372] In one aspect, the intracellular is designed to comprise the signaling domain of CD3-zeta and the signaling domain of CD28. In one aspect, the signaling domain of CD28 comprises an amino acid sequence of SEQ ID NO: 44. In one aspect, the signaling domain of CD28 is encoded by a nucleic acid sequence of SEQ ID NO: 45.

[00373] In one aspect, the intracellular is designed to comprise the signaling domain of CD3-zeta and the signaling domain of ICOS. In one aspect, the signaling domain of ICOS comprises an amino acid sequence of SEQ ID NO: 42. In one aspect, the signaling domain of ICOS is encoded by a nucleic acid sequence of SEQ ID NO: 43.

[00374] In one aspect, the cell of the invention, e.g., described herein, e.g., a cell expressing a CAR described herein, includes a CAR that includes an antigen binding domain that binds a target tumor antigen described herein (e.g., a solid tumor antigen or antigen expressed on a tumor associated with MDSCs or TAMs), a transmembrane domain, a primary signaling domain, and one or more (e.g., one) costimulatory signaling domain.

[00375] In one embodiment, the CAR-expressing cell may further comprise an inhibitory CAR. In one embodiment, the inhibitory CAR comprises an antigen binding domain that binds an antigen found on normal cells but not cancer cells, e.g., normal cells that also express the tumor antigen targeted by the CAR. In one embodiment, the inhibitory CAR comprises the antigen binding domain, a transmembrane domain and an intracellular domain of an inhibitory molecule. For example, the intracellular domain of the inhibitory CAR can be an intracellular domain of PD1, PD-L1, CTLA4, TIM3, LAG3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4, CD80, CD86, B7-H3 (CD276), B7-H4 (VTCN1), HVEM (TNFRSF14 or CD270), KIR, A2aR, MHC class I, MHC class II, GAL9, adenosine, or TGF beta.

[00376] In one embodiment, the antigen binding domains of the CARs can be such that the antigen binding domains do not interact with one another. For example, a cell expressing a first and second CAR can have an antigen binding domain of the first CAR, e.g., as a fragment, e.g.,

an scFv, that does not form an association with the antigen binding domain of the second CAR, e.g., the antigen binding domain of the second CAR is a VHH.

[00377] In some embodiments, the antigen binding domain comprises a single domain antigen binding (SDAB) molecules include molecules whose complementary determining regions are part of a single domain polypeptide. Examples include, but are not limited to, heavy chain variable domains, binding molecules naturally devoid of light chains, single domains derived from conventional 4-chain antibodies, engineered domains and single domain scaffolds other than those derived from antibodies. SDAB molecules may be any of the art, or any future single domain molecules. SDAB molecules may be derived from any species including, but not limited to mouse, human, camel, llama, lamprey, fish, shark, goat, rabbit, and bovine. This term also includes naturally occurring single domain antibody molecules from species other than Camelidae and sharks.

[00378] In one aspect, an SDAB molecule can be derived from a variable region of the immunoglobulin found in fish, such as, for example, that which is derived from the immunoglobulin isotype known as Novel Antigen Receptor (NAR) found in the serum of shark. Methods of producing single domain molecules derived from a variable region of NAR ("IgNARs") are described in WO 03/014161 and Streltsov (2005) Protein Sci. 14:2901-2909.

[00379] According to another aspect, an SDAB molecule is a naturally occurring single domain antigen binding molecule known as heavy chain devoid of light chains. Such single domain molecules are disclosed in WO 9404678 and Hamers-Casterman, C. et al. (1993) Nature 363:446-448, for example. For clarity reasons, this variable domain derived from a heavy chain molecule naturally devoid of light chain is known herein as a VHH or nanobody to distinguish it from the conventional VH of four chain immunoglobulins. Such a VHH molecule can be derived from Camelidae species, for example in camel, llama, dromedary, alpaca and guanaco. Other species besides Camelidae may produce heavy chain molecules naturally devoid of light chain; such VHHs are within the scope of the invention.

[00380] The SDAB molecules can be recombinant, CDR-grafted, humanized, camelized, de-immunized and/or in vitro generated (e.g., selected by phage display).

[00381] It has also been discovered, that cells having a plurality of chimeric membrane embedded receptors comprising an antigen binding domain that interactions between the

DEMANDE OU BREVET VOLUMINEUX

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

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JUMBO APPLICATIONS/PATENTS

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NOTE POUR LE TOME / VOLUME NOTE:

What is claimed is:

1. A CAR therapy comprising a cell, e.g., a population of immune effector cells, comprising, e.g., expressing, a chimeric antigen receptor (CAR) for use in combination with an inhibitor of a pro-M2 macrophage molecule in treating a subject having a disease associated with expression of a tumor antigen, wherein the CAR comprises a tumor antigen binding domain, a transmembrane domain, and an intracellular signaling domain.

2. A method of treating a subject having a disease associated with expression of a tumor antigen, comprising administering to the subject:

(i) a CAR therapy comprising a cell, e.g., a population of immune effector cells, comprising, e.g., expressing, a chimeric antigen receptor (CAR), wherein the CAR comprises a tumor antigen binding domain, a transmembrane domain, and an intracellular signaling domain; and

(ii) an inhibitor of a pro-M2 macrophage molecule.

3. The CAR therapy for use or the method of claim 1 or 2, wherein the CAR therapy and the inhibitor of a pro-M2 macrophage molecule are administered sequentially.

4. The CAR therapy for use or the method of any of claims 1-3, wherein the inhibitor of a pro-M2 macrophage molecule is administered prior to the CAR therapy.

5. The CAR therapy for use or the method of any of claims 1-4, wherein the inhibitor of a pro-M2 macrophage molecule and the CAR therapy are administered simultaneously or concurrently.

6. The CAR therapy for use or the method of any of claims 1-5, wherein the CAR therapy is administered as (a) single infusion or (b) multiple infusions (e.g., a single dose split into multiple infusions), and wherein the inhibitor of a pro-M2 macrophage molecule is administered as (a) a single dose, or (b) multiple doses (e.g., a first and second, and optionally one or more subsequent doses).

7. The CAR therapy for use or the method of any of claims 1-6, wherein a dose of the CAR therapy is administered after (e.g., at least 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 1 week, 2 weeks, 3 weeks, 4 weeks, 5 weeks, or more, after) administration of a first dose of the inhibitor of a pro-M2 macrophage molecule, e.g., but before administration of the second dose of the inhibitor.

8. The CAR therapy for use or the method of claims 1 or 5, wherein a dose of the CAR therapy is administered concurrently with (e.g., within 2 days (e.g., within 2 days, 1 day, 24 hours, 12 hours, 6 hours, 4 hours, 2 hours, or less) of), the administration of a first dose of the inhibitor of a pro-M2 macrophage molecule.

9. The CAR therapy for use or the method of any of claims 6-8, wherein one or more subsequent doses of the inhibitor of a pro-M2 macrophage molecule are administered after a second dose of the inhibitor of a pro-M2 macrophage molecule.

10. The CAR therapy for use or the method of any of claims 1-9, wherein the inhibitor of a pro-M2 macrophage molecule is administered in more than one dose, and the doses are administered twice a day (BID), once a day, once a week, once every 14 days, or once every month.

11. The CAR therapy for use or the method of any of claims 1-10, wherein the administering of the inhibitor of a pro-M2 macrophage molecule comprises multiple doses comprising a duration of at least 7 days, e.g., at least 7 days, 8 days, 9 days, 10 days, 1 week, 2 weeks, 3 weeks, 4 weeks, 5 weeks, 6 weeks, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, or more.

12. The CAR therapy for use or the method of any of claims 1-11, wherein the CAR therapy is administered at a dose comprising at least about 5 x 10^6, 1 x 10^7, 1.5 x 10^7, 2 x 10^7, 2.5 x 10^7, 3 x 10^7, 3.5 x 10^7, 4 x 10^7, 5 x 10^7, 1 x 10^8, 1.5 x 10^8, 2 x 10^8, 2.5 x 10^8, 3 x 10^8, 3.5 x 10^8, 4 x 10^8, 5 x 10^8, 1 x 10^9, 2 x 10^9, or 5 x 10^9 cells, e.g., CAR positive cells.

13. The CAR therapy for use or the method of any of claims 1-12, wherein the inhibitor of a pro-M2 macrophage molecule is an IL-13 inhibitor, an IL-4 inhibitor, an IL-13Rα1 inhibitor, an IL-4Rα inhibitor, an IL-10 inhibitor, a CSF-1 inhibitor, a TGF beta inhibitor, a JAK2 inhibitor, a cell surface molecule, an iron oxide, a small molecule inhibitor, a PI3K inhibitor, an HDAC inhibitor, an inhibitor of the glycolytic pathway, a mitochondria-targeted antioxidant, or combinations thereof.

14. The CAR therapy for use or the method of claim 13, wherein the inhibitor of a pro-M2 macrophage molecule is a small molecule, an antibody or antigen-binding fragment thereof, a protein (e.g., a fusion protein), a nucleic acid (e.g., an shRNA or siRNA), or a gene editing system.

15. The CAR therapy for use or the method of claim 13, wherein the inhibitor of a pro-M2 macrophage molecule is an antibody or antigen-binding fragment thereof.

16. The CAR therapy for use or the method of any of claims 1-15, wherein the tumor antigen binding domain of the CAR binds CD123.

17. A CAR therapy comprising a cell, e.g., a population of immune effector cells, comprising, e.g., expressing, a chimeric antigen receptor (CAR) for use in combination with a tumor targeting therapy in treating a subject having a disease associated with expression of a tumor antigen, wherein:

(i) the CAR comprises a tumor antigen binding domain that binds CD123 (CD123 CAR), a transmembrane domain, and an intracellular signaling domain; and

(ii) the tumor targeting therapy comprises a second CAR therapy that comprises a cell, e.g., a population of immune effector cells, compring, e.g., expressing, a CAR comprising a tumor antigen binding domain that binds to a tumor antigen other than CD123 (e.g., a CAR that binds to a solid tumor antigen or a hematologic tumor antigen other than CD123),

wherein the CD123 CAR is administered in an amount and/or time sufficient to result in inhibition of an M2 macrophage activity.

18. A method of treating a subject having a disease associated with expression of a tumor antigen, comprising administering to the subject:

(i) a CAR therapy comprising a cell, e.g., a population of immune effector cells, comprising, e.g., expressing, a chimeric antigen receptor (CAR), wherein the CAR comprises a tumor antigen binding domain that binds CD123 (CD123 CAR), a transmembrane domain, and an intracellular signaling domain; and

(ii) a tumor targeting therapy, wherein the tumor targeting therapy comprises a second CAR therapy that comprises a cell, e.g., a population of immune effector cells, compring, e.g., expressing, a CAR comprising a tumor antigen binding domain that binds to a tumor antigen other than CD123 (e.g., a CAR that binds to a solid tumor antigen or a hematologic tumor antigen other than CD123),

wherein the CD123 CAR is administered in an amount and/or time sufficient to result in inhibition of an M2 macrophage activity.

.

19. The CAR therapy for use or the method of claim 17 or 18, wherein the inhibition of the M2 macrophage activity comprises inhibition of polarization of a macrophage to an M2 phenotype, and/or reversal of a phenotype of an M2 macrophage.

20. The CAR therapy for use of any of claims 17-19, wherein the tumor antigen binding domain of the second CAR therapy binds to CD19, mesothelin, or EGFRviii.

21. The CAR therapy for use or the method of any of claims 16-20, wherein the tumor antigen binding domain of the CAR that binds to CD123 comprises a heavy chain complementary determining region 1 (HC CDR1), a heavy chain complementary determining region 2 (HC CDR2), and a heavy chain complementary determining region 3 (HC CDR3) of any CD123 heavy chain binding domain amino acid sequence listed in Table 16, Table 18, Table 20, Table 22, Table 24, Table 25, Table 26, Table 27 or Table 28; and

a light chain complementary determining region 1 (LC CDR1), a light chain complementary determining region 2 (LC CDR2), and a light chain complementary determining region 3 (LC CDR3) of any CD123 light chain binding domain amino acid sequence listed in Table 17, Table 19, Table 21, Table 23, Table 24, Table 25, Table 26, Table 27 or Table 28.

22. The CAR therapy for use or the method of any of claims 16-21, wherein the CD123 binding domain comprises a CD123 binding domain (e.g., scFv) amino acid sequence listed in Table 26, Table 27 or Table 28.

23. The CAR therapy for use or the method of any of claims 16-22, wherein the CAR comprises (e.g., consists of) a CAR amino acid sequence listed in Table 26 or Table 27.

24. The CAR therapy for use or the method of any of claims 1-15, 17, or 18, wherein the tumor antigen binding domain of the CAR binds mesothelin.

25. The CAR therapy for use or the method of claim 24, wherein the tumor antigen binding domain of the CAR comprises a heavy chain complementary determining region 1 (HC CDR1), a heavy chain complementary determining region 2 (HC CDR2), and a heavy chain complementary determining region 3 (HC CDR3) of any mesothelin heavy chain binding domain amino acid sequence listed in Table 2, Table 3 or Table 11; and

a light chain complementary determining region 1 (LC CDR1), a light chain complementary determining region 2 (LC CDR2), and a light chain complementary determining region 3 (LC CDR3) of any mesothelin light chain binding domain amino acid sequence listed in Table 2, Table 4 or Table 11.

26. The CAR therapy for use or the method of claim 24 or 25, wherein the mesothelin binding domain comprises a mesothelin binding domain (e.g., scFv) amino acid sequence listed in Table 2 or Table 11.

27. The CAR therapy for use or the method of any of claims 24-26, wherein the CAR comprises (e.g., consists of) a CAR amino acid sequence listed in Table 11.

28. The CAR therapy for use or the method of any of claims 1-15, 17, or 18, wherein the tumor antigen binding domain of the CAR binds EGFRvIII.

29. The CAR therapy for use or the method of claim 28, wherein the tumor antigen binding domain of the CAR comprises a heavy chain complementary determining region 1 (HC CDR1), a heavy chain complementary determining region 2 (HC CDR2), and a heavy chain complementary determining region 3 (HC CDR3) of any EGFRvIII heavy chain binding domain amino acid sequence listed in Table 5; and

a light chain complementary determining region 1 (LC CDR1), a light chain complementary determining region 2 (LC CDR2), and a light chain complementary determining region 3 (LC CDR3) of any EGFRvIII light chain binding domain amino acid sequence listed in Table 5.

30. The CAR therapy for use or the method of claim 28 or 29, wherein the EGFRvIII binding domain comprises a EGFRvIII binding domain (e.g., scFv) amino acid sequence listed in Table 5.

31. The CAR therapy for use or the method of any of claims 28-30, wherein the CAR comprises (e.g., consists of) a CAR amino acid sequence listed in Table 30.

32. The CAR therapy for use or the method of claims 1-15, 17, or 18, wherein the tumor antigen binding domain of the CAR binds CD19.

33. The CAR therapy for use or the method of claim 32, wherein the tumor antigen binding domain of the CAR comprises a heavy chain complementary determining region 1 (HC CDR1), a heavy chain complementary determining region 2 (HC CDR2), and a heavy chain complementary determining region 3 (HC CDR3) of any CD19 heavy chain binding domain amino acid sequence listed in Table 6, Table 7, or Table 9; and

a light chain complementary determining region 1 (LC CDR1), a light chain complementary determining region 2 (LC CDR2), and a light chain complementary determining region 3 (LC CDR3) of any CD19 light chain binding domain amino acid sequence listed in Table 6, Table 8, or Table 9.

