



(12) **DEMANDE DE BREVET CANADIEN**
CANADIAN PATENT APPLICATION

(13) **A1**

(22) Date de dépôt/Filing Date: 2014/12/19

(41) Mise à la disp. pub./Open to Public Insp.: 2015/06/25

(62) Demande originale/Original Application: 2 931 684

(30) Priorités/Priorities: 2013/12/19 (CN PCT/CN2013/089979);
2014/07/21 (CN PCT/CN2014/082610);
2014/11/06 (CN PCT/CN2014/090509)

(51) Cl.Int./Int.Cl. *C12N 15/62*(2006.01),
A61K 35/00(2006.01), *A61K 35/17*(2015.01),
C07K 14/705(2006.01), *C07K 16/28*(2006.01),
C07K 16/30(2006.01), *C07K 19/00*(2006.01),
C12N 15/64(2006.01), *C12N 15/85*(2006.01),
C12N 5/0783(2010.01), *C12N 5/10*(2006.01)

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(54) Titre : RECEPTEURS ANTIGENIQUES CHIMERIQUES DE LA MESOTHELIN HUMAINE ET LEURS
UTILISATIONS

(54) Title: HUMAN MESOTHELIN CHIMERIC ANTIGEN RECEPTORS AND USES THEREOF

(57) Abrégé/Abstract:

Provided are compositions and methods for treating diseases associated with expression of mesothelin. Also provided are a chimeric antigen receptor (CAR) specific to mesothelin, vectors encoding the same, and recombinant T cells comprising the mesothelin CAR. Further provided are methods of administering a genetically modified T cell expressing a CAR that comprises a mesothelin binding domain.

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Abstract

Provided are compositions and methods for treating diseases associated with expression of mesothelin. Also provided are a chimeric antigen receptor (CAR) specific to mesothelin, vectors encoding the same, and recombinant T cells comprising the mesothelin CAR. Further provided are methods of administering a genetically modified T cell expressing a CAR that comprises a mesothelin binding domain.

DEMANDE OU BREVET VOLUMINEUX

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**HUMAN MESOTHELIN
CHIMERIC ANTIGEN RECEPTORS AND USES THEREOF**

This application claims priority to International Application No. PCT/CN2013/089979, filed December 19, 2013, International Application No. PCT/CN2014/082610, filed July 21, 2014 and International Application No. PCT/CN2014/090509, filed November 6, 2014, the entire contents of each of these applications are incorporated herein by reference.

FIELD OF THE INVENTION

[001] The present invention relates generally to the use of T cells engineered to express a Chimeric Antigen Receptor (CAR) to treat a disease associated with expression of mesothelin.

BACKGROUND OF THE INVENTION

[002] Mesothelin was originally identified by Pastan and colleagues as a tumor associated antigen due to its limited expression by normal tissues and overexpression on tumors. Chang K, et al., *Cancer Res.* 1992;52(1):181-186 and Chang K, et al. *ProcNatlAcadSciUSA.* 1996;93(1):136-140. The mesothelin gene encodes a precursor 71-kDa protein that is processed to yield 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. A soluble splice variant of the 40-kDa carboxyl-terminal fragment called “soluble mesothelin/MPF-related” has been found in the sera of patients with pancreatic ductal adenocarcinoma (PDA). Johnston, F, et al. *Clinical Cancer Research.* 2009;15(21):6511. Mesothelin is currently being explored both as a therapeutic target as well as a bio-marker for disease activity and therapeutic response. Argani P, et al. *Clin Cancer Res.* 2001;7(12):3862-3868.

[003] Mesothelin is a differentiation antigen that is also present on normal tissues. Using the mouse anti-human mesothelin antibody K1 that was developed by the Pastan group, strong K1 reactivity has been demonstrated within mesothelial cells that line the peritoneal, pleural, and

pericardial cavities, although at lower levels than usually seen for malignant tissues. Chang K, et al., *Cancer Res.* 1992;52(1):181-186. Weak K1 reactivity has been detected within the Fallopian tube epithelium, tracheal basal epithelium and tonsils epithelium. Mesothelin has also been found on all layers of the cornea. Jirsova K, et al. *Experimental eye research.* 2010;91(5):623-629. However, K1 reactivity has not been detected in the majority of normal tissues including the liver, kidneys, spleen, bone marrow, lymph nodes, thymus, cardiac muscle, tongue, skeletal muscle, skin, cerebral cortex, cerebellum, spinal cord, peripheral nerve, pituitary, adrenal, salivary gland, mammary gland, thyroid, parathyroid, testis, prostate, epididymis, cervical epithelium, lung parenchyma, esophagus, small-bowel epithelium, colon epithelium, bladder epithelium, gall-bladder epithelium. Chang K, et al., *Cancer Res.* 1992;52(1):181-186.

[004] Mesothelin is overexpressed in the vast majority of primary pancreatic adenocarcinomas with rare and weak expression seen in benign pancreatic tissue. Argani P, et al. *Clin Cancer Res.* 2001;7(12):3862-3868. Epithelial malignant pleural mesothelioma (MPM) universally expresses mesothelin while sarcomatoid MPM does not express mesothelin. Most serous epithelial ovarian carcinomas, and the related primary peritoneal carcinomas, express mesothelin.

[005] Mesothelin is a target of a natural immune response in ovarian cancer, and has been proposed to be a target for cancer immunotherapy. Bracci L, et al. *Clin Cancer Res.* 2007;13(2 Pt 1):644-653; Moschella F, et al. *Cancer Res.* 2011;71(10):3528-3539; Gross G, et al. *FASEB J.* 1992;6(15):3370-3378; Sadelain M, et al. *Nat Rev Cancer.* 2003;3(1):35-45; Muul LM, et al. *Blood.* 2003;101(7):2563-2569; Yee C, et al. *Proc Natl Acad Sci U S A.* 2002;99(25):16168-16173. The presence of mesothelin-specific CTLs in patients with pancreatic cancer correlates with overall survival. Thomas AM, et al. *J Exp Med.* 2004;200:297-306. In addition, Pastan and coworkers have used soluble antibody fragments of an anti-mesothelin antibody conjugated to immunotoxins to treat cancer patients with mesothelin-positive tumors. This approach has demonstrated adequate safety and some clinical activity in pancreatic cancer. Hassan R, et al. *Cancer Immun.* 2007;7:20 and Hassan R, et al. *Clin Cancer Res.* 2007;13(17):5144-5149. In ovarian cancer, this therapeutic strategy produced one minor response by RECIST criteria and stable disease in a second patient who also had complete resolution of their ascites.

SUMMARY OF THE INVENTION

[006] The invention features, e.g., methods of providing an immune response in patients by administering an immune effector cell that is engineered to express a Chimeric Antigen Receptor (CAR) that comprises an antibody (e.g., scFv) that specifically targets mesothelin. In particular, the invention pertains to the use of an immune effector cell such as, e.g., a T cell or NK cell, engineered to express a CAR that includes an antibody such as antigen binding fragment thereof to treat a cancer associated with expression of mesothelin (or MSLN). In particular, the invention pertains to adoptive cell transfer that may be particularly suitable for patients with mesothelin-expressing cancers, such as, e.g., mesothelioma (e.g., malignant pleural mesothelioma, lung cancer (e.g., non-small cell lung cancer, small cell lung cancer, squamous cell lung cancer, or large cell lung cancer), pancreatic cancer (e.g., pancreatic ductal adenocarcinoma, pancreatic metatstatic), ovarian cancer, colorectal cancer and bladder cancer, or any combination thereof.

[007] Accordingly, in one aspect, the invention pertains to an isolated nucleic acid molecule encoding a chimeric antigen receptor (CAR), wherein the CAR comprises an anti-mesothelin binding domain (e.g., a human anti-mesothelin binding domain), a transmembrane domain, and an intracellular signaling domain comprising a stimulatory domain. In one embodiment, the encoded anti-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 human anti-mesothelin binding domain described herein, and 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 anti-mesothelin binding domain described herein. In one embodiment, the encoded human anti-mesothelin binding domain comprises, or consists of, a light chain variable region described herein (e.g., in Table 2, 4 or 5) and/or a heavy chain variable region described herein (e.g., in Table 2, 4, or 5). In one embodiment, the encoded anti-mesothelin binding domain is a scFv comprising or consisting of a light chain and a heavy chain of an amino acid sequence of Table 2. In an embodiment, the anti-mesothelin binding domain (e.g., an scFV) comprises or consists: 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 2, or a sequence with 95-99% identity with an amino acid sequence of Table 2; and/or a heavy chain variable region comprising, or consisting of, 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 2, or a sequence with 95-99% identity to an amino acid sequence of Table 2. In one embodiment, the human anti-mesothelin binding domain comprises, or consists of, a sequence selected from the group consisting of SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, 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, and SEQ ID NO: 62, or a sequence with 95-99% identity thereof. In one embodiment, the nucleic acid sequence encoding the human anti-mesothelin binding domain comprises, or consists of, a sequence selected from the group consisting of 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, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, and SEQ ID NO: 110, or a sequence with 95-99% identity thereof.

[008] In one embodiment, the isolated nucleic acid further comprises a sequence encoding a transmembrane domain, e.g., a transmembrane domain described herein. In one embodiment, the encoded transmembrane domain comprises, or consists of, a transmembrane domain of a protein selected from the alpha, beta or zeta chain of the T-cell receptor, CD28, CD3 epsilon, CD45, CD4, CD5, CD8, CD9, CD16, CD22, CD33, CD37, CD64, CD80, CD86, CD134, CD137 and CD154. In one embodiment, the encoded transmembrane domain comprises, or consists of, a sequence of SEQ ID NO: 12. In one embodiment, the transmembrane domain comprises, or consists of, an amino acid sequence having at least one, two or three modifications (e.g., substitutions) but not more than 20, 10 or 5 modifications (e.g., substitutions) of an amino acid sequence of SEQ ID NO: 12, or a sequence with 95-99% identity to an amino acid sequence of SEQ ID NO: 12.

[009] In one embodiment, the encoded CAR includes an anti-mesothelin binding domain, e.g., an anti-mesothelin binding domain described herein, connected to the transmembrane domain by a hinge region, e.g., a hinge region described herein. In one embodiment, the hinge region comprises, or consists of, SEQ ID NO: 6 or SEQ ID NO: 8.

[0010] In one embodiment, the isolated nucleic acid molecule further comprises a sequence encoding a costimulatory domain, e.g., a costimulatory domain described herein. In one embodiment, the costimulatory domain is a functional signaling domain obtained from a protein selected from the group consisting of OX40, CD27, CD28, CDS, ICAM-1, LFA-1 (CD11a/CD18), ICOS (CD278), and 4-1BB (CD137). In one embodiment, the encoded costimulatory domain comprises, or consists of, a sequence of SEQ ID NO: 14. In one embodiment, the costimulatory domain comprises, or consists of, an amino acid sequence having at least one, two or three modifications (e.g., substitutions) but not more than 20, 10 or 5 modifications (e.g., substitutions) of an amino acid sequence of SEQ ID NO: 14, or a sequence with 95-99% identity to an amino acid sequence of SEQ ID NO: 14.

[0011] In one embodiment, the isolated nucleic acid comprises a sequence encoding an intracellular signaling domain, e.g., an intracellular signaling domain described herein. In one embodiment, the isolated nucleic acid encodes a functional signaling domain of 4-1BB and/or a functional signaling domain of CD3 zeta. In one embodiment, the encoded intracellular signaling domain comprises the sequence of SEQ ID NO: 7 and/or the sequence of SEQ ID NO: 9 or SEQ ID NO: 10. In one embodiment, the intracellular signaling domain comprises an amino acid sequence having at least one, two or three modifications (e.g., substitutions) but not more than 20, 10 or 5 modifications (e.g., substitutions) of an amino acid sequence of SEQ ID NO: 7 and/or an amino acid sequence of SEQ ID NO: 9 or SEQ ID NO: 10, or a sequence with 95-99% identity to an amino acid sequence of SEQ ID NO: 7 and/or an amino acid sequence of SEQ ID NO: 9 or SEQ ID NO: 10. In one embodiment, the encoded intracellular signaling domain comprises, or consists of, the sequence of SEQ ID NO: 7 and the sequence of SEQ ID NO: 9 or SEQ ID NO: 10, wherein the sequences comprising the intracellular signaling domain are expressed in the same frame and as a single polypeptide chain.

[0012] In another aspect, the invention pertains to an isolated nucleic acid molecule encoding a CAR construct comprising a leader sequence, e.g., of SEQ ID NO: 1; an anti-mesothelin

binding domain described herein, e.g., having an amino acid sequence of Table 2, or a sequence with 95-99% identity thereof; a hinge region, e.g., of SEQ ID NO: 2; a transmembrane domain, e.g., having a sequence of SEQ ID NO: 6; a costimulatory domain, e.g., a 4-1BB costimulatory domain having a sequence of SEQ ID NO:7; and a primary signaling domain, e.g., CD3 zeta stimulatory domain having a sequence of SEQ ID NO:9 or 10. In one embodiment, the isolated nucleic acid molecule comprises (e.g., consists of) a nucleic acid sequence encoding a polypeptide having an amino acid sequence of Table 2. In one embodiment, the isolated nucleic acid molecule comprises (consists of) a nucleic acid encoding a polypeptide having 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 Table 2, or a sequence with 95-99% identity to an amino acid sequence of Table 2.

[0013] In another aspect, the invention pertains to an isolated polypeptide molecule encoded by the nucleic acid sequence, e.g., a nucleic acid described herein.

[0014] In another aspect, the invention pertains to an isolated polypeptide molecule comprising, or consisting of, a sequence selected from the group consisting of Table 2, 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 2, or a sequence with 95-99% identity to an amino acid sequence of Table 2. In one embodiment, the isolated polypeptide 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 anti-mesothelin binding domain described herein, and 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 anti-mesothelin binding domain described herein.

[0015] In another aspect, the invention pertains to an isolated chimeric antigen receptor (CAR) molecule comprising an anti-mesothelin binding domain described herein, e.g., a human anti-mesothelin binding domain described herein, a transmembrane domain, and an intracellular signaling domain comprising a stimulatory domain.

[0016] In one embodiment, the anti-mesothelin binding domain does not compete for binding to human mesothelin with an antigen binding domain comprising a sequence comprising SEQ ID NO: 279.

[0017] In one embodiment, the anti-mesothelin binding domain competes for binding to human mesothelin with an antigen binding domain comprising a LC CDR1, LC CDR2 and LC CDR3 of an anti-mesothelin light chain amino acid sequence selected from SEQ ID NO: 43 or SEQ ID NO: 49 and an HC CDR1, HC CDR2, and HC CDR3 of an anti-mesothelin heavy chain amino acid sequence selected from SEQ ID NO: 43 or SEQ ID NO: 49. In one embodiment, the anti-mesothelin binding domain competes for binding to human mesothelin with an antigen binding domain comprising SEQ ID NO:43 or SEQ ID NO:49.

[0018] In one embodiment, the anti-mesothelin binding domain binds to a different epitope of human mesothelin than the epitope of human mesothelin targeted by the antigen binding domain comprising a sequence comprising SEQ ID NO: 279. In an embodiment, the epitope comprises a sequence of amino acids selected from amino acids 314-315, 317-318, 346-349, and 369-375 of SEQ ID NO: 278, or any combination thereof. In an embodiment, the epitope comprises one or more amino acids selected from amino acids 314-315, 317-318, 346-349, and 369-375 of SEQ ID NO: 278, or any combination thereof.

[0019] In an embodiment, the anti-mesothelin binding domain described herein does not bind to the N-terminus of mesothelin as shown in SEQ ID NO: 278. In one embodiment, the anti-mesothelin binding domain binds to the C-terminus of human mesothelin. In one embodiment, the anti-mesothelin binding domain binds an epitope within amino acids 450-588 of SEQ ID NO: 278. In one embodiment, the epitope bound by the anti-mesothelin binding domain comprises a sequence selected from amino acids 485-490, 498-507, 532-537, and 545-572 of SEQ ID NO: 278, or a combination thereof. In one embodiment, the epitope bound by the anti-mesothelin binding domain comprises one or more amino acids selected from amino acids 485-490, 498-507, 532-537, and 545-572 of SEQ ID NO: 278, or any combination thereof. In these embodiments, SEQ ID NO: 278 represents amino acids 296-588 of human mesothelin, e.g., the first amino acid of SEQ ID NO: 278 is amino acid 296 and the last amino acid of SEQ ID NO: 278 is amino acid 588.

[0020] In one embodiment, the anti-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 human anti-mesothelin binding domain described herein, and 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 anti-mesothelin binding domain described herein. In one embodiment, the human anti-mesothelin binding domain comprises, or consists of, 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 anti-mesothelin binding domain is a scFv comprising, or consisting of, a light chain variable region and a heavy chain variable region of an amino acid sequence of Table 2. In an embodiment, the anti-mesothelin binding domain (e.g., an scFv) comprises, or consists of: 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 2, or a sequence with 95-99% identity to an amino acid sequence of 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) 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 2, or a sequence with 95-99% identity to an amino acid sequence of Table 2. In one embodiment, the human anti-mesothelin binding domain comprises, or consists of, a sequence selected from the group consisting of SEQ ID NO: 39; SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, 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, and SEQ ID NO: 62, or a sequence with 95-99% identity thereof.

[0021] In one embodiment, the transmembrane domain is a transmembrane domain of a protein selected from the group consisting of the alpha, beta or zeta chain of the T-cell receptor, CD28, CD3 epsilon, CD45, CD4, CD5, CD8, CD9, CD16, CD22, CD33, CD37, CD64, CD80, CD86, CD134, CD137 and CD154. In one embodiment, the transmembrane domain comprises a

transmembrane domain described herein, e.g., having a sequence of SEQ ID NO:6, an amino acid sequence having at least one, two or three modifications (e.g., substitutions) but not more than 20, 10 or 5 modifications (e.g., substitutions) of an amino acid sequence of SEQ ID NO:6, or a sequence with 95-99% identity to an amino acid sequence of SEQ ID NO:6.

[0022] In one embodiment, the anti-mesothelin binding domain is connected to the transmembrane domain by a hinge region. In one embodiment, the hinge region comprises a hinge region described herein, e.g., a hinge region of SEQ ID NO:2.

[0023] In one embodiment, the isolated CAR molecule further comprises a costimulatory domain, e.g., a costimulatory domain described herein. In one embodiment, the costimulatory domain is a functional signaling domain obtained from a protein selected from the group consisting of OX40, CD27, CD28, CDS, ICAM-1, LFA-1 (CD11a/CD18), ICOS (CD278), and 4-1BB (CD137) or functional variant thereof. In one embodiment, the costimulatory domain comprises, or consists of, a sequence of SEQ ID NO:7. In one embodiment, the costimulatory domain comprises, or consists of, an amino acid sequence having at least one, two or three modifications (e.g., substitutions) but not more than 20, 10 or 5 modifications (e.g., substitutions) of an amino acid sequence of SEQ ID NO:7, or a sequence with 95-99% identity to an amino acid sequence of SEQ ID NO:7.

[0024] In one embodiment, the isolated CAR molecule comprises an intracellular signaling domain, e.g., an intracellular signaling domain described herein. In one embodiment, the intracellular signaling domain comprises a functional signaling domain of 4-1BB and/or a functional signaling domain of CD3 zeta. In one embodiment, the intracellular signaling domain comprises, or consists of, the sequence of SEQ ID NO: 7 and/or the sequence of SEQ ID NO: 9 or SEQ ID NO: 10. In one embodiment, the intracellular signaling domain comprises, or consists of, an amino acid sequence having at least one, two or three modifications (e.g., substitutions) but not more than 20, 10 or 5 modifications (e.g., substitutions) of an amino acid sequence of SEQ ID NO:7 and/or an amino acid sequence of SEQ ID NO:9 or SEQ ID NO: 10, or a sequence with 95-99% identity to an amino acid sequence of SEQ ID NO:7 and/or an amino acid sequence of SEQ ID NO:9 or SEQ ID NO: 10. In one embodiment, the intracellular signaling domain comprises, or consists of, the sequence of SEQ ID NO: 9 and the sequence of

SEQ ID NO: 9 or SEQ ID NO: 10, wherein the sequences comprising the intracellular signaling domain are expressed in the same frame and as a single polypeptide chain.

[0025] In another aspect, the invention pertains to an isolated CAR molecule comprising a leader sequence, e.g., of SEQ ID NO: 1; an anti-mesothelin binding domain described herein, e.g., having an amino acid sequence of Table 2, or a sequence with 95-99% identify thereof; a hinge region, e.g., of SEQ ID NO: 2; a transmembrane domain, e.g., having a sequence of SEQ ID NO: 6; a costimulatory domain, e.g., a 4-1BB costimulatory domain having a sequence of SEQ ID NO: 7; and a primary signaling domain, e.g., CD3 zeta stimulatory domain having a sequence of SEQ ID NO: 9 or SEQ ID NO: 10. In one embodiment, the isolated CAR molecule comprises (e.g., consists of) a polypeptide having an amino acid sequence of Table 2. In one embodiment, the isolated CAR molecule comprises (consists of) a polypeptide having 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 Table 2, or a sequence with 95-99% identity to an amino acid sequence of Table 2. In one embodiment, the isolated CAR molecule comprises, or consists of, an amino acid sequence selected from the group consisting of 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, SEQ ID NO: 70, 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, SEQ ID NO: 79, SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 83, SEQ ID NO: 84, SEQ ID NO: 85, and SEQ ID NO: 86.

[0026] In another aspect, the invention pertains to a vector comprising a nucleic acid sequence described herein. In one embodiment, the nucleic acid sequence encodes a CAR molecule, e.g., a CAR molecule described herein. In one embodiment, the vector is selected from the group consisting of a DNA, a RNA, a plasmid, a lentivirus vector, adenoviral vector, or a retrovirus vector.

[0027] In one embodiment, the vector is a lentivirus vector, e.g., a lentivirus vector described herein. In one embodiment, the vector further comprises a promoter. In one embodiment, the promoter is an EF-1 α promoter. In one embodiment, the EF-1 α promoter comprises a sequence of SEQ ID NO: 11.

[0028] In one embodiment, the vector is an in vitro transcribed vector, e.g., a vector that transcribes RNA of a nucleic acid molecule described herein. In one embodiment, the RNA is transcribed from an in vitro transcription vector, wherein the vector is pD-A.anti-meso BD OF.2bg.150A, wherein the anti-meso BD is an anti-mesothelin binding domain described herein. In one embodiment, the nucleic acid sequence in the vector further comprises a poly(A) tail, e.g., a poly A tail described herein, e.g., comprising about 150 adenosine bases (SEQ ID NO: 271). In one embodiment, the nucleic acid sequence in the vector further comprises a 3'UTR, e.g., a 3'UTR described herein, e.g., comprising at least one repeat of a 3'UTR derived from human beta-globulin.

[0029] In another aspect, the invention pertains to a cell comprising the vector. The cell can be, e.g., a cell described herein. In one embodiment, the cell is a human T cell, e.g., a T cell described herein, or a human NK cell, e.g., a human NK cell described herein. In one embodiment, the human T cell is a CD8+ T cell. In one embodiment, the cell is an autologous T cell. In one embodiment, the cell is an allogeneic T cell. In one embodiment, the cell is a T cell and the T cell is diacylglycerol kinase (DGK) deficient. In one embodiment, the cell is a T cell and the T cell is Ikaros deficient. In one embodiment, the cell is a T cell and the T cell is both DGK and Ikaros deficient.

[0030] In one aspect, the CAR-expressing cell described herein can further comprise a second CAR, e.g., a second CAR that includes a different antigen binding domain, e.g., to the same target (mesothelin) or a different target (e.g., a target other than mesothelin on stroma cells, e.g., FAP; a target other than mesothelin on prostate cancer cells, e.g., androgen receptor, OR51E2, PSMA, PSCA, PDGRF- β , TARP, GloboH, MAD-CT-1, or MAD-CT-2; a target other than mesothelin on ovarian cancer cells, e.g., Tn, PRSS21, CD171, Lewis Y, folate receptor α , claudin6, GloboH, or sperm protein 17; e.g., a target other than mesothelin on lung cancer cells, e.g., VEGF, HER3, IGF-1R, EGFR, DLL4, or Trop-2). In one embodiment, the CAR-expressing cell comprises a first CAR that targets a first antigen and includes an intracellular signaling domain having a costimulatory signaling domain but not a primary signaling domain, and a second CAR that targets a second, different, antigen and includes an intracellular signaling domain having a primary signaling domain but not a costimulatory signaling domain. In one embodiment, the CAR expressing cell comprises a first mesothelin CAR that includes a mesothelin binding domain, a transmembrane domain and a costimulatory domain and a second

CAR that targets an antigen other than mesothelin (e.g., an antigen expressed on stroma cells, lung cancer cells, prostate cancer cells or ovarian cancer cells) and includes an antigen binding domain, a transmembrane domain and a primary signaling domain. In another embodiment, the CAR expressing cell comprises a first mesothelin CAR that includes a mesothelin binding domain, a transmembrane domain and a primary signaling domain and a second CAR that targets an antigen other than mesothelin (e.g., an antigen expressed on stroma cells, lung cancer cells, prostate cancer cells or ovarian cancer cells) and includes an antigen binding domain to the antigen, a transmembrane domain and a costimulatory signaling domain.

[0031] In one embodiment, the CAR-expressing cell comprises a mesothelin CAR described herein and 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 mesothelin. 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, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), LAG3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4 and TGFR beta.

[0032] In another embodiment, the CAR-expressing cell described herein can further express another agent, e.g., an agent which enhances the activity or fitness of a CAR-expressing cell, e.g., an agent described herein. For example, in one embodiment, the agent can be an agent which inhibits a molecule that modulates or regulates, e.g., inhibits, T cell function. In some embodiments, the molecule that modulates or regulates T cell function is an inhibitory molecule. Examples of inhibitory molecules include PD1, PD-L1, CTLA4, TIM3, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), LAG3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4 and TGFR beta. In embodiments, an agent, e.g., an inhibitory nucleic acid, e.g., a dsRNA, e.g., an siRNA or shRNA; or e.g., an inhibitory protein or system, e.g., a clustered regularly interspaced short palindromic repeats (CRISPR), a transcription-activator like effector nuclease (TALEN), or a zinc finger endonuclease (ZFN), e.g., as described herein, can be used to inhibit expression of a molecule that modulates or regulates, e.g., inhibits, T-cell function in the CAR-expressing cell. In an embodiment the agent is an shRNA, e.g., an shRNA described herein. In an embodiment, the agent that modulates or regulates, e.g., inhibits, T-cell function is inhibited within a CAR-expressing cell. For example, a dsRNA molecule that inhibits expression of a

molecule that modulates or regulates, e.g., inhibits, T-cell function is linked to the nucleic acid that encodes a component, e.g., all of the components, of the CAR.

[0033] In one embodiment, the agent which inhibits an inhibitory molecule comprises a first polypeptide, e.g., an inhibitory molecule, associated with a second polypeptide that provides a positive signal to the cell, e.g., an intracellular signaling domain described herein. In one embodiment, the agent comprises a first polypeptide, e.g., of an inhibitory molecule such as PD1, PD-L1, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), LAG3, CTLA4, , VISTA, CD160, BTLA, LAIR1, TIM3, 2B4, TGFR beta and TIGIT, or a fragment of any of these (e.g., at least a portion of the extracellular domain of any of these), and a second polypeptide which is an intracellular signaling domain described herein (e.g., comprising a costimulatory domain (e.g., 41BB, CD27 or CD28, e.g., as described herein) and/or a primary signaling domain (e.g., a CD3 zeta signaling domain described herein)). In one embodiment, the agent comprises a first polypeptide of PD1 or a fragment thereof (e.g., at least a portion of the extracellular domain of PD1), and a second polypeptide of an intracellular signaling domain described herein (e.g., a CD28 signaling domain described herein and/or a CD3 zeta signaling domain described herein).

[0034] In another aspect, the invention pertains to a method of making a cell comprising transducing a cell described herein, e.g., a T cell or a NK cell, with a vector comprising a nucleic acid encoding a CAR molecule, e.g., a CAR molecule described herein. In one embodiment, the vector is a lentiviral vector described herein.

[0035] The present invention also provides a method of generating a population of RNA-engineered cells, e.g., cells described herein, e.g., T cells or NK cells, transiently expressing exogenous RNA. The method comprises introducing an in vitro transcribed RNA or synthetic RNA into a cell, where the RNA comprises a nucleic acid encoding a CAR molecule described herein.

[0036] In another aspect, the invention pertains to a method of providing anti-tumor immunity in a subject comprising administering to the subject an effective amount of a cell comprising a CAR molecule, e.g., a cell expressing a CAR molecule described herein, a cell described herein. In one embodiment, the cell is an autologous T cell or NK cell. In one

embodiment, the cell is an allogeneic T cell or NK cell. In one embodiment, the subject is a human.

[0037] In another aspect, the invention pertains to a method of treating a subject having a disease associated with expression of mesothelin (e.g., a proliferative disease, a precancerous condition, and a noncancer related indication associated with the expression of mesothelin) comprising administering to the subject an effective amount of a cell comprising a CAR molecule, e.g., as described herein.

[0038] In one embodiment, the disease associated with mesothelin is cancer, e.g., a cancer described herein. In one embodiment, the disease associated with mesothelin is selected from the group consisting of: mesothelioma (e.g., malignant pleural mesothelioma), lung cancer (e.g., non-small cell lung cancer, small cell lung cancer, squamous cell lung cancer, or large cell lung cancer), pancreatic cancer (e.g., pancreatic ductal adenocarcinoma), ovarian cancer, colorectal cancer and bladder cancer or any combination thereof. In one embodiment, the disease is pancreatic cancer, e.g., metastatic pancreatic ductal adenocarcinoma (PDA), e.g., in a subject who has progressed on at least one prior standard therapy. In one embodiment, the disease is mesothelioma (e.g., malignant pleural mesothelioma), e.g., in a subject who has progressed on at least one prior standard therapy. In one embodiment, the disease is ovarian cancer, e.g., serous epithelial ovarian cancer, e.g., in a subject who has progressed after at least one prior regimen of standard therapy.

[0039] In one embodiment, the mesothelin CAR expressing cell, e.g., T cell or NK cell, is administered to a subject that has received a previous dose of melphalan.

[0040] In one embodiment, the cells expressing a CAR molecule, e.g., a CAR molecule described herein, are administered in combination with an agent that enhances the activity or fitness of a cell expressing a CAR molecule, e.g., an agent described herein.