34. The CAR therapy for use or the method of claim 32 or 33, wherein the CD19 binding domain comprises a CD19 binding domain (e.g., scFv) amino acid sequence listed in Table 6 or Table 9.

35. The CAR therapy for use or the method of any of claims 32-34, wherein the CD19 binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 83; SEQ ID NO: 84, SEQ ID NO: 85; SEQ ID NO: 86; SEQ ID NO: 87; SEQ ID NO: 88; SEQ ID NO: 89, SEQ ID NO: 90, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, and SEQ ID NO: 112.

36. The CAR therapy for use or the method of any of the preceding claims, wherein the tumor antigen binding domain of the CAR binds a solid tumor antigen.

37. The CAR therapy for use or the method of any of the preceding claims, wherein the tumor antigen binding domain of the CAR binds an antigen expressed on a tumor associated with tumor-associated macrophages (TAMs) and/or myeloid derived suppressor cells (MDSCs).

38. The CAR therapy for use or the method of claim 36 or 37, wherein the solid tumor antigen or the antigen expressed on a tumor associated with tumor-associated macrophages (TAMs) and/or myeloid derived suppressor cells (MDSCs) is CD123, EGFRvIII, mesothelin, GD2, Tn antigen, sTn antigen, Tn-O-Glycopeptides, sTn-O-Glycopeptides, PSMA, CD97, TAG72, CD44v6, CEA, EPCAM, KIT, IL-13Ra2, leguman, GD3, CD171, IL-11Ra, PSCA, MAD-CT-1, MAD-CT-2, VEGFR2, LewisY, CD24, PDGFR-beta, SSEA-4, folate receptor alpha, ERBBs (e.g., ERBB2), Her2/neu, MUC1, EGFR, NCAM, Ephrin B2, CAIX, LMP2, sLe, HMWMAA, o-acetyl-GD2, folate receptor beta, TEM1/CD248, TEM7R, FAP, Legumain, HPV E6 or E7, ML-IAP, CLDN6, TSHR, GPRC5D, ALK, Polysialic acid, Fos-related antigen, neutrophil elastase, TRP-2, CYP1B1, sperm protein 17, beta human chorionic gonadotropin, AFP, thyroglobulin, PLAC1, globoH, RAGE1, MN-CA IX, human telomerase reverse transcriptase, intestinal carboxyl esterase, mut hsp 70-2, NA-17, NY-BR-1, UPK2, HAVCR1, ADRB3,

PANX3, NY-ESO-1, GPR20, Ly6k, OR51E2, TARP, GFRα4, or a peptide of any of these antigens presented on MHC.

39. The CAR therapy for use or the method of any of the preceding claims, wherein the intracellular signaling domain comprises a primary signaling domain comprising a CD3-zeta stimulatory domain.

40. The CAR therapy for use or the method of any of the preceding claims, wherein the intracellular signaling domain comprises a costimulatory domain which is an intracellular domain of a costimulatory protein selected from the group consisting of CD27, CD28, 4-1BB (CD137), OX40, GITR, CD30, CD40, ICOS, BAFFR, HVEM, ICAM-1, lymphocyte function-associated antigen-1 (LFA-1), CD2, CDS, CD7, CD287, LIGHT, NKG2C, NKG2D, SLAMF7, NKp80, NKp30, NKp44, NKp46, CD160, B7-H3, and a ligand that specifically binds with CD83.

41. The CAR therapy for use or the method of claim 40, wherein the costimulatory domain comprises an intracellular domain of 4-1BB.

42. The CAR therapy for use or the method of claim 40, wherein the costimulatory domain comprises an intracellular domain of CD28.

43. The CAR therapy for use or the method of any of claims 40-42, wherein the intracellular signaling domain comprises two costimulatory domains, e.g., a 4-1BB costimulatory domain and a CD28 costimulatory domain.

44. The CAR therapy for use or the method of any of the preceding claims, wherein the disease associated with expression of a tumor antigen is cancer.

45. The method of claim 44, wherein the cancer is Hodgkin lymphoma.

46. The method of claim 44, wherein the cancer is a solid cancer.

47. The CAR therapy for use or the method of any of the preceding claims, wherein the cell comprising a CAR comprises a nucleic acid encoding the CAR.

48. The CAR therapy for use or the method of claim 47, wherein the nucleic acid encoding the CAR is a lentiviral vector.

49. The CAR therapy for use or the method of claim 47 or 48, wherein the nucleic acid encoding the CAR is introduced into the cells by lentiviral transduction.

50. The CAR therapy for use or the method of any of claims 47-49, wherein the nucleic acid encoding the CAR is an RNA, e.g., an in vitro transcribed RNA.

51. The CAR therapy for use or the method of any of claims 47-50, wherein the nucleic acid encoding the CAR is introduced into the cells by electroporation.

52. The CAR therapy for use or the method of any of claims 1-51, wherein the cell is a T cell or an NK cell.

53. The CAR therapy for use or the method of claim 52, wherein the T cell is an autologous or allogeneic T cell.

54. The CAR therapy for use or the method of any of claims 1-53, wherein the subject is a mammal, e.g., a human.

55. The CAR therapy for use or the method of claims 17-54, wherein the CD123 CAR therapy and the tumor targeting therapy are administered sequentially, simultaneously, or concurrently.

56. The CAR therapy for use or the method of claims 17-55, wherein the CD123 CAR therapy is administered prior to the tumor targeting therapy.

57. The CAR therapy for use or the method of claim 56, wherein the CD123 CAR therapy is administered at least 5 days, at least 7 days, at least 10 days, at least 15 days, at least 20 days, at least 1 month, at least 2 months, at least 3 months, at least 4 months, at least 5 months, at least 6 months, at least 7 months, at least 8 months, at least 9 months or at least 10 months, prior to administration of the tumor targeting therapy. .

58. The CAR therapy for use or the method of claims 17-57, wherein the CD123 CAR therapy is administered as (a) a single infusion or (b) multiple infusions (e.g., a single dose split into multiple infusions), and wherein the tumor targeting therapy is administered as (a) a single dose, or (b) multiple doses (e.g., a first and second, and optionally one or more subsequent doses).

59. The CAR therapy for use or the method of claims 17-58, wherein the CAR therapy or the tumor targeting therapy is administered at a dose comprising at least about 5×10^6, 1×10^7, 1.5×10^7, 2×10^7, 2.5×10^7, 3×10^7, 3.5×10^7, 4×10^7, 5×10^7, 1×10^8, 1.5×10^8, 2×10^8, 2.5×10^8, 3×10^8, 3.5×10^8, 4×10^8, 5×10^8, 1×10^9, 2×10^9, or 5×10^9 cells, e.g., CAR positive cells.

60. The CAR therapy for use or the method of claims 17-60, wherein the CAR therapy and the tumor targeting therapy are formulated in a pharmaceutical composition.

61. A pharmaceutical composition comprising (i) a cell, e.g., a population of immune effector cells, comprising, e.g., expressing, a chimeric antigen receptor (CAR), wherein the CAR comprises a tumor antigen binding domain, a transmembrane domain, and an intracellular signaling domain; and (ii) an inhibitor of a pro-M2 macrophage molecule.

62. A pharmaceutical composition comprising (i) a cell, e.g., a population of immune effector cells, comprising, e.g., expressing, a chimeric antigen receptor (CAR), wherein the CAR comprises a tumor antigen binding domain, a transmembrane domain, and an intracellular signaling domain; and (ii) an inhibitor of a pro-M2 macrophage molecule for use in treating a disease or disorder.

63 A method for stimulating a T cell-mediated immune response to a solid tumor cell in a mammal, the method comprising administering to a mammal an effective amount of the composition of claim 61.

64. A method of providing an anti-solid tumor immunity in a mammal, comprising administering to the mammal an effective amount of the composition of claim 61.

65. A method of treating a mammal having a disease associated with expression of a solid tumor antigen, said method comprising administering an effective amount of the composition of claim 61.

66. The method of any of claims 63-65, wherein the cell, e.g., the population of immune effector cells, and the inhibitor of a pro-M2 macrophage molecule are provided for separate administration (e.g., in two separate compositions).

67. The method of any of claims 63-65, wherein the cell, e.g., the population of immune effector cells, and the inhibitor of a pro-M2 macrophage molecule are provided for simultaneous administration (e.g., in one composition).

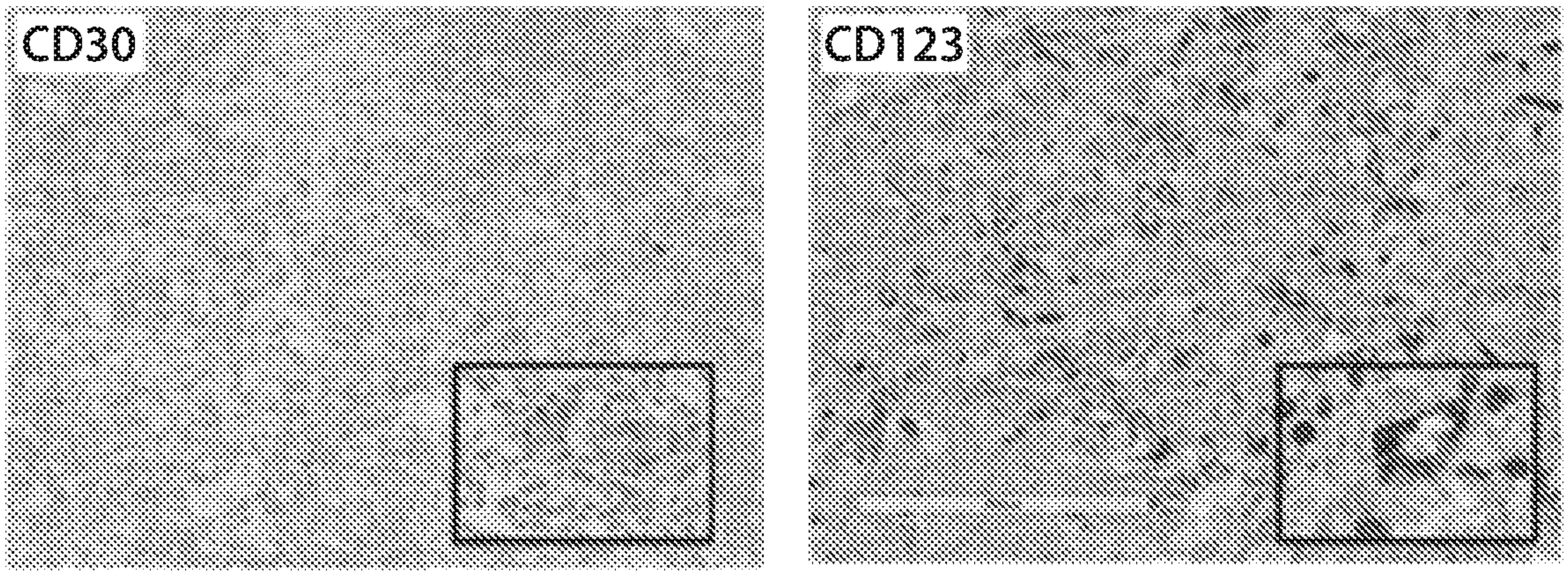
CD30
CD123

FIG. 1A

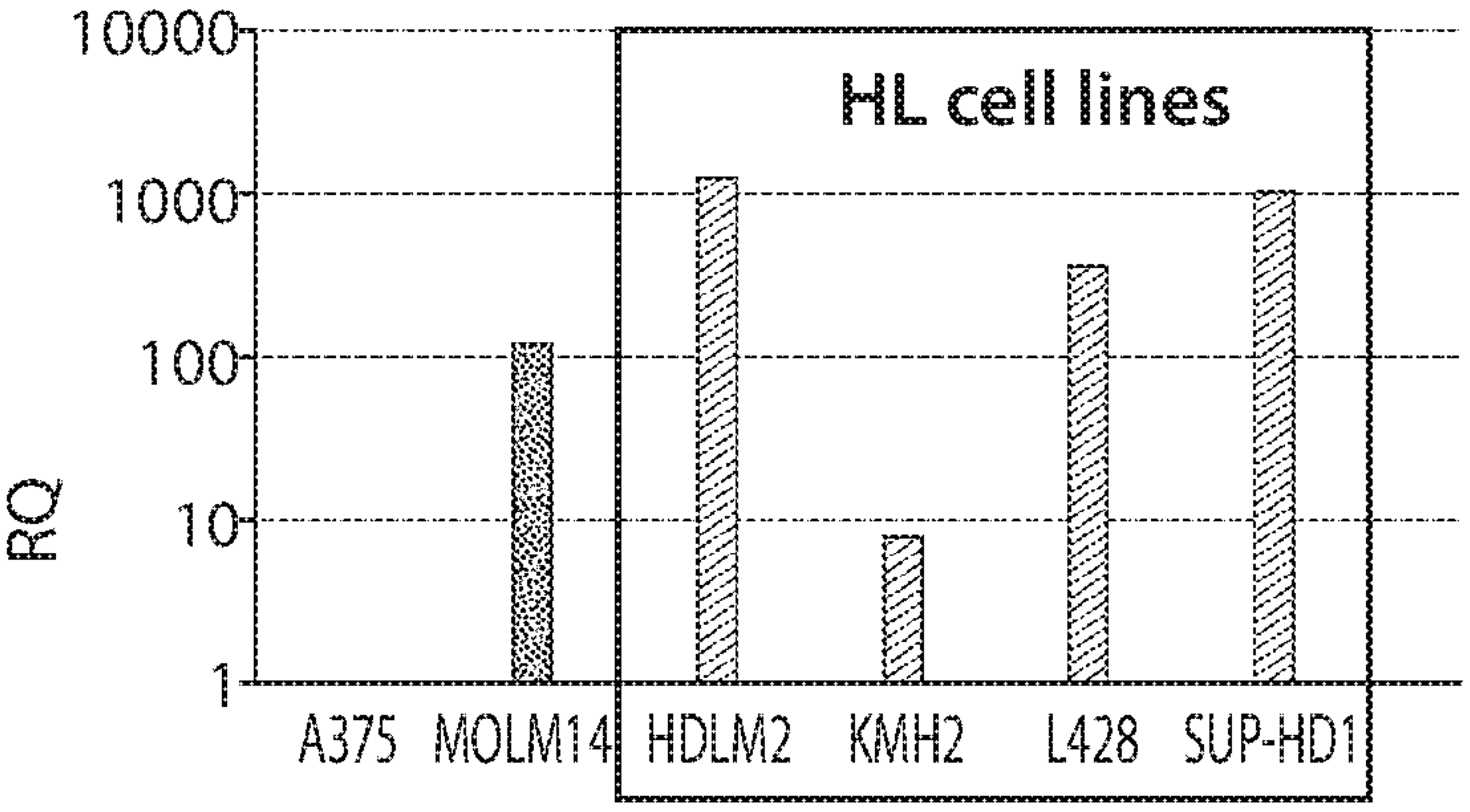
10000
1000
100
10
1
RQ
HL cell lines
A375
MOLM14
HDLM2
KMH2
L428
SUP-HD1

FIG. 1B

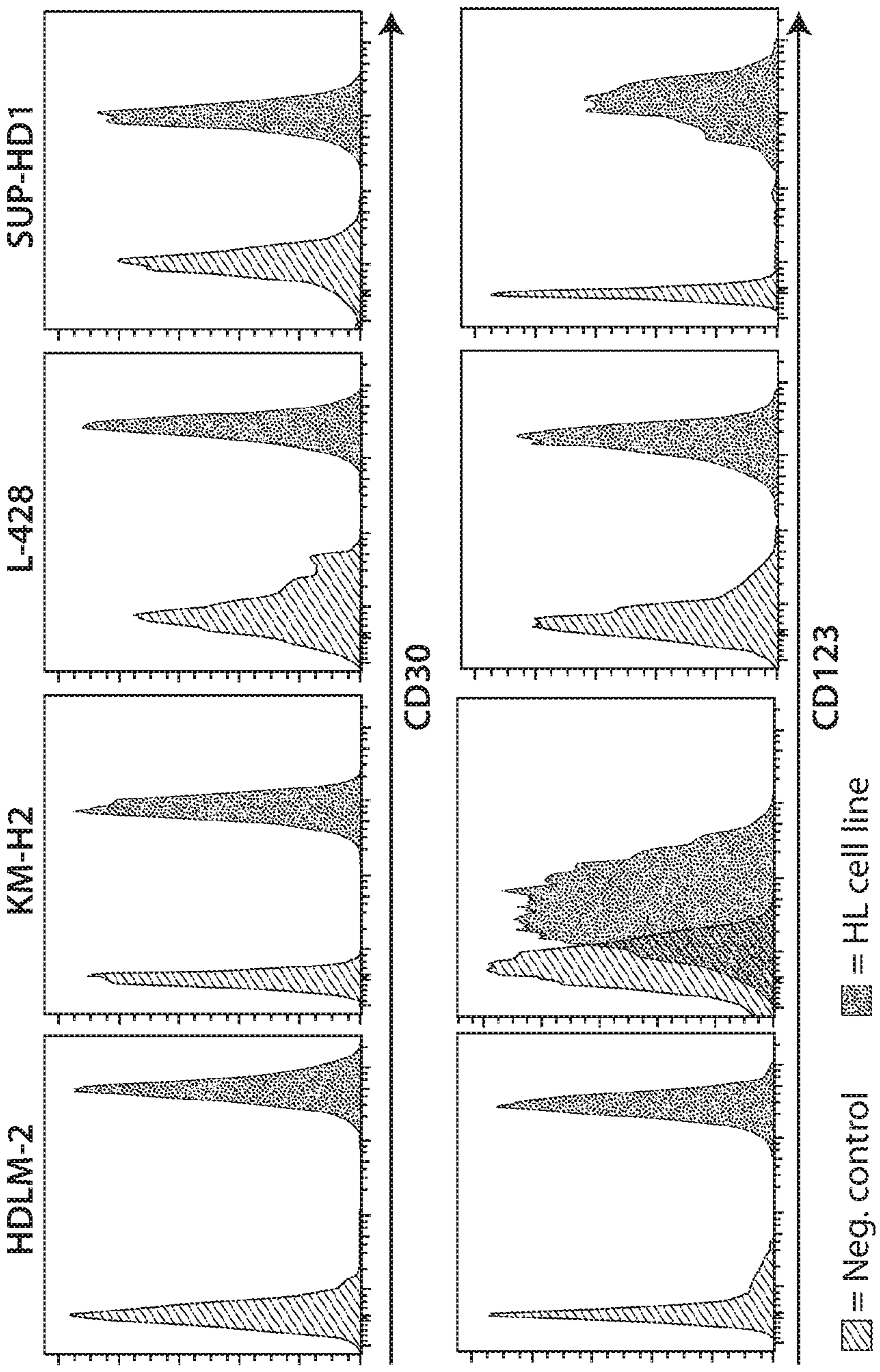

FIG. 1C

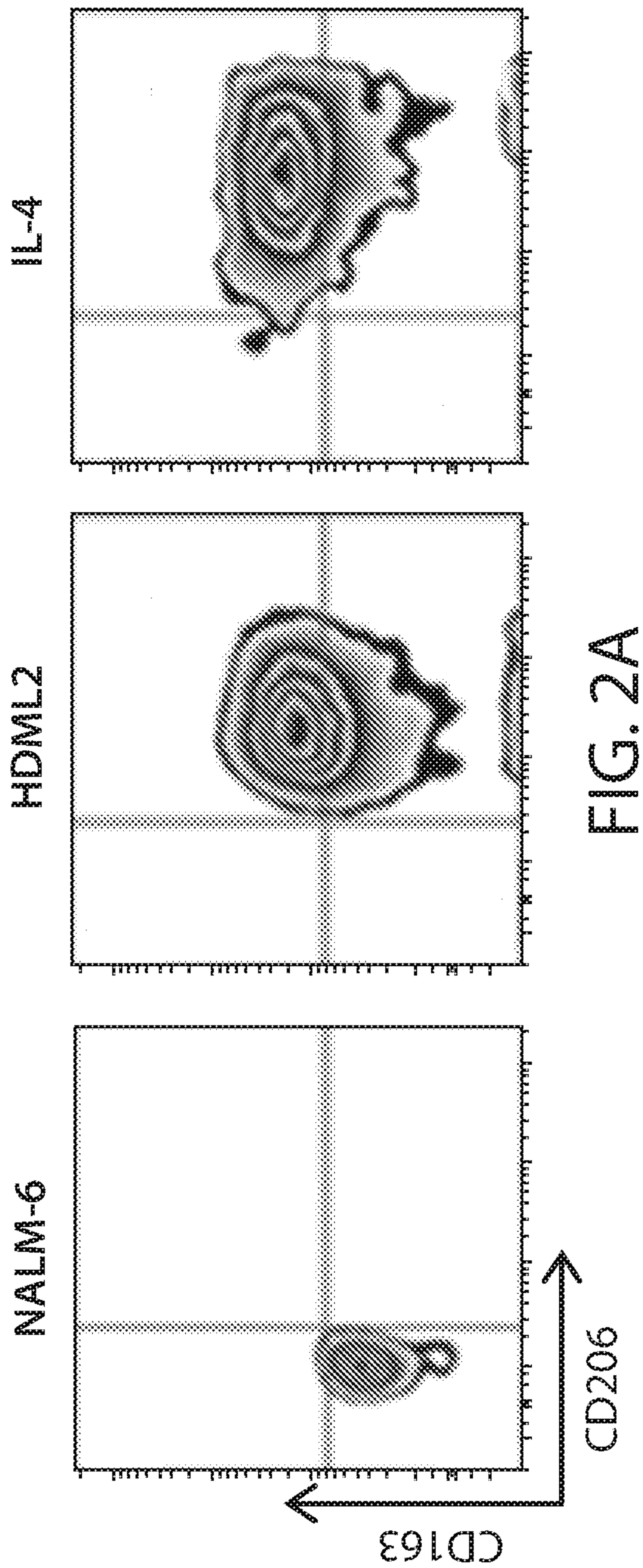

FIG. 2A

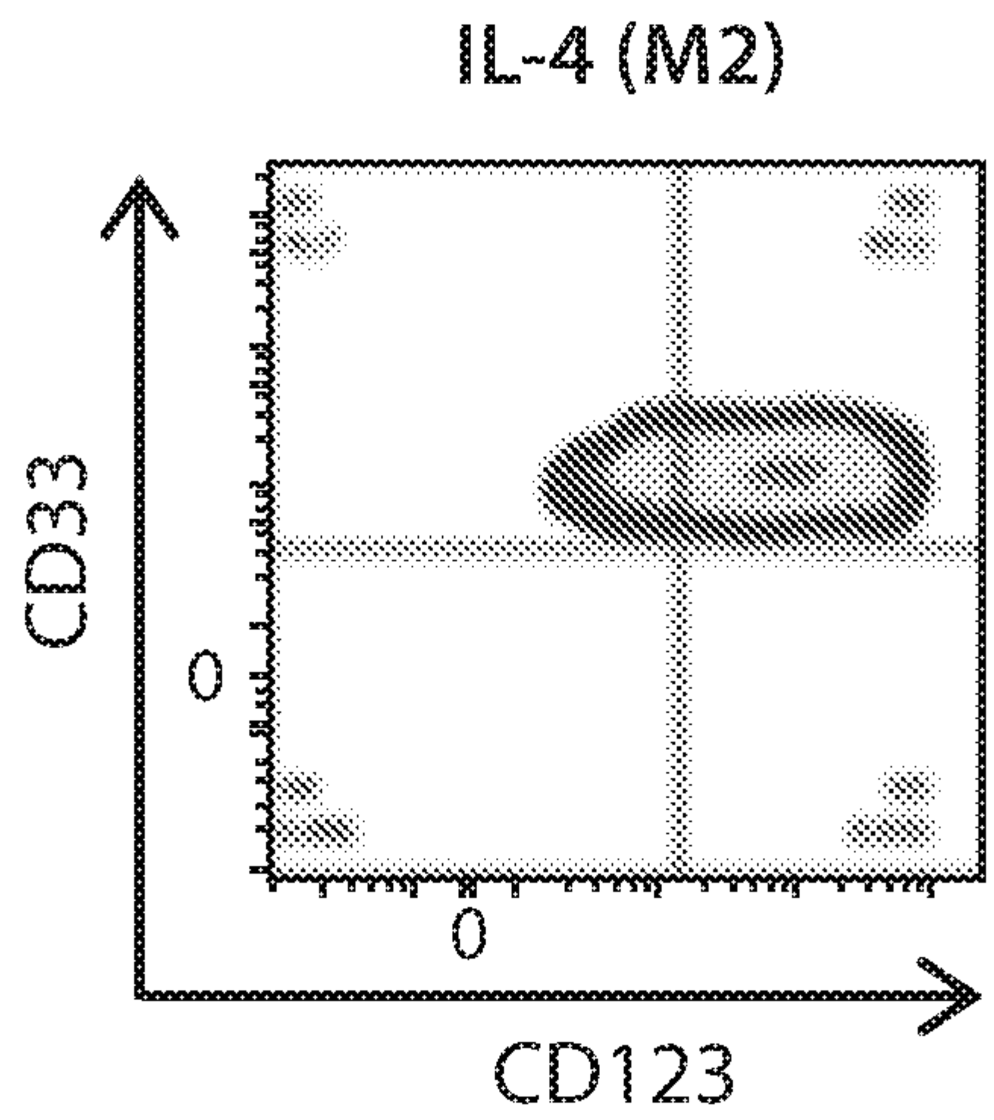
IL-4 (M2)
CD33
0
0
CD123

FIG. 2B

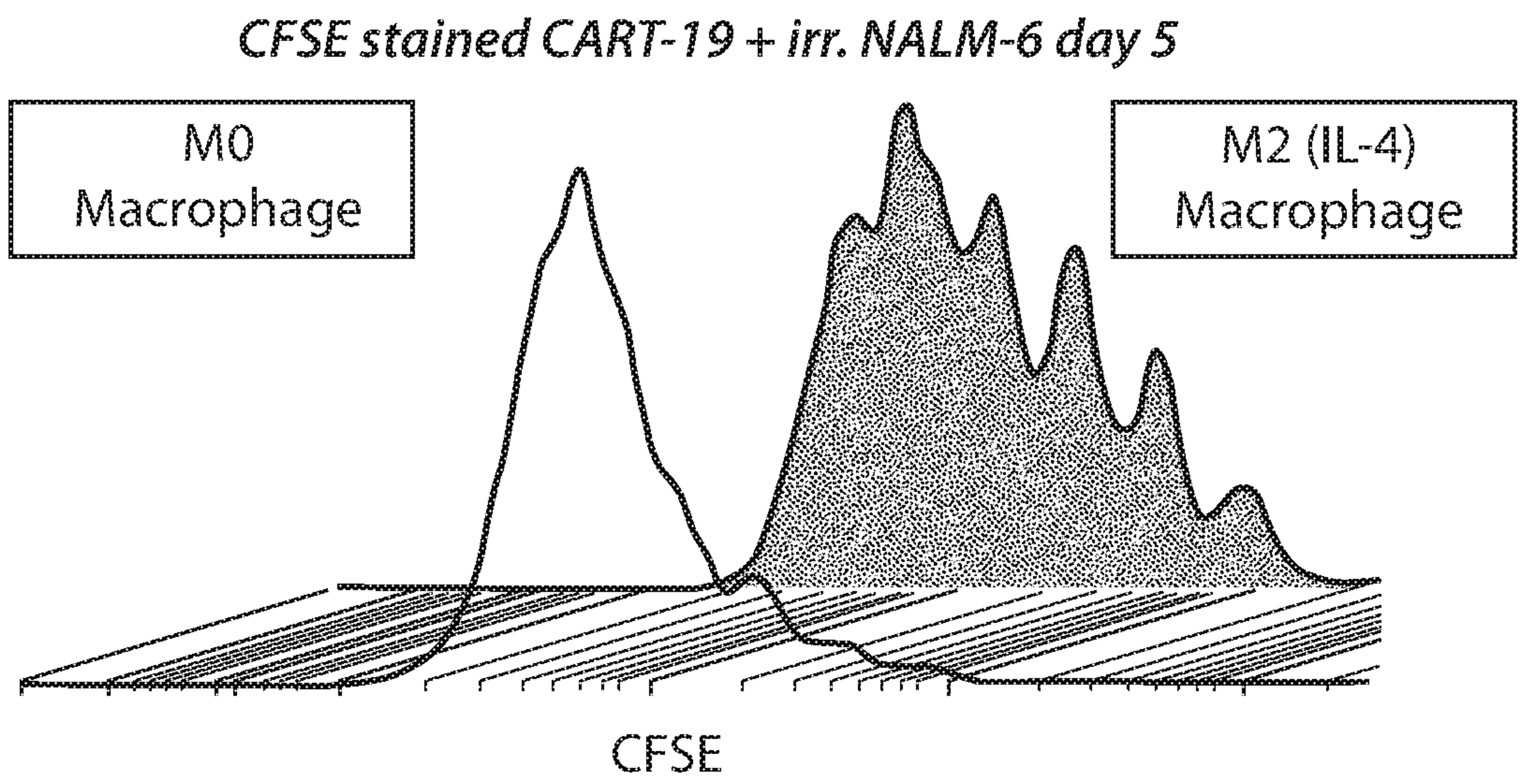
CFSE stained CART-19 + irr. NALM-6 day 5
M0
Macrophage
M2 (IL-4)
Macrophage
CFSE