[0041] In one embodiment, the cells expressing a CAR molecule, e.g., a CAR molecule described herein, are administered in combination with a low, immune enhancing dose of an mTOR inhibitor. While not wishing to be bound by theory, it is believed that treatment with a low, immune enhancing, dose (e.g., a dose that is insufficient to completely suppress the immune system but sufficient to improve immune function) is accompanied by a decrease in PD-1 positive T cells or an increase in PD-1 negative cells. PD-1 positive T cells, but not PD-1

negative T cells, can be exhausted by engagement with cells which express a PD-1 ligand, e.g., PD-L1 or PD-L2.

[0042] In an embodiment this approach can be used to optimize the performance of CAR cells described herein in the subject. While not wishing to be bound by theory, it is believed that, in an embodiment, the performance of endogenous, non-modified immune effector cells, e.g., T cells, is improved. While not wishing to be bound by theory, it is believed that, in an embodiment, the performance of a mesothelin CAR expressing cell is improved. In other embodiments, cells, e.g., T cells or NK cells, which have, or will be engineered to express a CAR, can be treated ex vivo by contact with an amount of an mTOR inhibitor that increases the number of PD1 negative immune effector cells, e.g., T cells or increases the ratio of PD1 negative immune effector cells, e.g., T cells/ PD1 positive immune effector cells, e.g., T cells.

[0043] In an embodiment, administration of a low, immune enhancing, dose of an mTOR inhibitor, e.g., an allosteric inhibitor, e.g., RAD001, or a catalytic inhibitor, is initiated prior to administration of an CAR expressing cell described herein, e.g., T cells or NK cells. In an embodiment, the CAR cells are administered after a sufficient time, or sufficient dosing, of an mTOR inhibitor, such that the level of PD1 negative immune effector cells, e.g., T cells, or the ratio of PD1 negative immune effector cells, e.g., T cells/ PD1 positive immune effector cells, e.g., T cells, has been, at least transiently, increased.

[0044] In an embodiment, the cell, e.g., T cell or NK cell, to be engineered to express a CAR, is harvested after a sufficient time, or after sufficient dosing of the low, immune enhancing, dose of an mTOR inhibitor, such that the level of PD1 negative immune effector cells, e.g., T cells, or the ratio of PD1 negative immune effector cells, e.g., T cells/ PD1 positive immune effector cells, e.g., T cells, in the subject or harvested from the subject has been, at least transiently, increased.

[0045] In one embodiment, the cells expressing a CAR molecule, e.g., a CAR molecule described herein, are administered in combination with an agent that ameliorates one or more side effect associated with administration of a cell expressing a CAR molecule, e.g., an agent described herein.

[0046] In one embodiment, the cells expressing a CAR molecule, e.g., a CAR molecule described herein, are administered in combination with an agent that treats the disease associated with mesothelin expression, e.g., an agent described herein.

[0047] In one embodiment, the cells expressing a CAR molecule, e.g., a CAR molecule described herein, are administered at a dose and/or dosing schedule described herein.

[0048] In one embodiment, the cells expressing a CAR molecule, e.g., a CAR molecule described herein, are administered as a first line treatment for the disease, e.g., the cancer, e.g., the cancer described herein. In another embodiment, the cells expressing a CAR molecule, e.g., a CAR molecule described herein, are administered as a second, third, fourth line treatment for the disease, e.g., the cancer, e.g., the cancer described herein.

[0049] In one embodiment, a population of cells described herein is administered.

[0050] In one embodiment, the CAR molecule is introduced into T cells or NK cells, e.g., using in vitro transcription, and the subject (e.g., human) receives an initial administration of cells comprising a CAR molecule, and one or more subsequent administrations of cells comprising a CAR molecule, wherein the one or more subsequent administrations are administered less than 15 days, e.g., 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, or 2 days after the previous administration. In one embodiment, more than one administration of cells comprising a CAR molecule are administered to the subject (e.g., human) per week, e.g., 2, 3, or 4 administrations of cells comprising a CAR molecule are administered per week. In one embodiment, the subject (e.g., human subject) receives more than one administration of cells comprising a CAR molecule per week (e.g., 2, 3 or 4 administrations per week) (also referred to herein as a cycle), followed by a week of no administration of cells comprising a CAR molecule, and then one or more additional administration of cells comprising a CAR molecule (e.g., more than one administration of the cells comprising a CAR molecule per week) is administered to the subject. In another embodiment, the subject (e.g., human subject) receives more than one cycle of cells comprising a CAR molecule, and the time between each cycle is less than 10, 9, 8, 7, 6, 5, 4, or 3 days. In one embodiment, the cells comprising a CAR molecule are administered every other day for 3 administrations per week. In one embodiment, the cells comprising a CAR molecule are administered for at least two, three, four, five, six, seven, eight or more weeks.

[0051] In one aspect, the invention includes a population of autologous or allogenic cells that are transfected or transduced with a vector comprising a nucleic acid molecule encoding a mesothelin-CAR molecule, e.g., as described herein. In one embodiment, the vector is a retroviral vector. In one embodiment, the vector is a self-inactivating lentiviral vector as

described elsewhere herein. In one embodiment, the vector is delivered (e.g., by transfecting or electroporating) to a cell, e.g., a T cell or a NK cell, wherein the vector comprises a nucleic acid molecule encoding a mesothelin CAR molecule as described herein, which is transcribed as an mRNA molecule, and the mesothelin CAR molecule is translated from the RNA molecule and expressed on the surface of the cell.

[0052] In another aspect, the present invention provides a population of CAR-expressing cells, e.g., CART cells. In some embodiments, the population of CAR-expressing cells comprises a mixture of cells expressing different CARs. For example, in one embodiment, the population of CART cells can include a first cell expressing a CAR having an anti-mesothelin binding domain described herein, and a second cell expressing a CAR having a different anti-mesothelin binding domain, e.g., an anti-mesothelin binding domain described herein that differs from the anti-mesothelin binding domain in the CAR expressed by the first cell. As another example, the population of CAR-expressing cells can include a first cell expressing a CAR that includes an anti-mesothelin binding domain, e.g., as described herein, and a second cell expressing a CAR that includes an antigen binding domain to a target other than mesothelin (e.g., a target other than mesothelin on stroma cells, e.g., FAP; a target other than mesothelin on prostate cancer cells, e.g., androgen receptor, OR51E2, PSMA, PSCA, PDGRF- β , TARP, GloboH, MAD-CT-1, or MAD-CT-2; a target other than mesothelin on ovarian cancer cells, e.g., Tn, PRSS21, CD171, Lewis Y, folate receptor α , claudin6, GloboH, or sperm protein 17; e.g., a target other than mesothelin on lung cancer cells, e.g., VEGF, HER3, IGF-1R, EGFR, DLL4, or Trop-2). In one embodiment, the population of CAR-expressing cells includes, e.g., a first cell expressing a CAR that includes a primary intracellular signaling domain, and a second cell expressing a CAR that includes a secondary signaling domain.

[0053] In another aspect, the present invention provides a population of cells wherein at least one cell in the population expresses a CAR having an anti- mesothelin binding domain described herein, and a second cell expressing another agent, e.g., an agent which enhances the activity or function of a CAR-expressing cell. For example, in one embodiment, the agent can be an agent which inhibits a molecule that modulates or regulates, e.g., inhibits, T cell function. In some embodiments, the molecule that modulates or regulates T cell function is an inhibitory molecule, e.g., an agent described herein. Examples of inhibitory molecules include PD1, PD-L1, CTLA4, TIM3, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), LAG3, VISTA, BTLA,

TIGIT, LAIR1, CD160, 2B4 and TGFR beta. In embodiments, an agent, e.g., an inhibitory nucleic acid, e.g., a dsRNA, e.g., an siRNA or shRNA; or e.g., an inhibitory protein or system, e.g., a clustered regularly interspaced short palindromic repeats (CRISPR), a transcription-activator like effector nuclease (TALEN), or a zinc finger endonuclease (ZFN), e.g., as described herein, can be used to inhibit expression of a molecule that modulates or regulates, e.g., inhibits, T-cell function in the CAR-expressing cell. In an embodiment the agent is an shRNA, e.g., an shRNA described herein. In an embodiment, the agent that modulates or regulates, e.g., inhibits, T-cell function is inhibited within a CAR-expressing cell. For example, a dsRNA molecule that inhibits expression of a molecule that modulates or regulates, e.g., inhibits, T-cell function is linked to the nucleic acid that encodes a component, e.g., all of the components, of the CAR.

[0054] In one embodiment, the agent which inhibits an inhibitory molecule comprises a first polypeptide, e.g., an inhibitory molecule, associated with a second polypeptide that provides a positive signal to the cell, e.g., an intracellular signaling domain described herein. In one embodiment, the agent comprises a first polypeptide, e.g., of an inhibitory molecule such as PD1, PD-L1, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), LAG3, CTLA4, , VISTA, CD160, BTLA, LAIR1, TIM3, 2B4, TGFR beta and TIGIT, or a fragment of any of these (e.g., at least a portion of an extracellular domain of any of these), and a second polypeptide which is an intracellular signaling domain described herein (e.g., comprising a costimulatory domain (e.g., 41BB, CD27 or CD28, e.g., as described herein) and/or a primary signaling domain (e.g., a CD3 zeta signaling domain described herein). In one embodiment, the agent comprises a first polypeptide of PD1 or a fragment thereof (e.g., at least a portion of the extracellular domain of PD1), and a second polypeptide of an intracellular signaling domain described herein (e.g., a CD28 signaling domain described herein and/or a CD3 zeta signaling domain described herein).

[0055] In one embodiment, the nucleic acid molecule encoding a mesothelin CAR molecule, e.g., as described herein, is expressed as an mRNA molecule. In one embodiment, the genetically modified mesothelin CAR-expressing cells, e.g., T cells or NK cells, can be generated by transfecting or electroporating an RNA molecule encoding the desired CARs (e.g., without a vector sequence) into the cell. In one embodiment, a mesothelin CAR molecule is translated from the RNA molecule once it is incorporated and expressed on the surface of the recombinant cell.

[0056] In another aspect, the invention pertains to the isolated nucleic acid molecule encoding a CAR molecule, e.g., a CAR molecule described herein, a CAR molecule described herein, a vector comprising a CAR molecule described herein, and/or a cell comprising a CAR molecule described herein for use as a medicament.

[0057] In another aspect, the invention pertains to a the isolated nucleic acid molecule encoding a CAR molecule described herein, a CAR molecule described herein, a vector comprising a CAR molecule described herein, and/or a cell comprising a CAR molecule described herein for use in the treatment of a disease expressing mesothelin, e.g., as described herein.

BRIEF DESCRIPTION OF THE DRAWINGS

[0058] FIG. 1 is a schematic of the pD-A.anti-meso BD.OF.BBZ.2bg.150A plasmid. Figure discloses "150A" as SEQ ID NO: 271.

[0059] FIG. 2 depicts cell manufacturing and treatment schedules that can be used. **(A)** Autologous cells are obtained by leukocyte apheresis and T cells are enriched by expansion with anti-CD3/CD28 mAb coated magnetic beads. Cells are expanded for 8 to 12 days. On the last day of culture, the beads are removed using a magnetic field and the cells are washed, electroporated with human meso CAR mRNA construct, and cryopreserved in infusible medium. **(B)** Three treatment infusion schedules are depicted. On Schedule 1, patients receive 1×10^8 human meso bearing CART cells by intravenous (i.v.) infusion on day 0 followed by 1×10^9 human meso bearing CART cells one week later. Safety can be monitored for a minimum of one month before patients are eligible for Schedule 2. On Schedule 2, patients receive 1×10^8 human meso bearing CART cells by i.v. infusion three times per week for one week followed by one week of rest and then 1×10^9 human meso bearing CART cells administered three times per week for one week. On Schedule 3, patients receive $3 \times 10^8/m^2$ human meso bearing CART cells by i.v. infusion three times per week for three weeks followed by intra-tumoral injection into a primary lesion of 2×10^8 human meso bearing CART cells on days +35 and +57.

[0060] FIG. 3A and 3B are graphic representations of cytotoxicity as assayed donor 2 (healthy donor) T cell transduced with mouse SS1 CAR or the anti-MSLN CARs M1 to M12 of

the invention and cultured with either control K562 cells that do not express MSLN as shown in FIG. 3A, or K562 cells transduced to express MSLN (K562-Meso) as shown in FIG. 3B.

[0061] FIG. 4A and 4B are graphs showing the IFN γ secretion of the mouse SS1 and CD19 CART and the anti-MSLN CARTs upon stimulation by MSLN+ cells. FIG. 4A shows reactivity to the transduced cell line K562-Meso and its MSLN-negative parental line K562. FIG. 4B shows reactivity toward cancer cells naturally expressing MSLN; the ovarian cancer line Ovcar8 and the pancreatic cancer lines SW1990 and Panc0203.

[0062] FIG. 5 shows a clinical trial design for mesothelin CARTs made by transducing a CAR construct with a lentiviral vector.

[0063] FIG. 6A, 6B, 6C, and 6D show anti-tumor activity of CART-meso cells.

[0064] FIG. 7A, 7B, and 7C show the *in vivo* persistence of CARTmeso cells and trafficking to primary and metastatic tumor sites.

[0065] FIG. 8 shows cytokine and chemokines in the serum after CARTmeso cell infusion.

[0066] FIG. 9A and 9B show CARTmeso cell induction of anti-tumor antibodies. Sera was obtained from the MPM patient (FIG. 9A) and the pancreatic cancer patient (FIG. 9B).

[0067] FIG. 10 shows tumor growth in NSG mice injected with EMMESO tumor cells. After tumors grew to ~ 200 mm 3 in size, mesoCAR T cells were injected via tail vein and measured for 39 days post injection.

[0068] FIG. 11A and 11B show the expression of mesoCAR by flow cytometry analysis at the time of injection (FIG. 11A) or after 40 days at the time of harvest from xenograft tumors.

[0069] FIG. 12 shows the functional capacity of mesoCAR T cells with regard to *in vitro* killing when isolated from the flank of NSG mice after 39 days, or cryo preserved after transduction.

[0070] FIG. 13 shows the expression of inhibitor enzymes DGK and SHP1 in TILs isolated from EMESO flank tumor compared to overnight-rested TILs.

[0071] FIG. 14A, 14B, 14C, 14D, 14E, and 14F show the effect of treatment with inhibitors (anti-PDL1, DGK inhibitor, and SSG) of inhibitory mechanisms that downregulate mesoCART

function on tumor cell killing (FIG. 14A, 14C and 14E) and IFNgamma cytokine secretion (FIG. 14B, 14C, and 14F).

[0072] FIG. 15A, 15B, 15C, and 15D show cytokine secretion from a small panel of human CART-MSLN after stimulation with various tumor cell lines. FIG. 15A shows IFNgamma secretion. FIG. 15B shows TNF. FIG. 15C shows IL-2. FIG. 15D shows IL-4.

[0073] FIG. 16A and 16B show the results of the killing assay of CART-MSLN-5, CART-MSLN-11, CART-MSLN17, and murine CART-MSLN-SS1 against Ovcar3 (FIG. 16A) and U87mg (FIG. 16B) tumor cells.

[0074] FIG. 17A and 17B show the results of the killing assay of the panel of CART-MSLN against Ovcar3 tumor cells.

[0075] FIG. 18 shows the anti-tumor activity of a first set of CART-MSLN (including M5, M11, M17, and M21) in the Ovcar8 xenograft model.

[0076] FIG. 19 shows the anti-tumor activity of a second set of CART-MSLN (including M12, M14, M16, and M23) in the Ovcar8 xenograft model.

[0077] FIG. 20A, 20B, and 20C depicts the loss of functionality of mesoCAR T cells in the tumor microenvironment (TILs) over time compared to fresh or thawed mesoCAR T cells. A) Cytotoxicity assay; B) IFN γ release assay; and C) western blot analysis of ERK signaling (via phosphorylation).

[0078] FIG. 21 depicts the effect of deletion of DGK on cytotoxicity of mesoCAR T cells. Percent target cell killing is assessed at different effector:target ratios.

[0079] FIG. 22 depicts the effect of deletion of DGK on IFN γ production and release from mesoCAR T cells. Concentration of IFN γ is assessed at different effector:target ratios.

[0080] FIG. 23 depicts the effect of deletion of DGK on ERK signaling, or T cell activation, mesoCAR T cells. B: albumin, M: mesothelin, 3/28: CD3/CD28 stimulated cells.

[0081] FIG. 24 depicts the effect of deletion of DGK on TGF β sensitivity of mesoCAR T cells with regard to cytotoxic activity.

[0082] FIG. 25A and 25B depict the effect of deletion of DGK on therapeutic efficacy of mesoCAR T cells in a tumor mouse model. A) Effect on anti-tumor activity is shown by tumor volume over time. B) Persistence and proliferation of tumor infiltrating cells.

[0083] FIG. 26A, 26B, 26C, 26D, 26E, and 26F shows the cytokine production and cytotoxic mediator release in CAR-expressing T cells with reduced levels of Ikaros. FIG. 26A shows Ikaros expression in wild-type and *Ikzf1*⁺⁻ CAR T cells as measured by flow cytometry (left panel) and western blot (right panel). Following stimulation with mesothelin-coated beads, PMA/Ionomycin (PMA/I), or BSA-coated beads (control), the percentage of cells producing IFN- γ (FIG. 26B), TNF- α (FIG. 26C), and IL-2 (FIG. 26D), the cytotoxic mediator granzyme B (FIG. 26E), and CD107a expression (FIG. 26F) was determined.

[0084] FIG. 27A, 27B, and 27C shows cytokine production and cytotoxic mediator release in CAR-expressing T cells with a dominant negative allele of Ikaros (IkDN). Following stimulation with mesothelin-coated beads, PMA/Ionomycin (PMA/I), or BSA-coated beads (control), the percentage of cells producing IFN- γ (FIG. 27A), IL-2 (FIG. 27B), and CD107a expression (FIG. 27C) was determined.

[0085] FIG. 28A, 28B, 28C, 28D, and 28E shows that the depletion of Ikaros did not augment activation and signaling of CAR T cells following antigen stimulation. The levels of CD69 (FIG. 28A), CD25 (FIG. 28B), and 4-1BB (FIG. 28C) was determined by flow cytometry at the indicated time points in *Ikzf1*⁺⁻ CAR T cells. In FIG. 28D, the RAS/ERK signaling pathways were examined in wild-type (WT) and Ikaros dominant negative cells (IkDN) after TCR stimulation with CD3/CD28 antibodies. The levels of phosphorylated TCR signaling proteins such as phosphorylated PLC γ , phosphorylated Lck, phosphorylated JNK, phosphorylated Akt, phosphorylated ERK, phosphorylated IKK α , and IkB α were assessed by western blot. In FIG. 28E, WT and IkDN cells transduced with mesoCAR were stimulated with BSA or mesothelin-coated beads, and downstream signaling pathways were examined by western blot by assessing the levels of phosphorylated ERK and phosphorylated PLC γ .

[0086] FIG. 29A, 29B, 29C, 29D, and 29E shows that the reduction of Ikaros in CAR T cells augments the response against target cells AE17 or mesothelin-expressing AE17 (AE17 meso) *in vitro*. FIG. 29A depicts IFN γ production in WT and *Ikzf1*⁺⁻ meso CART cells at the indicated effector:target cell ratios. Cytolysis of meso CAR-expressing WT and *Ikzf1*⁺⁻ (FIG. 29B) and IkDN (FIG. 29C) was measured at the indicated effector:target cell ratios. IFN γ production (FIG. 29D) and cytosis (FIG. 29E) of WT and *Ikzf1*⁺⁻ transduced with FAP-CAR was measured at the indicated effector:target cell ratios, where the target cells were FAP-expressing 3T3 cells.

[0087] FIG. 30A, 30B, and 30C shows the efficacy of CAR T cells with depletion of Ikaros against established tumors *in vivo*. CAR T cells were administered to mice bearing established mesothelin-expressing AE17 tumors. Tumor volume was measured after administration with mesoCAR-expressing WT and *Ikzf1*^{+/−} (FIG. 30A) or IkDN (FIG. 30B). Tumor volume was measured after administration of FAP-CAR-expressing WT and *Ikzf1*^{+/−} (FIG. 30C).

[0088] FIG. 31A, 31B, 31C, 31D, 31E, and 31F shows the increased persistence and resistance of *Ikzf1*^{+/−} CAR T cells in the immunosuppressive tumor microenvironment compared to WT CAR T cells. The percentage of CAR-expressing WT or *Ikzf1*^{+/−} cells (GFP positive) were detected by flow cytometry from harvested from the spleen (FIG. 31A) and the tumors (FIG. 31B). The functional capacity of the CAR T cells harvested 3 days after infusion from the spleen or tumors was assessed by measuring IFN γ production after stimulation with CD3/CD28 antibodies (FIG. 31C) or PMA/Ionomycin (PMA/I) (FIG. 31D). Regulatory T cells (CD4+FoxP3+ expression) and macrophages (CD206 expression) were assessed by measuring the expression of Treg or macrophage markers on CAR T cells harvested 9 days after infusion from the spleen or tumors.

[0089] FIG. 32A and 32B shows that T cells with reduced Ikaros levels are less sensitive to soluble inhibitory factors TGF β and adenosine. MesoCAR-expressing WT, *Ikzf1*^{+/−}, and IkDN cells were tested for their ability to produce IFN γ (FIG. 32A) and cytotoxicity (FIG. 32B) in response to TGF- β or adenosine.

[0090] FIG. 33A and 33B are graphs showing an increase in titers to influenza vaccine strains as compared to placebo. In FIG. 33A, the increase above baseline in influenza geometric mean titers to each of the 3 influenza vaccine strains (H1N1 A/California/ 07/2009, H3N2 A/Victoria/210/2009, B/Brisbane/60/ 2008) relative to the increase in the placebo cohort 4 weeks after vaccination is shown for each of the RAD001 dosing cohorts in the intention to treat population. The bold black line indicates the 1.2 fold increase in titers relative to placebo that is required to be met for 2 out of 3 influenza vaccine strains to meet the primary endpoint of the study. The star “*” indicates that the increase in GMT titer relative to placebo exceeds 1 with posterior probability of at least 80%. FIG 33B is a graph of the same data as in FIG. 33A for the subset of subjects with baseline influenza titers \leq 1:40.

[0091] FIG. 34 shows a scatter plot of RAD001 concentration versus fold increase in geometric mean titer to each influenza vaccine strain 4 weeks after vaccination. RAD001

concentrations (1 hour post dose) were measured after subjects had been dosed for 4 weeks. All subjects who had pharmacokinetic measurements were included in the analysis set. The fold increase in geometric mean titers at 4 weeks post vaccination relative to baseline is shown on the y axis.

[0092] FIG. 35 is a graphic representation showing increase in titers to heterologous influenza strains as compared to placebo. The increase above baseline in influenza geometric mean titers to 2 heterologous influenza strains (A/H1N1 strain A/New Jersey/8/76 and A/H3N2 strain A/Victoria/361/11) not contained in the influenza vaccine relative to the increase in the placebo cohort 4 weeks after vaccination is shown for each of the RAD001 dosing cohorts in the intention to treat population. * indicates increase in titer relative to placebo exceeds 1 with a posterior probability of at least 80%.

[0093] FIG. 36A and 36B are graphic representations of IgG and IgM levels before and after influenza vaccination. Levels of anti-A/H1N1/California/07/2009 influenza IgG and IgM were measured in serum obtained from subjects before and 4 weeks post influenza vaccination. No significant difference in the change from baseline to 4 weeks post vaccination in anti-H1N1 influenza IgG and IgM levels were detected between the RAD001 and placebo cohorts (all p values > 0.05 by Kruskal-Wallis rank sum test).

[0094] FIG. 37A, 37B, and 37C are graphic representations of the decrease in percent of PD-1-positive CD4 and CD8 and increase in PD-1-negative CD4 T cells after RAD001 treatment. The percent of PD-1-positive CD4, CD8 and PD-1-negative CD4 T cells was determined by FACS analysis of PBMC samples at baseline, after 6 weeks of study drug treatment (Week 6) and 6 weeks after study drug discontinuation and 4 weeks after influenza vaccination (Week 12). FIG. 37A shows there was a significant decrease (-37.1 – -28.5%) in PD-1-positive CD4 T cells at week 12 in cohorts receiving RAD001 at dose levels 0.5mg/Day (n=25), 5mg/Week (n=29) and 20 mg/Week (n=30) as compared to the placebo cohort (n=25) with p=0.002 (0.02), p=0.003 (q=0.03), and p= 0.01 (q=0.05) respectively. FIG. 37B shows there was a significant decrease (-43.3 – -38.5%) in PD-1-positive CD8 T cells at week 12 in cohorts receiving RAD001 (n=109) at dose levels 0.5mg/Day (n=25), 5mg/Week (n=29) and 20 mg/Week (n=30) as compared to the placebo cohort (n=25) with p=0.01 (0.05), p=0.007 (q=0.04), and p= 0.01 (q=0.05) respectively. FIG. 37C shows was a significant increase (3.0 – 4.9%) in PD-1-negative CD4 T cells at week 12 in cohorts receiving RAD001 (n=109) at dose levels 0.5mg/Day (n=25), 5mg/Week (n=29)

and 20 mg/Week (n=30) as compared to the placebo cohort (n=25) with p=0.0007 (0.02), p=0.03 (q=0.07), and p= 0.03 (q=0.08) respectively.

[0095] FIG. 38A and 38B are graphic representations of the decrease in percent of PD-1-positive CD4 and CD8 and increase in PD-1-negative CD4 T cells after RAD001 treatment adjusted for differences in baseline PD-1 expression. The percent of PD-1-positive CD4, CD8 and PD-1-negative CD4 T cells was determined by FACS analysis of PBMC samples at baseline, after 6 weeks of study drug treatment (Week 6) and 6 weeks after study drug discontinuation and 4 weeks after influenza vaccination (Week 12). FIG. 38A shows a significant decrease of 30.2% in PD-1+ CD4 T cells at week 6 in the pooled RAD cohort (n=84) compared to placebo cohort (n=25) with p=0.03 (q=0.13). The decrease in PD-1-positive CD4 T cells at week 12 in the pooled RAD as compared to the placebo cohort is 32.7% with p=0.05 (q=0.19). FIG. 38B shows a significant decrease of 37.4% in PD-1-positive CD8 T cells at week 6 in the pooled RAD001 cohort (n=84) compared to placebo cohort (n=25) with p=0.008 (q=0.07). The decrease in PD-1-positive CD8 T cells at week 12 in the pooled RAD001 as compared to the placebo cohort is 41.4% with p=0.066 (q=0.21). FIG. 38A and 38B represent the data in FIG. 37A, 37B, and 37C but with the different RAD001 dosage groups of FIG. 37A, 37B, and 37C pooled into the single RAD001-treated group in FIG. 38A and 38B.

[0096] FIG. 39 depicts increases in exercise and energy in elderly subjects in response to RAD001.

[0097] FIG. 40A and 40B depict the predicted effect of RAD001 on P70 S6K activity in cells. FIG. 40A depicts P70 S6 kinase inhibition with higher doses of weekly and daily RAD001; FIG. 40B depicts P70 S6 kinase inhibition with lower doses of weekly RAD001.

[0098] FIG. 41A, 41B, and 41C are Biacore T200 SPR sensograms for the scFvs SS1 (FIG. 41A), M5 (FIG. 41B), and M11 (FIG. 41C).

[0099] FIG. 42A, 42B, and 42C are epitope binning SPR sensograms for the anti-human mesothelin scFvs in comparison to the murine SS1 scFv. Competitive binding was observed for scFvs M12, M14, M16, M17, M21, and M23 (FIG. 42A). ScFv M5 (FIG. 42B) and M11 (FIG. 42C) bind to a different epitope than SS1.

[0100] FIG. 43 is a graph depicting tumor growth after various mesothelin CAR T treatments in the OVCAR8 tumor model. Mean tumor volume +/- SEM to day 62 post tumor implantation. T cells were administered on days 14 and 19. Small circles: mice treated with 100ul of PBS via

the lateral tail vein; black squares: mice treated with Isotype control T cells; gray triangles: mice treated with one dose of SS1 CAR T cells; inverted triangles: mice treated with a double dose of SS1 CAR T cells; diamonds: mice treated with a single dose of M5 CAR T cells; large circles: mice treated with a double dose of M5 CAR T cells; gray squares: mice treated with a single dose of M11 CAR T cells; and black triangles: mice treated with a double dose of M11 CAR T cells.

[00101] FIG. 44 is a schematic representation of the human mesothelin peptide coverage in hydrogen deuterium exchange mass spectrometry analysis. Each black bar represents a peptide.

[00102] FIG. 45A and 45B are graphic representations showing the difference in deuterium uptake of human mesothelin when in complex with SS1 (black bars) and M5 (grey bars). The difference in deuterium uptake upon antibody binding (represented on the y-axis) is depicted for each peptide fragment detected (represented on the x-axis), with peptides at amino acids 297-464 in FIG. 45A and peptides at amino acids 458-586 in FIG. 45B. All differences are relative to the deuterium uptake of unbound mesothelin (control). * denote regions of statistical significance using the Tukey test for peptides with a difference less than 0.75 Da.

[00103] FIG. 46 is a schematic representation showing the primary sequence of antigen human mesothelin (amino acids 296-588) and the regions protected by SS1 and M5. The black bars designate the amino acids protected when complexed with SS1 (amino acids 314-315, 317-318, 346-349, and 369-375). The grey bars designate the amino acids protected when complexed with M5 (amino acids 485-490, 498-507, 532-537, and 545-572). FIG. 47 shows a generic map showing different configurations of constructs encoding a CAR with a shRNA for coexpression of the CAR and an shRNA. FIG. 47A-47D show the various configurations on a single vector, e.g., where the U6 regulated shRNA is upstream or downstream of the EF1 alpha regulated CAR encoding elements. In the exemplary constructs depicted in FIG. 47A and 47B, the transcription occurs through the U6 and EF1 alpha promoters in the same direction. In the exemplary constructs depicted in FIG. 47C and 47D, the transcription occurs through the U6 and EF1 alpha promoters in different directions. In FIGURE 47E, the shRNA (and corresponding U6 promoter) is on a first vector, and the CAR (and corresponding EF1 alpha promoter) is on a second vector (FIG. 16E).

[00104] FIG. 48 depicts the structures of two exemplary RCAR configurations. The antigen binding members comprise an antigen binding domain, a transmembrane domain, and a switch domain. The intracellular binding members comprise a switch domain, a co-stimulatory signaling domain and a primary signaling domain. The two configurations demonstrate that the first and second switch domains described herein can be in different orientations with respect to the antigen binding member and the intracellular binding member. Other RCAR configurations are further described herein.

DETAILED DESCRIPTION

Definitions

[00105] 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.

[00106] 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.

[00107] 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 $\pm 20\%$ or in some instances $\pm 10\%$, or in some instances $\pm 5\%$, or in some instances $\pm 1\%$, or in some instances $\pm 0.1\%$ from the specified value, as such variations are appropriate to perform the disclosed methods.

[00108] 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. 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.

[00109] 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.

[00110] 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.

[00111] 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.

[00112] 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).

[00113] 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.

[00114] 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.

[00115] 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.

[00116] 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.

[00117] 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.

[00118] 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.

[00119] The term “compete” refers to the ability of an antigen binding domain, e.g., an antibody or fragment thereof, to interfere with binding directly or indirectly of another antigen binding domain, e.g., an antigen binding domain provided herein, e.g., an antibody or fragment thereof provided herein, to the target, e.g., mesothelin. The extent to which an antigen binding domain, e.g., an antibody or fragment thereof, is able to interfere with the binding of another antigen binding domain, e.g., an antibody or fragment thereof, to the target, and therefore whether it can be said to compete, can be determined using a competition binding assay. In some embodiments, a competition binding assay is a quantitative competition assay. For example, one particularly suitable quantitative competition assay uses a surface plasmon resonance (SPR)-based approach to measure binding, e.g., competition, between one antibody or fragment thereof and another antibody or fragment thereof for binding to an immobilized target. An exemplary SPR-based competition assay is described in Example 2 herein. Another suitable quantitative competition assay uses a FACS-based approach to measure competition between a labelled (e.g., His tagged, biotinylated or radioactively labeled, among others) antibody or fragment thereof and another antibody or fragment thereof for binding to the target.

[00120] 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.

[00121] The term “autologous” refers to any material derived from the same individual to whom it is later to be re-introduced into the individual.

[00122] 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.

[00123] The term “xenogeneic” refers to a graft derived from an animal of a different species.

[00124] 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, mesothelioma, 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.

[00125] The phrase “disease associated with expression of mesothelin” 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, lung cancer, ovarian cancer, pancreatic cancer, and the like.

[00126] 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, e.g., for the ability to bind mesothelin using the functional assays described herein.

[00127] 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.

[00128] 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:9, 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:10, or the equivalent residues from a non-human species, e.g., mouse, rodent, monkey, ape and the like.

[00129] 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.

[00130] 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.

[00131] 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 stimulation. 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.

[00132] 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.

[00133] 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:9. In one aspect, the “zeta stimulatory domain” or a “CD3-zeta stimulatory domain” is the sequence provided as SEQ ID NO:10.

[00134] The term a “costimulatory molecule” refers to a 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, and a ligand that specifically binds with CD83

[00135] A costimulatory intracellular signaling domain can be an 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, SLAMF7, NKp80, CD160, B7-H3, and a ligand that specifically binds with CD83, and the like.

[00136] 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.

[00137] 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. In one aspect a “4-1BB costimulatory domain” is defined as amino acid residues 214-255 of GenBank Acc. No.. 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:7 or the equivalent residues from a non-human species, e.g., mouse, rodent, monkey, ape and the like.

[00138] An “antigen presenting cell,” as used herein, means an immune system cell such as an accessory cell (e.g., a B-cell, a dendritic cell, and the like) that displays foreign antigens complexed with major histocompatibility complexes (MHC's) on their surfaces. T-cells may recognize these complexes using their T-cell receptors (TCRs). APCs process antigens and present them to T-cells.

[00139] 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 (i.e., 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.

[00140] 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).

[00141] The term “effective amount” or “therapeutically effective amount” is 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. The term “endogenous” refers to any material from or produced inside an organism, cell, tissue or system.

[00142] The term “exogenous” refers to any material introduced from or produced outside an organism, cell, tissue or system.

[00143] The term “expression” refers to the transcription and/or translation of a particular nucleotide sequence driven by its promoter.

[00144] 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.

[00145] 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.

[00146] 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. 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.

[00147] 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.

[00148] The term “humanized” refers to those 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 a significant portion 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 substantially all 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.

[00149] The term “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.

[00150] 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.

[00151] In the context of the present invention, the following abbreviations for the commonly occurring nucleic acid bases are used. “A” refers to adenine, “C” refers to cytosine, “G” refers to guanosine, “T” refers to thymidine, and “U” refers to uridine.

[00152] 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, where necessary to join two protein coding regions, are in the same reading frame.

[00153] 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.

[00154] 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)).

[00155] 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, a recombinant peptide, or a combination thereof.

[00156] 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.

[00157] 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.

[00158] 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.

[00159] 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.

[00160] 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.

[00161] The term “flexible polypeptide 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 (SEQ ID NO: 38), where n is a positive integer equal to or greater than 1. For example, n=1, n=2, n=3, n=4, n=5 and n=6, n=7, n=8, n=9 and n=10. In one embodiment, the flexible polypeptide linkers include, but are not limited to, (Gly₄ Ser)₄ (SEQ ID NO: 27) or (Gly₄

Ser)₃ (SEQ ID NO: 28) In another embodiment, the linkers include multiple repeats of (Gly₂Ser), (GlySer) or (Gly₃Ser) (SEQ ID NO: 29). Also included within the scope of the invention are linkers described in WO2012/138475, incorporated herein by reference).

[00162] As used herein, a 5' cap (also termed an RNA cap, an RNA 7-methylguanosine cap or an RNA m⁷G 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.

[00163] 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.

[00164] 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: 30), 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.

[00165] 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.

[00166] 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.

[00167] As used herein, the terms “treat”, “treatment” and “treating” refer to the reduction or amelioration of the progression, severity and/or duration of a proliferative disorder, or the amelioration of one or more symptoms (preferably, one or more discernible symptoms) of a proliferative disorder resulting from the administration of one or more therapies (e.g., one or more therapeutic agents such as a CAR of the invention). In specific embodiments, the terms “treat”, “treatment” and “treating” refer to the amelioration of at least one measurable physical parameter of a proliferative disorder, such as growth of a tumor, not necessarily discernible by the patient. In other embodiments the terms “treat”, “treatment” and “treating” -refer to the inhibition of the progression of a proliferative disorder, either physically by, e.g., stabilization of a discernible symptom, physiologically by, e.g., stabilization of a physical parameter, or both. In other embodiments the terms “treat”, “treatment” and “treating” refer to the reduction or stabilization of tumor size or cancerous cell count.

[00168] 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.

[00169] The term “subject” is intended to include living organisms in which an immune response can be elicited (e.g., mammals, human).

[00170] 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.

[00171] The term “therapeutic” as used herein means a treatment. A therapeutic effect is obtained by reduction, suppression, remission, or eradication of a disease state.

[00172] The term “prophylaxis” as used herein means the prevention of or protective treatment for a disease or disease state.

[00173] The terms “cancer associated antigen” or “tumor antigen” interchangeably refers to a molecule (typically a protein, carbohydrate or lipid) that is expressed on the surface of a cancer cell, either entirely or as a fragment (e.g., MHC/peptide), and which is useful for the preferential targeting of a pharmacological agent to the cancer cell. In some embodiments, a tumor antigen is a marker expressed by both normal cells and cancer cells, e.g., a lineage marker, e.g., CD19 on B cells. In some embodiments, a tumor antigen is a cell surface molecule that is overexpressed in a cancer cell in comparison to a normal cell, for instance, 1-fold over expression, 2-fold overexpression, 3-fold overexpression or more in comparison to a normal cell. In some embodiments, a tumor antigen is a cell surface molecule that is inappropriately synthesized in the cancer cell, for instance, a molecule that contains deletions, additions or mutations in comparison to the molecule expressed on a normal cell. In some embodiments, a tumor antigen will be expressed exclusively on the cell surface of a cancer cell, entirely or as a fragment (e.g., MHC/peptide), and not synthesized or expressed on the surface of a normal cell. In some embodiments, the CARs of the present invention includes CARs comprising an antigen binding domain (e.g., antibody or antibody fragment) that binds to a MHC presented peptide. Normally, peptides derived from endogenous proteins fill the pockets of Major histocompatibility complex (MHC) class I molecules, and are recognized by T cell receptors (TCRs) on CD8 + T

lymphocytes. The MHC class I complexes are constitutively expressed by all nucleated cells. In cancer, virus-specific and/or tumor-specific peptide/MHC complexes represent a unique class of cell surface targets for immunotherapy. TCR-like antibodies targeting peptides derived from viral or tumor antigens in the context of human leukocyte antigen (HLA)-A1 or HLA-A2 have been described (see, e.g., Sastry et al., *J Virol.* 2011 85(5):1935-1942; Sergeeva et al., *Blood*, 2011 117(16):4262-4272; Verma et al., *J Immunol* 2010 184(4):2156-2165; Willemse et al., *Gene Ther* 2001 8(21):1601-1608; Dao et al., *Sci Transl Med* 2013 5(176):176ra33; Tashev et al., *Cancer Gene Ther* 2012 19(2):84-100). For example, TCR-like antibody can be identified from screening a library, such as a human scFv phage displayed library.

[00174] 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.

[00175] The term “specifically binds,” refers to an antibody, or a ligand, which recognizes and binds with a binding partner (e.g., tumor antigen) protein present in a sample, but which antibody or ligand does not substantially recognize or bind other molecules in the sample.

[00176] “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.

[00177] “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.

[00178] “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.

[00179] “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.

[00180] The term “bioequivalent” refers to an amount of an agent other than the reference compound (e.g., RAD001), required to produce an effect equivalent to the effect produced by the reference dose or reference amount of the reference compound (e.g., RAD001). In an embodiment the effect is the level of mTOR inhibition, e.g., as measured by P70 S6 kinase inhibition, e.g., as evaluated in an in vivo or in vitro assay, e.g., as measured by an assay described herein, e.g., the Boulay assay, or measurement of phosphorylated S6 levels by western blot. In an embodiment, the effect is alteration of the ratio of PD-1 positive/PD-1 negative T

cells, as measured by cell sorting. In an embodiment a bioequivalent amount or dose of an mTOR inhibitor is the amount or dose that achieves the same level of P70 S6 kinase inhibition as does the reference dose or reference amount of a reference compound. In an embodiment, a bioequivalent amount or dose of an mTOR inhibitor is the amount or dose that achieves the same level of alteration in the ratio of PD-1 positive/PD-1 negative T cells as does the reference dose or reference amount of a reference compound.

[00181] The term ‘low, immune enhancing, dose’ when used in conjunction with an mTOR inhibitor, e.g., an allosteric mTOR inhibitor, e.g., RAD001 or rapamycin, or a catalytic mTOR inhibitor, refers to a dose of mTOR inhibitor that partially, but not fully, inhibits mTOR activity, e.g., as measured by the inhibition of P70 S6 kinase activity. Methods for evaluating mTOR activity, e.g., by inhibition of P70 S6 kinase, are discussed herein. The dose is insufficient to result in complete immune suppression but is sufficient to enhance the immune response. In an embodiment, the low, immune enhancing, dose of mTOR inhibitor results in a decrease in the number of PD-1 positive T cells and/or an increase in the number of PD-1 negative T cells, or an increase in the ratio of PD-1 negative T cells/PD-1 positive T cells. In an embodiment, the low, immune enhancing, dose of mTOR inhibitor results in an increase in the number of naive T cells. In an embodiment, the low, immune enhancing, dose of mTOR inhibitor results in one or more of the following:

an increase in the expression of one or more of the following markers: CD62L^{high}, CD127^{high}, CD27⁺, and BCL2, e.g., on memory T cells, e.g., memory T cell precursors;

a decrease in the expression of KLRG1, e.g., on memory T cells, e.g., memory T cell precursors; and

an increase in the number of memory T cell precursors, e.g., cells with any one or combination of the following characteristics: increased CD62L^{high}, increased CD127^{high}, increased CD27⁺, decreased KLRG1, and increased BCL2;

wherein any of the changes described above occurs, e.g., at least transiently, e.g., as compared to a non-treated subject.

[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 using anti-mesothelin chimeric antigen receptors (CAR), e.g., human mesothelin CAR.

[00184] In one aspect, the invention provides a number of chimeric antigen receptors comprising an antibody or antibody fragment engineered for specific binding to a mesothelin protein. In one aspect, the invention provides a cell (e.g., T cell or NK cell) engineered to express a CAR, e.g., 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 or NK 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 or NK 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.

[00185] In one aspect, the mesothelin protein 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, i.e., 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 mesothelin antigen binding domain of the CAR is a scFv antibody fragment that is human or humanized compared to the murine sequence of the scFv from which it is derived. In one embodiment, the human anti-mesothelin scFv antibody fragment comprises a light chain variable region and/or a heavy chain variable region provided in Table 2, or a sequence with substantial identity thereto, e.g., 95-99% identity.

[00186] In some aspects, the antibodies of the invention are incorporated into a chimeric antigen receptor (CAR). In one aspect, the CAR comprises the polypeptide sequence provided herein as SEQ ID NO: 39; SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, 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, and SEQ ID NO: 62, or a sequence with 95-99% identity thereof.

[00187] In one aspect, the human scFv portion of a CAR 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.

[00188] In one aspect, the human mesothelin CAR molecule comprises the scFv portion provided in SEQ ID NO: 39. In one aspect, the human mesothelin CAR molecule comprises the scFv portion provided in SEQ ID NO: 40. In one aspect, the human mesothelin CAR molecule comprises the scFv portion provided in SEQ ID NO: 41. In one aspect, the human mesothelin CAR molecule comprises the scFv portion provided in SEQ ID NO: 42. In one aspect, the human mesothelin CAR molecule comprises the scFv portion provided in SEQ ID NO: 43. In one aspect, the human mesothelin CAR molecule comprises the scFv portion provided in SEQ ID NO: 44. In one aspect, the human mesothelin CAR molecule comprises the scFv portion provided in SEQ

ID NO: 45. In one aspect, the human mesothelin CAR molecule comprises the scFv portion provided in SEQ ID NO: 46. In one aspect, the human mesothelin CAR molecule comprises the scFv portion provided in SEQ ID NO: 47. In one aspect, the human mesothelin CAR molecule comprises the scFv portion provided in SEQ ID NO: 48. In one aspect, the human mesothelin CAR molecule comprises the scFv portion provided in SEQ ID NO: 49. In one aspect, the human mesothelin CAR molecule comprises the scFv portion provided in SEQ ID NO: 50. In one aspect, the human mesothelin CAR molecule comprises the scFv portion provided in SEQ ID NO: 51. In one aspect, the human mesothelin CAR molecule comprises the scFv portion provided in SEQ ID NO: 52. In one aspect, the human mesothelin CAR molecule comprises the scFv portion provided in SEQ ID NO: 53. In one aspect, the human mesothelin CAR molecule comprises the scFv portion provided in SEQ ID NO: 54. In one aspect, the human mesothelin CAR molecule comprises the scFv portion provided in SEQ ID NO: 55. In one aspect, the human mesothelin CAR molecule comprises the scFv portion provided in SEQ ID NO: 56. In one aspect, the human mesothelin CAR molecule comprises the scFv portion provided in SEQ ID NO: 57. In one aspect, the human mesothelin CAR molecule comprises the scFv portion provided in SEQ ID NO: 58. In one aspect, the human mesothelin CAR molecule comprises the scFv portion provided in SEQ ID NO: 59. In one aspect, the human mesothelin CAR molecule comprises the scFv portion provided in SEQ ID NO: 60. In one aspect, the human mesothelin CAR molecule comprises the scFv portion provided in SEQ ID NO: 61. In one aspect, the human mesothelin CAR molecule comprises the scFv portion provided in SEQ ID NO: 62.

[00189] In one aspect, the CAR disclosed herein 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. In one aspect, the antigen binding domain binds to mesothelin. In one aspect, the -mesothelin CAR comprises the sequence provided in Table 2.

[00190] In one aspect, the mesothelin CAR comprises a CAR selected from the sequence provided in one or more of SEQ ID NOS: 63-86. In one aspect, themesothelin CAR comprises the sequence provided in SEQ ID NO: 63. In one aspect, themesothelin CAR comprises the sequence provided in SEQ ID NO: 64. In one aspect, themesothelin CAR comprises the sequence provided in SEQ ID NO: 65. In one aspect, themesothelin CAR comprises the sequence provided in SEQ ID NO: 66. In one aspect, themesothelin CAR comprises the

sequence provided in SEQ ID NO: 67. In one aspect, themesothelin CAR comprises the sequence provided in SEQ ID NO: 68. In one aspect, themesothelin CAR comprises the sequence provided in SEQ ID NO: 69. In one aspect, themesothelin CAR comprises the sequence provided in SEQ ID NO: 70. In one aspect, themesothelin CAR comprises the sequence provided in SEQ ID NO: 71. In one aspect, themesothelin CAR comprises the sequence provided in SEQ ID NO: 72. In one aspect, themesothelin CAR comprises the sequence provided in SEQ ID NO: 73. In one aspect, themesothelin CAR comprises the sequence provided in SEQ ID NO: 74. In one aspect, themesothelin CAR comprises the sequence provided in SEQ ID NO: 75. In one aspect, themesothelin CAR comprises the sequence provided in SEQ ID NO: 76. In one aspect, themesothelin CAR comprises the sequence provided in SEQ ID NO: 77. In one aspect, themesothelin CAR comprises the sequence provided in SEQ ID NO: 78. In one aspect, themesothelin CAR comprises the sequence provided in SEQ ID NO: 79. In one aspect, themesothelin CAR comprises the sequence provided in SEQ ID NO: 80. In one aspect, themesothelin CAR comprises the sequence provided in SEQ ID NO: 81. In one aspect, themesothelin CAR comprises the sequence provided in SEQ ID NO: 82. In one aspect, themesothelin CAR comprises the sequence provided in SEQ ID NO: 83. In one aspect, themesothelin CAR comprises the sequence provided in SEQ ID NO: 84. In one aspect, themesothelin CAR comprises the sequence provided in SEQ ID NO: 85. In one aspect, themesothelin CAR comprises the sequence provided in SEQ ID NO: 86.

[00191] Furthermore, the present invention provides mesothelin 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 mesothelin.

[00192] In one aspect, the invention provides a cell (e.g., T cell or NK cell) engineered to express a chimeric antigen receptor (CAR), wherein the CAR T cell (“CART”) exhibits an antitumor property. A preferred antigen is mesothelin. In one aspect, the antigen binding domain of the CAR comprises a human anti-mesothelin antibody fragment. In one aspect, the antigen binding domain of the CAR comprises a human anti-mesothelin antibody fragment comprising an scFv. Accordingly, the invention provides an mesothelin CAR that comprises a human anti-mesothelin binding domain and is engineered into a T cell or NK cell and methods of their use for adoptive therapy.

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

[00194] Furthermore, the present invention provides mesothelin 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 mesothelin.

Chimeric Antigen Receptor (CAR)

[00195] The present invention encompasses a recombinant nucleic acid construct comprising sequences encoding a CAR, wherein the CAR comprises an antibody that binds specifically to mesothelin, e.g., a human antibody fragment that specifically binds to mesothelin. In one aspect, the mesothelin is human mesothelin, and 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.

[00196] In specific aspects, a CAR construct of the invention comprises a scFv domain selected from the group consisting of SEQ ID NOS: 39-62, wherein the scFv may be preceded by an optional leader sequence such as provided in SEQ ID NO: 1, and followed by an optional hinge sequence such as provided in SEQ ID NO:2 or SEQ ID NO: 3 or SEQ ID NO:4 or SEQ ID NO:5, a transmembrane region such as provided in SEQ ID NO:6, an intracellular signalling domain that includes SEQ ID NO:7 or SEQ ID NO:8 and a CD3 zeta sequence that includes SEQ ID NO:9 or SEQ ID NO: 10, wherein the domains are contiguous with and in the same reading frame to form a single fusion protein. Also included in the invention is a nucleotide sequence that encodes the polypeptide selected from the group consisting of 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, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, and SEQ ID NO: 110, or a sequence with 95-99% identify thereof. Also included in the invention is a nucleotide sequence that encodes the polypeptide of each of the scFv fragments selected from the group consisting of SEQ ID NO: 39; SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, 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, and SEQ ID NO: 62, or a sequence with 95-99% identify thereof, and each of the domains of SEQ ID NOS: 1, 2, and 6-9, plus the encoded mesothelin CAR fusion protein of the invention. In one aspect an exemplary mesothelin CAR constructs comprise an optional leader sequence, an extracellular mesothelin binding domain, a hinge, a transmembrane domain, and an intracellular stimulatory domain. In one aspect, the mesothelin CAR construct comprises an optional leader sequence, a mesothelin binding domain, a hinge, a transmembrane domain, an intracellular costimulatory domain and an intracellular stimulatory domain. Specific mesothelin CAR constructs containing human scFv domains are provided as SEQ ID NOS: 87-110.

[00197] Full-length CAR sequences are also provided herein as 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, SEQ ID NO: 70, 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, SEQ ID NO: 79, SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 83, SEQ ID NO: 84, SEQ ID NO: 85, or SEQ ID NO: 86. An exemplary leader sequence is provided as SEQ ID NO: 1. An exemplary hinge/spacer sequence is provided as SEQ ID NO: 2 or SEQ ID NO: 3 or SEQ ID NO: 4 or SEQ ID NO: 5. An exemplary transmembrane domain sequence is provided as SEQ ID NO: 6. An exemplary sequence of the intracellular signaling domain of the 4-1BB protein is provided as SEQ ID NO: 7. An exemplary sequence of the intracellular signaling domain of CD27 is provided as SEQ ID NO: 8. An exemplary CD3zeta domain sequence is provided as SEQ ID NO: 9 or SEQ ID NO: 10.

[00198] 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 anti-mesothelin 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 anti-mesothelin binding domain is selected from one or more of SEQ ID NOS: 87-110. In one aspect, the anti-mesothelin binding domain comprises SEQ ID NO: 87. In one aspect, the anti-mesothelin binding domain comprises SEQ ID NO: 88. In one aspect, the anti-mesothelin binding domain comprises SEQ ID NO: 89. In one aspect, the anti-mesothelin binding domain comprises SEQ ID NO: 90. In one aspect, the anti-mesothelin binding domain comprises SEQ ID NO: 91. In one aspect, the anti-mesothelin binding domain comprises SEQ ID NO: 92. In one aspect, the anti-mesothelin binding domain comprises SEQ ID NO: 93. In one aspect, the anti-mesothelin binding domain comprises SEQ ID NO: 94. In one aspect, the anti-mesothelin binding domain comprises SEQ ID NO: 95. In one aspect, the anti-mesothelin binding domain comprises SEQ ID NO: 96. In one aspect, the anti-mesothelin binding domain comprises SEQ ID NO: 97. In one aspect, the anti-mesothelin binding domain comprises SEQ ID NO: 98. In one aspect, the anti-mesothelin binding domain comprises SEQ ID NO: 99. In one aspect, the anti-mesothelin binding domain comprises SEQ ID NO: 100. In one aspect, the anti-mesothelin binding domain comprises SEQ ID NO: 101. In one aspect, the anti-mesothelin binding domain comprises SEQ ID NO: 102. In one aspect, the anti-mesothelin binding domain comprises SEQ ID NO: 103. In one aspect, the anti-mesothelin binding domain comprises SEQ ID NO: 104. In one aspect, the anti-mesothelin binding domain comprises SEQ ID NO: 105. In one aspect, the anti-mesothelin binding domain comprises SEQ ID NO: 106. In one aspect, the anti-mesothelin binding domain comprises SEQ ID NO: 107. In one aspect, the anti-mesothelin binding domain comprises SEQ ID NO: 108. In one aspect, the anti-mesothelin binding domain comprises SEQ ID NO: 109. In one aspect, the anti-mesothelin binding domain comprises SEQ ID NO: 110. In one aspect, the present invention encompasses a recombinant DNA construct comprising a transgene encoding a CAR, wherein the transgene comprises the nucleic acid sequence encoding an anti-mesothelin binding domain described herein, e.g., a human anti-mesothelin binding domain selected from one or more of SEQ ID NOS: 87-110, wherein the sequence is contiguous with and in the same reading frame as the nucleic acid sequence encoding an intracellular signaling

domain. 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. In one aspect the nucleic acid sequence of a CAR construct of the invention is selected from one or more of SEQ ID NOS: 111-134. In one aspect the nucleic acid sequence of a CAR construct is SEQ ID NO: 111. In one aspect the nucleic acid sequence of a CAR construct is SEQ ID NO: 112. In one aspect the nucleic acid sequence of a CAR construct is SEQ ID NO: 113. In one aspect the nucleic acid sequence of a CAR construct is SEQ ID NO: 114. In one aspect the nucleic acid sequence of a CAR construct is SEQ ID NO: 115. In one aspect the nucleic acid sequence of a CAR construct is SEQ ID NO: 116. In one aspect the nucleic acid sequence of a CAR construct is SEQ ID NO: 117. In one aspect the nucleic acid sequence of a CAR construct is SEQ ID NO: 118. In one aspect the nucleic acid sequence of a CAR construct is SEQ ID NO: 119. In one aspect the nucleic acid sequence of a CAR construct is SEQ ID NO: 120. In one aspect the nucleic acid sequence of a CAR construct is SEQ ID NO: 121. In one aspect the nucleic acid sequence of a CAR construct is SEQ ID NO: 122. In one aspect the nucleic acid sequence of a CAR construct is SEQ ID NO: 123. In one aspect the nucleic acid sequence of a CAR construct is SEQ ID NO: 124. In one aspect the nucleic acid sequence of a CAR construct is SEQ ID NO: 125. In one aspect the nucleic acid sequence of a CAR construct is SEQ ID NO: 126. In one aspect the nucleic acid sequence of a CAR construct is SEQ ID NO: 127. In one aspect the nucleic acid sequence of a CAR construct is SEQ ID NO: 128. In one aspect the nucleic acid sequence of a CAR construct is SEQ ID NO: 129. In one aspect the nucleic acid sequence of a CAR construct is SEQ ID NO: 130. In one aspect the nucleic acid sequence of a CAR construct is SEQ ID NO: 131. In one aspect the nucleic acid sequence of a CAR construct is SEQ ID NO: 132. In one aspect the nucleic acid sequence of a CAR construct is SEQ ID NO: 133. In one aspect the nucleic acid sequence of a CAR construct is SEQ ID NO: 134.

[00199] 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.

[00200] The present invention includes retroviral and lentiviral vector constructs expressing a CAR that can be directly transduced into a cell. 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: 35). 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.

Antigen binding domain

[00201] 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 antigen binding domain depends upon the type and number of antigens that define the surface of a target cell. For example, the antigen binding domain may be chosen to recognize a antigen that acts as a cell surface marker on target cells associated with a particular disease state.

[00202] In one aspect, the CAR-mediated immune effector cell response can be directed to cells that express an antigen of interest, where the CAR comprises an antigen binding domain that specifically binds to the antigen of interest. In one aspect, the portion of the CAR comprising the antigen binding domain comprises an antigen binding domain that targets mesothelin. In one aspect, the antigen binding domain targets human mesothelin.

[00203] 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 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 an antigen binding domain, such as a recombinant fibronectin domain, and the like. In some instances, it is beneficial for the antigen binding domain to be derived from the same species in which the CAR will ultimately be used in. For example, for use in humans, it may be beneficial for the antigen binding domain of the CAR to

comprise human or humanized residues for the antigen binding domain of an antibody or antibody fragment. Thus, in one aspect, the antigen binding domain comprises a human antibody or an antibody fragment.

[00204] In one embodiment, the anti-mesothelin binding domain does not compete, or competes poorly, for binding to human mesothelin with an antigen binding domain comprising an amino acid sequence comprising SEQ ID NO: 279, e.g., murine SS1 scFv, e.g., in a competition assay described herein.

[00205] The amino acid sequence of murine SS1 scFv is provided below (SEQ ID NO: 279):

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QVQLQQSGPELEKPGASVKISCKASGYSFTGYTMNWKQSHGKSLEWIGLITPYNGASSYNQKFRGKATLT  
VDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSGGGSGGGSGGGSDIELTQSP  
AIMSASPGEKVTMTCASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPGRFSGSGNSYSLTISSVEA  
EDDATYYCQQWSGYPLTFGAGTKLEI
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[00206] In one embodiment, the anti-mesothelin binding domain competes for binding to human mesothelin with an antigen binding domain comprising a LC CDR1, LC CDR2 and LC CDR3 of an anti-mesothelin light chain amino acid sequence selected from SEQ ID NO: 43 or SEQ ID NO: 49 and an HC CDR1, HC CDR2, and HC CDR3 of an anti-mesothelin heavy chain amino acid sequence selected from SEQ ID NO: 43 or SEQ ID NO: 49, e.g., in a competition assay described herein. In one embodiment, the anti-mesothelin binding domain competes for binding to human mesothelin with an antigen binding domain comprising a LC CDR1 selected from SEQ ID NO: 203 or SEQ ID NO: 209, a LC CDR2 selected from SEQ ID NO: 227 or SEQ ID NO: 233, and a LC CDR3 selected from SEQ ID NO: 251 or SEQ ID NO: 257; and a HC CDR1 selected from SEQ ID NO: 138 or SEQ ID NO: 144, a HC CDR2 selected from SEQ ID NO: 156 or SEQ ID NO: 162, and a HC CDR3 selected from SEQ ID NO: 179 or SEQ ID NO: 185, e.g., in a competition assay described herein.

[00207] In one embodiment, the anti-mesothelin binding domain competes for binding to human mesothelin with an antigen binding domain comprising a sequence selected from SEQ ID NO: 43 or SEQ ID NO: 49, e.g., in a competition assay described herein.

[00208] In embodiments, the competition assay is an SPR-based assay. Briefly, the antigen, e.g., human mesothelin, is immobilized on a surface. Through a microflow system, a reference antibody is injected over the antigen layer. Upon binding of the reference antibody to the

antigen, an increase in signal, typically expressed in response units (RU) is detected, e.g., reference signal. After a desired time, a test antibody is injected over the antigen layer. If the test antibody binds to a different region or epitope of the antigen, then an additional increase in signal is detected, e.g., a 5% or more, 10% or more, 15% or more, 20% or more, 25% or more, 30% or more, 35% or more, 40% or more, 45% or more, 50% or more, 55% or more, 60% or more, 65% or more, 70% or more, 75% or more, 80% or more, 85% or more, 90% or more, or 95% or more increase in signal, e.g., RU, as compared to the highest signal detected upon binding of the reference antibody, e.g., the reference signal. If the test antibody binds to the same region or epitope of the antigen, then little or no increase in signal, e.g., RU, will be detected, e.g., less than 20%, less than 15%, less than 10%, less than 5%, less than 4%, less than 3%, less than 2 %, or less than 1% increase in signal, e.g., RU, as compared to the highest signal detected upon binding of the reference antibody, e.g., the reference signal. When using this SPR-based competition assay, an antibody is said to compete with the reference antibody when less than 20%, less than 15%, less than 10%, less than 5%, less than 4%, less than 3%, less than 2 %, or less than 1% increase in signal, e.g., RU, is detected when compared to the reference signal detected upon binding of the reference antibody to the antigen. An antibody is said to not compete, or compete poorly, with a reference antibody when a 5% or more, 10% or more, 15% or more, 20% or more, 25% or more, 30% or more, 35% or more, 40% or more, 45% or more, 50% or more, 55% or more, 60% or more, 65% or more, 70% or more, 75% or more, 80% or more, 85% or more, 90% or more, or 95% or more increase in signal, e.g., RU, is detected when compared to the reference signal detected upon binding of the reference antibody to the antigen.