FIG. 2C

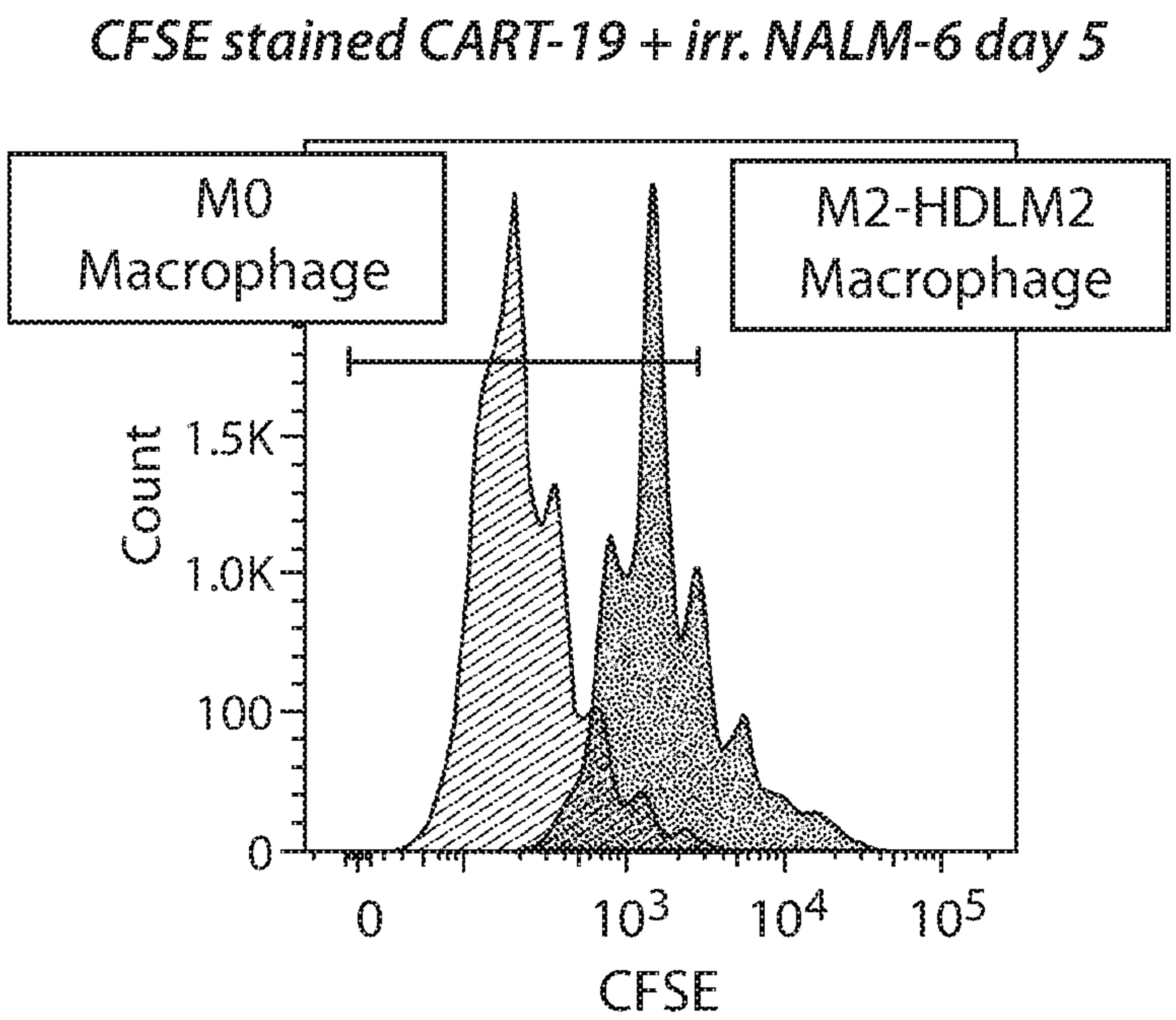
CFSE stained CART-19 + irr. NALM-6 day 5
M0
Macrophage
M2-HDLM2
Macrophage
Count
1.5K
1.0K
100
0
0
10^3
10^4
10^5
CFSE

FIG. 2D

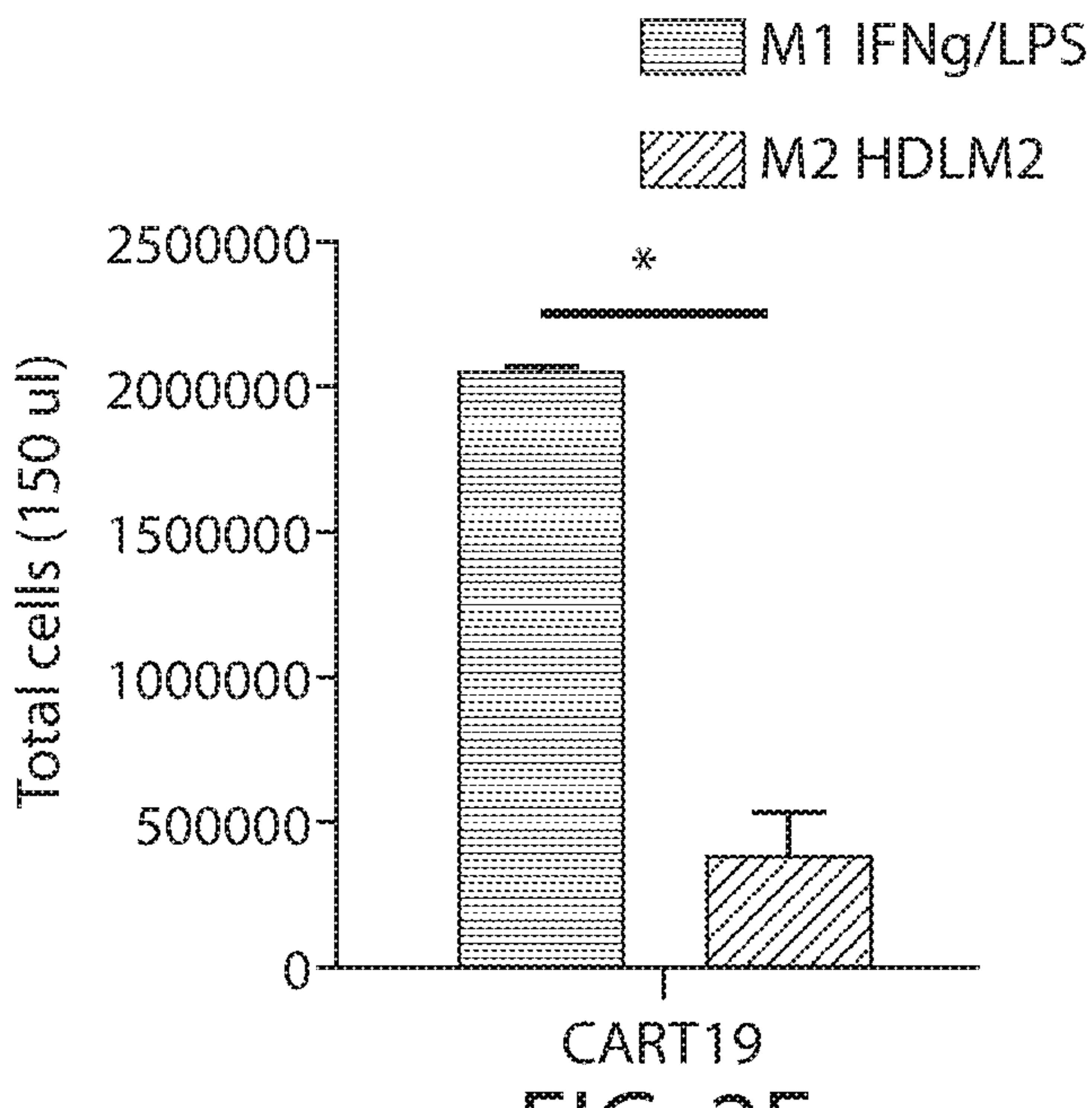
M1 IFNg/LPS
M2 HDLM2
*
Total cells (150 ul)
2500000
2000000
1500000
1000000
500000
0
CART19

FIG. 2E

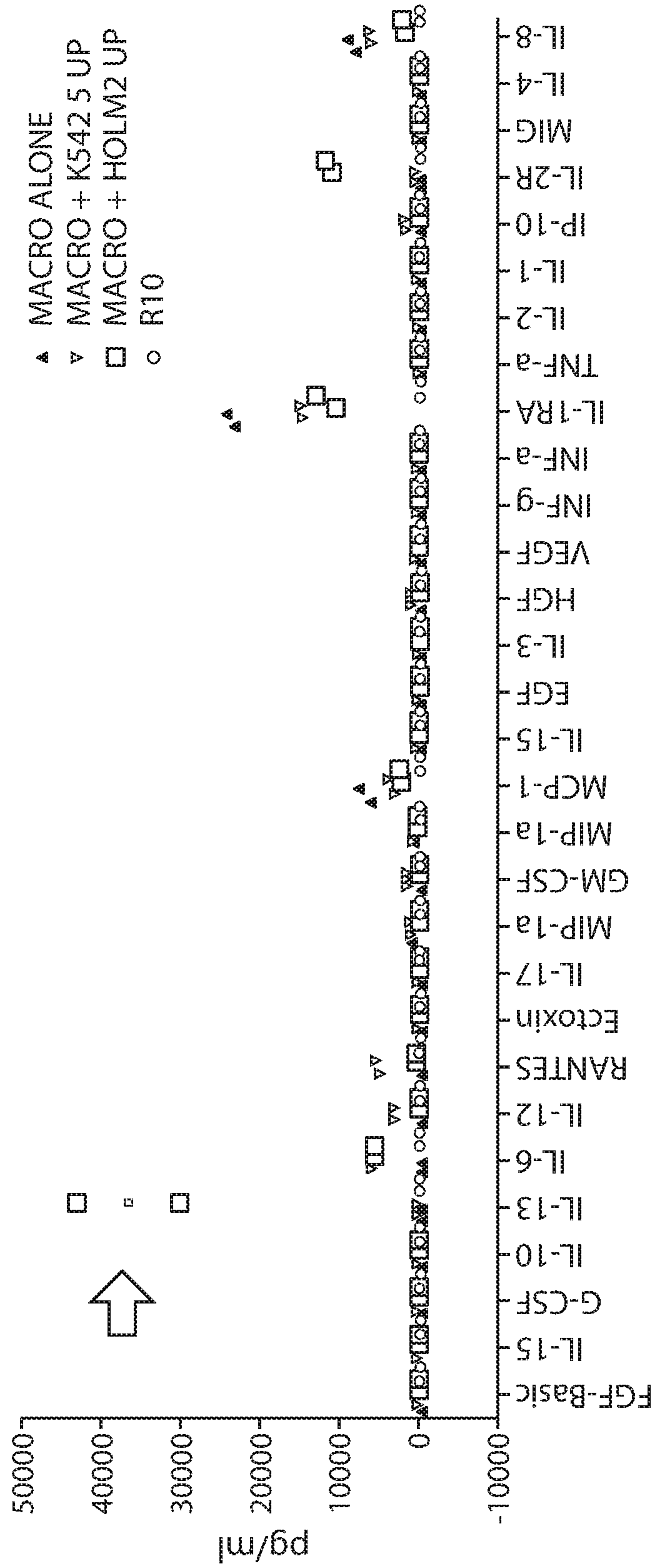
MACRO ALONE
MACRO + K542 5 UP
MACRO + HOLM2 UP
R10
pg/ml
50000
40000
30000
20000
10000
0
-10000
FGF-Basic
IL-15
G-CSF
IL-10
IL-13
IL-6
IL-12
RANTES
Ectoxin
IL-17
MIP-1a
GM-CSF
MIP-1a
MCP-1
IL-15
EGF
IL-3
HGF
VEGF
INF-g
INF-a
IL-1RA
TNF-a
IL-2
IL-1
IP-10
IL-2R
MIG
IL-4
IL-8

FIG. 2F

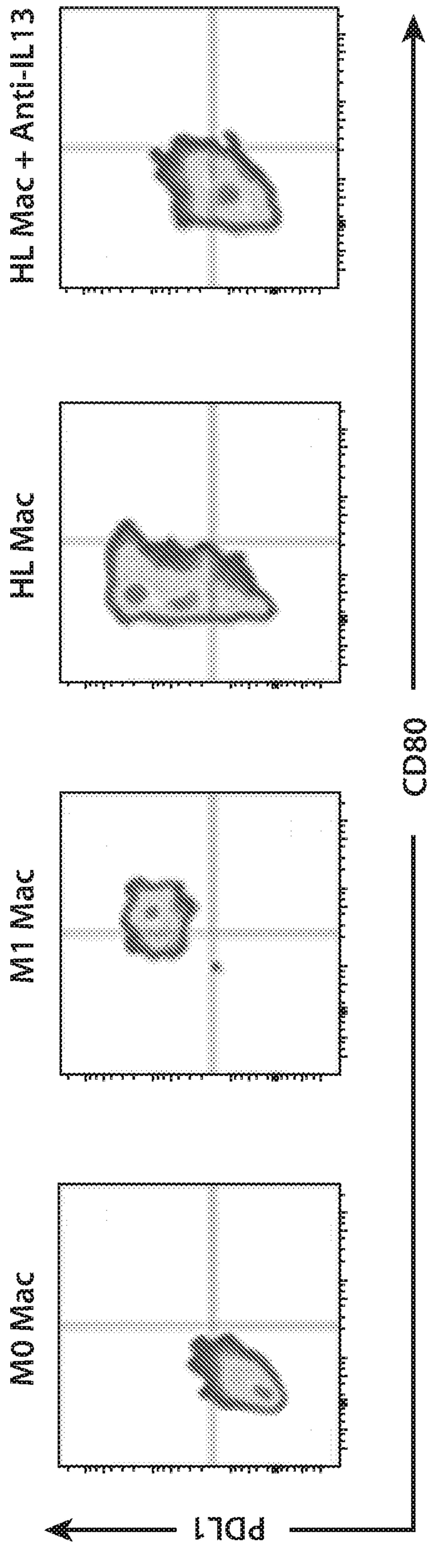

FIG. 2G

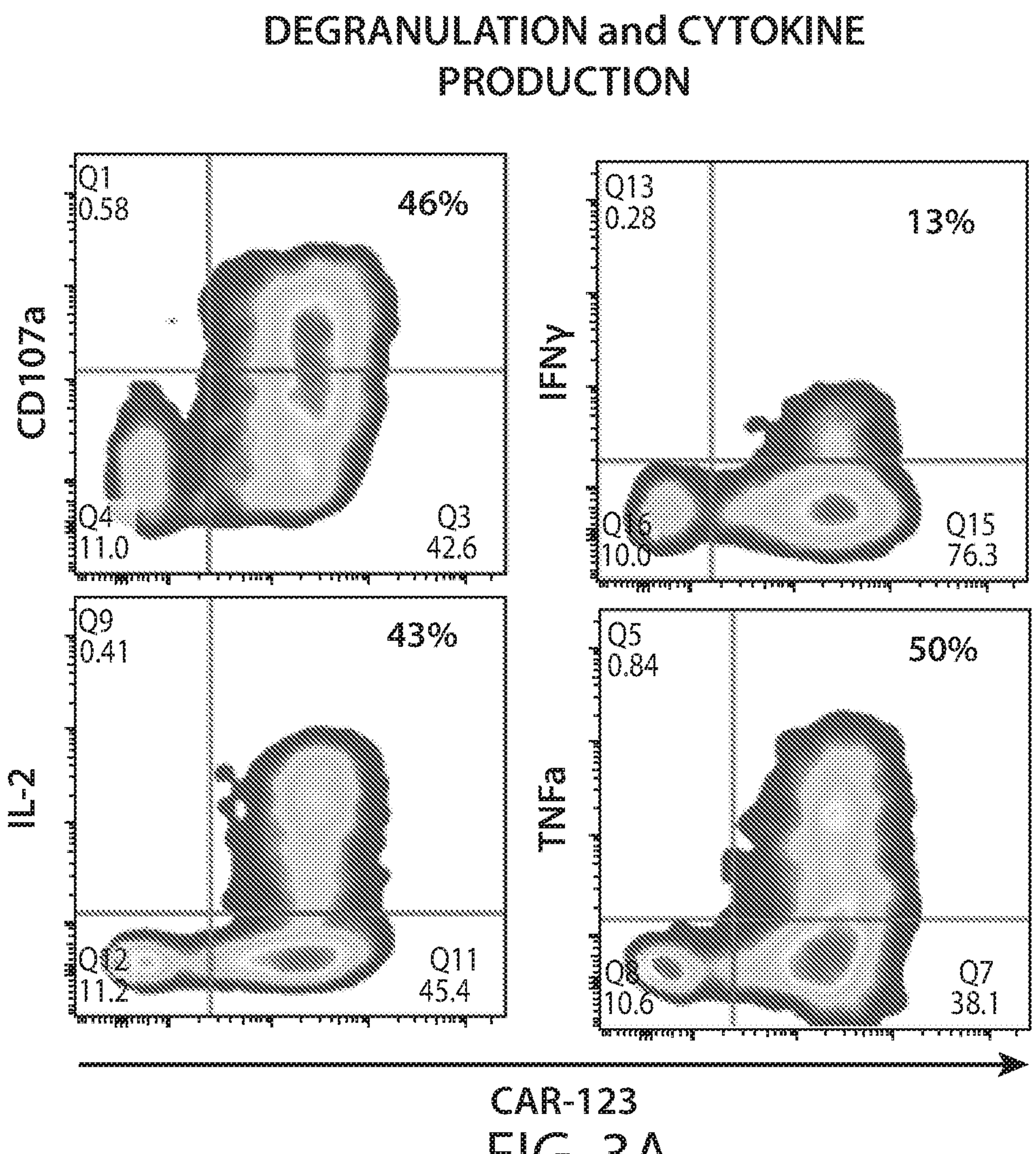
DEGRANULATION and CYTOKINE PRODUCTION
CD107a
Q1
0.58
46%
Q4
11.0
Q3
42.6
IFNγ
Q13
0.28
13%
Q16
10.0
Q15
76.3
IL-2
Q9
0.41
43%
Q12
11.2
Q11
45.4
TNFa
Q5
0.84
50%
Q8
10.6
Q7
38.1
CAR-123

FIG. 3A

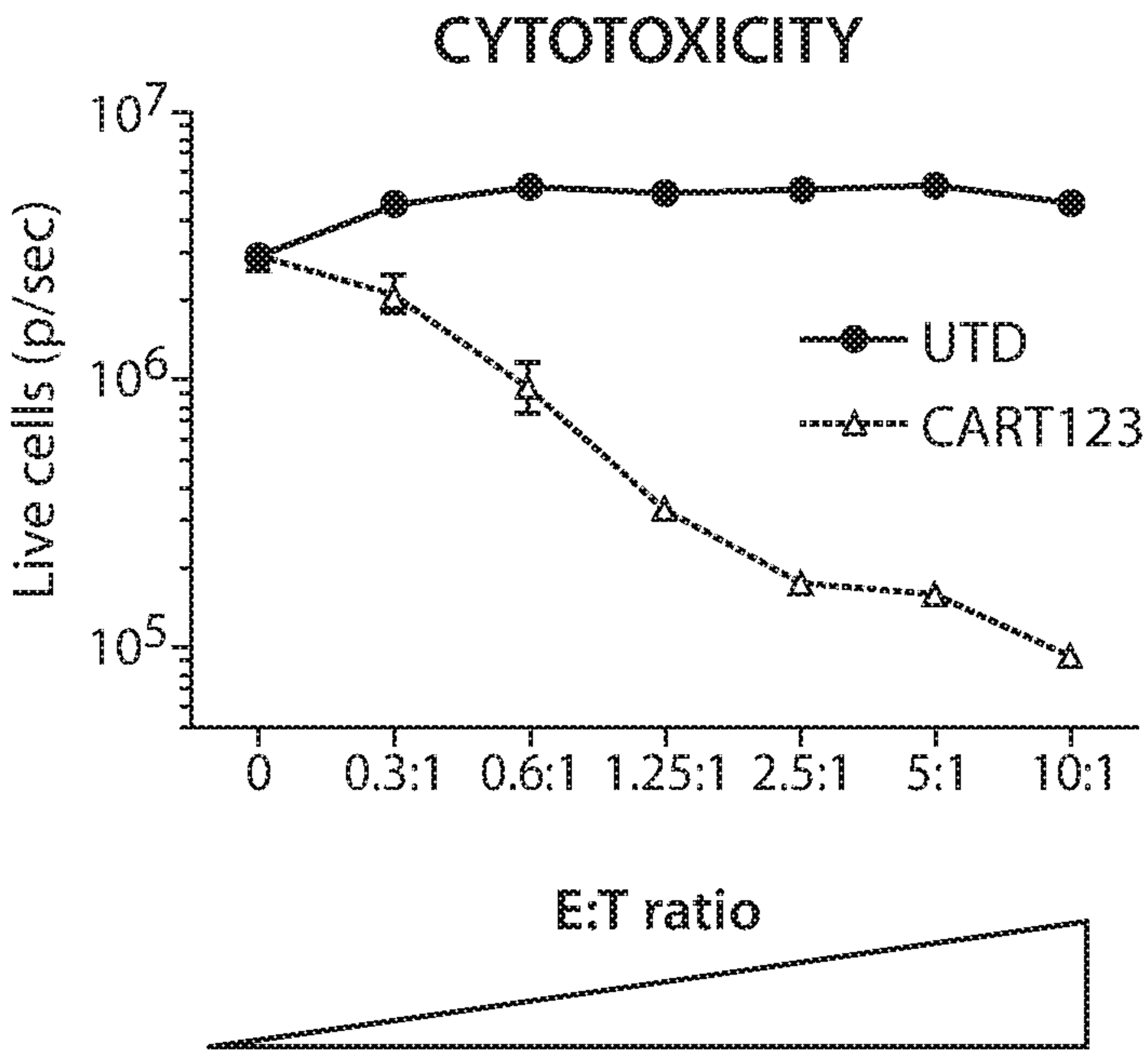
CYTOTOXICITY
10^7
10^6
10^5
Live cells (p/sec)
UTD
CART123
0
0.3:1
0.6:1
1.25:1
2.5:1
5:1
10:1
E:T ratio

FIG. 3B

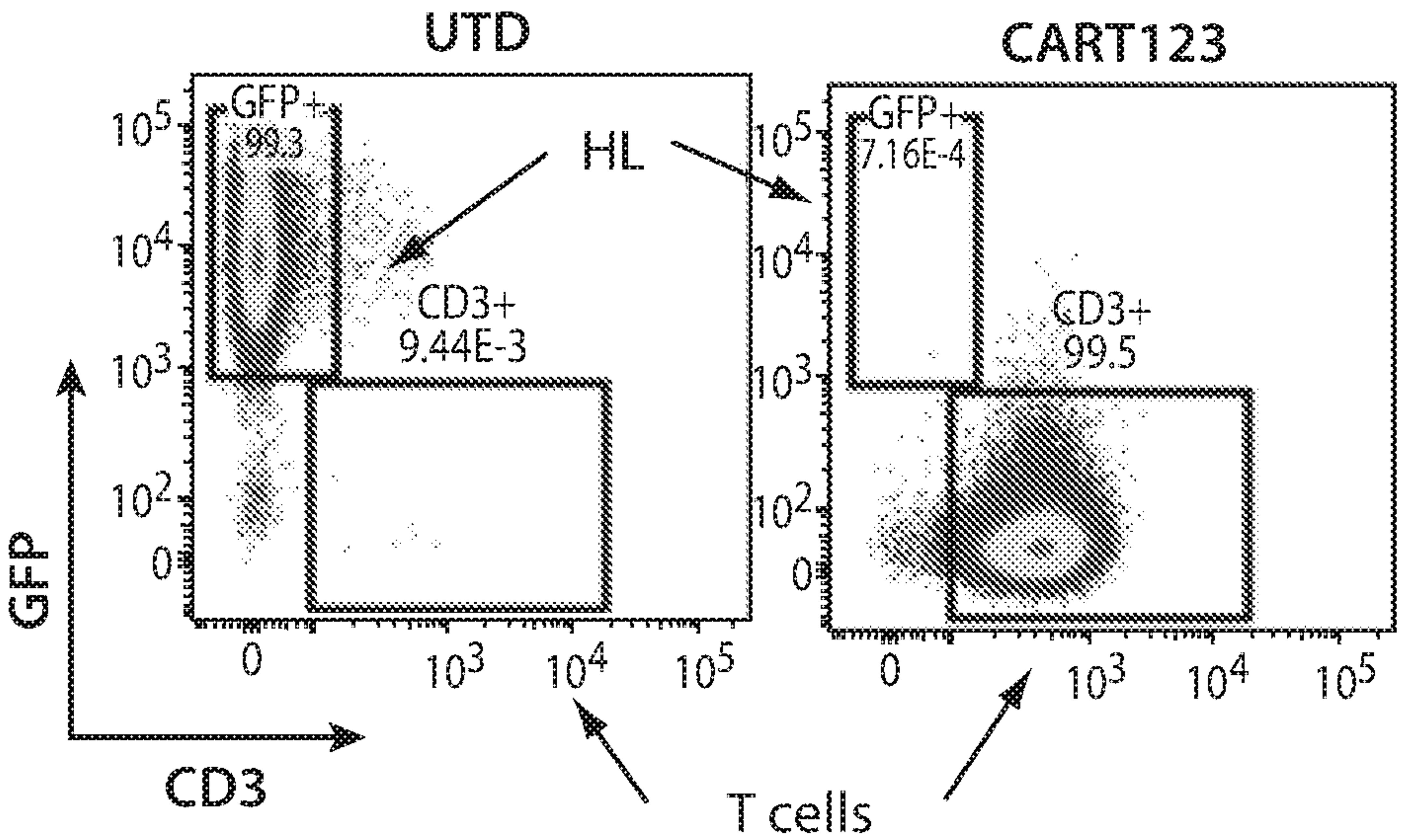
UTD
CART123
GFP+
99.3
GFP+
7.16E-4
HL
CD3+
9.44E-3
CD3+
99.5
10^5
10^4
10^3
10^2
0
10^3
10^4
10^5
GFP
CD3
T cells

FIG. 3C

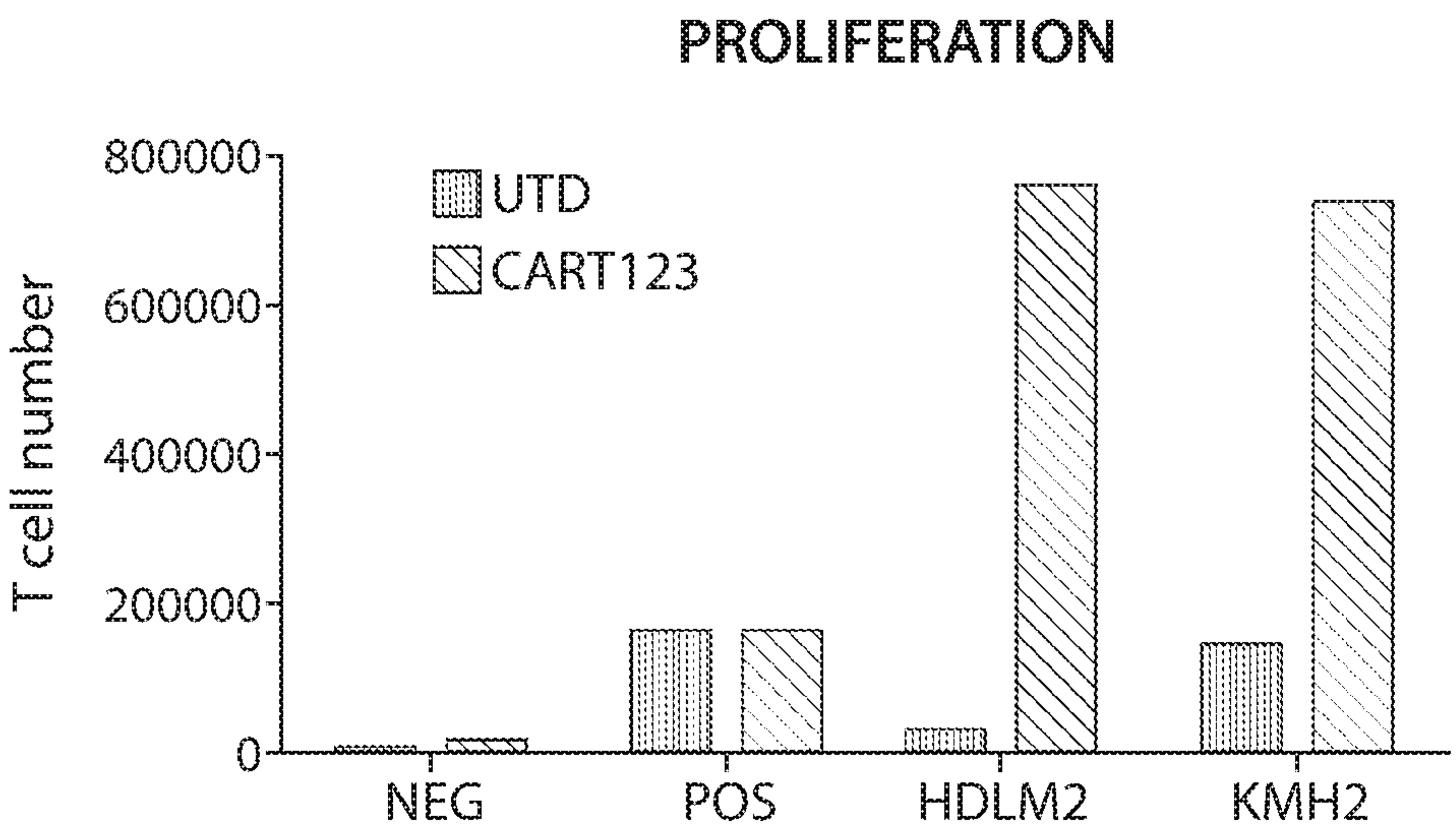
PROLIFERATION
800000
600000
400000
200000
0
T cell number
UTD
CART123
NEG
POS
HDLM2
KMH2