[00209] Identification of the epitope bound by the antigen binding domains described herein can be determined by various methods known in the art. For example, crystal structures can be generated containing the antigen binding domain bound to, or in complex with, the antigen. In another example, assays, e.g., a protection assay, can be performed to identify the regions of the antigen contribute to the epitope, or to identify the epitope. An exemplary protection assay, a hydrogen/deuterium exchange (HDX) mass spectrometry assay, is described further in Example 18. The HDX mass spectrometry was performed to identify the putative epitopes on human MSLN, e.g., hMSLN₂₉₆₋₅₈₈, e.g., SEQ ID NO: 278, for murine SS1, e.g., SEQ ID NO: 279, and the M5 scFv described herein, e.g., SEQ ID NO: 43. hMSLN₂₉₆₋₅₈₈, e.g., SEQ ID NO: 278, represents amino acids 296-588 of human mesothelin, e.g., the first amino acid of SEQ ID NO:

278 is amino acid 296 and the last amino acid of SEQ ID NO: 278 is amino acid 588. The amino acid sequence for human mesothelin, amino acids 296-588 is provided below: (SEQ ID NO: 278)

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EVEKTACPSGKKAREIDESLIFYKKWELEACVDAALLATQMDRVNAIPFTYEQLDVLKHKLDELYPQG  
YPESVIQHLGYLFLKMSPEDIRKWNVTSLETLKALLEVNKGHEMSPQAPRRLPLPQVATLIDRFVKGRG  
QLDKDTLDTLTAFYPGYLCLSPEELSSVPPSSIWAVRPQDLDTCPRQLDVLYPKARLAFQNMNGSE  
YFVKIQSFLGGAPTEDLKALSQQNVSMIDLATFMKLRTDAVLPLTVAEVQKLLGPHVEGLKAEERHRPV  
RDWILRQRQDDLDTLGLGLQG
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[00210] The results of the HDX mass spectrometry assay indicated that one or more amino acids of 314-315, 317-318, 346-349, and 369-375 of hMSLN₂₉₆₋₅₈₈, e.g., SEQ ID NO: 278 contribute to the epitope recognized by SS1. The results of the HDX mass spectrometry assay indicated that one or more amino acids of 485-490, 498-507, 532-537, or 545-572 of hMSLN₂₉₆₋₅₈₈, e.g., SEQ ID NO: 278, contribute to the epitope recognized by an anti-mesothelin antigen binding domain described herein, e.g., M5 scFv, e.g., SEQ ID NO: 43.

[00211] In one embodiment, the anti-mesothelin binding domain described herein binds to a different epitope of human mesothelin, e.g., SEQ ID NO: 278, than the epitope of human mesothelin targeted by the antigen binding domain comprising a sequence comprising SEQ ID NO: 279, e.g., murine SS1.

[00212] In one embodiment, the epitope recognized by SS1 comprises a sequence selected from amino acids 314-315, 317-318, 346-349, or 369-375 of hMSLN₂₉₆₋₅₈₈, e.g., SEQ ID NO: 278, or any combination thereof. In one embodiment, the epitope recognized by SS1 comprises one or more amino acids selected from amino acids 314-315, 317-318, 346-349, or 369-375 of hMSLN₂₉₆₋₅₈₈, e.g., SEQ ID NO: 278.

[00213] In one embodiment, the anti-mesothelin binding domain described herein binds to the C-terminus of human mesothelin. In one embodiment, the anti-mesothelin binding domain described herein binds an epitope within amino acids 450-588 of SEQ ID NO: 278, e.g., wherein the epitope, in part or in whole, can be found within amino acids 450-588, within amino acids 480-580, or within amino acids 485-572 of SEQ ID NO: 278. In one embodiment, the epitope recognized by an anti-mesothelin binding domain described herein comprises a sequence selected from amino acids 485-490, 498-507, 532-537, or 545-572 of hMSLN₂₉₆₋₅₈₈, e.g., SEQ ID NO: 278, or any combination thereof. In one embodiment, the epitope recognized by an anti-

mesothelin binding domain described herein comprises one or more amino acids selected from 485-490, 498-507, 532-537, or 545-572 of hMSLN₂₉₆₋₅₈₈, e.g., SEQ ID NO: 278, or any combination thereof.

[00214] In one embodiment, the anti-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 human anti-mesothelin binding domain selected from SEQ ID NOS: 39-62 and 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 anti-mesothelin binding domain selected from SEQ ID NOS: 39-62. In one embodiment, the human anti-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 anti-mesothelin binding domain is a scFv comprising a light chain variable region and a heavy chain variable region of an amino acid sequence of Table 2. In an embodiment, the anti-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) 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 2, or a sequence with 95-99% identity to an amino acid sequence of 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) 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 2, or a sequence with 95-99% identity to an amino acid sequence of Table 2.

[00215] In one embodiment, the human anti-mesothelin binding domain comprises a sequence selected from a group consisting of SEQ ID NOS: 39-62, or a sequence with 95-99% identify thereof. In one embodiment, the nucleic acid sequence encoding the human anti-mesothelin binding domain comprises a sequence selected from a group consisting of SEQ ID NO: 87-110, or a sequence with 95-99% identify thereof. In one embodiment, the human anti-mesothelin binding domain is a scFv, and a light chain variable region comprising an amino acid sequence described herein, e.g., in Table 2 or 3, is attached to a heavy chain variable region comprising an amino acid sequence described herein, e.g., in Table 2 or 3, via a linker, e.g., a linker described

herein. In one embodiment, the humanized anti-mesothelin binding domain includes a (Gly4-Ser)n linker (SEQ ID NO: 26), wherein n is 1, 2, 3, 4, 5, or 6, preferably 3 or 4. 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.

[00216] In one aspect, the antigen binding domain portion comprises one or more sequence selected from SEQ ID NOS:39-62. In one aspect the CAR is selected from one or more sequence selected from SEQ ID NOS: 63-86.

[00217] In one aspect, the antibodies of the invention may exist in a variety of other forms including, for example, 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. In one aspect, the antibody fragment provided herein is a scFv. In some instances, a human scFv may also be derived from a yeast display library.

[00218] A display library is a collection of entities; each entity includes an accessible polypeptide component and a recoverable component that encodes or identifies the polypeptide component. The polypeptide component is varied so that different amino acid sequences are represented. The polypeptide component can be of any length, e.g. from three amino acids to over 300 amino acids. A display library entity can include more than one polypeptide component, for example, the two polypeptide chains of a Fab. In one exemplary embodiment, a display library can be used to identify an anti-mesothelin binding domain. In a selection, the polypeptide component of each member of the library is probed with mesothelin, or a fragment thereof, and if the polypeptide component binds to the mesothelin, the display library member is identified, typically by retention on a support.

[00219] Retained display library members are recovered from the support and analyzed. The analysis can include amplification and a subsequent selection under similar or dissimilar conditions. For example, positive and negative selections can be alternated. The analysis can also include determining the amino acid sequence of the polypeptide component, i.e., the anti-

mesothelin binding domain, and purification of the polypeptide component for detailed characterization.

[00220] A variety of formats can be used for display libraries. Examples include the phage display. In phage display, the protein component is typically covalently linked to a bacteriophage coat protein. The linkage results from translation of a nucleic acid encoding the protein component fused to the coat protein. The linkage can include a flexible peptide linker, a protease site, or an amino acid incorporated as a result of suppression of a stop codon. Phage display is described, for example, in U.S. 5,223,409; Smith (1985) *Science* 228:1315-1317; WO 92/18619; WO 91/17271; WO 92/20791; WO 92/15679; WO 93/01288; WO 92/01047; WO 92/09690; WO 90/02809; de Haard *et al.* (1999) *J. Biol. Chem.* 274:18218-30; Hoogenboom *et al.* (1998) *Immunotechnology* 4:1-20; Hoogenboom *et al.* (2000) *Immunol Today* 2:371-8 and Hoet *et al.* (2005) *Nat Biotechnol.* 23(3)344-8. Bacteriophage displaying the protein component can be grown and harvested using standard phage preparatory methods, e.g. PEG precipitation from growth media. After selection of individual display phages, the nucleic acid encoding the selected protein components can be isolated from cells infected with the selected phages or from the phage themselves, after amplification. Individual colonies or plaques can be picked, the nucleic acid isolated and sequenced.

[00221] Other display formats include cell based display (see, e.g., WO 03/029456), protein-nucleic acid fusions (see, e.g., US 6,207,446), ribosome display (See, e.g., Mattheakis *et al.* (1994) *Proc. Natl. Acad. Sci. USA* 91:9022 and Hanes *et al.* (2000) *Nat Biotechnol.* 18:1287-92; Hanes *et al.* (2000) *Methods Enzymol.* 328:404-30; and Schaffitzel *et al.* (1999) *J Immunol Methods.* 231(1-2):119-35), and *E. coli* periplasmic display (*J Immunol Methods.* 2005 Nov 22; PMID: 16337958).

[00222] In addition to the use of display libraries, other methods can be used to obtain an anti-mesothelin binding domain. For example, mesothelin or a fragment thereof can be used as an antigen in a non-human animal, e.g., a rodent.

[00223] In one embodiment, the non-human animal includes at least a part of a human immunoglobulin gene. For example, it is possible to engineer mouse strains deficient in mouse antibody production with large fragments of the human Ig loci. Using the hybridoma technology, antigen-specific monoclonal antibodies (Mabs) derived from the genes with the desired

specificity may be produced and selected. See, e.g., XENOMOUSE™, Green et al., 1994, *Nat. Gen.* 7:13-21; U.S. 2003-0070185, WO 96/34096, published Oct. 31, 1996, and PCT Application No. PCT/US96/05928, filed Apr. 29, 1996.

[00224] 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, e.g., using flexible polypeptide linkers. The scFv molecules can 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 an 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.

[00225] 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 (Gly₄Ser)_n, where n is a positive integer equal to or greater than 1. (SEQ ID NO: 135) In one embodiment, the linker can be (Gly₄Ser)₄ (SEQ ID NO: 27) or (Gly₄Ser)₃ (SEQ ID NO: 28). Variation in the linker length may retain or enhance activity, giving rise to superior efficacy in activity studies.

Stability and Mutations

[00226] The stability of an anti-mesothelin binding domain, e.g., scFv molecules (e.g., soluble scFv), can be evaluated in reference to the biophysical properties (e.g., thermal stability) of a conventional control scFv molecule or a full length antibody. In one embodiment, the human scFv has a thermal stability that is greater than about 0.1, about 0.25, about 0.5, about 0.75, about 1, about 1.25, about 1.5, about 1.75, about 2, about 2.5, about 3, about 3.5, about 4, about 4.5,

about 5, about 5.5, about 6, about 6.5, about 7, about 7.5, about 8, about 8.5, about 9, about 9.5, about 10 degrees, about 11 degrees, about 12 degrees, about 13 degrees, about 14 degrees, or about 15 degrees Celsius than a control binding molecule (e.g. a conventional scFv molecule) in the described assays.

[00227] The improved thermal stability of the anti-mesothelin binding domain, e.g., scFv, is subsequently conferred to the entire mesothelin CAR construct, leading to improved therapeutic properties of the mesothelin CAR construct. The thermal stability of the anti-mesothelin binding domain, e.g., scFv, can be improved by at least about 2°C or 3°C as compared to a conventional antibody. In one embodiment, the anti-mesothelin binding domain, e.g., scFv, has a 1°C improved thermal stability as compared to a conventional antibody. In another embodiment, the anti-mesothelin binding domain, e.g., scFv, has a 2°C improved thermal stability as compared to a conventional antibody. In another embodiment, the anti-mesothelin binding domain, e.g., scFv, has a 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15°C improved thermal stability as compared to a conventional antibody. Comparisons can be made, for example, between the scFv molecules disclosed herein and scFv molecules or Fab fragments of an antibody from which the scFv VH and VL were derived. Thermal stability can be measured using methods known in the art. For example, in one embodiment, Tm can be measured. Methods for measuring Tm and other methods of determining protein stability are described in more detail below.

[00228] Mutations in scFv (arising through direct mutagenesis of the soluble scFv) alter the stability of the scFv and improve the overall stability of the scFv and the CART construct. Stability of the humanized scFv is compared against the murine scFv using measurements such as Tm, temperature denaturation and temperature aggregation.

[00229] In one embodiment, the anti-mesothelin binding domain, e.g., scFv, comprises at least one mutation such that the mutated anti-mesothelin binding domain, e.g., scFv, confers improved stability to the anti-mesothelin construct. In another embodiment, the anti-mesothelin binding domain, e.g., scFv, comprises at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 mutations such that the mutated anti-mesothelin binding domain, e.g., scFv, confers improved stability to the anti-mesothelin construct. The binding capacity of the mutant scFvs can be determined using assays described in the Examples.

Binding Affinity

[00230] A wide variety of methods for determining binding affinity are known in the art. An exemplary method for determining binding affinity employs surface plasmon resonance. Surface plasmon resonance is an optical phenomenon that allows for the analysis of real-time biospecific interactions by detection of alterations in protein concentrations within a biosensor matrix, for example using the BIACore system (Pharmacia Biosensor AB, Uppsala, Sweden and Piscataway, N.J.). For further descriptions, see Jonsson, U., *et al.* (1993) Ann. Biol. Clin. 51:19-26; Jonsson, U., *et al.* (1991) Biotechniques 11:620-627; Johnsson, B., *et al.* (1995) J. Mol. Recognit. 8:125-131; and Johnnson, B., *et al.* (1991) Anal. Biochem. 198:268-277.

[00231] In one aspect, the portion of a CAR composition of the invention comprising an antibody or fragment thereof comprises amino acid sequences that are homologous to the amino acid sequences described herein, and wherein the antibody or fragment thereof retains the desired functional properties of the anti-mesothelin antibody fragments of the invention. In one specific aspect, the CAR composition of the invention comprises an antibody fragment. In a further aspect, that antibody fragment comprises an scFv.

[00232] In various aspects, the portion comprising an antibody or antibody fragment of the CAR composition of the invention is engineered by modifying one or more amino acids within one or both variable regions (i.e., 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, that antibody fragment comprises an scFv.

[00233] 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, i.e., a conservative substitution, in

which an amino acid residue is replaced with an amino acid residue having a similar side chain, may be made.

[00234] 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).

[00235] 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 (i.e., 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.

[00236] 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).

[00237] 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.

[00238] 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.

[00239] In one aspect, the present invention 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 anti-mesothelin binding domain, 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 anti-mesothelin binding domain, e.g., scFv. The present invention 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.

Transmembrane domain

[00240] 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. 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 is used, e.g., in one embodiment, the transmembrane domain may be from the same protein that the signaling domain, costimulatory domain or the hinge domain is derived from. In another aspect, the transmembrane domain is not derived from the same protein that any other domain of the CAR is derived from. 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.

[00241] 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 domain(s) of, e.g., the alpha, beta or zeta chain of the T-cell receptor, CD28,

CD3 epsilon, CD45, CD4, CD5, CD8 (e.g., CD8 alpha, CD8 beta), 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, and NKG2C.

[00242] 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, an IgD hinge), a GS linker (e.g., a GS linker described herein), a KIR2DS2 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:2. In one aspect, the transmembrane domain comprises (e.g., consists of) a transmembrane domain of SEQ ID NO: 6.

[00243] 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 as follows:

ESKYGPPCPPCPAPEFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWY
VDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIS
KAKGQPQREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPP
VLDSDGSFFLYSRLTVDKSRWQEGNVFCSVVMHEALHNHYTQKSLSLSGKM (SEQ ID NO:3).

[00244] In some embodiments, the hinge or spacer comprises a hinge encoded by a nucleotide sequence as follows:

GAGAGCAAGTACGGCCCTCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGGAGTTCCCTGGCGGA
CCCAGCGTGTCCCTGTTCCCCCCCCAAGCCCAAGGACACCCCTGATGATCAGCCGGACC
CCCGAGGTGACCTGTGTGGTGGACGTGTCCCAGGAGGACCCGAGGTCCAGTT

CAACTGGTACGTGGACGGCGTGGAGGTGCACAACGCCAAGACCAAGCCCCGGGAG
 GAGCAGTTCAATAGCACCTACCGGGTGGTCCGTGCTGACCGTGCTGCACCAGGA
 CTGGCTGAACGGCAAGGAATACAAGTGTAAAGGTGTCCAACAAAGGGCCTGCCAGCA
 GCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCTCGGGAGCCCCAGGTGTAC
 ACCCTGCCCCCTAGCCAAGAGGAGATGACCAAGAACCAAGGTGTCCCTGACCTGCCT
 GGTGAAGGGCTTCTACCCCAGCGACATGCCGTGGAGTGGAGAGCAACGCCAGC
 CCGAGAACAACTACAAGACCACCCCCCTGTGCTGGACAGCGACGGCAGCTCTTC
 CTGTACAGCCGGCTGACCGTGGACAAGAGCCGGTGGCAGGAGGGCAACGTCTTAG
 CTGCTCCGTATGCACGAGGCCCTGCACAACCACTACACCCAGAACAGAGCCTGAGCC
 TGTCCCTGGCAAGATG (SEQ ID NO:14).

[00245] 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
 RWPESPKAQASSVPTAQPQAEGSLAKATTAPATTRNTGRGEEKKEKEKEEQQERETK
 TPECPHSHTQPLGVYLLPAVQDLWLRDKATFTCFVVGSDLKDAHTWEVAGKVPTGGV
 EEGLLERHSNGSQHSRLLPRSLWNAGTSVTCTLNHPSLPPQRLMALREPAQAPVK
 LSLNLLASSDPPEAASWLLCEVSGFSPPNILLMWLEDQREVNTSGFAPARPPPQPGSTTF
 WAWSVLRVPAPPSPQPATYTCVVSHEDSRTLLNASRSLEVSYVTDH (SEQ ID NO:4).

[00246] In some embodiments, the hinge or spacer comprises a hinge encoded by a nucleotide sequence of

AGGTGGCCGAAAGTCCAAGGCCAGGCATCTAGTGTCCCTACTGCACAGCCCCA
 GGCAGAACGCAGCCTAGCCAAAGCTACTACTGCACCTGCCACTACGCGCAATACTG
 GCCGTGGCGGGGAGGAGAAGAAAAAGGAGAAAGAGAAAGAACAGGAAGAGA
 GGGAGACCAAGACCCCTGAATGTCCATCCCATAACCCAGCCGTGGCGTCTATCTCT
 TGACTCCCGCAGTACAGGACTGTGGCTTAGAGATAAGGCCACCTTACATGTTCG
 TCGTGGGCTCTGACCTGAAGGATGCCATTGACTTGGGAGGTTGCCGGAAAGGTAC
 CCACAGGGGGGTTGAGGAAGGGTTGCTGGAGCGCCATTCCAATGGCTCTCAGAGC
 CAGCACTCAAGACTCACCCCTCCGAGATCCCTGTGGAACGCCGGACCTCTGTCACA
 TGTACTCTAAATCATCCTAGCCTGCCACAGCGTCTGATGCCCTAGAGAGCCA
 GCCGCCAGGCACCAGTTAAGCTTAGCCTGAATCTGCTGCCAGTAGTGTACCCCCA
 GAGGCCGCCAGCTGGCTTTATGCGAAGTGTCCGGTTAGCCGCCAACATCTG
 CTCATGTGGCTGGAGGACCAGCGAGAAGTGAACACCAGCGGCTCGCTCCAGCCCCG

GCCCCCACCCAGCCGGTTCTACCACATTCTGGGCCTGGAGTGTCTTAAGGGTCCC
AGCACCCACCTAGCCCCAGCCAGCCACATACACCTGTGTTGTCCCAGAAGATAG
CAGGACCCTGCTAAATGCTCTAGGAGTCTGGAGGTTCCCTACGTGACTGACCATT
(SEQ ID NO:15).

[00247] 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.

[00248] 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 signaling 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:5). In some embodiments, the linker is encoded by a nucleotide sequence of GGTGGCGGAGGTTCTGGAGGTGGAGGTTCC (SEQ ID NO:16).

[00249] In one aspect, the hinge or spacer comprises a KIR2DS2 hinge and portions thereof.

Cytoplasmic domain

[00250] 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.

[00251] 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.

[00252] 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).

[00253] A primary cytoplasmic 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.

[00254] Examples of ITAM containing primary intracellular signaling domains that are of particular use in the invention include those of 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 one embodiment, a CAR of the invention comprises an intracellular signaling domain, e.g., a primary signaling domain of CD3-zeta.

[00255] 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.

[00256] Further examples of molecules containing a primary intracellular signaling domain that are of particular use in the invention include those of DAP10, DAP12, and CD32.

[00257] The intracellular 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 (also known as PD1), 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 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, TNFR2, TRANCE/RANKL, DNAM1 (CD226), SLAMF4 (CD244, 2B4), CD84, CD96 (Tactile), NKG2D, 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, and PAG/Cbp.

[00258] The intracellular signaling domains 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 domains. 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.

[00259] 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.

[00260] 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: 16. In one aspect, the signaling domain of CD3-zeta is a signaling domain of SEQ ID NO: 17.

[00261] 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

QRRKYRSNKGESPVEPAEPCRYSCPREEGSTIPIQEDYRKPEPACSP (SEQ ID NO:8). In one aspect, the signalling domain of CD27 is encoded by a nucleic acid sequence of AGGAGTAAGAGGGAGCAGGCTCCTGCACAGTGAATGAACTGACTCCCCGCCG CCCCGGGCCCACCCGCAAGCATTACCAGCCCTATGCCACCACGCGACTTCGCAGC CTATCGCTCC (SEQ ID NO:19).

[00262] In one aspect, the CAR-expressing cell described herein can further comprise a second CAR, e.g., a second CAR that includes a different antigen binding domain, e.g., to the same target (mesothelin) or a different target (e.g., a target other than mesothelin on stroma cells, e.g., FAP; a target other than mesothelin on prostate cancer cells, e.g., androgen receptor, OR51E2, PSMA, PSCA, PDGRF- β , TARP, GloboH, MAD-CT-1, or MAD-CT-2; a target other than mesothelin on ovarian cancer cells, e.g., Tn, PRSS21, CD171, Lewis Y, folate receptor α , claudin6, GloboH, or sperm protein 17, e.g., a target other than mesothelin on lung cancer cells, e.g., VEGF, HER3, IGF-1R, EGFR, DLL4, or Trop-2). In one embodiment, the CAR-expressing cell comprises a first CAR that targets a first antigen and includes an intracellular signaling domain having a costimulatory signaling domain but not a primary signaling domain, and a second CAR that targets a second, different, antigen and includes an intracellular signaling

domain having a primary signaling domain but not a costimulatory signaling domain. Placement of a costimulatory signaling domain, e.g., 4-1BB, CD28, CD27 or OX-40, onto the first CAR, and the primary signaling domain, e.g., CD3 zeta, on the second CAR can limit the CAR activity to cells where both targets are expressed. In one embodiment, the CAR expressing cell comprises a first mesothelin CAR that includes a mesothelin binding domain, a transmembrane domain and a costimulatory domain and a second CAR that targets an antigen other than mesothelin (e.g., a target other than mesothelin on stroma cells, e.g., FAP; a target other than mesothelin on prostate cancer cells, e.g., androgen receptor, OR51E2, PSMA, PSCA, PDGRF- β , TARP, GloboH, MAD-CT-1, or MAD-CT-2; a target other than mesothelin on ovarian cancer cells, e.g., Tn, PRSS21, CD171, Lewis Y, folate receptor α , claudin6, GloboH, or sperm protein 17, e.g., a target other than mesothelin on lung cancer cells, e.g., VEGF, HER3, IGF-1R, EGFR, DLL4, or Trop-2) and includes an antigen binding domain, a transmembrane domain and a primary signaling domain. In another embodiment, the CAR expressing cell comprises a first mesothelin CAR that includes a mesothelin binding domain, a transmembrane domain and a primary signaling domain and a second CAR that targets an antigen other than mesothelin (e.g., a target other than mesothelin on stroma cells, e.g., FAP; a target other than mesothelin on prostate cancer cells, e.g., androgen receptor, OR51E2, PSMA, PSCA, PDGRF- β , TARP, GloboH, MAD-CT-1, or MAD-CT-2; a target other than mesothelin on ovarian cancer cells, e.g., Tn, PRSS21, CD171, Lewis Y, folate receptor α , claudin6, GloboH, or sperm protein 17, e.g., a target other than mesothelin on lung cancer cells, e.g., VEGF, HER3, IGF-1R, EGFR, DLL4, or Trop-2) and includes an antigen binding domain to the antigen, a transmembrane domain and a costimulatory signaling domain.

[00263] In one embodiment, the CAR-expressing cell comprises a mesothelin CAR described herein and 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 mesothelin. 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, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), LAG3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4 and TGFR beta.

[00264] In one embodiment, when the CAR-expressing cell comprises two or more different CARs, the antigen binding domains of the different 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.

[00265] 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.

[00266] 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.

[00267] 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.

[00268] The SDAB molecules can be recombinant, CDR-grafted, humanized, camelized, de-immunized and/or in vitro generated (e.g., selected by phage display).

[00269] It has also been discovered, that cells having a plurality of chimeric membrane embedded receptors comprising an antigen binding domain that interactions between the antigen binding domain of the receptors can be undesirable, e.g., because it inhibits the ability of one or more of the antigen binding domains to bind its cognate antigen. Accordingly, disclosed herein are cells having a first and a second non-naturally occurring chimeric membrane embedded receptor comprising antigen binding domains that minimize such interactions. Also disclosed herein are nucleic acids encoding a first and a second non-naturally occurring chimeric membrane embedded receptor comprising an antigen binding domains that minimize such interactions, as well as methods of making and using such cells and nucleic acids. In an embodiment the antigen binding domain of one of the first and the second non-naturally occurring chimeric membrane embedded receptor, comprises an scFv, and the other comprises a single VH domain, e.g., a camelid, shark, or lamprey single VH domain, or a single VH domain derived from a human or mouse sequence.

[00270] In some embodiments, the claimed invention comprises a first and second CAR, wherein the antigen binding domain of one of the first and the second CAR does not comprise a variable light domain and a variable heavy domain. In some embodiments, the antigen binding domain of one of the first and the second CAR is an scFv, and the other is not an scFv. In some embodiments, the antigen binding domain of one of the first and the second CAR comprises a single VH domain, e.g., a camelid, shark, or lamprey single VH domain, or a single VH domain derived from a human or mouse sequence. In some embodiments, the antigen binding domain of one of the first and the second CAR comprises a nanobody. In some embodiments, the antigen binding domain of one of the first and the second CAR comprises a camelid VHH domain.

[00271] In some embodiments, the antigen binding domain of one of the first and the second CAR comprises an scFv, and the other comprises a single VH domain, e.g., a camelid, shark, or lamprey single VH domain, or a single VH domain derived from a human or mouse sequence. In some embodiments, the antigen binding domain of one of the first and the second CAR comprises an scFv, and the other comprises a nanobody. In some embodiments, the antigen

binding domain of one of the first and the second CAR comprises comprises an scFv, and the other comprises a camelid VHH domain.

[00272] In some embodiments, when present on the surface of a cell, binding of the antigen binding domain of the first CAR to its cognate antigen is not substantially reduced by the presence of the second CAR. In some embodiments, binding of the antigen binding domain of the first CAR to its cognate antigen in the presence of the second CAR is 85%, 90%, 95%, 96%, 97%, 98% or 99% of binding of the antigen binding domain of the first CAR to its cognate antigen in the absence of the second CAR.

[00273] In some embodiments, when present on the surface of a cell, the antigen binding domains of the first and the second CAR, associate with one another less than if both were scFv antigen binding domains. In some embodiments, the antigen binding domains of the first and the second CAR, associate with one another 85%, 90%, 95%, 96%, 97%, 98% or 99% less than if both were scFv antigen binding domains.

[00274] In another aspect, the CAR-expressing cell described herein can further express another agent, e.g., an agent which enhances the activity or fitness of a CAR-expressing cell. For example, in one embodiment, the agent can be an agent which inhibits a molecule that modulates or regulates, e.g., inhibits, T cell function. In some embodiments, the molecule that modulates or regulates T cell function is an inhibitory molecule. Inhibitory molecules, e.g., PD1, can, in some embodiments, decrease the ability of a CAR-expressing cell to mount an immune effector response. Examples of inhibitory molecules include PD1, PD-L1, CTLA4, TIM3, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), LAG3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4 and TGFR beta. In embodiments, an agent, e.g., an inhibitory nucleic acid, e.g., a dsRNA, e.g., an siRNA or shRNA; or e.g., an inhibitory protein or system, e.g., a clustered regularly interspaced short palindromic repeats (CRISPR), a transcription-activator like effector nuclease (TALEN), or a zinc finger endonuclease (ZFN), e.g., as described herein, can be used to inhibit expression of a molecule that modulates or regulates, e.g., inhibits, T-cell function in the CAR-expressing cell. In an embodiment the agent is an shRNA, e.g., an shRNA described herein. In an embodiment, the agent that modulates or regulates, e.g., inhibits, T-cell function is inhibited within a CAR-expressing cell. For example, a dsRNA molecule that

inhibits expression of a molecule that modulates or regulates, e.g., inhibits, T-cell function is linked to the nucleic acid that encodes a component, e.g., all of the components, of the CAR.

[00275] In one embodiment, the agent which inhibits an inhibitory molecule comprises a first polypeptide, e.g., an inhibitory molecule, associated with a second polypeptide that provides a positive signal to the cell, e.g., an intracellular signaling domain described herein. In one embodiment, the agent comprises a first polypeptide, e.g., of an inhibitory molecule such as PD1, PD-L1, CTLA4, TIM3, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), LAG3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4 and TGFR beta T, or a fragment of any of these (e.g., at least a portion of an extracellular domain of any of these), and a second polypeptide which is an intracellular signaling domain described herein (e.g., comprising a costimulatory domain (e.g., 41BB, CD27 or CD28, e.g., as described herein) and/or a primary signaling domain (e.g., a CD3 zeta signaling domain described herein)). In one embodiment, the agent comprises a first polypeptide of PD1 or a fragment thereof (e.g., at least a portion of an extracellular domain of PD1), and a second polypeptide of an intracellular signaling domain described herein (e.g., a CD28 signaling domain described herein and/or a CD3 zeta signaling domain described herein). PD1 is an inhibitory member of the CD28 family of receptors that also includes CD28, CTLA-4, ICOS, and BTLA. PD-1 is expressed on activated B cells, T cells and myeloid cells (Agata et al. 1996 *Int. Immunol* 8:765-75). Two ligands for PD1, PD-L1 and PD-L2 have been shown to downregulate T cell activation upon binding to PD1 (Freeman et al. 2000 *J Exp Med* 192:1027-34; Latchman et al. 2001 *Nat Immunol* 2:261-8; Carter et al. 2002 *Eur J Immunol* 32:634-43). PD-L1 is abundant in human cancers (Dong et al. 2003 *J Mol Med* 81:281-7; Blank et al. 2005 *Cancer Immunol. Immunother* 54:307-314; Konishi et al. 2004 *Clin Cancer Res* 10:5094). Immune suppression can be reversed by inhibiting the local interaction of PD1 with PD-L1.

[00276] In one embodiment, the agent comprises the extracellular domain (ECD) of an inhibitory molecule, e.g., Programmed Death 1 (PD1), can be fused to a transmembrane domain and intracellular signaling domains such as 41BB and CD3 zeta (also referred to herein as a PD1 CAR). In one embodiment, the PD1 CAR, when used in combinations with a mesothelin CAR described herein, improves the persistence of the T cell. In one embodiment, the CAR is a PD1 CAR comprising the extracellular domain of PD1 indicated as underlined in SEQ ID NO: 24 and a signal sequence at amino acids 1-21 of SEQ ID NO:24. In one embodiment, the PD1 CAR comprises the amino acid sequence of SEQ ID NO:24.

[00277] Malpvtallplalllhaarppgwfdspdrpwnpptfspallvvtegdnatftcsfsntsesfvlnwyrmspsnqtdkl
aafpedrsqpgqdcfrfrvtqlpngrdfhmsvvrarrndsgtylegaislapkaqikesraelrvterraevptahpspsprpagqfqtlvt
ttppaprpptpaptiasqplslrpeacrpaggavhtrgldfacdiyiwaplagtcgvllslvitlyckrgrkklyifkqpfmrpvqtqeed
gcscrfpeeeeeggcelrvkfsrsadapaykqgqnqlynelnlgrreeydvldkrrgrdpemggkprrknpqeglynelqdkmaea
yseimgmkerrgkghdglyqglstatkdydalhmqalppr (SEQ ID NO:24).

[00278] In one embodiment, the PD1 CAR without the N-terminal signal sequence comprises the amino acid sequence provided below (SEQ ID NO:22).

[00279] pgwfldspdrpwnpptspallvvtegdnatftcsfsntsesfvlnwyrmspsnqtdklaafpedrsqpgqdcrfrvtqlpngrdfhmssvrrarrndsgtlycgaislapkaqikesraelrvterraevptahtpspsprpagqfqtlvttppaprptaptiasqlsrlpeacrpaggavhtrgldfacdiyiwiaplagtcgvlls1vitlyckrgrkklyifkqpfmrpvqtqeedgcscrfpeeeeeggcelrvfksrsadapaykqgqnqlynelngrreeydvlkrrgrdpemggkprrknpqeglynelqdkmaeayseigmkgerrrgkghdgyqqlstatkdydalhmqalppr (SEQ ID NO:22).

[00280] In one embodiment, the agent comprises a nucleic acid sequence encoding the PD1 CAR with the N-terminal signal sequence, e.g., the PD1 CAR described herein. In one embodiment, the nucleic acid sequence for the PD1 CAR is shown below, with the PD1 ECD underlined below in SEQ ID NO: 23

[00281] atggccctccctgtcactgccctgttctcccccgcactcctgtccacgcccgttagaccacccggatgttctggacttcggatcgccctggaaatcccccaacccatcaccggcactctgggttgactgaggcgataatgcgacccatcagtgctcggttctccaacacctccgaatcattcgtctgaactgttcccgcatgagccctcaaaaccagaccgacaagctcgccgcgttccggaaagatcggtcgcaaccggacaggattgtcgttcccgctgactcaactgccgaatggcagagacttccacatgagcgtgtcccgctgaccgaaacgactccgggacacctacatcgccgttcccgcatgcacatccatccccatcgccctgcggggcagttcagaccctggtcacgaccactccggccgcgcgcgactccggcccaactatcgcgagccagccctgtcgctgaggccgaaagcatgccgcctgcccggagggtgtgcataccggggattggacttcgcatgcgacatctacattggctctcgccggaaactgtggcgtgtccctgtccctggtcataccctgtactgcaagegggggtcgaaaaagttctgtacatttcaagcagccctcatgaggcccgtgcaaaaccacccaggaggaggacgggtgtccctggccgttcccgaaagaggaaggagggtgcgagctgcgcgtgaagttctccggagcggcgcgcgttcccgctataagcagggccgaaccagctgtacaacgaactgaacctggacggcgaaagagtgatgtgtccatggacaagcggcgccggggacccgaaatggcgggaaacctagaagaaagaaccctcaggaaggcctgtataacgagactgcagaaggacaagatggccgaggcctactccgaaattgggatgaagggagagcggcgagggaaagggcactgcacggcctgtaccaaggactgtccaccgcccaccaaggacacatacgatgcctgcacatgcaggccct (SEQ ID NO: 23).

[00282] In another aspect, the present invention provides a population of CAR-expressing cells, e.g., CART cells. In some embodiments, the population of CAR-expressing cells comprises a mixture of cells expressing different CARs. For example, in one embodiment, the population of CART cells can include a first cell expressing a CAR having an anti-CD19 binding domain described herein, and a second cell expressing a CAR having a different anti-CD19 binding domain, e.g., an anti-mesothelin binding domain described herein that differs from the anti-mesothelin binding domain in the CAR expressed by the first cell. As another example, the population of CAR-expressing cells can include a first cell expressing a CAR that includes an anti-mesothelin binding domain, e.g., as described herein, and a second cell expressing a CAR that includes an antigen binding domain to a target other than mesothelin (e.g., a target other than mesothelin on stroma cells, e.g., FAP; a target other than mesothelin on prostate cancer cells, e.g., androgen receptor, OR51E2, PSMA, PSCA, PDGRF- β , TARP, GloboH, MAD-CT-1, or MAD-CT-2; a target other than mesothelin on ovarian cancer cells, e.g., Tn, PRSS21, CD171, Lewis Y, folate receptor α , claudin6, GloboH, or sperm protein 17, e.g., a target other than mesothelin on lung cancer cells, e.g., VEGF, HER3, IGF-1R, EGFR, DLL4, or Trop-2). In one embodiment, the population of CAR-expressing cells includes, e.g., a first cell expressing a CAR that includes a primary intracellular signaling domain, and a second cell expressing a CAR that includes a secondary signaling domain.

[00283] In another aspect, the present invention provides a population of cells wherein at least one cell in the population expresses a CAR having an anti-mesothelin binding domain described herein, and a second cell expressing another agent, e.g., an agent which enhances the activity or function of a CAR-expressing cell. For example, in one embodiment, the agent can be an agent which modulates or regulates, e.g., inhibits, T cell function. In some embodiments, the molecule that modulates or regulates T cell function is an inhibitory molecule, e.g., an agent described herein. Inhibitory molecules, e.g., can, in some embodiments, decrease the ability of a CAR-expressing cell to mount an immune effector response. Examples of inhibitory molecules include PD1, PD-L1, CTLA4, TIM3, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), LAG3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4 and TGFR beta. In one embodiment, the agent which inhibits an inhibitory molecule comprises a first polypeptide, e.g., an inhibitory molecule, associated with a second polypeptide that provides a positive signal to the cell, e.g., an intracellular signaling domain described herein. In one embodiment, the agent

comprises a first polypeptide, e.g., of an inhibitory molecule such as PD1, PD-L1, CTLA4, TIM3, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), LAG3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4 and TGFR beta, or a fragment of any of these (e.g., at least a portion of an extracellular domain of any of these), and a second polypeptide which is an intracellular signaling domain described herein (e.g., comprising a costimulatory domain (e.g., 41BB, CD27 or CD28, e.g., as described herein) and/or a primary signaling domain (e.g., a CD3 zeta signaling domain described herein). In one embodiment, the agent comprises a first polypeptide of PD1 or a fragment thereof (e.g., at least a portion of the extracellular domain of PD1), and a second polypeptide of an intracellular signaling domain described herein (e.g., a CD28 signaling domain described herein and/or a CD3 zeta signaling domain described herein).

[00284] In one aspect, the present invention provides methods comprising administering a population of CAR-expressing cells, e.g., CART cells, e.g., a mixture of cells expressing different CARs, in combination with another agent, e.g., a kinase inhibitor, such as a kinase inhibitor described herein. In another aspect, the present invention provides methods comprising administering a population of cells wherein at least one cell in the population expresses a CAR having an anti-mesothelinbinding domain as described herein, and a second cell expressing another agent, e.g., an agent which enhances the activity or fitness of a CAR-expressing cell, in combination with another agent, e.g., a kinase inhibitor, such as a kinase inhibitor described herein.

Regulatable Chimeric Antigen Receptors

[00285] In some embodiments, a regulatable CAR (RCAR) where the CAR activity can be controlled is desirable to optimize the safety and efficacy of a CAR therapy. There are many ways CAR activities can be regulated. For example, inducible apoptosis using, e.g., a caspase fused to a dimerization domain (see, e.g., Di et al., N Engl. J. Med. 2011 Nov. 3; 365(18):1673-1683), can be used as a safety switch in the CAR therapy of the instant invention. In an aspect, a RCAR comprises a set of polypeptides, typically two in the simplest embodiments, in which the components of a standard CAR described herein, e.g., an antigen binding domain and an intracellular signaling domain, are partitioned on separate polypeptides or members. 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.

[00286] In an aspect, an RCAR comprises two polypeptides or members: 1) an intracellular signaling member comprising an intracellular signaling domain, e.g., a primary intracellular signaling domain described herein, and a first switch domain; 2) an antigen binding member comprising an antigen binding domain, e.g., that targets mesothelin as described herein, and a second switch domain. Optionally, the RCAR comprises a transmembrane domain described herein. In an embodiment, a transmembrane domain can be disposed on the intracellular signaling member, on the antigen binding member, or on both. (Unless otherwise indicated, when members or elements of an RCAR are described herein, the order can be as provided, but other orders are included as well. In other words, in an embodiment, the order is as set out in the text, but in other embodiments, the order can be different. E.g., the order of elements on one side of a transmembrane region can be different from the example, e.g., the placement of a switch domain relative to a intracellular signaling domain can be different, e.g., reversed).

[00287] In an embodiment, the first and second switch domains can form an intracellular or an extracellular dimerization switch. In an embodiment, the dimerization switch can be a homodimerization switch, e.g., where the first and second switch domain are the same, or a heterodimerization switch, e.g., where the first and second switch domain are different from one another.

[00288] In embodiments, an RCAR can comprise a “multi switch.” A multi switch can comprise heterodimerization switch domains or homodimerization switch domains. A multi switch comprises a plurality of, e.g., 2, 3, 4, 5, 6, 7, 8, 9, or 10, switch domains, independently, on a first member, e.g., an antigen binding member, and a second member, e.g., an intracellular signaling member. In an embodiment, the first member can comprise a plurality of first switch domains, e.g., FKBP-based switch domains, and the second member can comprise a plurality of second switch domains, e.g., FRB-based switch domains. In an embodiment, the first member can comprise a first and a second switch domain, e.g., a FKBP-based switch domain and a FRB-based switch domain, and the second member can comprise a first and a second switch domain, e.g., a FKBP-based switch domain and a FRB-based switch domain.

[00289] In an embodiment, the intracellular signaling member comprises one or more intracellular signaling domains, e.g., a primary intracellular signaling domain and one or more costimulatory signaling domains.

[00290] In an embodiment, the antigen binding member may comprise one or more intracellular signaling domains, e.g., one or more costimulatory signaling domains. In an embodiment, the antigen binding member comprises a plurality, e.g., 2 or 3 costimulatory signaling domains described herein, e.g., selected from 41BB, CD28, CD27, ICOS, and OX40, and in embodiments, no primary intracellular signaling domain. In an embodiment, the antigen binding member comprises the following costimulatory signaling domains, from the extracellular to intracellular direction: 41BB-CD27; 41BB-CD27; CD27-41BB; 41BB-CD28; CD28-41BB; OX40-CD28; CD28-OX40; CD28-41BB; or 41BB-CD28. In such embodiments, the intracellular binding member comprises a CD3zeta domain. In one such embodiment the RCAR comprises (1) an antigen binding member comprising, an antigen binding domain, e.g., described herein, a transmembrane domain, and two costimulatory domains and a first switch domain; and (2) an intracellular signaling domain comprising a transmembrane domain or membrane tethering domain and at least one primary intracellular signaling domain, and a second switch domain.

[00291] An embodiment provides RCARs wherein the antigen binding member is not tethered to the surface of the CAR cell. This allows a cell having an intracellular signaling member to be conveniently paired with one or more antigen binding domains, without transforming the cell with a sequence that encodes the antigen binding member. In such embodiments, the RCAR comprises: 1) an intracellular signaling member comprising: a first switch domain, a transmembrane domain, an intracellular signaling domain, e.g., a primary intracellular signaling domain, and a first switch domain; and 2) an antigen binding member comprising: an antigen binding domain, e.g., described herein, and a second switch domain, wherein the antigen binding member does not comprise a transmembrane domain or membrane tethering domain, and, optionally, does not comprise an intracellular signaling domain. In some embodiments, the RCAR may further comprise 3) a second antigen binding member comprising: a second antigen binding domain, e.g., a second antigen binding domain that binds a different antigen than is bound by the antigen binding domain; and a second switch domain.

[00292] Also provided herein are RCARs wherein the antigen binding member comprises bispecific activation and targeting capacity. In this embodiment, the antigen binding member can comprise a plurality, e.g., 2, 3, 4, or 5 antigen binding domains, e.g., scFvs, wherein each antigen binding domain binds to a target antigen, e.g. different antigens or the same antigen, e.g., the same or different epitopes on the same antigen. In an embodiment, the plurality of antigen binding domains are in tandem, and optionally, a linker or hinge region is disposed between each of the antigen binding domains. Suitable linkers and hinge regions are described herein.

[00293] An embodiment provides RCARs having a configuration that allows switching of proliferation. In this embodiment, the RCAR comprises: 1) an intracellular signaling member comprising: optionally, a transmembrane domain or membrane tethering domain; one or more co-stimulatory signaling domain, e.g., selected from 41BB, CD28, CD27, ICOS, and OX40, and a switch domain; and 2) an antigen binding member comprising: an antigen binding domain, e.g., described herein, a transmembrane domain, and a primary intracellular signaling domain, e.g., a CD3zeta domain, wherein the antigen binding member does not comprise a switch domain, or does not comprise a switch domain that dimerizes with a switch domain on the intracellular signaling member. In an embodiment, the antigen binding member does not comprise a co-stimulatory signaling domain. In an embodiment, the intracellular signaling member comprises a switch domain from a homodimerization switch. In an embodiment, the intracellular signaling member comprises a first switch domain of a heterodimerization switch and the RCAR comprises a second intracellular signaling member which comprises a second switch domain of the heterodimerization switch. In such embodiments, the second intracellular signaling member comprises the same intracellular signaling domains as the intracellular signaling member. In an embodiment, the dimerization switch is intracellular. In an embodiment, the dimerization switch is extracellular.

[00294] In any of the RCAR configurations described here, the first and second switch domains comprise a FKBP/FRB-based switch as described herein.

[00295] Also provided herein are cells comprising an RCAR described herein. Any cell that is engineered to express a RCAR can be used as a RCARX cell. In an embodiment the RCARX cell is a T cell, and is referred to as a RCART cell. In an embodiment the RCARX cell is an NK cell, and is referred to as a RCARN cell.

[00296] Also provided herein are nucleic acids and vectors comprising RCAR encoding sequences. Sequence encoding various elements of an RCAR can be disposed on the same nucleic acid molecule, e.g., the same plasmid or vector, e.g., viral vector, e.g., lentiviral vector. In an embodiment, (i) sequence encoding an antigen binding member and (ii) sequence encoding an intracellular signaling member, can be present on the same nucleic acid, e.g., vector. Production of the corresponding proteins can be achieved, e.g., by the use of separate promoters, or by the use of a bicistronic transcription product (which can result in the production of two proteins by cleavage of a single translation product or by the translation of two separate protein products). In an embodiment, a sequence encoding a cleavable peptide, e.g., a P2A or F2A sequence, is disposed between (i) and (ii). In an embodiment, a sequence encoding an IRES, e.g., an EMCV or EV71 IRES, is disposed between (i) and (ii). In these embodiments, (i) and (ii) are transcribed as a single RNA. In an embodiment, a first promoter is operably linked to (i) and a second promoter is operably linked to (ii), such that (i) and (ii) are transcribed as separate mRNAs.

[00297] Alternatively, the sequence encoding various elements of an RCAR can be disposed on the different nucleic acid molecules, e.g., different plasmids or vectors, e.g., viral vector, e.g., lentiviral vector. E.g., the (i) sequence encoding an antigen binding member can be present on a first nucleic acid, e.g., a first vector, and the (ii) sequence encoding an intracellular signaling member can be present on the second nucleic acid, e.g., the second vector.

Dimerization switches

[00298] Dimerization switches can be non-covalent or covalent. In a non-covalent dimerization switch, the dimerization molecule promotes a non-covalent interaction between the switch domains. In a covalent dimerization switch, the dimerization molecule promotes a covalent interaction between the switch domains.

[00299] In an embodiment, the RCAR comprises a FKBP/FRAP, or FKBP/FRB,-based dimerization switch. FKBP12 (FKBP, or FK506 binding protein) is an abundant cytoplasmic protein that serves as the initial intracellular target for the natural product immunosuppressive drug, rapamycin. Rapamycin binds to FKBP and to the large PI3K homolog FRAP (RAFT, mTOR). FRB is a 93 amino acid portion of FRAP, that is sufficient for binding the FKBP-rapamycin complex (Chen, J., Zheng, X. F., Brown, E. J. & Schreiber, S. L. (1995) *Identification*

of an 11-kDa FKBP12-rapamycin-binding domain within the 289-kDa FKBP12-rapamycin-associated protein and characterization of a critical serine residue. Proc Natl Acad Sci U S A 92: 4947-51.)

[00300] In embodiments, an FKBP/FRAP, e.g., an FKBP/FRB, based switch can use a dimerization molecule, e.g., rapamycin or a rapamycin analog.

[00301] The amino acid sequence of FKBP is as follows:

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D V P D Y A S L G G P S S P K K K R K V S R G V Q V E T I S P G D G R T F P K
R G Q T C V V H Y T G M L E D G K K F D S S R D R N K P F K F M L G K Q E V I
R G W E E G V A Q M S V G Q R A K L T I S P D Y A Y G A T G H P G I I P P H A
T L V F D V E L L K L E T S Y (SEQ ID NO: 382)
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[00302] In embodiments, an FKBP switch domain can comprise a FRB binding fragment of FKBP, e.g., the underlined portion of SEQ ID NO: 382, which is:

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V Q V E T I S P G D G R T F P K R G Q T C V V H Y T G M L E D G K K F D S S R
D R N K P F K F M L G K Q E V I R G W E E G V A Q M S V G Q R A K L T I S P D
Y A Y G A T G H P G I I P P H A T L V F D V E L L K L E T S (SEQ ID NO: 383)
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[00303] The amino acid sequence of FRB is as follows:

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I L W H E M W H E G L E E A S R L Y F G E R N V K G M F E V L E P L H A M M E R G P Q T L K E T S F N Q A Y G R D L M E A Q E W C R K Y M K
S G N V K D L T Q A W D L Y Y H V F R R I S K (SEQ ID NO: 384)
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[00304] “FKBP/FRAP, e.g., an FKPP/FRB, based switch” as that term is used herein, refers to a dimerization switch comprising: a first switch domain, comprises an FRB binding fragment or an FKBP analog, e.g., RAD001, and has at least 70, 75, 80, 85, 90, 95, 96, 97, 98, or 99% identity with, or differs by no more than 30, 25, 20, 15, 10, 5, 4, 3, 2, or 1 amino acid residues from, the FKBP sequence of SEQ ID NO: 382 or 383; and a second switch domain, which comprises an FKBP binding fragment or an FRB analog, and has at least 70, 75, 80, 85, 90, 95, 96, 97, 98, or 99% identity with, or differs by no more than 30, 25, 20, 15, 10, 5, 4, 3, 2, or 1 amino acid residues from, the FRB sequence of SEQ ID NO: 384. In an embodiment, a RCAR described herein comprises one switch domain comprises amino acid residues disclosed in SEQ ID NO: 382 (or SEQ ID NO: 383), and one switch domain comprises amino acid residues disclosed in SEQ ID NO: 384.

[00305] In embodiments, the FKBP/FRB dimerization switch comprises a modified FRB switch domain that exhibits altered, e.g., increased, affinity for the dimerization molecule, e.g., rapamycin or a rapalogue, e.g., RAD001. In an embodiment, the modified FRB switch domain comprises one or more mutations, e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10 or more, selected from mutations at amino acid position(s) L2031, E2032, S2035, R2036, F2039, G2040, T2098, W2101, D2102, Y2105, and F2108, where the wild-type amino acid is mutated to any other naturally-occurring amino acid. In an embodiment, a mutant FRB comprises a mutation at E2032, where E2032 is mutated to phenylalanine (E2032F), methionine (E2032M), arginine (E2032R), valine (E2032V), tyrosine (E2032Y), isoleucine (E2032I), e.g., SEQ ID NO: 385, or leucine (E2032L), e.g., SEQ ID NO: 386. In an embodiment, a mutant FRB comprises a mutation at T2098, where T2098 is mutated to phenylalanine (T2098F) or leucine (T2098L), e.g., SEQ ID NO: 387. In an embodiment, a mutant FRB comprises a mutation at E2032 and at T2098, where E2032 is mutated to any amino acid, and where T2098 is mutated to any amino acid, e.g., SEQ ID NO: 388. In an embodiment, a mutant FRB comprises an E2032I and a T2098L mutation, e.g., SEQ ID NO: 389. In an embodiment, a mutant FRB comprises an E2032L and a T2098L mutation, e.g., SEQ ID NO: 340.

[00306] Table 15. Exemplary mutant FRB having increased affinity for a dimerization molecule.

FRB mutant	Amino Acid Sequence	SEQ ID NO:
E2032I mutant	ILWHEMWHEGLIEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETSFNQAYGR DLMEAQEWCRCRKYMKSGNVKDLTQAWDLYYHVFRRISKTS	385
E2032L mutant	ILWHEMWHEGLLEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETSFNQAYGR DLMEAQEWCRCRKYMKSGNVKDLTQAWDLYYHVFRRISKTS	386
T2098L mutant	ILWHEMWHEGLEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETSFNQAYGR DLMEAQEWCRCRKYMKSGNVKDLQAWDLYYHVFRRISKTS	387
E2032, T2098 mutant	ILWHEMWHEGL X ASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETSFNQAYGR DLMEAQEWCRCRKYMKSGNVKDL X QAWDLYYHVFRRISKTS	388
E2032I, T2098L mutant	ILWHEMWHEGLIEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETSFNQAYGR DLMEAQEWCRCRKYMKSGNVKDLQAWDLYYHVFRRISKTS	389
E2032L, T2098L mutant	ILWHEMWHEGLLEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETSFNQAYGR DLMEAQEWCRCRKYMKSGNVKDLQAWDLYYHVFRRISKTS	390

[00307] Other suitable dimerization switches include a GyrB-GyrB based dimerization switch, a Gibberellin-based dimerization switch, a tag/binder dimerization switch, and a halo-tag/snap-

tag dimerization switch. Following the guidance provided herein, such switches and relevant dimerization molecules will be apparent to one of ordinary skill.

Dimerization molecule

[00308] Association between the switch domains is promoted by the dimerization molecule. In the presence of dimerization molecule interaction or association between switch domains allows for signal transduction between a polypeptide associated with, e.g., fused to, a first switch domain, and a polypeptide associated with, e.g., fused to, a second switch domain. In the presence of non-limiting levels of dimerization molecule signal transduction is increased by 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 5, 10, 50, 100 fold, e.g., as measured in a system described herein.

[00309] Rapamycin and rapamycin analogs (sometimes referred to as rapalogues), e.g., RAD001, can be used as dimerization molecules in a FKBP/FRB-based dimerization switch described herein. In an embodiment the dimerization molecule can be selected from rapamycin (sirolimus), RAD001 (everolimus), zotarolimus, temsirolimus, AP-23573 (ridaforolimus), biolimus and AP21967. Additional rapamycin analogs suitable for use with FKBP/FRB-based dimerization switches are further described in the section entitled “Combination Therapies”, or in the subsection entitled “Exemplary mTOR inhibitors”.

RNA Transfection

[00310] Disclosed herein are methods for producing an in vitro transcribed RNA CAR. The present invention also includes a CAR encoding RNA construct that can be directly transfected into a cell. A method for generating mRNA for use in transfection can involve 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:35). RNA so produced can efficiently transfect different kinds of cells. In one aspect, the template includes sequences for the CAR.

[00311] In one aspect the mesothelin CAR is encoded by a messenger RNA (mRNA). In one aspect the mRNA encoding the mesothelin CAR is introduced into a T cell for production of a CART cell.

[00312] In one embodiment, the in vitro transcribed RNA CAR can be introduced to a cell as a form of transient transfection. The RNA is produced by in vitro transcription using a polymerase chain reaction (PCR)-generated template. DNA of interest from any source can be directly converted by PCR into a template for in vitro mRNA synthesis using appropriate primers and RNA polymerase. The source of the DNA can be, for example, genomic DNA, plasmid DNA, phage DNA, cDNA, synthetic DNA sequence or any other appropriate source of DNA. The desired template for in vitro transcription is a CAR of the present invention. For example, the template for the RNA CAR comprises an extracellular region comprising a single chain variable domain of an anti-tumor antibody; a hinge region, a transmembrane domain (e.g., a transmembrane domain of CD8a); and a cytoplasmic region that includes an intracellular signaling domain, e.g., comprising the signaling domain of CD3-zeta and the signaling domain of 4-1BB.

[00313] In one embodiment, the DNA to be used for PCR contains an open reading frame. The DNA can be from a naturally occurring DNA sequence from the genome of an organism. In one embodiment, the nucleic acid can include some or all of the 5' and/or 3' untranslated regions (UTRs). The nucleic acid can include exons and introns. In one embodiment, the DNA to be used for PCR is a human nucleic acid sequence. In another embodiment, the DNA to be used for PCR is a human nucleic acid sequence including the 5' and 3' UTRs. The DNA can alternatively be an artificial DNA sequence that is not normally expressed in a naturally occurring organism. An exemplary artificial DNA sequence is one that contains portions of genes that are ligated together to form an open reading frame that encodes a fusion protein. The portions of DNA that are ligated together can be from a single organism or from more than one organism.

[00314] PCR is used to generate a template for in vitro transcription of mRNA which is used for transfection. Methods for performing PCR are well known in the art. Primers for use in PCR are designed to have regions that are substantially complementary to regions of the DNA to be used as a template for the PCR. The term "substantially complementary" refers to sequences of nucleotides where a majority or all of the bases in the primer sequence are complementary, or one or more bases are non-complementary, or mismatched. Substantially complementary sequences are able to anneal or hybridize with the intended DNA target under annealing conditions used for PCR. The primers can be designed to be substantially complementary to any portion of the DNA template. For example, the primers can be designed to amplify the portion of

a nucleic acid that is normally transcribed in cells (the open reading frame), including 5' and 3' UTRs. The primers can also be designed to amplify a portion of a nucleic acid that encodes a particular domain of interest. In one embodiment, the primers are designed to amplify the coding region of a human cDNA, including all or portions of the 5' and 3' UTRs. Primers useful for PCR can be generated by synthetic methods that are well known in the art. "Forward primers" are primers that contain a region of nucleotides that are substantially complementary to nucleotides on the DNA template that are upstream of the DNA sequence that is to be amplified. The term "upstream" refers to a location 5' to the DNA sequence to be amplified relative to the coding strand. "Reverse primers" are primers that contain a region of nucleotides that are substantially complementary to a double-stranded DNA template that are downstream of the DNA sequence that is to be amplified. The term "downstream" refers to a location 3' to the DNA sequence to be amplified relative to the coding strand.

[00315] Any DNA polymerase useful for PCR can be used in the methods disclosed herein. The reagents and polymerase are commercially available from a number of sources.

[00316] Chemical structures with the ability to promote stability and/or translation efficiency may also be used. The RNA preferably has 5' and 3' UTRs. In one embodiment, the 5' UTR is between one and 3000 nucleotides in length. The length of 5' and 3' UTR sequences to be added to the coding region can be altered by different methods, including, but not limited to, designing primers for PCR that anneal to different regions of the UTRs. Using this approach, one of ordinary skill in the art can modify the 5' and 3' UTR lengths required to achieve optimal translation efficiency following transfection of the transcribed RNA.

[00317] The 5' and 3' UTRs can be the naturally occurring, endogenous 5' and 3' UTRs for the nucleic acid of interest. Alternatively, UTR sequences that are not endogenous to the nucleic acid of interest can be added by incorporating the UTR sequences into the forward and reverse primers or by any other modifications of the template. The use of UTR sequences that are not endogenous to the nucleic acid of interest can be useful for modifying the stability and/or translation efficiency of the RNA. For example, it is known that AU-rich elements in 3' UTR sequences can decrease the stability of mRNA. Therefore, 3' UTRs can be selected or designed to increase the stability of the transcribed RNA based on properties of UTRs that are well known in the art.

[00318] In one embodiment, the 5' UTR can contain the Kozak sequence of the endogenous nucleic acid. Alternatively, when a 5' UTR that is not endogenous to the nucleic acid of interest is being added by PCR as described above, a consensus Kozak sequence can be redesigned by adding the 5' UTR sequence. Kozak sequences can increase the efficiency of translation of some RNA transcripts, but does not appear to be required for all RNAs to enable efficient translation. The requirement for Kozak sequences for many mRNAs is known in the art. In other embodiments the 5' UTR can be 5'UTR of an RNA virus whose RNA genome is stable in cells. In other embodiments various nucleotide analogues can be used in the 3' or 5' UTR to impede exonuclease degradation of the mRNA.