FIG. 3D

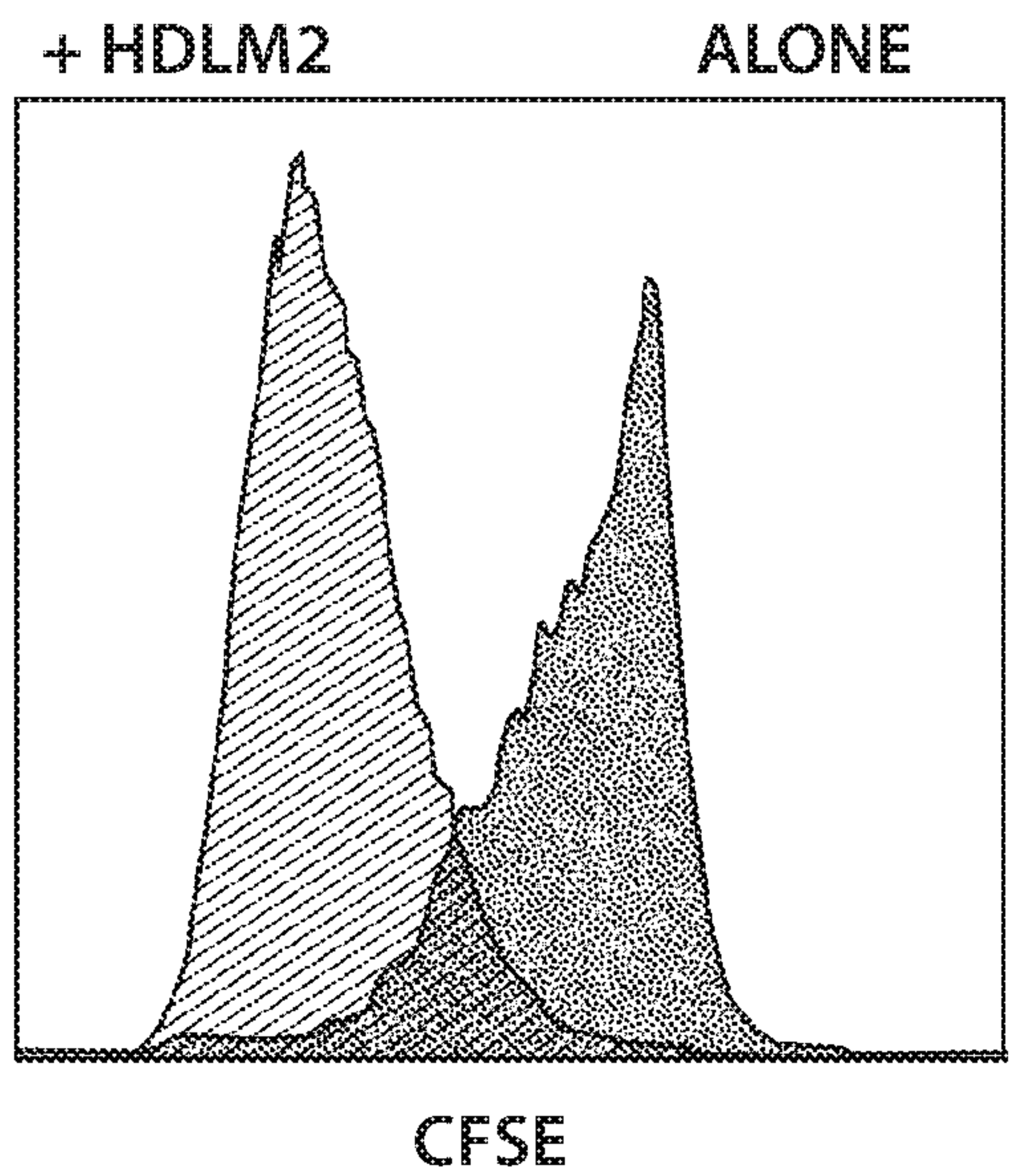
+ HDLM2
ALONE
CFSE

FIG. 3E

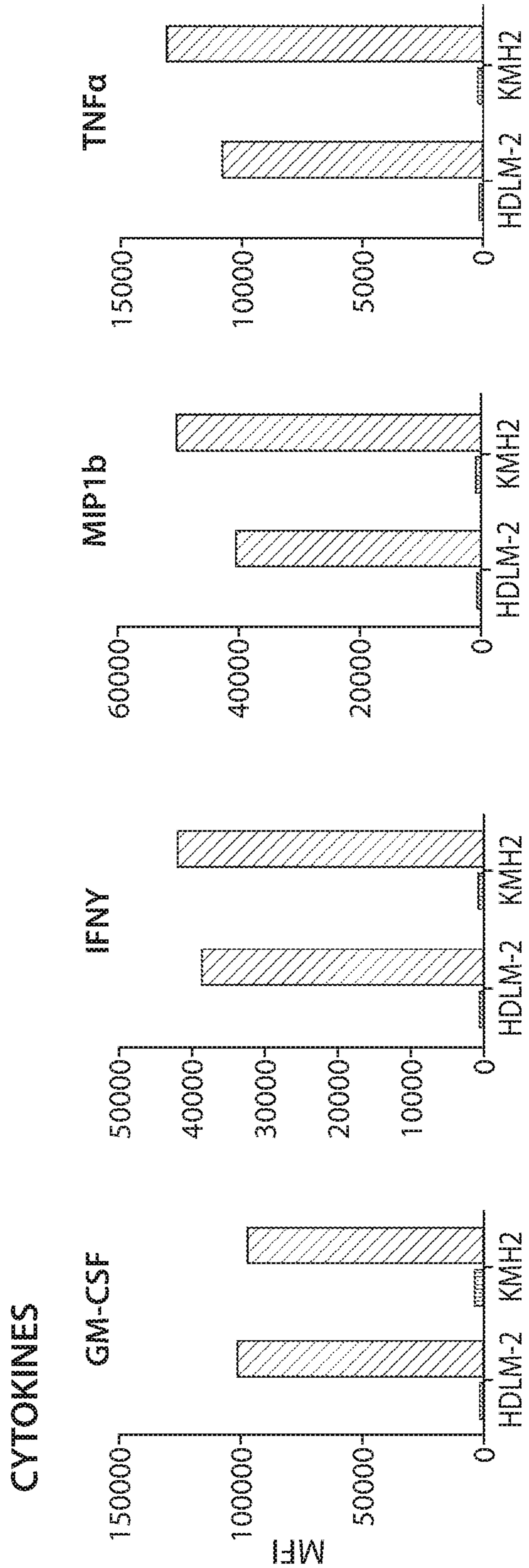
CYTOKINES
GM-CSF
IFNY
MIP1b
TNFa
MFI
150000
100000
50000
0
50000
40000
30000
20000
10000
60000
15000
10000
5000
HDLM-2
KMH2

FIG. 3F

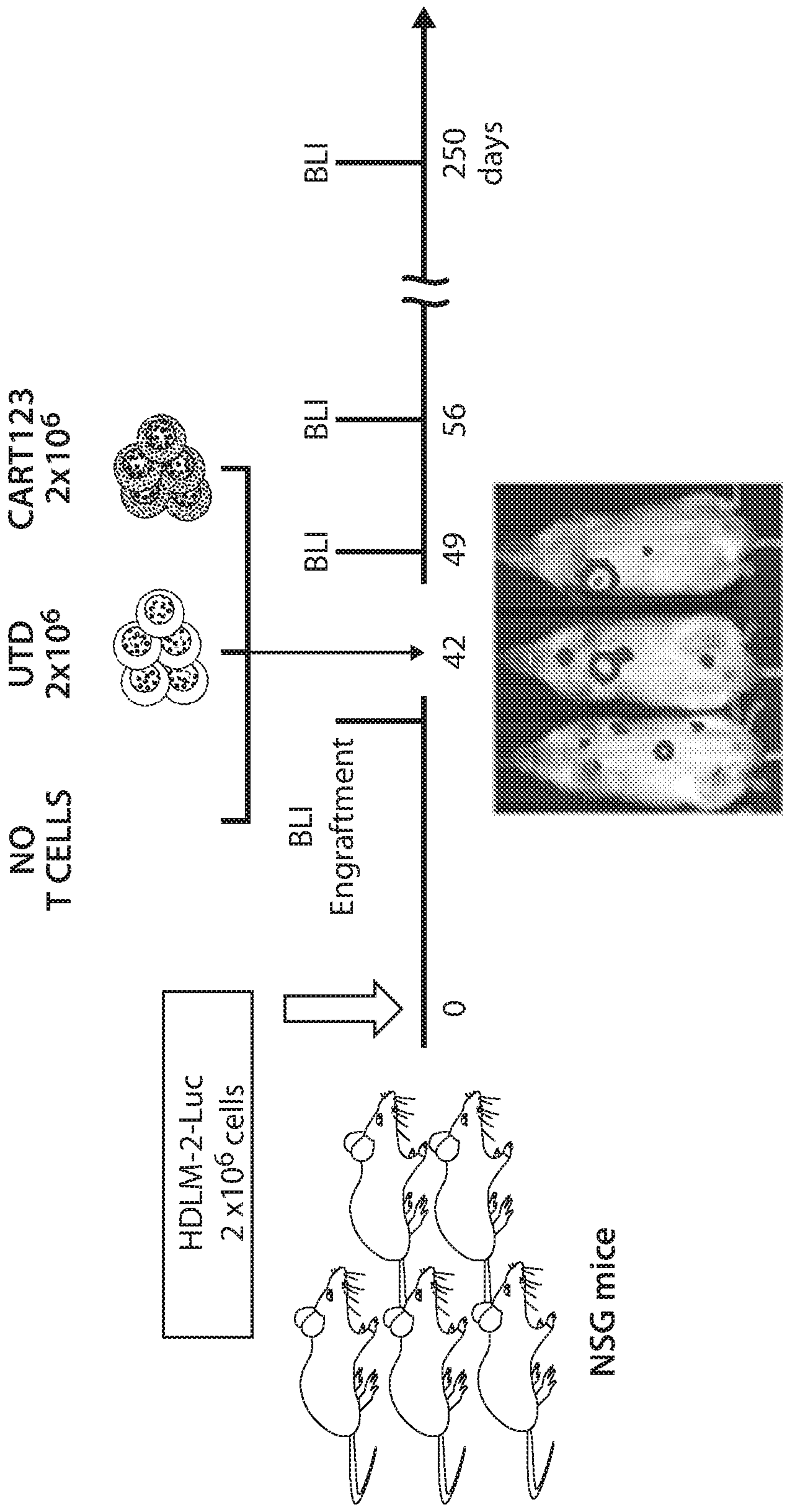
HDLM-2-Luc
2 x10^6 cells
NSG mice
0
BLI
Engraftment
NO
T CELLS
UTD
2x10^6
CART123
2x10^6
42
BLI
49
BLI
56
BLI
250
days

FIG. 4A

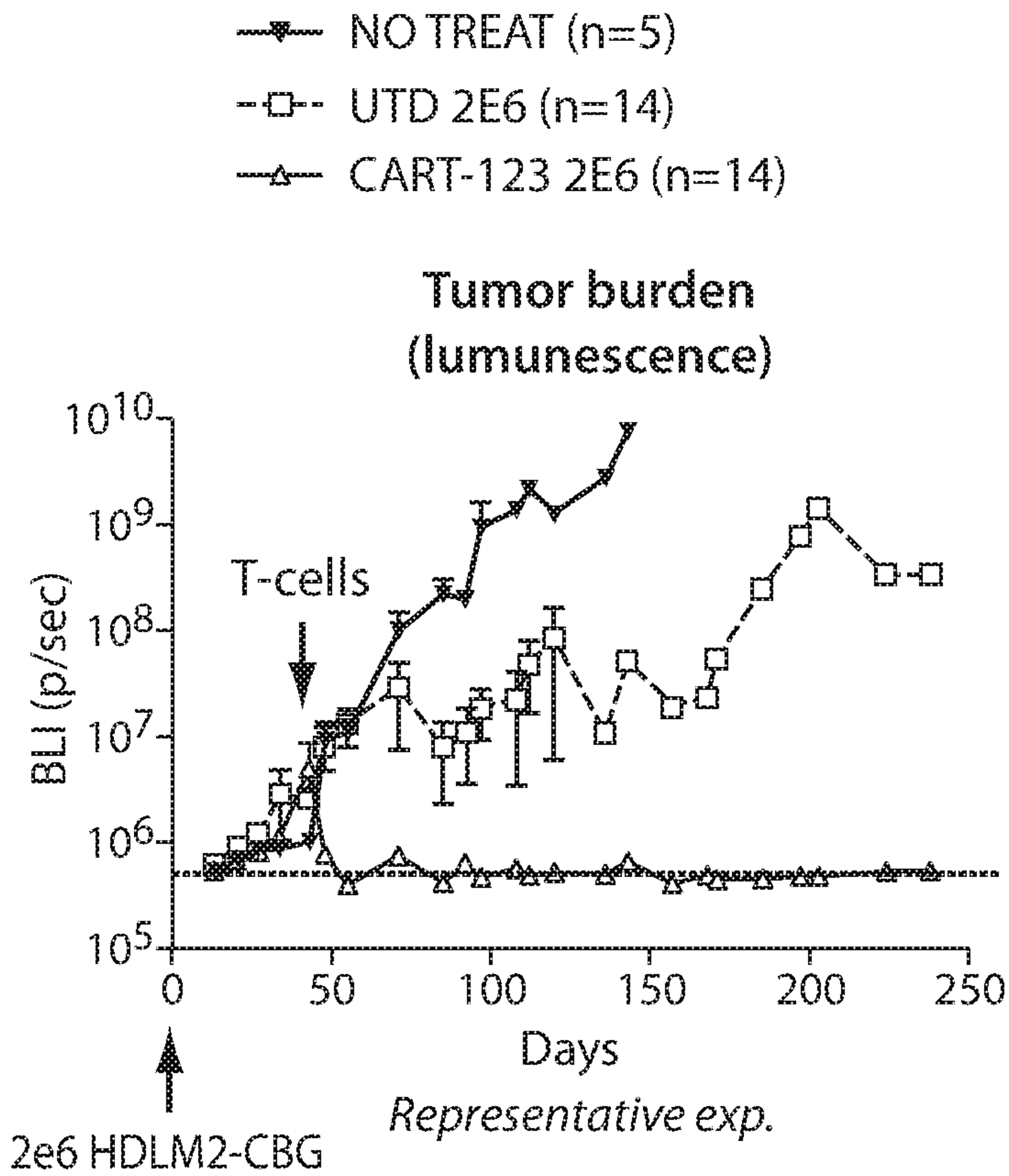
NO TREAT (n=5)
UTD 2E6 (n=14)
CART-123 2E6 (n=14)
Tumor burden
(lumunescence)
BLI (p/sec)
10^{10}
10^{9}
10^{8}
10^{7}
10^{6}
10^{5}
T-cells
0
50
100
150
200
250
Days
2e6 HDLM2-CBG
Representative exp.

FIG. 4B

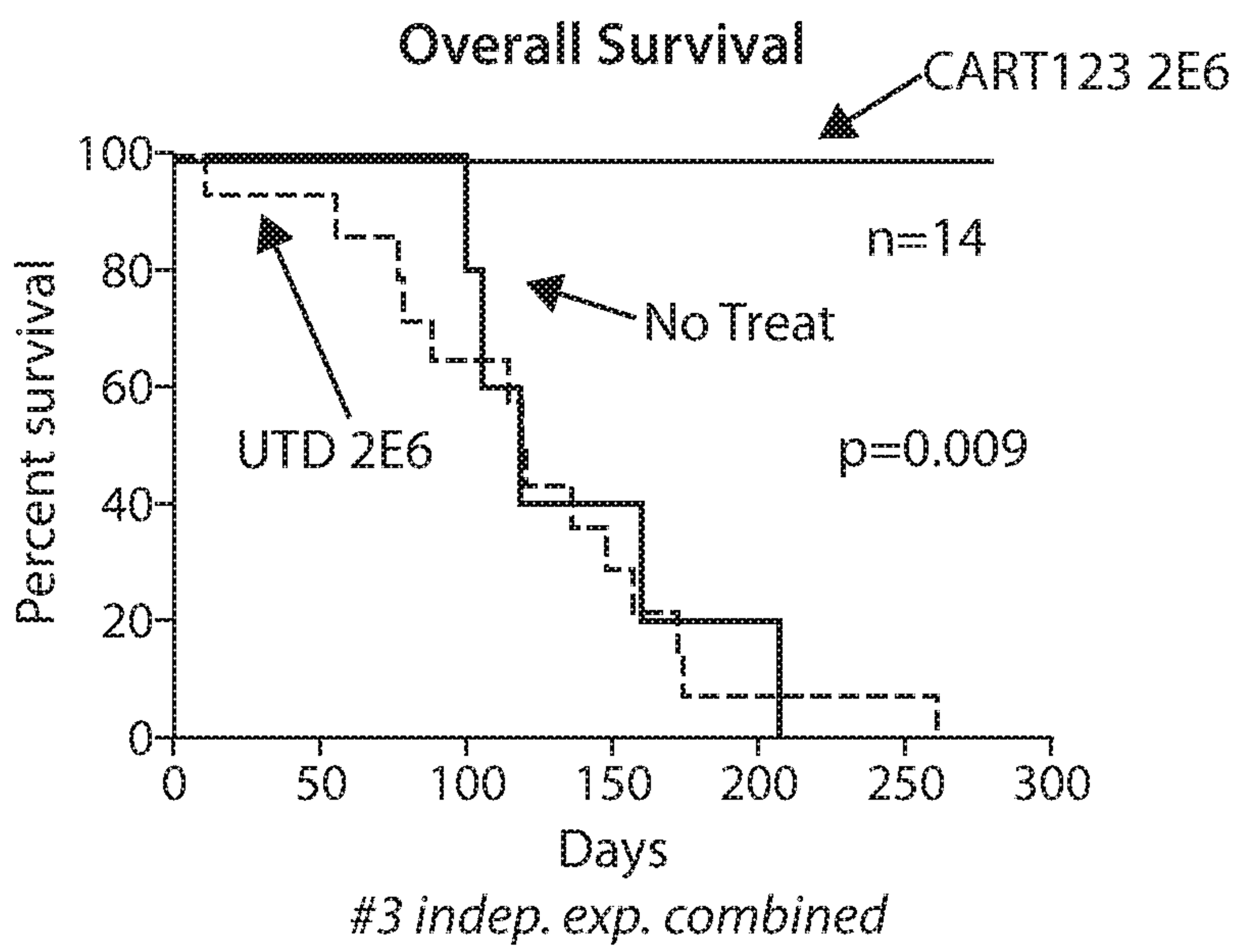
Overall Survival
CART123 2E6
n=14
No Treat
UTD 2E6
p=0.009
Percent survival
100
80
60
40
20
0
0
50
100
150
200
250
300
Days
#3 indep. exp. combined