[00319] To enable synthesis of RNA from a DNA template without the need for gene cloning, a promoter of transcription should be attached to the DNA template upstream of the sequence to be transcribed. When a sequence that functions as a promoter for an RNA polymerase is added to the 5' end of the forward primer, the RNA polymerase promoter becomes incorporated into the PCR product upstream of the open reading frame that is to be transcribed. In one preferred embodiment, the promoter is a T7 polymerase promoter, as described elsewhere herein. Other useful promoters include, but are not limited to, T3 and SP6 RNA polymerase promoters. Consensus nucleotide sequences for T7, T3 and SP6 promoters are known in the art.

[00320] In a preferred embodiment, the mRNA has both a cap on the 5' end and a 3' poly(A) tail which determine ribosome binding, initiation of translation and stability mRNA in the cell. On a circular DNA template, for instance, plasmid DNA, RNA polymerase produces a long concatameric product which is not suitable for expression in eukaryotic cells. The transcription of plasmid DNA linearized at the end of the 3' UTR results in normal sized mRNA which is not effective in eukaryotic transfection even if it is polyadenylated after transcription.

[00321] On a linear DNA template, phage T7 RNA polymerase can extend the 3' end of the transcript beyond the last base of the template (Schenborn and Mierendorf, Nuc Acids Res., 13:6223-36 (1985); Nacheva and Berzal-Herranz, Eur. J. Biochem., 270:1485-65 (2003)).

[00322] The conventional method of integration of polyA/T stretches into a DNA template is molecular cloning. However polyA/T sequence integrated into plasmid DNA can cause plasmid instability, which is why plasmid DNA templates obtained from bacterial cells are often highly contaminated with deletions and other aberrations. This makes cloning procedures not only

laborious and time consuming but often not reliable. That is why a method which allows construction of DNA templates with polyA/T 3' stretch without cloning highly desirable.

[00323] The polyA/T segment of the transcriptional DNA template can be produced during PCR by using a reverse primer containing a polyT tail, such as 100T tail (SEQ ID NO: 31) (size can be 50-5000 T (SEQ ID NO: 32)), or after PCR by any other method, including, but not limited to, DNA ligation or in vitro recombination. Poly(A) tails also provide stability to RNAs and reduce their degradation. Generally, the length of a poly(A) tail positively correlates with the stability of the transcribed RNA. In one embodiment, the poly(A) tail is between 100 and 5000 adenosines (SEQ ID NO: 33).

[00324] Poly(A) tails of RNAs can be further extended following in vitro transcription with the use of a poly(A) polymerase, such as *E. coli* polyA polymerase (E-PAP). In one embodiment, increasing the length of a poly(A) tail from 100 nucleotides to between 300 and 400 nucleotides (SEQ ID NO: 34) results in about a two-fold increase in the translation efficiency of the RNA. Additionally, the attachment of different chemical groups to the 3' end can increase mRNA stability. Such attachment can contain modified/artificial nucleotides, aptamers and other compounds. For example, ATP analogs can be incorporated into the poly(A) tail using poly(A) polymerase. ATP analogs can further increase the stability of the RNA.

[00325] 5' caps on also provide stability to RNA molecules. In a preferred embodiment, RNAs produced by the methods disclosed herein include a 5' cap. The 5' cap is provided using techniques known in the art and described herein (Cougot, et al., *Trends in Biochem. Sci.*, 29:436-444 (2001); Stepinski, et al., *RNA*, 7:1468-95 (2001); Elango, et al., *Biochim. Biophys. Res. Commun.*, 330:958-966 (2005)).

[00326] The RNAs produced by the methods disclosed herein can also contain an internal ribosome entry site (IRES) sequence. The IRES sequence may be any viral, chromosomal or artificially designed sequence which initiates cap-independent ribosome binding to mRNA and facilitates the initiation of translation. Any solutes suitable for cell electroporation, which can contain factors facilitating cellular permeability and viability such as sugars, peptides, lipids, proteins, antioxidants, and surfactants can be included.

[00327] RNA can be introduced into target cells using any of a number of different methods, for instance, commercially available methods which include, but are not limited to,

electroporation (Amaxa Nucleofector-II (Amaxa Biosystems, Cologne, Germany)), (ECM 830 (BTX) (Harvard Instruments, Boston, Mass.) or the Gene Pulser II (BioRad, Denver, Colo.), Multiporator (Eppendorf, Hamburg Germany), cationic liposome mediated transfection using lipofection, polymer encapsulation, peptide mediated transfection, or biolistic particle delivery systems such as “gene guns” (see, for example, Nishikawa, et al. *Hum Gene Ther.*, 12(8):861-70 (2001).

Nucleic Acid Constructs Encoding a CAR

[00328] The present invention provides CAR transgenes comprising nucleic acid sequences encoding one or more CAR constructs of the invention. In one aspect, the CAR transgene is provided as a messenger RNA transcript. In one aspect, the CAR transgene is provided as a DNA construct.

[00329] Accordingly, in one aspect, the invention pertains to an isolated nucleic acid molecule encoding a chimeric antigen receptor (CAR), wherein the CAR comprises an anti-mesothelin binding domain (e.g., a human anti-mesothelin binding domain), a transmembrane domain, and an intracellular signaling domain comprising a stimulatory domain. In one embodiment, the anti-mesothelin binding domain is an anti-mesothelin binding domain described herein, e.g., an anti-mesothelin binding domain which comprises a sequence selected from a group consisting of SEQ ID NO: 87-111, or a sequence with 95-99% identity thereof. In one embodiment, the isolated nucleic acid molecule further comprises a sequence encoding a costimulatory domain. In one embodiment, the transmembrane domain is a transmembrane domain of a protein selected from the group consisting of the alpha, beta or zeta chain of the T-cell receptor, CD28, CD3 epsilon, CD45, CD4, CD5, CD8, CD9, CD16, CD22, CD33, CD37, CD64, CD80, CD86, CD134, CD137 and CD154. In one embodiment, the transmembrane domain comprises a sequence of SEQ ID NO: 6, or a sequence with 95-99% identity thereof. In one embodiment, the anti-mesothelin binding domain is connected to the transmembrane domain by a hinge region, e.g., a hinge described herein. In one embodiment, the hinge region comprises SEQ ID NO:2 or SEQ ID NO:3 or SEQ ID NO:4 or SEQ ID NO:5, or a sequence with 95-99% identity thereof. In one embodiment, the isolated nucleic acid molecule further comprises a sequence encoding a costimulatory domain. In one embodiment, the costimulatory domain is a functional signaling domain of a protein selected from the group consisting of 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, and PAG/Cbp. In one embodiment, the costimulatory domain comprises a sequence of SEQ ID NO: 7, or a sequence with 95-99% identity thereof. In one embodiment, the intracellular signaling domain comprises a functional signaling domain of 4-1BB and a functional signaling domain of CD3 zeta. In one embodiment, the intracellular signaling domain comprises the sequence of SEQ ID NO: 7 or SEQ ID NO: 8, or a sequence with 95-99% identity thereof, and the sequence of SEQ ID NO: 9 or SEQ ID NO: 10, or a sequence with 95-99% identity thereof, wherein the sequences comprising the intracellular signaling domain are expressed in the same frame and as a single polypeptide chain. In another aspect, the invention pertains to an isolated nucleic acid molecule encoding a CAR construct comprising a leader sequence of SEQ ID NO: 1, a scFv domain having a sequence selected from the group consisting of SEQ ID NO: 39; SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, 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, and SEQ ID NO: 62, (or a sequence with 95-99% identity thereof), a hinge region of SEQ ID NO: 2 or SEQ ID NO: 3 or SEQ ID NO: 4 or SEQ ID NO: 5 (or a sequence with 95-99% identity thereof), a transmembrane domain having a sequence of SEQ ID NO: 6 (or a sequence with 95-99% identity thereof), a 4-1BB costimulatory domain having a sequence of SEQ ID NO: 7 (or a sequence with 95-99% identity thereof) or a CD27 costimulatory domain having a sequence of SEQ ID NO: 8 (or a sequence with 95-99% identity thereof), and a CD3 zeta stimulatory domain having a sequence of SEQ ID NO: 9 or SEQ ID NO: 10 (or a sequence with 95-99% identity thereof).

[00330] In another aspect, the invention pertains to an isolated polypeptide molecule encoded by the nucleic acid molecule. In one embodiment, the isolated polypeptide molecule comprises a sequence selected from the group consisting of 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, SEQ ID NO: 70, 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, SEQ ID NO: 79, SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 83, SEQ ID NO: 84, SEQ ID NO: 85, and SEQ ID NO: 86, or a sequence with 95-99% identity thereof.

[00331] In another aspect, the invention pertains to an isolated nucleic acid molecule encoding a chimeric antigen receptor (CAR) molecule that comprises an anti-mesothelin binding domain, a transmembrane domain, and an intracellular signaling domain comprising a stimulatory domain, and wherein the nucleic acid encoding the anti-mesothelin binding domain comprises a sequence selected from the group consisting of SEQ ID NO: 111; SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 132, SEQ ID NO: 133, SEQ ID NO: 134, or a sequence with 95-99% identity thereof.

[00332] In one embodiment, the encoded CAR molecule further comprises a sequence encoding a costimulatory domain. In one embodiment, the costimulatory domain is a functional signaling domain of a protein selected from the group consisting of OX40, CD27, CD28, CDS, ICAM-1, LFA-1 (CD11a/CD18) and 4-1BB (CD137). In one embodiment, the costimulatory domain comprises a sequence of SEQ ID NO: 7. In one embodiment, the transmembrane domain is a transmembrane domain of a protein selected from the group consisting of the alpha, beta or zeta chain of the T-cell receptor, CD28, CD3 epsilon, CD45, CD4, CD5, CD8, CD9, CD16, CD22, CD33, CD37, CD64, CD80, CD86, CD134, CD137 and CD154. In one embodiment, the transmembrane domain comprises a sequence of SEQ ID NO: 6. In one embodiment, the intracellular signaling domain comprises a functional signaling domain of 4-1BB and a functional signaling domain of zeta. In one embodiment, the intracellular signaling domain comprises the sequence of SEQ ID NO: 7 and the sequence of SEQ ID NO: 9, wherein the sequences comprising the intracellular signaling domain are expressed in the same frame and as

a single polypeptide chain. In one embodiment, the anti-mesothelin binding domain is connected to the transmembrane domain by a hinge region. In one embodiment, the hinge region comprises SEQ ID NO:2. In one embodiment, the hinge region comprises SEQ ID NO: 3, SEQ ID NO: 4, or SEQ ID NO: 5.

[00333] In another aspect, the invention pertains to an isolated CAR molecule comprising a leader sequence of SEQ ID NO: 1, a scFv domain having a sequence selected from the group consisting of SEQ ID NOS: 39-62, or a sequence with 95-99% identify thereof, a hinge region of SEQ ID NO:2 or SEQ ID NO: 3 or SEQ ID NO: 4 or SEQ ID NO: 5, a transmembrane domain having a sequence of SEQ ID NO: 6, a 4-1BB costimulatory domain having a sequence of SEQ ID NO:7 or a CD27 costimulatory domain having a sequence of SEQ ID NO: 8, and a CD3 zeta stimulatory domain having a sequence of SEQ ID NO:9 or SEQ ID NO: 10. In one embodiment, the encoded CAR molecule comprises a sequence selected from the group consisting of SEQ ID NOS: 63-86, or a sequence with 95-99% identify thereof.

[00334] The present invention further provides vectors comprising CAR transgenes. In one aspect, a CAR vectors can be directly transduced into a cell, *e.g.*, a T cell or NK cell. In one aspect, the vector is a cloning or expression vector, *e.g.*, a vector including, but not limited to, one or more plasmids (*e.g.*, expression plasmids, cloning vectors, minicircles, minivectors, double minute chromosomes), retroviral and lentiviral vector constructs. In one aspect, the vector is capable of expressing the CAR construct in mammalian T cells or NK cells. In one aspect, the mammalian T cell is a human T cell or a human NK cell.

[00335] The present invention also includes a CAR encoding RNA construct that can be directly transfected into a cell, *e.g.*, a T cell or a NK 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 gene to be expressed, and a polyA tail, typically 50-2000 bases in length. RNA so produced can efficiently transfect different kinds of cells. In one aspect, the template includes sequences for the CAR.

[00336] In one aspect the mesothelin CAR transgene is encoded by a messenger RNA (mRNA). In one aspect the mRNA encoding the mesothelin CAR transgene is introduced into a T cell for production of a CART cell, or a NK cell.

Vectors

[00337] The present invention also provides vectors in which a DNA of the present invention is inserted. Vectors derived from retroviruses such as the lentivirus are suitable tools to achieve long-term gene transfer since they allow long-term, stable integration of a transgene and its propagation in daughter cells. Lentiviral vectors have the added advantage over vectors derived from onco-retroviruses such as murine leukemia viruses in that they can transduce non-proliferating cells, such as hepatocytes. They also have the added advantage of low immunogenicity.

[00338] In one embodiment, the vector comprising the nucleic acid encoding the desired CAR of the invention is a DNA, a RNA, a plasmid, an adenoviral vector, a lentivirus vector, or a retrovirus vector.

[00339] In another embodiment, the vector comprising the nucleic acid encoding the desired CAR of the invention is an adenoviral vector (A5/35). In another embodiment, the expression of nucleic acids encoding CARs can be accomplished using of transposons such as sleeping beauty, CRISPR, CAS9, and zinc finger nucleases. See, e.g., June *et al.* 2009 *Nature Reviews Immunology* 9:10: 704-716, incorporated herein by reference in its entirety.

[00340] In brief summary, the expression of natural or synthetic nucleic acids encoding CARs is typically achieved by operably linking a nucleic acid encoding the CAR polypeptide or portions thereof to a promoter, and incorporating the construct into an expression vector. The vectors can be suitable for replication and integration eukaryotes. Typical cloning vectors contain transcription and translation terminators, initiation sequences, and promoters useful for regulation of the expression of the desired nucleic acid sequence.

[00341] The expression constructs of the present invention may also be used for nucleic acid immunization and gene therapy, using standard gene delivery protocols. Methods for gene delivery are known in the art. See, e.g., U.S. Pat. Nos. 5,399,346, 5,580,859, 5,589,466, incorporated by reference herein in their entireties. In another embodiment, the invention provides a gene therapy vector.

[00342] The nucleic acid can be cloned into a number of types of vectors. For example, the nucleic acid can be cloned into a vector including, but not limited to a plasmid, a phagemid, a

phage derivative, an animal virus, and a cosmid. Vectors of particular interest include expression vectors, replication vectors, probe generation vectors, and sequencing vectors.

[00343] Further, the expression vector may be provided to a cell in the form of a viral vector. Viral vector technology is well known in the art and is described, for example, in Sambrook *et al.*, 2012, MOLECULAR CLONING: A LABORATORY MANUAL, volumes 1 -4, Cold Spring Harbor Press, NY), and in other virology and molecular biology manuals. Viruses, which are useful as vectors include, but are not limited to, retroviruses, adenoviruses, adeno- associated viruses, herpes viruses, and lentiviruses. In general, a suitable vector contains an origin of replication functional in at least one organism, a promoter sequence, convenient restriction endonuclease sites, and one or more selectable markers, (e.g., WO 01/96584; WO 01/29058; and U.S. Pat. No. 6,326,193).

[00344] A number of viral based systems have been developed for gene transfer into mammalian cells. For example, retroviruses provide a convenient platform for gene delivery systems. A selected gene can be inserted into a vector and packaged in retroviral particles using techniques known in the art. The recombinant virus can then be isolated and delivered to cells of the subject either *in vivo* or *ex vivo*. A number of retroviral systems are known in the art. In some embodiments, adenovirus vectors are used. A number of adenovirus vectors are known in the art. In one embodiment, lentivirus vectors are used.

[00345] Additional promoter elements, e.g., enhancers, regulate the frequency of transcriptional initiation. Typically, these are located in the region 30-110 bp upstream of the start site, although a number of promoters have been shown to contain functional elements downstream of the start site as well. The spacing between promoter elements frequently is flexible, so that promoter function is preserved when elements are inverted or moved relative to one another. In the thymidine kinase (tk) promoter, the spacing between promoter elements can be increased to 50 bp apart before activity begins to decline. Depending on the promoter, it appears that individual elements can function either cooperatively or independently to activate transcription. Exemplary promoters include the CMV IE gene, EF-1 α , ubiquitin C, or phosphoglycerokinase (PGK) promoters.

[00346] An example of a promoter that is capable of expressing a CAR transgene in a mammalian T cell is the EF1alpha promoter (EF1a or EF α). The native EF1a promoter drives

expression of the alpha subunit of the elongation factor-1 complex, which is responsible for the enzymatic delivery of aminoacyl tRNAs to the ribosome. The EF1a promoter has been extensively used in mammalian expression plasmids and has been shown to be effective in driving CAR expression from transgenes cloned into a lentiviral vector. See, e.g., Milone *et al.*, Mol. Ther. 17(8): 1453–1464 (2009). In one aspect, the EF1a promoter comprises the sequence provided as SEQ ID NO:11.

[00347] Another example of a promoter is the immediate early cytomegalovirus (CMV) promoter sequence. This promoter sequence is a strong constitutive promoter sequence capable of driving high levels of expression of any polynucleotide sequence operatively linked thereto. However, other constitutive promoter sequences may also be used, including, but not limited to the simian virus 40 (SV40) early promoter, mouse mammary tumor virus (MMTV), human immunodeficiency virus (HIV) long terminal repeat (LTR) promoter, MoMuLV promoter, an avian leukemia virus promoter, an Epstein-Barr virus immediate early promoter, a Rous sarcoma virus promoter, as well as human gene promoters such as, but not limited to, the actin promoter, the myosin promoter, the elongation factor-1 α promoter, the hemoglobin promoter, and the creatine kinase promoter. Further, the invention should not be limited to the use of constitutive promoters. Inducible promoters are also contemplated as part of the invention. The use of an inducible promoter provides a molecular switch capable of turning on expression of the polynucleotide sequence which it is operatively linked when such expression is desired, or turning off the expression when expression is not desired. Examples of inducible promoters include, but are not limited to a metallothioneine promoter, a glucocorticoid promoter, a progesterone promoter, and a tetracycline promoter.

[00348] In order to assess the expression of a CAR polypeptide or portions thereof, the expression vector to be introduced into a cell can also contain either a selectable marker gene or a reporter gene or both to facilitate identification and selection of expressing cells from the population of cells sought to be transfected or infected through viral vectors. In other aspects, the selectable marker may be carried on a separate piece of DNA and used in a co- transfection procedure. Both selectable markers and reporter genes may be flanked with appropriate regulatory sequences to enable expression in the host cells. Useful selectable markers include, for example, antibiotic-resistance genes, such as neo and the like.

[00349] Reporter genes are used for identifying potentially transfected cells and for evaluating the functionality of regulatory sequences. In general, a reporter gene is a gene that is not present in or expressed by the recipient organism or tissue and that encodes a polypeptide whose expression is manifested by some easily detectable property, e.g., enzymatic activity. Expression of the reporter gene is assayed at a suitable time after the DNA has been introduced into the recipient cells. Suitable reporter genes may include genes encoding luciferase, beta-galactosidase, chloramphenicol acetyl transferase, secreted alkaline phosphatase, or the green fluorescent protein gene (e.g., Ui-Tei *et al.*, 2000 FEBS Letters 479: 79-82). Suitable expression systems are well known and may be prepared using known techniques or obtained commercially. In general, the construct with the minimal 5' flanking region showing the highest level of expression of reporter gene is identified as the promoter. Such promoter regions may be linked to a reporter gene and used to evaluate agents for the ability to modulate promoter- driven transcription.

[00350] In one embodiment, the vector can further comprise a nucleic acid encoding a second CAR. In one embodiment, the second CAR includes an antigen binding domain to, e.g., a target other than mesothelin on stroma cells, e.g., FAP; a target other than mesothelin on prostate cancer cells, e.g., androgen receptor, OR51E2, PSMA, PSCA, PDGRF- β , TARP, GloboH, MAD-CT-1, or MAD-CT-2; a target other than mesothelin on ovarian cancer cells, e.g., Tn, PRSS21, CD171, Lewis Y, folate receptor α , claudin6, GloboH, or sperm protein 17; e.g., a target other than mesothelin on lung cancer cells, e.g., VEGF, HER3, IGF-1R, EGFR, DLL4, or Trop-2. In one embodiment, the vector comprises a nucleic acid sequence encoding a first CAR that targets a first antigen and includes an intracellular signaling domain having a costimulatory signaling domain but not a primary signaling domain, and a nucleic acid encoding a second CAR that targets a second, different, antigen and includes an intracellular signaling domain having a primary signaling domain but not a costimulatory signaling domain. In one embodiment, the vector comprises a nucleic acid encoding a first mesothelin CAR that includes a mesothelin binding domain, a transmembrane domain and a costimulatory domain and a nucleic acid encoding a second CAR that targets an antigen other than mesothelin (e.g., a target other than mesothelin on stroma cells, e.g., FAP; a target other than mesothelin on prostate cancer cells, e.g., androgen receptor, OR51E2, PSMA, PSCA, PDGRF- β , TARP, GloboH, MAD-CT-1, or MAD-CT-2; a target other than mesothelin on ovarian cancer cells, e.g., Tn, PRSS21, CD171, Lewis Y, folate receptor α , claudin6, GloboH, or sperm protein 17;

e.g., a target other than mesothelin on lung cancer cells, e.g., VEGF, HER3, IGF-1R, EGFR, DLL4, or Trop-2) and includes an antigen binding domain, a transmembrane domain and a primary signaling domain. In another embodiment, the vector comprises a nucleic acid encoding a first mesothelin CAR that includes a mesothelin binding domain, a transmembrane domain and a primary signaling domain and a nucleic acid encoding a second CAR that targets an antigen other than mesothelin (e.g., a target other than mesothelin on stroma cells, e.g., FAP; a target other than mesothelin on prostate cancer cells, e.g., androgen receptor, OR51E2, PSMA, PSCA, PDGRF- β , TARP, GloboH, MAD-CT-1, or MAD-CT-2; a target other than mesothelin on ovarian cancer cells, e.g., Tn, PRSS21, CD171, Lewis Y, folate receptor α , claudin6, GloboH, or sperm protein 17; e.g., a target other than mesothelin on lung cancer cells, e.g., VEGF, HER3, IGF-1R, EGFR, DLL4, or Trop-2) and includes an antigen binding domain to the antigen, a transmembrane domain and a costimulatory signaling domain.

[00351] In one embodiment, the vector comprises a nucleic acid encoding a mesothelin CAR described herein and a nucleic acid encoding 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 CLL. 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, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), LAG3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4 and TGFR beta.

[00352] In one embodiment, the vector comprises a nucleic acid encoding a mesothelin CAR described herein and an inhibitory nucleic acid, e.g., a dsRNA, e.g., an siRNA or shRNA, e.g., as described herein.

[00353] Methods of introducing and expressing genes into a cell are known in the art. In the context of an expression vector, the vector can be readily introduced into a host cell, e.g., mammalian, bacterial, yeast, or insect cell by any method in the art. For example, the expression vector can be transferred into a host cell by physical, chemical, or biological means.

[00354] Physical methods for introducing a polynucleotide into a host cell include calcium phosphate precipitation, lipofection, particle bombardment, microinjection, electroporation, and

the like. Methods for producing cells comprising vectors and/or exogenous nucleic acids are well-known in the art. See, for example, Sambrook *et al.*, 2012, MOLECULAR CLONING: A LABORATORY MANUAL, volumes 1 -4, Cold Spring Harbor Press, NY). A preferred method for the introduction of a polynucleotide into a host cell is lipofection, e.g., using Lipofectamine (Life Technologies).

[00355] Biological methods for introducing a polynucleotide of interest into a host cell include the use of DNA and RNA vectors. Viral vectors, and especially retroviral vectors, have become the most widely used method for inserting genes into mammalian, e.g., human cells. Other viral vectors can be derived from lentivirus, poxviruses, herpes simplex virus I, adenoviruses and adeno-associated viruses, and the like. See, for example, U.S. Pat. Nos. 5,350,674 and 5,585,362.

[00356] Chemical means for introducing a polynucleotide into a host cell include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. An exemplary colloidal system for use as a delivery vehicle in vitro and in vivo is a liposome (e.g., an artificial membrane vesicle). Other methods of state-of-the-art targeted delivery of nucleic acids are available, such as delivery of polynucleotides with targeted nanoparticles or other suitable sub-micron sized delivery system.

[00357] In the case where a non-viral delivery system is utilized, an exemplary delivery vehicle is a liposome. The use of lipid formulations is contemplated for the introduction of the nucleic acids into a host cell (in vitro, ex vivo or in vivo). In another aspect, the nucleic acid may be associated with a lipid. The nucleic acid associated with a lipid may be encapsulated in the aqueous interior of a liposome, interspersed within the lipid bilayer of a liposome, attached to a liposome via a linking molecule that is associated with both the liposome and the oligonucleotide, entrapped in a liposome, complexed with a liposome, dispersed in a solution containing a lipid, mixed with a lipid, combined with a lipid, contained as a suspension in a lipid, contained or complexed with a micelle, or otherwise associated with a lipid. Lipid, lipid/DNA or lipid/expression vector associated compositions are not limited to any particular structure in solution. For example, they may be present in a bilayer structure, as micelles, or with a “collapsed” structure. They may also simply be interspersed in a solution, possibly forming

aggregates that are not uniform in size or shape. Lipids are fatty substances which may be naturally occurring or synthetic lipids. For example, lipids include the fatty droplets that naturally occur in the cytoplasm as well as the class of compounds which contain long-chain aliphatic hydrocarbons and their derivatives, such as fatty acids, alcohols, amines, amino alcohols, and aldehydes.

[00358] Lipids suitable for use can be obtained from commercial sources. For example, dimyristyl phosphatidylcholine (“DMPC”) can be obtained from Sigma, St. Louis, MO; dicetyl phosphate (“DCP”) can be obtained from K & K Laboratories (Plainview, NY); cholesterol (“Choi”) can be obtained from Calbiochem-Behring; dimyristyl phosphatidylglycerol (“DMPG”) and other lipids may be obtained from Avanti Polar Lipids, Inc. (Birmingham, AL.). Stock solutions of lipids in chloroform or chloroform/methanol can be stored at about -20°C. Chloroform is used as the only solvent since it is more readily evaporated than methanol. “Liposome” is a generic term encompassing a variety of single and multilamellar lipid vehicles formed by the generation of enclosed lipid bilayers or aggregates. Liposomes can be characterized as having vesicular structures with a phospholipid bilayer membrane and an inner aqueous medium. Multilamellar liposomes have multiple lipid layers separated by aqueous medium. They form spontaneously when phospholipids are suspended in an excess of aqueous solution. The lipid components undergo self-rearrangement before the formation of closed structures and entrap water and dissolved solutes between the lipid bilayers (Ghosh *et al.*, 1991 *Glycobiology* 5: 505-10). However, compositions that have different structures in solution than the normal vesicular structure are also encompassed. For example, the lipids may assume a micellar structure or merely exist as nonuniform aggregates of lipid molecules. Also contemplated are lipofectamine-nucleic acid complexes.

[00359] Regardless of the method used to introduce exogenous nucleic acids into a host cell or otherwise expose a cell to the inhibitor of the present invention, in order to confirm the presence of the recombinant DNA sequence in the host cell, a variety of assays may be performed. Such assays include, for example, “molecular biological” assays well known to those of skill in the art, such as Southern and Northern blotting, RT-PCR and PCR; “biochemical” assays, such as detecting the presence or absence of a particular peptide, e.g., by immunological means (ELISAs and Western blots) or by assays described herein to identify agents falling within the scope of the invention.

[00360] The present invention further provides a vector comprising a CAR encoding nucleic acid molecule. In one aspect, a CAR vector can be directly transduced into a cell, *e.g.*, a T cell or a NK cell. In one aspect, the vector is a cloning or expression vector, *e.g.*, a vector including, but not limited to, one or more plasmids (*e.g.*, expression plasmids, cloning vectors, minicircles, minivectors, double minute chromosomes), retroviral and lentiviral vector constructs. In one aspect, the vector is capable of expressing the CAR construct in mammalian T cells. In one aspect, the mammalian T cell is a human T cell. In one aspect, the mammalian cell is a human NK cell.

Sources of Cells

[00361] Prior to expansion and genetic modification, a source of cells (*e.g.*, T cells or NK cells) is obtained from a subject. The term “subject” is intended to include living organisms in which an immune response can be elicited (*e.g.*, mammals). Examples of subjects include humans, dogs, cats, mice, rats, and transgenic species thereof. T cells can be obtained from a number of sources, including peripheral blood mononuclear cells, bone marrow, lymph node tissue, cord blood, thymus tissue, tissue from a site of infection, ascites, pleural effusion, spleen tissue, and tumors. In certain aspects of the present invention, any number of T cell lines available in the art, may be used. In certain aspects of the present invention, T cells can be obtained from a unit of blood collected from a subject using any number of techniques known to the skilled artisan, such as Ficoll™ separation. In one preferred aspect, cells from the circulating blood of an individual are obtained by apheresis. The apheresis product typically contains lymphocytes, including T cells, monocytes, granulocytes, B cells, other nucleated white blood cells, red blood cells, and platelets. In one aspect, the cells collected by apheresis may be washed to remove the plasma fraction and to place the cells in an appropriate buffer or media for subsequent processing steps. In one aspect of the invention, the cells are washed with phosphate buffered saline (PBS). In an alternative aspect, the wash solution lacks calcium and may lack magnesium or may lack many if not all divalent cations. Initial activation steps in the absence of calcium can lead to magnified activation. As those of ordinary skill in the art would readily appreciate a washing step may be accomplished by methods known to those in the art, such as by using a semi-automated “flow-through” centrifuge (for example, the Cobe 2991 cell processor, the Baxter CytoMate, or the Haemonetics Cell Saver 5) according to the manufacturer’s instructions. After washing, the cells may be resuspended in a variety of biocompatible buffers,

such as, for example, Ca-free, Mg-free PBS, PlasmaLyte A, or other saline solution with or without buffer. Alternatively, the undesirable components of the apheresis sample may be removed and the cells directly resuspended in culture media.

[00362] In one aspect, T cells are isolated from peripheral blood lymphocytes by lysing the red blood cells and depleting the monocytes, for example, by centrifugation through a PERCOLL™ gradient or by counterflow centrifugal elutriation. A specific subpopulation of T cells, such as CD3+, CD28+, CD4+, CD8+, CD45RA+, and CD45RO+T cells, can be further isolated by positive or negative selection techniques. For example, in one aspect, T cells are isolated by incubation with anti-CD3/anti-CD28 (e.g., 3x28)-conjugated beads, such as DYNABEADS® M-450 CD3/CD28 T, for a time period sufficient for positive selection of the desired T cells. In one aspect, the time period is about 30 minutes. In a further aspect, the time period ranges from 30 minutes to 36 hours or longer and all integer values there between. In a further aspect, the time period is at least 1, 2, 3, 4, 5, or 6 hours. In yet another preferred aspect, the time period is 10 to 24 hours. In one aspect, the incubation time period is 24 hours. For isolation of T cells from patients with leukemia, use of longer incubation times, such as 24 hours, can increase cell yield. Longer incubation times may be used to isolate T cells in any situation where there are few T cells as compared to other cell types, such as in isolating tumor infiltrating lymphocytes (TIL) from tumor tissue or from immunocompromised individuals. Further, use of longer incubation times can increase the efficiency of capture of CD8+ T cells. Thus, by simply shortening or lengthening the time T cells are allowed to bind to the CD3/CD28 beads and/or by increasing or decreasing the ratio of beads to T cells (as described further herein), subpopulations of T cells can be preferentially selected for or against at culture initiation or at other time points during the process. Additionally, by increasing or decreasing the ratio of anti-CD3 and/or anti-CD28 antibodies on the beads or other surface, subpopulations of T cells can be preferentially selected for or against at culture initiation or at other desired time points. The skilled artisan would recognize that multiple rounds of selection can also be used in the context of this invention. In certain aspects, it may be desirable to perform the selection procedure and use the “unselected” cells in the activation and expansion process. “Unselected” cells can also be subjected to further rounds of selection.

[00363] Enrichment of a T cell population by negative selection can be accomplished with a combination of antibodies directed to surface markers unique to the negatively selected cells.

One method is cell sorting and/or selection via negative magnetic immunoadherence or flow cytometry that uses a cocktail of monoclonal antibodies directed to cell surface markers present on the cells negatively selected. For example, to enrich for CD4+ cells by negative selection, a monoclonal antibody cocktail typically includes antibodies to CD14, CD20, CD11b, CD16, HLA-DR, and CD8. In certain aspects, it may be desirable to enrich for or positively select for regulatory T cells which typically express CD4+, CD25+, CD62Lhi, GITR+, and FoxP3+. Alternatively, in certain aspects, T regulatory cells are depleted by anti-C25 conjugated beads or other similar method of selection.

[00364] In one embodiment, a T cell population can be selected that expresses one or more of IFN- \square , TNF α , IL-17A, IL-2, IL-3, IL-4, GM-CSF, IL-10, IL-13, granzyme B, and perforin, or other appropriate molecules, e.g., other cytokines. Methods for screening for cell expression can be determined, e.g., by the methods described in PCT Publication No.: WO 2013/126712.

[00365] In one embodiment, a T cell population is diacylglycerol kinase (DGK)-deficient. DGK-deficient cells include cells that do not express DGK RNA or protein, or have reduced or inhibited DGK activity. DGK-deficient cells can be generated by genetic approaches, e.g., administering RNA-interfering agents, e.g., siRNA, shRNA, miRNA, to reduce or prevent DGK expression. Alternatively, DGK-deficient cells can be generated by treatment with DGK inhibitors described herein.

[00366] In one embodiment, a T cell population is Ikaros-deficient. Ikaros-deficient cells include cells that do not express Ikaros RNA or protein, or have reduced or inhibited Ikaros activity. Ikaros-deficient cells can be generated by genetic approaches, e.g., administering RNA-interfering agents, e.g., siRNA, shRNA, miRNA, to reduce or prevent Ikaros expression. Alternatively, Ikaros-deficient cells can be generated by treatment with Ikaros inhibitors, e.g., lenalidomide.

[00367] In embodiments, a T cell population is DGK-deficient and Ikaros-deficient, e.g., does not express DGK and Ikaros, or has reduced or inhibited DGK and Ikaros activity. Such DGK and Ikaros-deficient cells can be generated by any of the methods described herein.

[00368] For isolation of a desired population of cells by positive or negative selection, the concentration of cells and surface (e.g., particles such as beads) can be varied. In certain aspects, it may be desirable to significantly decrease the volume in which beads and cells are mixed

together (e.g., increase the concentration of cells), to ensure maximum contact of cells and beads. For example, in one aspect, a concentration of 2 billion cells/ml is used. In one aspect, a concentration of 1 billion cells/ml is used. In a further aspect, greater than 100 million cells/ml is used. In a further aspect, a concentration of cells of 10, 15, 20, 25, 30, 35, 40, 45, or 50 million cells/ml is used. In yet one aspect, a concentration of cells from 75, 80, 85, 90, 95, or 100 million cells/ml is used. In further aspects, concentrations of 125 or 150 million cells/ml can be used. Using high concentrations can result in increased cell yield, cell activation, and cell expansion. Further, use of high cell concentrations allows more efficient capture of cells that may weakly express target antigens of interest, such as CD28-negative T cells, or from samples where there are many tumor cells present (e.g., leukemic blood, tumor tissue, etc.). Such populations of cells may have therapeutic value and would be desirable to obtain. For example, using high concentration of cells allows more efficient selection of CD8+ T cells that normally have weaker CD28 expression.

[00369] In a related aspect, it may be desirable to use lower concentrations of cells. By significantly diluting the mixture of T cells and surface (e.g., particles such as beads), interactions between the particles and cells is minimized. This selects for cells that express high amounts of desired antigens to be bound to the particles. For example, CD4+ T cells express higher levels of CD28 and are more efficiently captured than CD8+ T cells in dilute concentrations. In one aspect, the concentration of cells used is 5×10^6 /ml. In other aspects, the concentration used can be from about 1×10^5 /ml to 1×10^6 /ml, and any integer value in between.

[00370] In other aspects, the cells may be incubated on a rotator for varying lengths of time at varying speeds at either 2-10°C or at room temperature.

[00371] T cells for stimulation can also be frozen after a washing step. Wishing not to be bound by theory, the freeze and subsequent thaw step provides a more uniform product by removing granulocytes and to some extent monocytes in the cell population. After the washing step that removes plasma and platelets, the cells may be suspended in a freezing solution. While many freezing solutions and parameters are known in the art and will be useful in this context, one method involves using PBS containing 20% DMSO and 8% human serum albumin, or culture media containing 10% Dextran 40 and 5% Dextrose, 20% Human Serum Albumin and

7.5% DMSO, or 31.25% Plasmalyte-A, 31.25% Dextrose 5%, 0.45% NaCl, 10% Dextran 40 and 5% Dextrose, 20% Human Serum Albumin, and 7.5% DMSO or other suitable cell freezing media containing for example, Hespan and PlasmaLyte A, the cells then are frozen to -80°C at a rate of 1° per minute and stored in the vapor phase of a liquid nitrogen storage tank. Other methods of controlled freezing may be used as well as uncontrolled freezing immediately at -20° C or in liquid nitrogen.

[00372] In certain aspects, cryopreserved cells are thawed and washed as described herein and allowed to rest for one hour at room temperature prior to activation using the methods of the present invention.

[00373] Also contemplated in the context of the invention is the collection of blood samples or apheresis product from a subject at a time period prior to when the expanded cells as described herein might be needed. As such, the source of the cells to be expanded can be collected at any time point necessary, and desired cells, such as T cells, isolated and frozen for later use in T cell therapy for any number of diseases or conditions that would benefit from T cell therapy, such as those described herein. In one aspect a blood sample or an apheresis is taken from a generally healthy subject. In certain aspects, a blood sample or an apheresis is taken from a generally healthy subject who is at risk of developing a disease, but who has not yet developed a disease, and the cells of interest are isolated and frozen for later use. In certain aspects, the T cells may be expanded, frozen, and used at a later time. In certain aspects, samples are collected from a patient shortly after diagnosis of a particular disease as described herein but prior to any treatments. In a further aspect, the cells are isolated from a blood sample or an apheresis from a subject prior to any number of relevant treatment modalities, including but not limited to treatment with agents such as natalizumab, efalizumab, antiviral agents, chemotherapy, radiation, immunosuppressive agents, such as cyclosporin, azathioprine, methotrexate, mycophenolate, and FK506, antibodies, or other immunoablative agents such as CAMPATH, anti-CD3 antibodies, cytoxin, fludarabine, cyclosporin, FK506, rapamycin, mycophenolic acid, steroids, FR901228, and irradiation. These drugs inhibit either the calcium dependent phosphatase calcineurin (cyclosporine and FK506) or inhibit the p70S6 kinase that is important for growth factor induced signaling (rapamycin). (Liu *et al.*, Cell 66:807-815, 1991; Henderson *et al.*, Immun. 73:316-321, 1991; Bierer *et al.*, Curr. Opin. Immun. 5:763-773, 1993). In a further aspect, the cells are isolated for a patient and frozen for later use in conjunction with (e.g., before, simultaneously or

following) bone marrow or stem cell transplantation, T cell ablative therapy using either chemotherapy agents such as, fludarabine, external-beam radiation therapy (XRT), cyclophosphamide, or antibodies such as OKT3 or CAMPATH. In one aspect, the cells are isolated prior to and can be frozen for later use for treatment following B-cell ablative therapy such as agents that react with CD20, e.g., Rituxan.

[00374] In a further aspect of the present invention, T cells are obtained from a patient directly following treatment that leaves the subject with functional T cells. In this regard, it has been observed that following certain cancer treatments, in particular treatments with drugs that damage the immune system, shortly after treatment during the period when patients would normally be recovering from the treatment, the quality of T cells obtained may be optimal or improved for their ability to expand ex vivo. Likewise, following ex vivo manipulation using the methods described herein, these cells may be in a preferred state for enhanced engraftment and in vivo expansion. Thus, it is contemplated within the context of the invention to collect blood cells, including T cells, dendritic cells, or other cells of the hematopoietic lineage, during this recovery phase. Further, in certain aspects, mobilization (for example, mobilization with GM-CSF) and conditioning regimens can be used to create a condition in a subject wherein repopulation, recirculation, regeneration, and/or expansion of particular cell types is favored, especially during a defined window of time following therapy. Illustrative cell types include T cells, B cells, dendritic cells, and other cells of the immune system.

[00375] In an embodiment, the NK cells are obtained from the subject. In another embodiment, the NK cells are an NK cell line, e.g., NK-92 cell line (Conkwest).

Allogeneic CAR

[00376] In embodiments described herein, the immune effector cell can be an allogeneic immune effector cell, e.g., T cell or NK cell. For example, the cell can be an allogeneic T cell, e.g., an allogeneic T cell lacking expression of a functional T cell receptor (TCR) and/or human leukocyte antigen (HLA), e.g., HLA class I and/or HLA class II.

[00377] A T cell lacking a functional TCR can be, e.g., engineered such that it does not express any functional TCR on its surface, engineered such that it does not express one or more subunits that comprise a functional TCR or engineered such that it produces very little functional TCR on its surface. Alternatively, the T cell can express a substantially impaired TCR, e.g., by

expression of mutated or truncated forms of one or more of the subunits of the TCR. The term “substantially impaired TCR” means that this TCR will not elicit an adverse immune reaction in a host.

[00378] A T cell described herein can be, e.g., engineered such that it does not express a functional HLA on its surface. For example, a T cell described herein, can be engineered such that cell surface expression HLA, e.g., HLA class I and/or HLA class II, is downregulated.

[00379] In some embodiments, the T cell can lack a functional TCR and a functional HLA, e.g., HLA class I and/or HLA class II.

[00380] Modified T cells that lack expression of a functional TCR and/or HLA can be obtained by any suitable means, including a knock out or knock down of one or more subunit of TCR or HLA. For example, the T cell can include a knock down of TCR and/or HLA using siRNA, shRNA, clustered regularly interspaced short palindromic repeats (CRISPR) transcription-activator like effector nuclease (TALEN), or zinc finger endonuclease (ZFN).

[00381] In some embodiments, the allogeneic cell can be a cell which does not express or expresses at low levels an inhibitory molecule, e.g. by any method described herein. For example, the cell can be a cell that does not express or expresses at low levels an inhibitory molecule, e.g., that can decrease the ability of a CAR-expressing cell to mount an immune effector response. Examples of inhibitory molecules include PD1, PD-L1, CTLA4, TIM3, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), LAG3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4 and TGFR beta. Inhibition of an inhibitory molecule, e.g., by inhibition at the DNA, RNA or protein level, can optimize a CAR-expressing cell performance. In embodiments, an inhibitory nucleic acid, e.g., an inhibitory nucleic acid, e.g., a dsRNA, e.g., an siRNA or shRNA, a clustered regularly interspaced short palindromic repeats (CRISPR), a transcription-activator like effector nuclease (TALEN), or a zinc finger endonuclease (ZFN), e.g., as described herein, can be used.

siRNA and shRNA to inhibit TCR or HLA

[00382] In some embodiments, TCR expression and/or HLA expression can be inhibited using siRNA or shRNA that targets a nucleic acid encoding a TCR and/or HLA in a T cell.

[00383] Expression of siRNA and shRNAs in T cells can be achieved using any conventional expression system, e.g., such as a lentiviral expression system.

[00384] Exemplary shRNAs that downregulate expression of components of the TCR are described, e.g., in US Publication No.: 2012/0321667. Exemplary siRNA and shRNA that downregulate expression of HLA class I and/or HLA class II genes are described, e.g., in U.S. publication No.: US 2007/0036773.

CRISPR to inhibit TCR or HLA

[00385] “CRISPR” or “CRISPR to TCR and/or HLA” or “CRISPR to inhibit TCR and/or HLA” as used herein refers to a set of clustered regularly interspaced short palindromic repeats, or a system comprising such a set of repeats. “Cas”, as used herein, refers to a CRISPR-associated protein. A “CRISPR/Cas” system refers to a system derived from CRISPR and Cas which can be used to silence or mutate a TCR and/or HLA gene.

[00386] Naturally-occurring CRISPR/Cas systems are found in approximately 40% of sequenced eubacteria genomes and 90% of sequenced archaea. Grissa *et al.* (2007) *BMC Bioinformatics* 8: 172. This system is a type of prokaryotic immune system that confers resistance to foreign genetic elements such as plasmids and phages and provides a form of acquired immunity. Barrangou *et al.* (2007) *Science* 315: 1709-1712; Marragini *et al.* (2008) *Science* 322: 1843-1845.

[00387] The CRISPR/Cas system has been modified for use in gene editing (silencing, enhancing or changing specific genes) in eukaryotes such as mice or primates. Wiedenheft *et al.* (2012) *Nature* 482: 331-8. This is accomplished by introducing into the eukaryotic cell a plasmid containing a specifically designed CRISPR and one or more appropriate Cas.

[00388] The CRISPR sequence, sometimes called a CRISPR locus, comprises alternating repeats and spacers. In a naturally-occurring CRISPR, the spacers usually comprise sequences foreign to the bacterium such as a plasmid or phage sequence; in the TCR and/or HLA CRISPR/Cas system, the spacers are derived from the TCR or HLA gene sequence.

[00389] RNA from the CRISPR locus is constitutively expressed and processed by Cas proteins into small RNAs. These comprise a spacer flanked by a repeat sequence. The RNAs guide other Cas proteins to silence exogenous genetic elements at the RNA or DNA level.

Horvath *et al.* (2010) *Science* 327: 167-170; Makarova *et al.* (2006) *Biology Direct* 1: 7. The spacers thus serve as templates for RNA molecules, analogously to siRNAs. Pennisi (2013) *Science* 341: 833-836.

[00390] As these naturally occur in many different types of bacteria, the exact arrangements of the CRISPR and structure, function and number of Cas genes and their product differ somewhat from species to species. Haft *et al.* (2005) *PLoS Comput. Biol.* 1: e60; Kunin *et al.* (2007) *Genome Biol.* 8: R61; Mojica *et al.* (2005) *J. Mol. Evol.* 60: 174-182; Bolotin *et al.* (2005) *Microbiol.* 151: 2551-2561; Pourcel *et al.* (2005) *Microbiol.* 151: 653-663; and Stern *et al.* (2010) *Trends. Genet.* 28: 335-340. For example, the Cse (Cas subtype, *E. coli*) proteins (e.g., CasA) form a functional complex, Cascade, that processes CRISPR RNA transcripts into spacer-repeat units that Cascade retains. Brouns *et al.* (2008) *Science* 321: 960-964. In other prokaryotes, Cas6 processes the CRISPR transcript. The CRISPR-based phage inactivation in *E. coli* requires Cascade and Cas3, but not Cas1 or Cas2. The Cmr (Cas RAMP module) proteins in *Pyrococcus furiosus* and other prokaryotes form a functional complex with small CRISPR RNAs that recognizes and cleaves complementary target RNAs. A simpler CRISPR system relies on the protein Cas9, which is a nuclease with two active cutting sites, one for each strand of the double helix. Combining Cas9 and modified CRISPR locus RNA can be used in a system for gene editing. Pennisi (2013) *Science* 341: 833-836.

[00391] The CRISPR/Cas system can thus be used to edit a TCR and/or HLA gene (adding or deleting a basepair), or introducing a premature stop which thus decreases expression of a TCR and/or HLA. The CRISPR/Cas system can alternatively be used like RNA interference, turning off TCR and/or HLA gene in a reversible fashion. In a mammalian cell, for example, the RNA can guide the Cas protein to a TCR and/or HLA promoter, sterically blocking RNA polymerases.

[00392] Artificial CRISPR/Cas systems can be generated which inhibit TCR and/or HLA, using technology known in the art, e.g., that described in U.S. Publication No.20140068797, and Cong (2013) *Science* 339: 819-823. Other artificial CRISPR/Cas systems that are known in the art may also be generated which inhibit TCR and/or HLA, e.g., that described in Tsai (2014) *Nature Biotechnol.*, 32:6 569-576, U.S. Patent No.: 8,871,445; 8,865,406; 8,795,965; 8,771,945; and 8,697,359.

TALEN to inhibit TCR and/or HLA

[00393] “TALEN” or “TALEN to HLA and/or TCR” or “TALEN to inhibit HLA and/or TCR” refers to a transcription activator-like effector nuclease, an artificial nuclease which can be used to edit the HLA and/or TCR gene.

[00394] TALENs are produced artificially by fusing a TAL effector DNA binding domain to a DNA cleavage domain. Transcription activator-like effects (TALEs) can be engineered to bind any desired DNA sequence, including a portion of the HLA or TCR gene. By combining an engineered TALE with a DNA cleavage domain, a restriction enzyme can be produced which is specific to any desired DNA sequence, including a HLA or TCR sequence. These can then be introduced into a cell, wherein they can be used for genome editing. Boch (2011) *Nature Biotech.* 29: 135-6; and Boch et al. (2009) *Science* 326: 1509-12; Moscou et al. (2009) *Science* 326: 3501.

[00395] TALEs are proteins secreted by *Xanthomonas* bacteria. The DNA binding domain contains a repeated, highly conserved 33-34 amino acid sequence, with the exception of the 12th and 13th amino acids. These two positions are highly variable, showing a strong correlation with specific nucleotide recognition. They can thus be engineered to bind to a desired DNA sequence.

[00396] To produce a TALEN, a TALE protein is fused to a nuclease (N), which is a wild-type or mutated FokI endonuclease. Several mutations to FokI have been made for its use in TALENs; these, for example, improve cleavage specificity or activity. Cermak et al. (2011) *Nucl. Acids Res.* 39: e82; Miller et al. (2011) *Nature Biotech.* 29: 143-8; Hockemeyer et al. (2011) *Nature Biotech.* 29: 731-734; Wood et al. (2011) *Science* 333: 307; Doyon et al. (2010) *Nature Methods* 8: 74-79; Szczepek et al. (2007) *Nature Biotech.* 25: 786-793; and Guo et al. (2010) *J. Mol. Biol.* 200: 96.

[00397] The FokI domain functions as a dimer, requiring two constructs with unique DNA binding domains for sites in the target genome with proper orientation and spacing. Both the number of amino acid residues between the TALE DNA binding domain and the FokI cleavage domain and the number of bases between the two individual TALEN binding sites appear to be important parameters for achieving high levels of activity. Miller et al. (2011) *Nature Biotech.* 29: 143-8.

[00398] A HLA or TCR TALEN can be used inside a cell to produce a double-stranded break (DSB). A mutation can be introduced at the break site if the repair mechanisms improperly

repair the break via non-homologous end joining. For example, improper repair may introduce a frame shift mutation. Alternatively, foreign DNA can be introduced into the cell along with the TALEN; depending on the sequences of the foreign DNA and chromosomal sequence, this process can be used to correct a defect in the HLA or TCR gene or introduce such a defect into a wt HLA or TCR gene, thus decreasing expression of HLA or TCR.

[00399] TALENs specific to sequences in HLA or TCR can be constructed using any method known in the art, including various schemes using modular components. Zhang et al. (2011) *Nature Biotech.* 29: 149-53; Geibler et al. (2011) *PLoS ONE* 6: e19509.

Zinc finger nuclease to inhibit HLA and/or TCR

[00400] “ZFN” or “Zinc Finger Nuclease” or “ZFN to HLA and/or TCR” or “ZFN to inhibit HLA and/or TCR” refer to a zinc finger nuclease, an artificial nuclease which can be used to edit the HLA and/or TCR gene.

[00401] Like a TALEN, a ZFN comprises a FokI nuclease domain (or derivative thereof) fused to a DNA-binding domain. In the case of a ZFN, the DNA-binding domain comprises one or more zinc fingers. Carroll et al. (2011) *Genetics Society of America* 188: 773-782; and Kim et al. (1996) *Proc. Natl. Acad. Sci. USA* 93: 1156-1160.

[00402] A zinc finger is a small protein structural motif stabilized by one or more zinc ions. A zinc finger can comprise, for example, Cys2His2, and can recognize an approximately 3-bp sequence. Various zinc fingers of known specificity can be combined to produce multi-finger polypeptides which recognize about 6, 9, 12, 15 or 18-bp sequences. Various selection and modular assembly techniques are available to generate zinc fingers (and combinations thereof) recognizing specific sequences, including phage display, yeast one-hybrid systems, bacterial one-hybrid and two-hybrid systems, and mammalian cells.

[00403] Like a TALEN, a ZFN must dimerize to cleave DNA. Thus, a pair of ZFNs are required to target non-palindromic DNA sites. The two individual ZFNs must bind opposite strands of the DNA with their nucleases properly spaced apart. Bitinaite et al. (1998) *Proc. Natl. Acad. Sci. USA* 95: 10570-5.

[00404] Also like a TALEN, a ZFN can create a double-stranded break in the DNA, which can create a frame-shift mutation if improperly repaired, leading to a decrease in the expression

and amount of HLA and/or TCR in a cell. ZFNs can also be used with homologous recombination to mutate in the HLA or TCR gene.

[00405] ZFNs specific to sequences in HLA AND/OR TCR can be constructed using any method known in the art. See, e.g., Provasi (2011) *Nature Med.* 18: 807-815; Torikai (2013) *Blood* 122: 1341-1349; Cathomen et al. (2008) *Mol. Ther.* 16: 1200-7; and Guo et al. (2010) *J. Mol. Biol.* 400: 96; U.S. Patent Publication 2011/0158957; U.S. Patent Publication 2012/0060230.

Activation and Expansion of Cells

[00406] Cells may be activated and expanded generally using methods as described, for example, in U.S. Patents 6,352,694; 6,534,055; 6,905,680; 6,692,964; 5,858,358; 6,887,466; 6,905,681; 7,144,575; 7,067,318; 7,172,869; 7,232,566; 7,175,843; 5,883,223; 6,905,874; 6,797,514; 6,867,041; and U.S. Patent Application Publication No. 20060121005.

[00407] Generally, the T cells of the invention may be expanded by contact with a surface having attached thereto an agent that stimulates a CD3/TCR complex associated signal and a ligand that stimulates a costimulatory molecule on the surface of the T cells. In particular, T cell populations may be stimulated as described herein, such as by contact with an anti-CD3 antibody, or antigen-binding fragment thereof, or an anti-CD2 antibody immobilized on a surface, or by contact with a protein kinase C activator (e.g., bryostatin) in conjunction with a calcium ionophore. For co-stimulation of an accessory molecule on the surface of the T cells, a ligand that binds the accessory molecule is used. For example, a population of T cells can be contacted with an anti-CD3 antibody and an anti-CD28 antibody, under conditions appropriate for stimulating proliferation of the T cells. To stimulate proliferation of either CD4+ T cells or CD8+ T cells, an anti-CD3 antibody and an anti-CD28 antibody. Examples of an anti-CD28 antibody include 9.3, B-T3, XR-CD28 (Diaclone, Besançon, France) can be used as can other methods commonly known in the art (Berg *et al.*, *Transplant Proc.* 30(8):3975-3977, 1998; Haanen *et al.*, *J. Exp. Med.* 190(9):13191328, 1999; Garland *et al.*, *J. Immunol Meth.* 227(1-2):53-63, 1999).

[00408] In certain aspects, the primary stimulatory signal and the costimulatory signal for the T cell may be provided by different protocols. For example, the agents providing each signal may be in solution or coupled to a surface. When coupled to a surface, the agents may be coupled to the same surface (i.e., in “cis” formation) or to separate surfaces (i.e., in “trans” formation). Alternatively, one agent may be coupled to a surface and the other agent in solution. In one aspect, the agent providing the costimulatory signal is bound to a cell surface and the agent providing the primary activation signal is in solution or coupled to a surface. In certain aspects, both agents can be in solution. In one aspect, the agents may be in soluble form, and then cross-linked to a surface, such as a cell expressing Fc receptors or an antibody or other binding agent which will bind to the agents. In this regard, see for example, U.S. Patent Application Publication Nos. 20040101519 and 20060034810 for artificial antigen presenting cells (aAPCs) that are contemplated for use in activating and expanding T cells in the present invention.

[00409] In one aspect, the two agents are immobilized on beads, either on the same bead, i.e., “cis,” or to separate beads, i.e., “trans.” By way of example, the agent providing the primary activation signal is an anti-CD3 antibody or an antigen-binding fragment thereof and the agent providing the costimulatory signal is an anti-CD28 antibody or antigen-binding fragment thereof; and both agents are co-immobilized to the same bead in equivalent molecular amounts. In one aspect, a 1:1 ratio of each antibody bound to the beads for CD4+ T cell expansion and T cell growth is used. In certain aspects of the present invention, a ratio of anti CD3:CD28 antibodies bound to the beads is used such that an increase in T cell expansion is observed as compared to the expansion observed using a ratio of 1:1. In one particular aspect an increase of from about 1 to about 3 fold is observed as compared to the expansion observed using a ratio of 1:1. In one aspect, the ratio of CD3:CD28 antibody bound to the beads ranges from 100:1 to 1:100 and all integer values there between. In one aspect of the present invention, more anti-CD28 antibody is bound to the particles than anti-CD3 antibody, i.e., the ratio of CD3:CD28 is less than one. In certain aspects of the invention, the ratio of anti CD28 antibody to anti CD3 antibody bound to the beads is greater than 2:1. In one particular aspect, a 1:100 CD3:CD28 ratio of antibody bound to beads is used. In one aspect, a 1:75 CD3:CD28 ratio of antibody bound to beads is used. In a further aspect, a 1:50 CD3:CD28 ratio of antibody bound to beads is used. In one aspect, a 1:30 CD3:CD28 ratio of antibody bound to beads is used. In one preferred aspect, a 1:10 CD3:CD28

ratio of antibody bound to beads is used. In one aspect, a 1:3 CD3:CD28 ratio of antibody bound to the beads is used. In yet one aspect, a 3:1 CD3:CD28 ratio of antibody bound to the beads is used.

[00410] Ratios of particles to cells from 1:500 to 500:1 and any integer values in between may be used to stimulate T cells or other target cells. As those of ordinary skill in the art can readily appreciate, the ratio of particles to cells may depend on particle size relative to the target cell. For example, small sized beads could only bind a few cells, while larger beads could bind many. In certain aspects the ratio of cells to particles ranges from 1:100 to 100:1 and any integer values in-between and in further aspects the ratio comprises 1:9 to 9:1 and any integer values in-between, can also be used to stimulate T cells. The ratio of anti-CD3- and anti-CD28-coupled particles to T cells that result in T cell stimulation can vary as noted above, however certain preferred values include 1:100, 1:50, 1:40, 1:30, 1:20, 1:10, 1:9, 1:8, 1:7, 1:6, 1:5, 1:4, 1:3, 1:2, 1:1, 2:1, 3:1, 4:1, 5:1, 6:1, 7:1, 8:1, 9:1, 10:1, and 15:1 with one preferred ratio being at least 1:1 particles per T cell. In one aspect, a ratio of particles to cells of 1:1 or less is used. In one particular aspect, a preferred particle: cell ratio is 1:5. In further aspects, the ratio of particles to cells can be varied depending on the day of stimulation. For example, in one aspect, the ratio of particles to cells is from 1:1 to 10:1 on the first day and additional particles are added to the cells every day or every other day thereafter for up to 10 days, at final ratios of from 1:1 to 1:10 (based on cell counts on the day of addition). In one particular aspect, the ratio of particles to cells is 1:1 on the first day of stimulation and adjusted to 1:5 on the third and fifth days of stimulation. In one aspect, particles are added on a daily or every other day basis to a final ratio of 1:1 on the first day, and 1:5 on the third and fifth days of stimulation. In one aspect, the ratio of particles to cells is 2:1 on the first day of stimulation and adjusted to 1:10 on the third and fifth days of stimulation. In one aspect, particles are added on a daily or every other day basis to a final ratio of 1:1 on the first day, and 1:10 on the third and fifth days of stimulation. One of skill in the art will appreciate that a variety of other ratios may be suitable for use in the present invention. In particular, ratios will vary depending on particle size and on cell size and type. In one aspect, the most typical ratios for use are in the neighborhood of 1:1, 2:1 and 3:1 on the first day.

[00411] In further aspects of the present invention, the cells, such as T cells, are combined with agent-coated beads, the beads and the cells are subsequently separated, and then the cells

are cultured. In an alternative aspect, prior to culture, the agent-coated beads and cells are not separated but are cultured together. In a further aspect, the beads and cells are first concentrated by application of a force, such as a magnetic force, resulting in increased ligation of cell surface markers, thereby inducing cell stimulation.