FIG. 4C

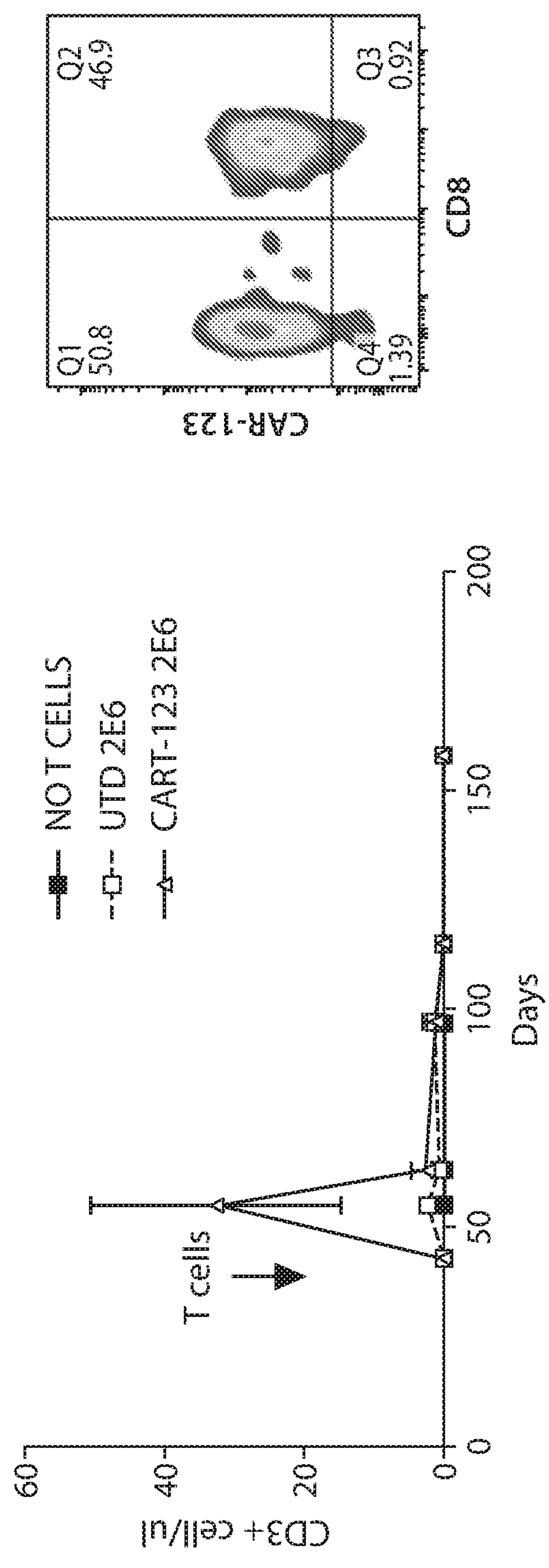
Q1
50.8
Q2
46.9
Q3
0.92
Q4
1.39
CAR-123
CD8
NOT CELLS
UTD 2E6
CART-123 2E6
T cells
CD3+ cell/ul
Days
0
20
40
60
0
50
100
150
200

FIG. 4D

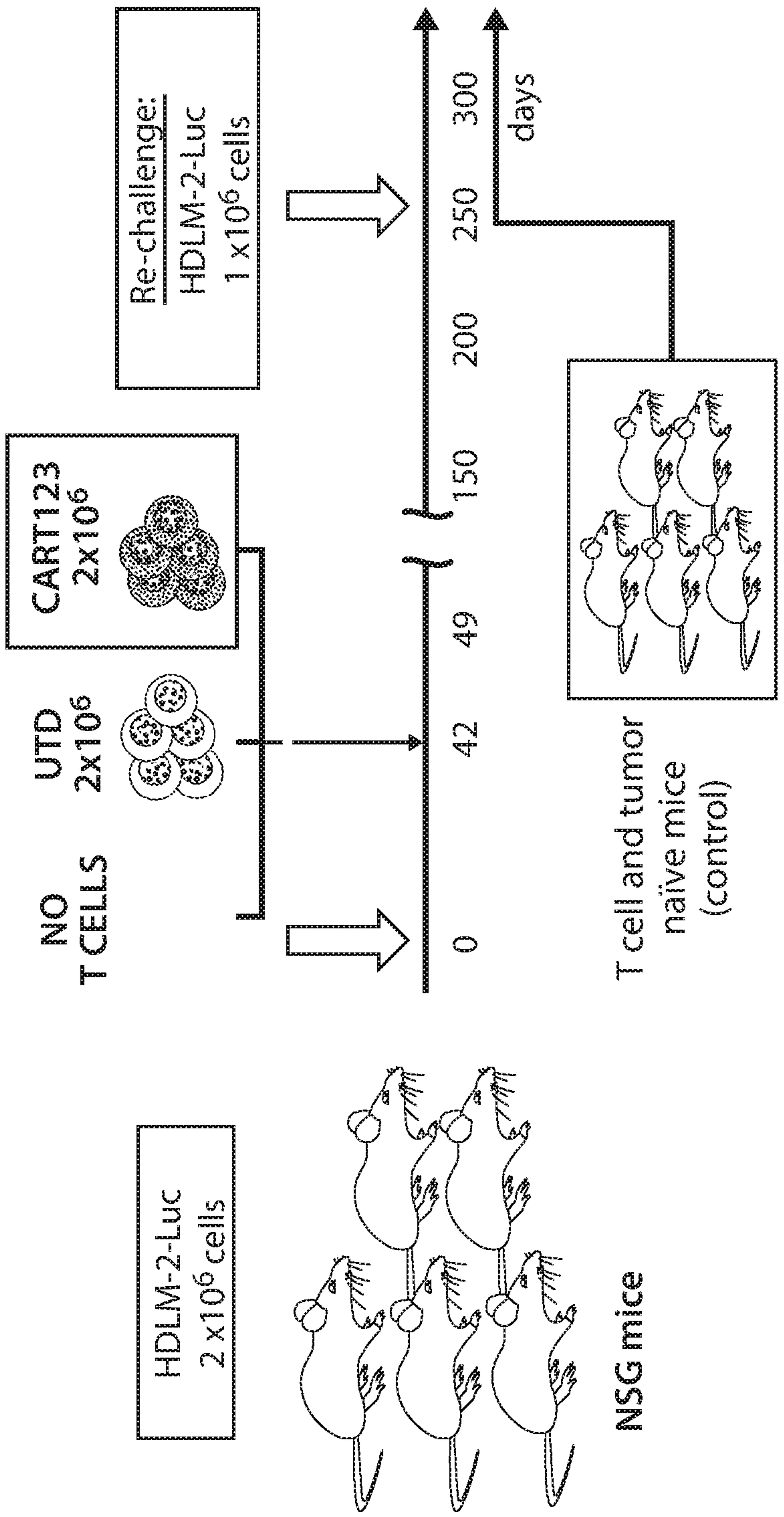
HDLM-2-Luc
2x10^6 cells
NSG mice
NO
T CELLS
UTD
2x10^6
CART123
2x10^6
Re-challenge:
HDLM-2-Luc
1 x10^6 cells
0
42
49
150
200
250
300
days
T cell and tumor
naïve mice
(control)

FIG. 5A

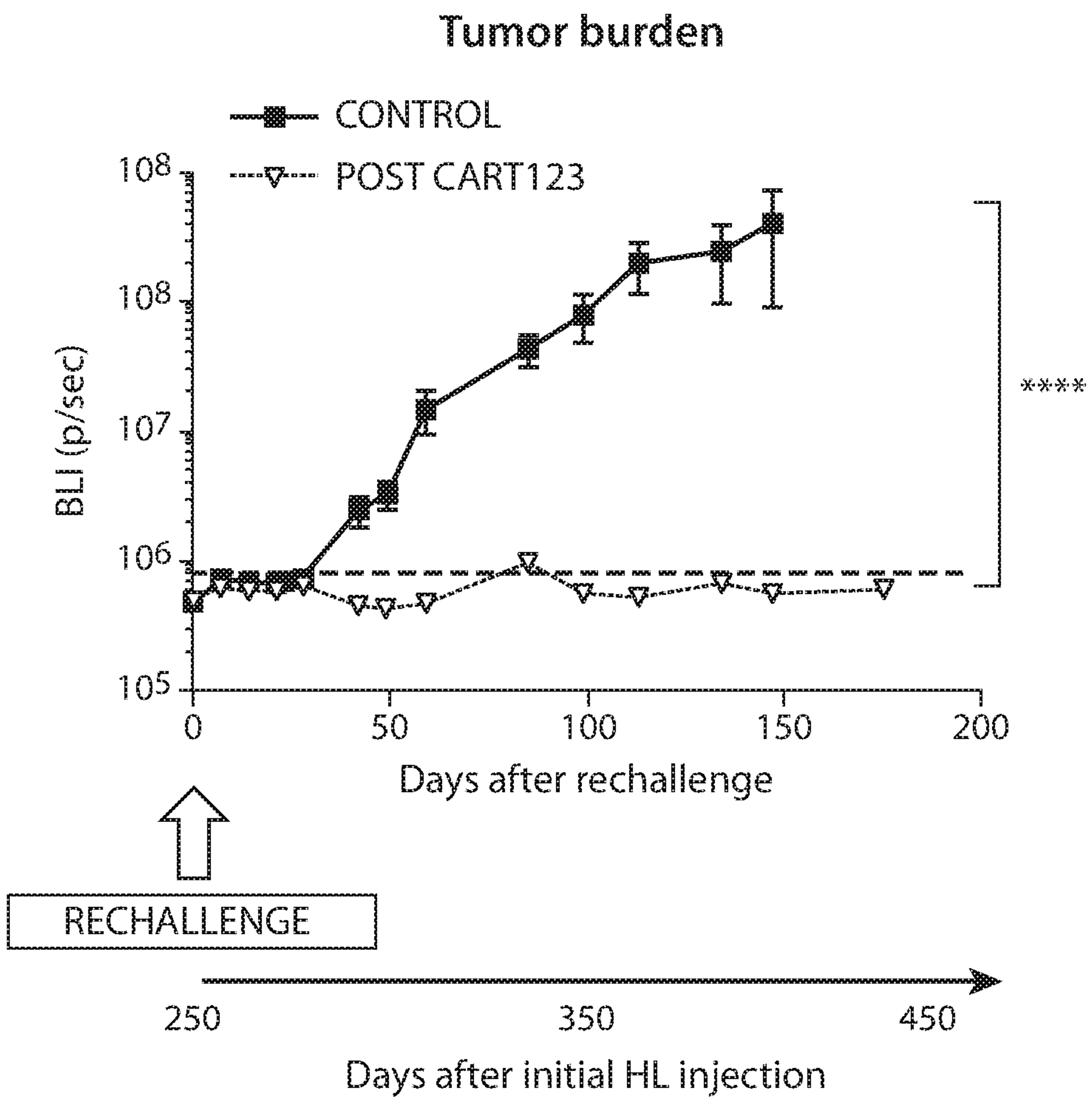
Tumor burden
CONTROL
POST CART123
BLI (p/sec)
10^8
10^8
10^7
10^6
10^5
0
50
100
150
200
Days after rechallenge
****
RECHALLENGE
250
350
450
Days after initial HL injection

FIG. 5B

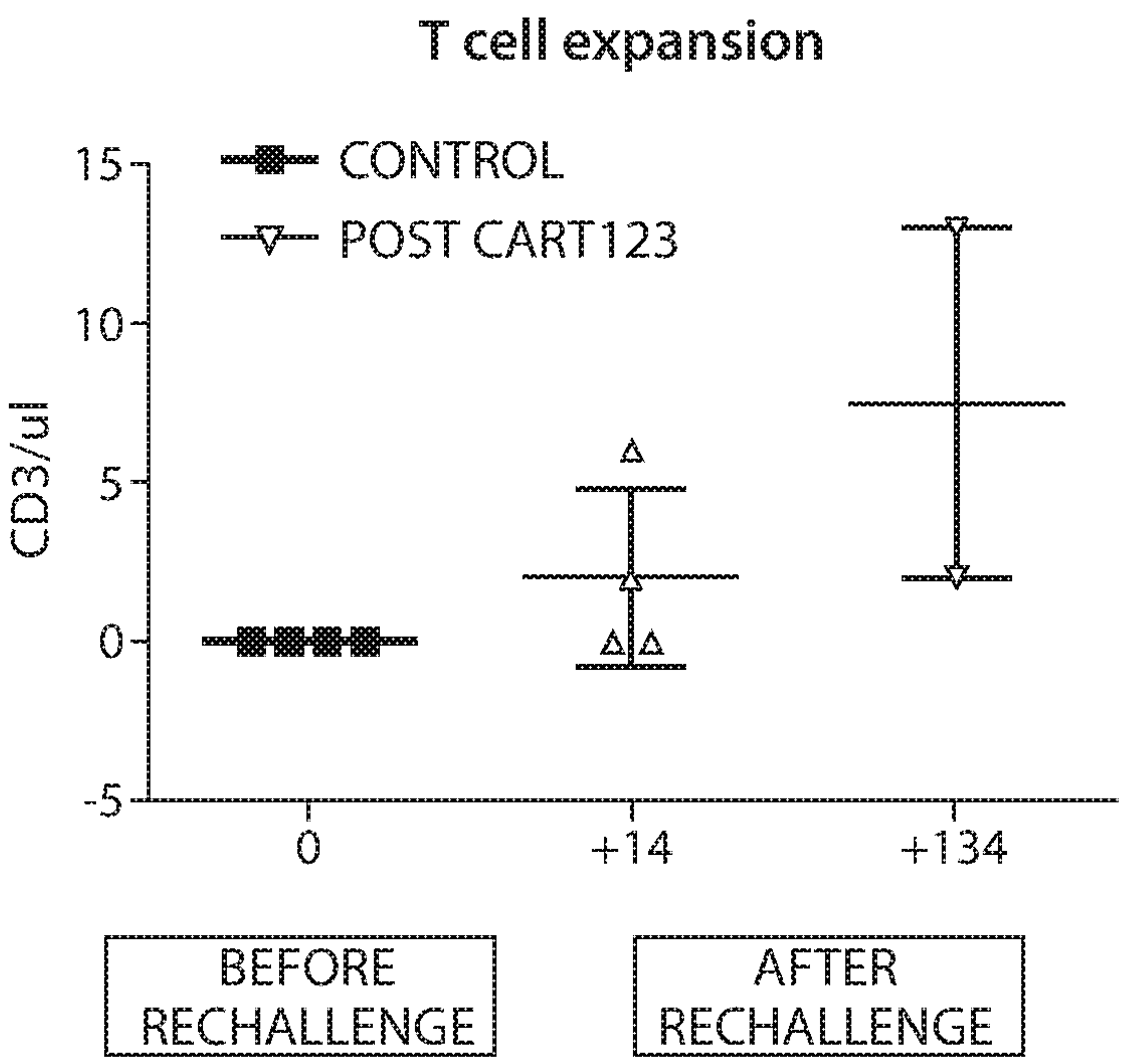
T cell expansion
CONTROL
POST CART123
CD3/ul
15
10
5
0
-5
0
+14
+134
BEFORE RECHALLENGE
AFTER RECHALLENGE

FIG. 5C

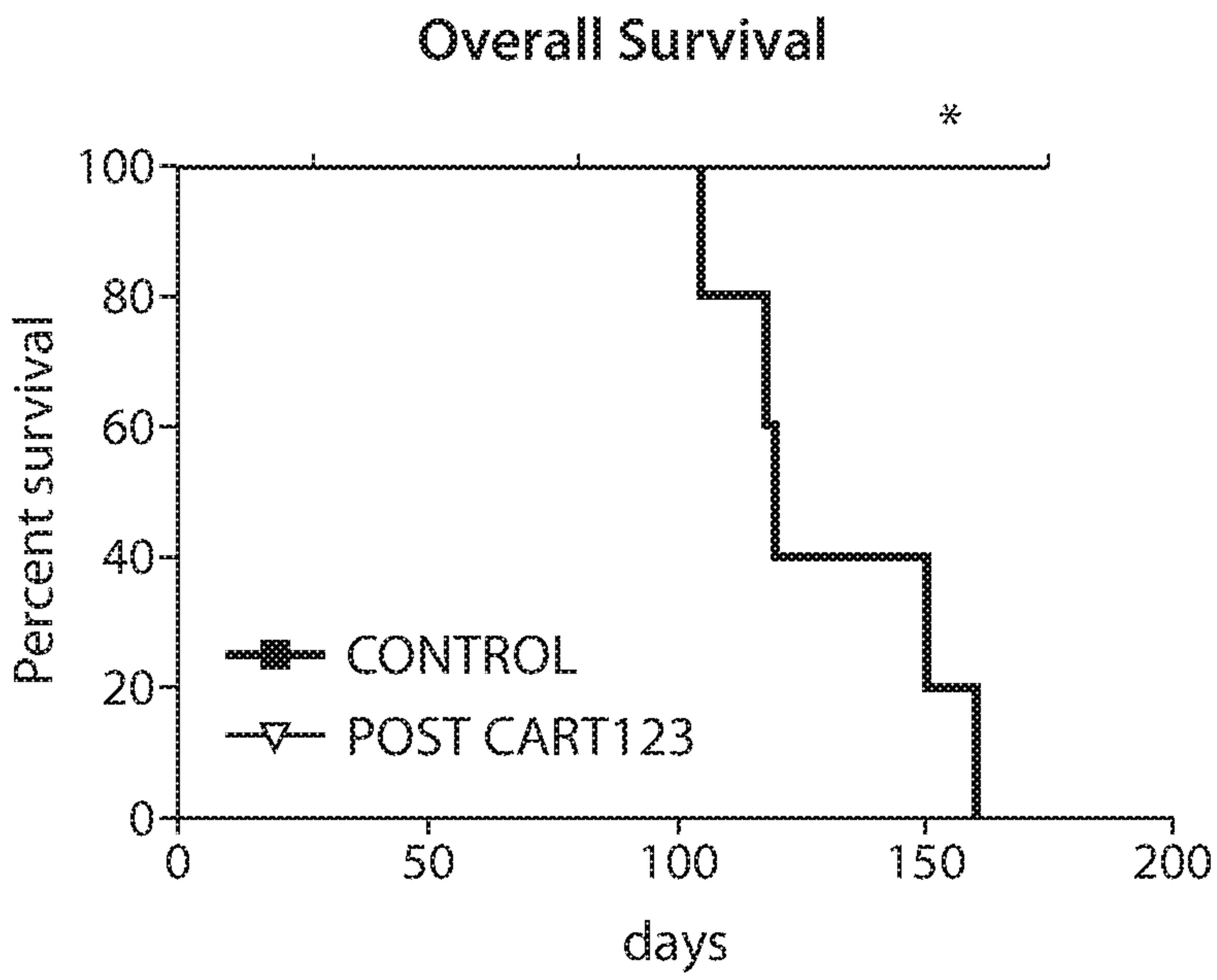
Overall Survival
*
Percent survival
100
80
60
40
20
0
CONTROL
POST CART123
0
50
100
150
200
days

FIG. 5D

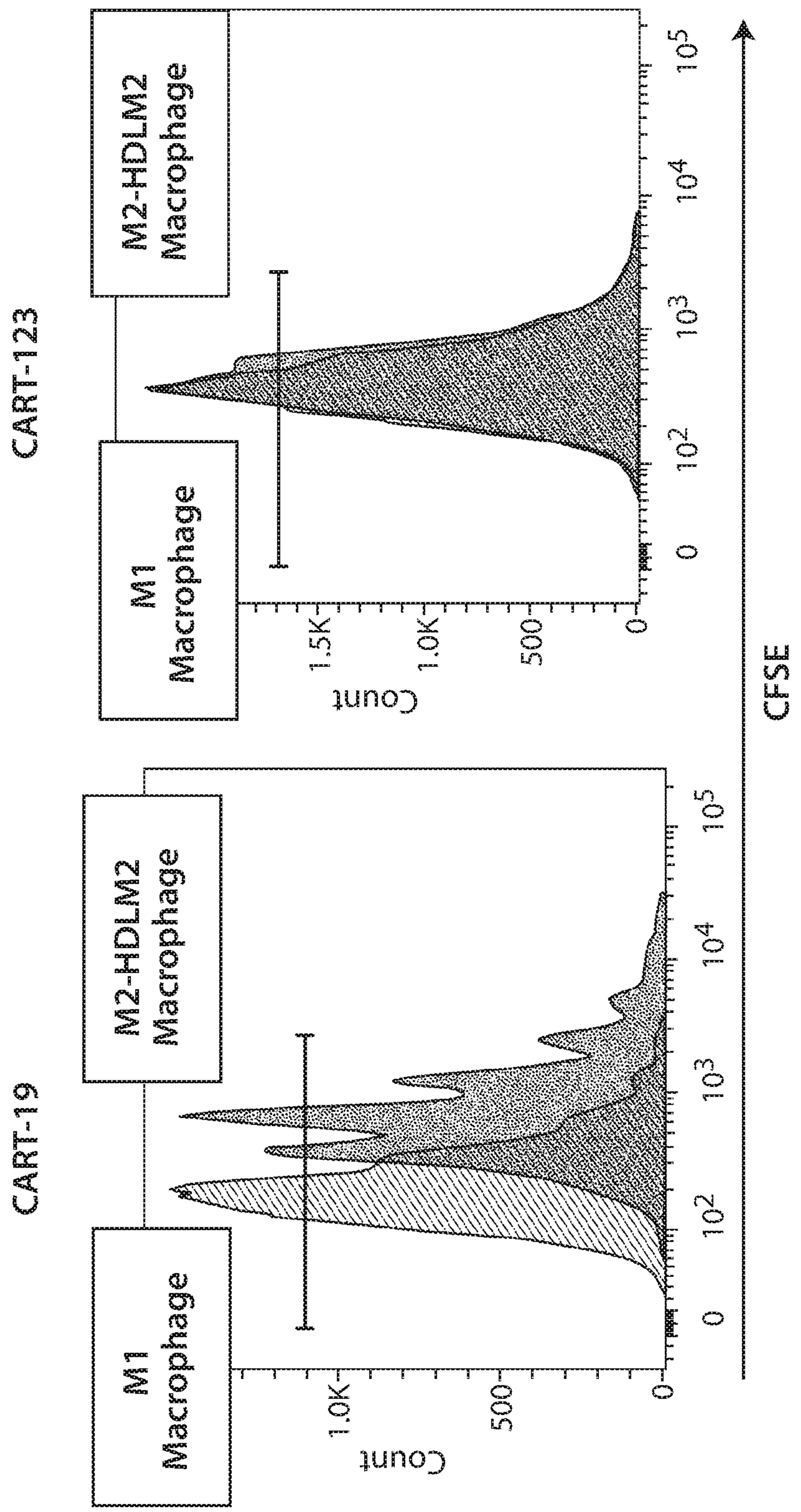
CART-19
CART-123
M1 Macrophage
M2-HDLM2 Macrophage
Count
0
500
1.0K
1.5K
0
10^2
10^3
10^4
10^5
CFSE

FIG. 6A

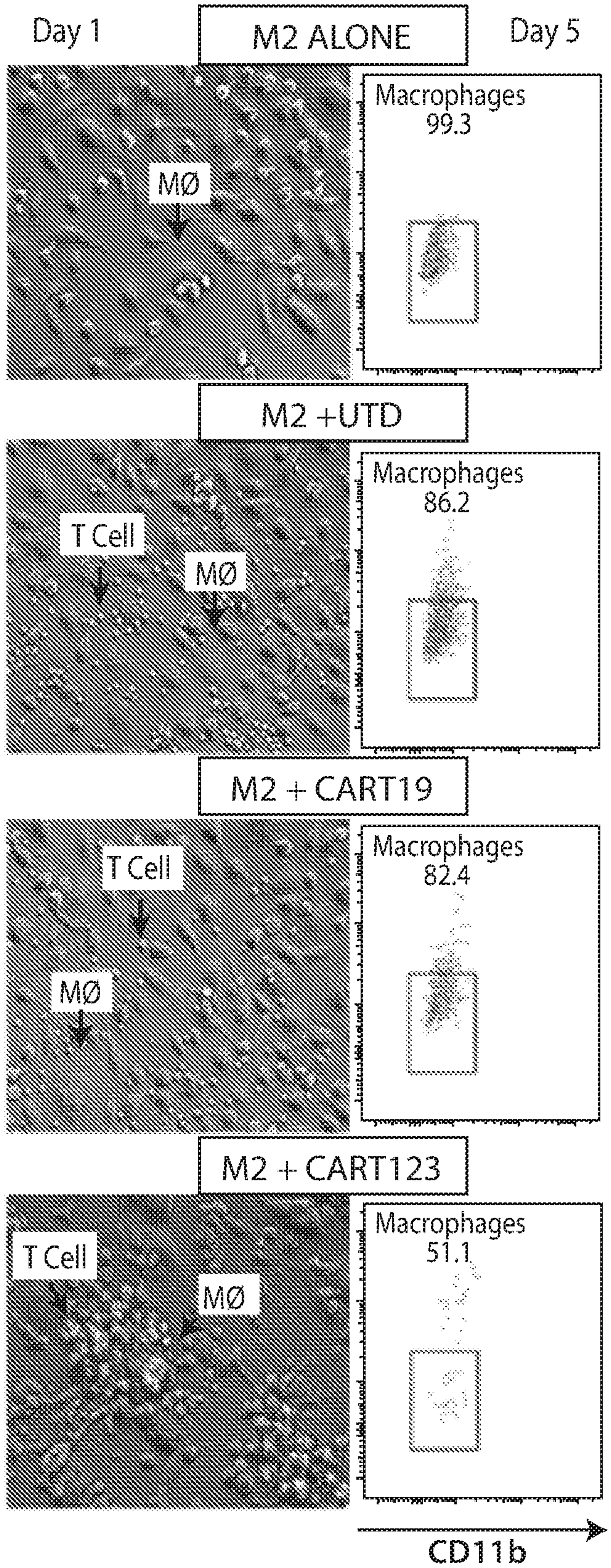
Day 1
M2 ALONE
Day 5
MØ
Macrophages
99.3
M2 +UTD
T Cell
MØ
Macrophages
86.2
M2 + CART19
T Cell
MØ
Macrophages
82.4
M2 + CART123
T Cell
MØ
Macrophages
51.1
CD11b

FIG. 6B

20/20

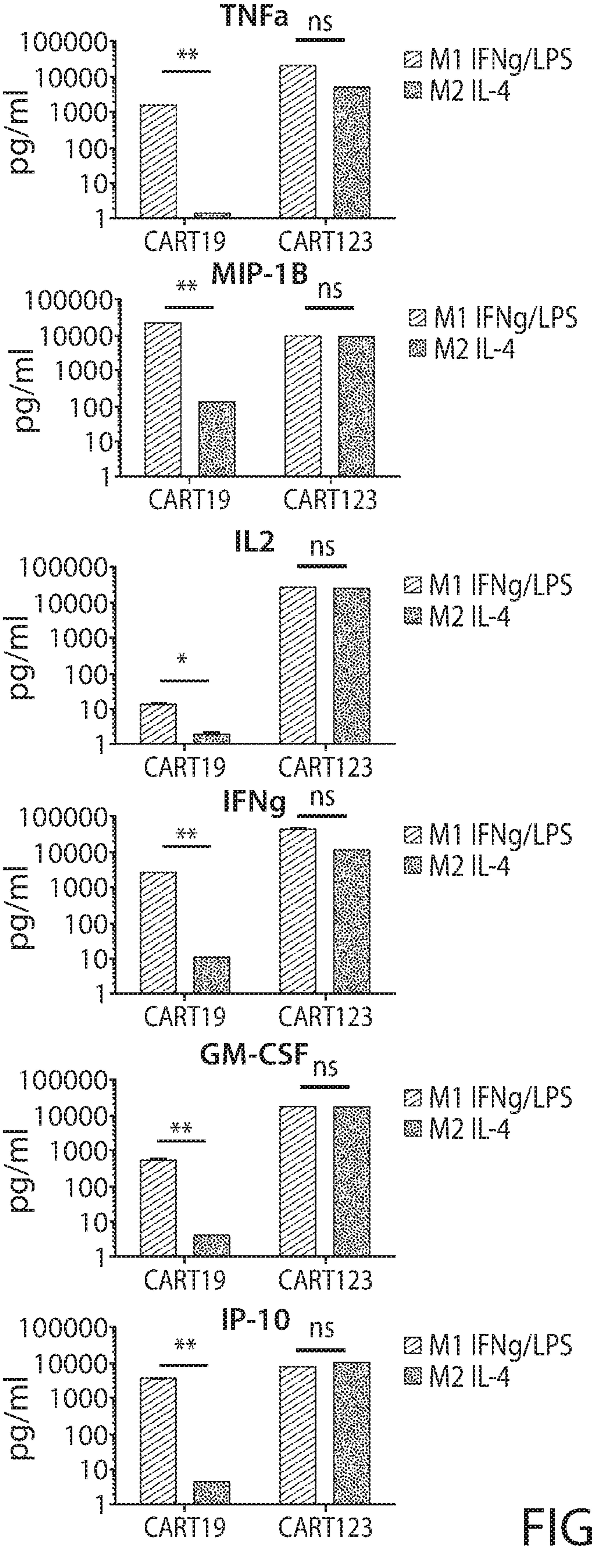
TNFa
ns
**
100000
10000
1000
100
10
1
pg/ml
CART19
CART123
M1 IFNg/LPS
M2 IL-4
MIP-1B
IL2
*
IFNg
GM-CSF
IP-10

FIG. 6C