[00412] By way of example, cell surface proteins may be ligated by allowing paramagnetic beads to which anti-CD3 and anti-CD28 are attached (3x28 beads) to contact the T cells. In one aspect the cells (for example, 10^4 to 10^9 T cells) and beads (for example, DYNABEADS® M-450 CD3/CD28 T paramagnetic beads at a ratio of 1:1) are combined in a buffer, for example PBS (without divalent cations such as, calcium and magnesium). Again, those of ordinary skill in the art can readily appreciate any cell concentration may be used. For example, the target cell may be very rare in the sample and comprise only 0.01% of the sample or the entire sample (i.e., 100%) may comprise the target cell of interest. Accordingly, any cell number is within the context of the present invention. In certain aspects, it may be desirable to significantly decrease the volume in which particles and cells are mixed together (i.e., increase the concentration of cells), to ensure maximum contact of cells and particles. For example, in one aspect, a concentration of about 2 billion cells/ml is used. In one aspect, greater than 100 million cells/ml is used. In a further aspect, a concentration of cells of 10, 15, 20, 25, 30, 35, 40, 45, or 50 million cells/ml is used. In yet one aspect, a concentration of cells from 75, 80, 85, 90, 95, or 100 million cells/ml is used. In further aspects, concentrations of 125 or 150 million cells/ml can be used. Using high concentrations can result in increased cell yield, cell activation, and cell expansion. Further, use of high cell concentrations allows more efficient capture of cells that may weakly express target antigens of interest, such as CD28-negative T cells. Such populations of cells may have therapeutic value and would be desirable to obtain in certain aspects. For example, using high concentration of cells allows more efficient selection of CD8+ T cells that normally have weaker CD28 expression.

[00413] In one aspect of the present invention, the mixture may be cultured for several hours (about 3 hours) to about 14 days or any hourly integer value in between. In one aspect, the mixture may be cultured for 21 days. In one aspect of the invention the beads and the T cells are cultured together for about eight days. In one aspect, the beads and T cells are cultured together for 2-3 days. Several cycles of stimulation may also be desired such that culture time of T cells can be 60 days or more. Conditions appropriate for T cell culture include an appropriate media

(e.g., Minimal Essential Media or RPMI Media 1640 or, X-vivo 15, (Lonza)) that may contain factors necessary for proliferation and viability, including serum (e.g., fetal bovine or human serum), interleukin-2 (IL-2), insulin, IFN- γ , IL-4, IL-7, GM-CSF, IL-10, IL-12, IL-15, TGF β , and TNF- α or any other additives for the growth of cells known to the skilled artisan. Other additives for the growth of cells include, but are not limited to, surfactant, plasmanate, and reducing agents such as N-acetyl-cysteine and 2-mercaptoethanol. Media can include RPMI 1640, AIM-V, DMEM, MEM, α -MEM, F-12, X-Vivo 15, and X-Vivo 20, Optimizer, with added amino acids, sodium pyruvate, and vitamins, either serum-free or supplemented with an appropriate amount of serum (or plasma) or a defined set of hormones, and/or an amount of cytokine(s) sufficient for the growth and expansion of T cells. Antibiotics, e.g., penicillin and streptomycin, are included only in experimental cultures, not in cultures of cells that are to be infused into a subject. The target cells are maintained under conditions necessary to support growth, for example, an appropriate temperature (e.g., 37° C) and atmosphere (e.g., air plus 5% CO₂).

[00414] T cells that have been exposed to varied stimulation times may exhibit different characteristics. For example, typical blood or apheresed peripheral blood mononuclear cell products have a helper T cell population (TH, CD4+) that is greater than the cytotoxic or suppressor T cell population (TC, CD8+). Ex vivo expansion of T cells by stimulating CD3 and CD28 receptors produces a population of T cells that prior to about days 8-9 consists predominately of TH cells, while after about days 8-9, the population of T cells comprises an increasingly greater population of TC cells. Accordingly, depending on the purpose of treatment, infusing a subject with a T cell population comprising predominately of TH cells may be advantageous. Similarly, if an antigen-specific subset of TC cells has been isolated it may be beneficial to expand this subset to a greater degree.

[00415] Further, in addition to CD4 and CD8 markers, other phenotypic markers vary significantly, but in large part, reproducibly during the course of the cell expansion process. Thus, such reproducibility enables the ability to tailor an activated T cell product for specific purposes.

[00416] Once a mesothelin CAR is constructed, various assays can be used to evaluate the activity of the molecule, such as but not limited to, the ability to expand T cells following antigen stimulation, sustain T cell expansion in the absence of re-stimulation, and anti-cancer

activities in appropriate in vitro and animal models. Assays to evaluate the effects of a mesothelin CAR are described in further detail below

[00417] Western blot analysis of CAR expression in primary T cells can be used to detect the presence of monomers and dimers. See, e.g., Milone *et al.*, Molecular Therapy 17(8): 1453-1464 (2009). Very briefly, T cells (1:1 mixture of CD4⁺ and CD8⁺ T cells) expressing the CARs are expanded *in vitro* for more than 10 days followed by lysis and SDS-PAGE under reducing conditions. CARs containing the full length TCR- ζ cytoplasmic domain and the endogenous TCR- ζ chain are detected by western blotting using an antibody to the TCR- ζ chain. The same T cell subsets are used for SDS-PAGE analysis under non-reducing conditions to permit evaluation of covalent dimer formation.

[00418] *In vitro* expansion of CAR⁺ T cells following antigen stimulation can be measured by flow cytometry. For example, a mixture of CD4⁺ and CD8⁺ T cells are stimulated with α CD3/ α CD28 aAPCs followed by transduction with lentiviral vectors expressing GFP under the control of the promoters to be analyzed. Exemplary promoters include the CMV IE gene, EF-1 α , ubiquitin C, or phosphoglycerokinase (PGK) promoters. GFP fluorescence is evaluated on day 6 of culture in the CD4⁺ and/or CD8⁺ T cell subsets by flow cytometry. See, e.g., Milone *et al.*, Molecular Therapy 17(8): 1453-1464 (2009). Alternatively, a mixture of CD4⁺ and CD8⁺ T cells are stimulated with α CD3/ α CD28 coated magnetic beads on day 0, and transduced with CAR on day 1 using a bicistronic lentiviral vector expressing CAR along with eGFP using a 2A ribosomal skipping sequence. Cultures are re-stimulated, e.g., with K562 cells expressing hCD32 and 4-1BBL in the presence of anti-CD3 and anti-CD28 antibody (K562-BBL-3/28) following washing. Exogenous IL-2 is added to the cultures every other day at 100 IU/ml. GFP⁺ T cells are enumerated by flow cytometry using bead-based counting. See, e.g., Milone *et al.*, Molecular Therapy 17(8): 1453-1464 (2009).

[00419] Sustained CAR⁺ T cell expansion in the absence of re-stimulation can also be measured. See, e.g., Milone *et al.*, Molecular Therapy 17(8): 1453-1464 (2009). Briefly, mean T cell volume (fl) is measured on day 8 of culture using a Coulter Multisizer III particle counter following stimulation with α CD3/ α CD28 coated magnetic beads on day 0, and transduction with the indicated CAR on day 1.

[00420] Assessment of cell proliferation and cytokine production has been previously described, e.g., at Milone *et al.*, Molecular Therapy 17(8): 1453-1464 (2009). Briefly, assessment of CAR-mediated proliferation is performed in microtiter plates by mixing washed T cells with target cells, such as K562-Meso, Ovcar3, Ovcar8, SW1990, Panc02.03 cells expressing mesothelin or CD32 and CD137 (KT32-BBL) for a final T-cell:target cell ratio of 1:1. Anti-CD3 (clone OKT3) and anti-CD28 (clone 9.3) monoclonal antibodies are added to cultures with KT32-BBL cells to serve as a positive control for stimulating T-cell proliferation since these signals support long-term CD8⁺ T cell expansion *ex vivo*. T cells are enumerated in cultures using CountBright™ fluorescent beads (Invitrogen, Carlsbad, CA) and flow cytometry as described by the manufacturer. CAR⁺ T cells are identified by GFP expression using T cells that are engineered with eGFP-2A linked CAR-expressing lentiviral vectors. For CAR+ T cells not expressing GFP, the CAR+ T cells are detected with biotinylated recombinant mesothelin protein and a secondary avidin-PE conjugate. CD4+ and CD8⁺ expression on T cells are also simultaneously detected with specific monoclonal antibodies (BD Biosciences). Cytokine measurements are performed on supernatants collected 24 hours following re-stimulation using the human TH1/TH2 cytokine cytometric bead array kit (BD Biosciences, San Diego, CA) according the manufacturer's instructions. Fluorescence is assessed using a FACScalibur flow cytometer, and data is analyzed according to the manufacturer's instructions.

[00421] Cytotoxicity can be assessed by methods described herein, e.g., in the examples, or by a standard 51Cr-release assay. See, e.g., Milone *et al.*, Molecular Therapy 17(8): 1453-1464 (2009). Briefly, target cells (e.g., BHK or CHO cells expressing mesothelin) are loaded with 51Cr (as NaCrO₄, New England Nuclear, Boston, MA) at 37°C for 2 hours with frequent agitation, washed twice in complete RPMI and plated into microtiter plates. Effector T cells are mixed with target cells in the wells in complete RPMI at varying ratios of effector cell:target cell (E:T). Additional wells containing media only (spontaneous release, SR) or a 1% solution of triton-X 100 detergent (total release, TR) are also prepared. After 4 hours of incubation at 37°C, supernatant from each well is harvested. Released ⁵¹Cr is then measured using a gamma particle counter (Packard Instrument Co., Waltham, MA). Each condition is performed in at least triplicate, and the percentage of lysis is calculated using the formula: % Lysis = (ER - SR) / (TR - SR), where ER represents the average 51Cr released for each experimental condition. Alternative cytotoxicity assays may also be used, such as flow based cytotoxicity assays.

[00422] Click beetle red and click beetle green luciferase can be used to simultaneously follow tumor progression and T cell trafficking, as each use the same luciferin substrate but emit light at the opposite ends of the visible light spectrum.

[00423] Other assays, including those described in the Example section herein as well as those that are known in the art can also be used to evaluate the mesothelin CAR constructs of the invention.

Therapeutic Application for Mesothelin Expressing Diseases and Disorders

[00424] The present invention provides compositions and methods for treating diseases and disorders associated with mesothelin. An example of a disease or disorder associated with mesothelin is mesothelioma.

[00425] Malignant mesothelioma is a type of cancer that occurs in the thin layer of cells lining the body's internal organs, known as the mesothelium. There are three recognized types of mesothelioma. Pleural mesothelioma (e.g., malignant pleural mesothelioma, or MPM) is the most common form of the disease, accounting for roughly 70% of cases, and occurs in the lining of the lung known as the pleura. Peritoneal mesothelioma occurs in the lining of the abdominal cavity, known as the peritoneum. Pericardial mesothelioma originates in the pericardium, which lines the heart.

[00426] A subject may be at risk to develop mesothelioma if the subject was exposed to asbestos. Exposure to asbestos and the inhalation of asbestos particles can cause mesothelioma. In most cases, mesothelioma symptoms will not appear in a subject exposed to asbestos until many years after the exposure has occurred.

[00427] Symptoms of pleural mesothelioma include, e.g., lower back pain or side chest pain, and shortness of breath. Other symptoms include difficulty swallowing, persistent cough, fever, weight loss or fatigue. Additional symptoms that some patients experience are muscle weakness, loss of sensory capability, coughing up blood, facial and arm swelling, and hoarseness. In the early stages of the disease, such as stage 1 mesothelioma, symptoms may be mild. Patients usually report pain in one area of the chest that never seems to go away, weight loss and fever.

[00428] Peritoneal mesothelioma originates in the abdomen and as a result, symptoms often include abdominal pain, weight loss, nausea, and vomiting. Fluid buildup may occur in the

abdomen as well as a result of the cancer. Peritoneal mesothelioma originates in the abdomen and will frequently spread to other organs in area including the liver, spleen or bowel. Severe abdominal pain is the most common complaint that patients first experience. There may also be a discomfort level with fluid buildup in the abdomen as well. Other symptoms of peritoneal mesothelioma may include difficult bowel movements, nausea and vomiting, fever and swollen feet.

[00429] Pericardial mesothelioma is the least common form of mesothelioma. Pericardial mesothelioma, as the name suggests, involves the heart. This rare type of mesothelioma cancer invades the pericardium, the sac that surrounds the heart. As the cancer progresses, the heart is not able to deliver oxygen as efficiently to the body causing further decline in health at an increasingly rapid rate. The symptoms most commonly associated with pericardial mesothelioma mimic those of a heart attack: nausea, pain in the chest and shortness of breath.

[00430] Subjects benefiting from treatment according to the invention include subjects with a mesothelioma, or subjects suspected of having mesothelioma, e.g., as evidenced by the presence of one or more of the symptoms described herein and/or exposure to asbestos. In particular embodiments, the mesothelioma is pleural mesothelioma (e.g., malignant pleural mesothelioma). In other aspects, the subject may be treated that has a precancerous condition such as, e.g., pleural plaques, benign mesothelioma or mesothelial hyperplasia.

[00431] Another example of a disease or disorder associated with mesothelin is pancreatic cancer. Pancreatic cancers that can be treated with methods described herein include, but are not limited to, exocrine pancreatic cancers and endocrine pancreatic cancers. Exocrine pancreatic cancers include, but are not limited to, adenocarcinomas, acinar cell carcinomas, adenosquamous carcinomas, colloid carcinomas, undifferentiated carcinomas with osteoclast-like giant cells, hepatoid carcinomas, intraductal papillary-mucinous neoplasms, mucinous cystic neoplasms, pancreatoblastomas, serous cystadenomas, signet ring cell carcinomas, solid and pseudopapillary tumors, pancreatic ductal carcinomas, and undifferentiated carcinomas. In some embodiments, the exocrine pancreatic cancer is pancreatic ductal carcinoma. Endocrine pancreatic cancers include, but are not limited to, insulinomas and glucagonomas.

[00432] In some embodiments, the pancreatic cancer is any of early stage pancreatic cancer, non-metastatic pancreatic cancer, primary pancreatic cancer, resected pancreatic cancer,

advanced pancreatic cancer, locally advanced pancreatic cancer, metastatic pancreatic cancer, unresectable pancreatic cancer, pancreatic cancer in remission, recurrent pancreatic cancer, pancreatic cancer in an adjuvant setting, or pancreatic cancer in a neoadjuvant setting. In some embodiments, the pancreatic cancer is locally advanced pancreatic cancer, unresectable pancreatic cancer, or metastatic pancreatic ductal carcinoma. In some embodiments, the pancreatic cancer is resistant to the gemcitabine-based therapy. In some embodiments, the pancreatic cancer is refractory to the gemcitabine-based therapy.

[00433] In other aspects, the disorder associated with mesothelin expression is ovarian cancer. Ovarian cancer is classified according to the histology of the tumor. Surface epithelial-stromal tumor, also known as ovarian epithelial carcinoma, is the most common type of ovarian cancer. It includes serous tumor (including serous papillary cystadenocarcinoma), endometrioid tumor and mucinous cystadenocarcinoma.

[00434] The methods described herein can be used to treat various stages of ovarian cancer, e.g., stage I, stage II, stage III or stage IV. Staging can be performed, e.g., when the ovarian cancer is removed. Ovarian cancer is staged as follows:

[00435] Stage I cancer is confined to one or both ovaries. The cancer is stage II if either one or both of the ovaries is involved and has spread to the uterus and/or the fallopian tubes or other sites in the pelvis. The cancer is stage III cancer if one or both of the ovaries is involved and has spread to lymph nodes or other sites outside of the pelvis but is still within the abdominal cavity, such as the surface of the intestine or liver. The cancer is stage IV cancer if one or both ovaries are involved and the cancer has spread outside the abdomen or to the inside of the liver.

[00436] In some embodiments, the ovarian cancer is resistant to one or more chemotherapeutic agent. In some embodiments, the ovarian cancer is refractory to the one or more chemotherapeutic agent.

[00437] Other cancers that can be treated with the CAR compositions described herein include, e.g., brain cancer, bladder cancer, breast cancer, cervical cancer, colorectal cancer, liver cancer, kidney cancer, lymphoma, leukemia, lung cancer (e.g., lung adenocarcinoma), melanoma, metastatic melanoma, mesothelioma, neuroblastoma, ovarian cancer, prostate cancer, pancreatic cancer, renal cancer, skin cancer, thymoma, sarcoma, non-Hodgkin's lymphoma, Hodgkin's lymphoma, uterine cancer, and any combination thereof.

[00438] The present invention provides methods for inhibiting the proliferation or reducing a mesothelin-expressing cell population, the methods comprising contacting a population of cells comprising a mesothelin expressing cell with a mesothelin CAR-expressing cell of the invention that binds to the mesothelin-expressing cell. In a specific embodiment, the invention provides methods for inhibiting the proliferation or reducing the population of cancer cells expressing mesothelin, the methods comprising contacting the mesothelin -expressing cancer cell population with a mesothelin CAR-expressing cell of the invention that binds to the mesothelin-expressing cell. In another embodiment, the invention provides methods for inhibiting the proliferation or reducing the population of cancer cells expressing mesothelin, the methods comprising contacting the mesothelin -expressing cancer cell population with a mesothelin CAR-expressing cell of the invention that binds to the mesothelin-expressing cell. In certain embodiments, the mesothelin CAR-expressing cell of the invention reduces the quantity, number, amount or percentage of cells and/or cancer cells by at least 25%, at least 30%, at least 40%, at least 50%, at least 65%, at least 75%, at least 85%, at least 95%, or at least 99% in a subject with or animal model of mesothelioma or another cancer associated with mesothelin -expressing cells relative to a negative control. In one aspect, the subject is a human.

[00439] The invention also provides methods for preventing, treating and/or managing a disorder associated with mesothelin -expressing cells (e.g., mesothelioma), the methods comprising administering to a subject in need a mesothelioma CAR-expressing cell of the invention that binds to the mesothelin -expressing cell. In one aspect, the subject is a human.

[00440] The invention provides methods for preventing relapse of cancer associated with mesothelin-expressing cells, the methods comprising administering to a subject in need thereof a mesothelin CAR-expressing cell of the invention that binds to the mesothelin-expressing cell. In another embodiment, the methods comprise administering to the subject in need thereof an effective amount of a mesothelin CAR-expressing cell of the invention that binds to the mesothelin-expressing cell in combination with an effective amount of another therapy.

[00441] In one aspect, the invention pertains to a vector comprising a sequence encoding a mesothelin CAR operably linked to promoter for expression in mammalian immune effector cells. In one aspect, the invention provides a recombinant immune effector cell expressing the mesothelin CAR for use in treating mesothelin -expressing tumors. In one aspect, the mesothelin

CAR-expressing cell of the invention is capable of contacting a tumor cell with at least one mesothelin CAR of the invention expressed on its surface such that the mesothelin CAR-expressing cell is activated in response to the antigen and the CAR-expressing cell targets the cancer cell and growth of the cancer is inhibited.

[00442] In one aspect, the invention pertains to a method of inhibiting growth of a mesothelin-expressing cancer cell, comprising contacting the tumor cell with a-mesothelin CAR-expressing cell such that the CAR-expressing cell is activated in response to the antigen and targets the cancer cell, wherein the growth of the cancer is inhibited. In one aspect, the activated CART targets and kills the cancer cell.

[00443] In one aspect, the invention pertains to a method of treating cancer in a subject. The method comprises administering to the subject a mesothelin CAR-expressing cell such that the cancer is treated in the subject. An example of a cancer that is treatable by the mesothelin CAR-expressing cell of the invention is a cancer associated with expression of mesothelin. In one aspect, the cancer associated with expression of mesothelin is selected from mesothelioma, pancreatic cancer, ovarian cancer and lung cancer.

[00444] The invention includes a type of cellular therapy where immune effector cells, e.g., T cells or NK cells, are genetically modified to express a chimeric antigen receptor (CAR) and the CAR-expressing cell is infused to a recipient in need thereof. The infused cell is able to kill tumor cells in the recipient. Unlike antibody therapies, CAR-modified immune effector cells are able to replicate in vivo resulting in long-term persistence that can lead to sustained tumor control. In various aspects, the cells administered to the patient, or their progeny, persist in the patient for at least four months, five months, six months, seven months, eight months, nine months, ten months, eleven months, twelve months, thirteen months, fourteen month, fifteen months, sixteen months, seventeen months, eighteen months, nineteen months, twenty months, twenty-one months, twenty-two months, twenty-three months, two years, three years, four years, or five years after administration of the cell to the patient.

[00445] The invention also includes a type of cellular therapy where immune effector cells are modified, e.g., by in vitro transcribed RNA, to transiently express a chimeric antigen receptor (CAR) and the CAR-expressing cell is infused to a recipient in need thereof. The infused cell is able to kill cancer cells in the recipient. Thus, in various aspects, the cells administered to the

patient, is present for less than one month, e.g., three weeks, two weeks, one week, after administration of the cell to the patient.

[00446] Without wishing to be bound by any particular theory, the anti-cancer immunity response elicited by the CAR-modified immune effector cells may be an active or a passive immune response, or alternatively may be due to a direct vs indirect immune response. In one aspect, the CAR transduced T cells exhibit specific proinflammatory cytokine secretion and potent cytolytic activity in response to human cancer cells expressing mesothelin, and mediate bystander killing and mediate regression of an established human tumor. For example, antigen-less tumor cells within a heterogeneous field of mesothelin-expressing tumor may be susceptible to indirect destruction by mesothelin redirected T cells that has previously reacted against adjacent antigen-positive cancer cells.

[00447] In one aspect, the fully-human scFv bearing CAR-modified immune effector cells of the invention may be a type of vaccine for ex vivo immunization and/or in vivo therapy in a mammal. In one aspect, the mammal is a human.

[00448] With respect to ex vivo immunization, at least one of the following occurs in vitro prior to administering the cell into a mammal: i) expansion of the cells, ii) introducing a nucleic acid encoding a CAR to the cells or iii) cryopreservation of the cells.

[00449] Ex vivo procedures are well known in the art and are discussed more fully below. Briefly, cells are isolated from a mammal (e.g., a human) and genetically modified (i.e., transduced or transfected in vitro) with a vector expressing a CAR disclosed herein. The CAR-modified cell can be administered to a mammalian recipient to provide a therapeutic benefit. The mammalian recipient may be a human and the CAR-modified cell can be autologous with respect to the recipient. Alternatively, the cells can be allogeneic, syngeneic or xenogeneic with respect to the recipient.

[00450] The procedure for ex vivo expansion of hematopoietic stem and progenitor cells is described in U.S. Pat. No. 5,199,942, incorporated herein by reference, can be applied to the cells of the present invention. Other suitable methods are known in the art therefore the present invention is not limited to any particular method of ex vivo expansion of the cells. Briefly, ex vivo culture and expansion of T cells comprises: (1) collecting CD34+ hematopoietic stem and progenitor cells from a mammal from peripheral blood harvest or bone marrow explants; and (2)

expanding such cells ex vivo. In addition to the cellular growth factors described in U.S. Pat. No. 5,199,942, other factors such as flt3-L, IL-1, IL-3 and c-kit ligand, can be used for culturing and expansion of the cells.

[00451] In addition to using a cell-based vaccine in terms of ex vivo immunization, the present invention also provides compositions and methods for in vivo immunization to elicit an immune response directed against an antigen in a patient.

[00452] Generally, the cells activated and expanded as described herein may be utilized in the treatment and prevention of diseases that arise in individuals who are immunocompromised. In particular, the CAR-modified immune effector cells of the invention are used in the treatment of diseases, disorders and conditions associated with expression of mesothelin. In certain aspects, the cells of the invention are used in the treatment of patients at risk for developing diseases, disorders and conditions associated with expression of mesothelin. Thus, the invention provides methods for the treatment or prevention of diseases, disorders and conditions associated with expression of mesothelin comprising administering to a subject in need thereof, a therapeutically effective amount of the CAR-modified T cells of the invention.

[00453] The CAR-modified T cells of the present invention may be administered either alone, or as a pharmaceutical composition in combination with diluents and/or with other components such as IL-2 or other cytokines or cell populations.

[00454] The present invention also provides methods for inhibiting the proliferation or reducing a mesothelin-expressing cell population, the methods comprising contacting a population of cells comprising a mesothelin-expressing cell with a mesothelin CAR-expressing cell (, e.g., a mesothelin CART also referred to as “CART-MSLN”) of the invention that binds to the mesothelin-expressing cell. In a specific aspect, the invention provides methods for inhibiting the proliferation or reducing the population of cancer cells expressing mesothelin, the methods comprising contacting the mesothelin-expressing cancer cell population with a mesothelin CAR-expressing cell of the invention that binds to the mesothelin-expressing cell. In one aspect, the present invention provides methods for inhibiting the proliferation or reducing the population of cancer cells expressing mesothelin, the methods comprising contacting the mesothelin-expressing cancer cell population with a mesothelin CAR-expressing cell of the invention that binds to the mesothelin-expressing cell. In certain aspects, the mesothelin CAR-expressing cell

of the invention reduces the quantity, number, amount or percentage of cells and/or cancer cells by at least 25%, at least 30%, at least 40%, at least 50%, at least 65%, at least 75%, at least 85%, at least 95%, or at least 99% in a subject with or animal model for mesothelioma or another cancer associated with mesothelin-expressing cells relative to a negative control. In one aspect, the subject is a human.

[00455] The present invention also provides methods for preventing, treating and/or managing a disease associated with mesothelin-expressing cells (e.g., mesothelioma), the methods comprising administering to a subject in need a mesothelin CAR-expressing cell of the invention that binds to the mesothelin-expressing cell. In one aspect, the subject is a human.

[00456] The present invention provides methods for preventing relapse of cancer associated with mesothelin-expressing cells, the methods comprising administering to a subject in need thereof a mesothelin CAR-expressing cell of the invention that binds to the mesothelin-expressing cell. In one aspect, the methods comprise administering to the subject in need thereof an effective amount of a mesothelin CAR-expressing cell of the invention that binds to the mesothelin-expressing cell in combination with an effective amount of another therapy.

Combination Therapies

[00457] A CAR-expressing cell described herein may be used in combination with other known agents and therapies. Administered “in combination”, as used herein, means that two (or more) different treatments are delivered to the subject during the course of the subject's affliction with the disorder, e.g., the two or more treatments are delivered after the subject has been diagnosed with the disorder and before the disorder has been cured or eliminated or treatment has ceased for other reasons. In some embodiments, the delivery of one treatment is still occurring when the delivery of the second begins, so that there is overlap in terms of administration. This is sometimes referred to herein as “simultaneous” or “concurrent delivery”. In other embodiments, the delivery of one treatment ends before the delivery of the other treatment begins. In some embodiments of either case, the treatment is more effective because of combined administration. For example, the second treatment is more effective, e.g., an equivalent effect is seen with less of the second treatment, or the second treatment reduces symptoms to a greater extent, than would be seen if the second treatment were administered in the absence of the first treatment, or the analogous situation is seen with the first treatment. In

some embodiments, delivery is such that the reduction in a symptom, or other parameter related to the disorder is greater than what would be observed with one treatment delivered in the absence of the other. The effect of the two treatments can be partially additive, wholly additive, or greater than additive. The delivery can be such that an effect of the first treatment delivered is still detectable when the second is delivered.

[00458] A CAR-expressing cell described herein and the at least one additional therapeutic agent can be administered simultaneously, in the same or in separate compositions, or sequentially. For sequential administration, the CAR-expressing cell described herein can be administered first, and the additional agent can be administered second, or the order of administration can be reversed.

[00459] In further aspects, a CAR-expressing cell described herein may be used in a treatment regimen in combination with surgery, chemotherapy, radiation, immunosuppressive agents, such as cyclosporin, azathioprine, methotrexate, mycophenolate, and FK506, antibodies, or other immunoablative agents such as CAMPATH, anti-CD3 antibodies or other antibody therapies, cytoxin, fludarabine, cyclosporin, FK506, rapamycin, mycophenolic acid, steroids, FR901228, cytokines, and irradiation. peptide vaccine, such as that described in Izumoto et al. 2008 J Neurosurg 108:963-971.

[00460] In one embodiment, a CAR-expressing cell described herein can be used in combination with a chemotherapeutic agent. Exemplary chemotherapeutic agents include an anthracycline (e.g., doxorubicin (e.g., liposomal doxorubicin)), a vinca alkaloid (e.g., vinblastine, vincristine, vindesine, vinorelbine), an alkylating agent (e.g., cyclophosphamide, decarbazine, melphalan, ifosfamide, temozolomide), an immune cell antibody (e.g., alemtuzumab, gemtuzumab, rituximab, tositumomab), an antimetabolite (including, e.g., folic acid antagonists, pyrimidine analogs, purine analogs and adenosine deaminase inhibitors (e.g., fludarabine)), an mTOR inhibitor, a TNFR glucocorticoid induced TNFR related protein (GITR) agonist, a proteasome inhibitor (e.g., aclaranomycin A, gliotoxin or bortezomib), an immunomodulator such as thalidomide or a thalidomide derivative (e.g., lenalidomide).

[00461] General Chemotherapeutic agents considered for use in combination therapies include anastrozole (Arimidex®), bicalutamide (Casodex®), bleomycin sulfate (Blenoxane®), busulfan (Myleran®), busulfan injection (Busulfex®), capecitabine (Xeloda®), N4-

pentoxycarbonyl-5-deoxy-5-fluorocytidine, carboplatin (Paraplatin®), carmustine (BiCNU®), chlorambucil (Leukeran®), cisplatin (Platinol®), cladribine (Leustatin®), cyclophosphamide (Cytoxan® or Neosar®), cytarabine, cytosine arabinoside (Cytosar-U®), cytarabine liposome injection (DepoCyt®), dacarbazine (DTIC-Dome®), dactinomycin (Actinomycin D, Cosmegen), daunorubicin hydrochloride (Cerubidine®), daunorubicin citrate liposome injection (DaunoXome®), dexamethasone, docetaxel (Taxotere®), doxorubicin hydrochloride (Adriamycin®, Rubex®), etoposide (Vepesid®), fludarabine phosphate (Fludara®), 5-fluorouracil (Adrucil®, Efudex®), flutamide (Eulexin®), tezacitibine, Gemcitabine (difuorodeoxycytidine), hydroxyurea (Hydrea®), Idarubicin (Idamycin®), ifosfamide (IFEX®), irinotecan (Camptosar®), L-asparaginase (ELSPAR®), leucovorin calcium, melphalan (Alkeran®), 6-mercaptopurine (Purinethol®), methotrexate (Folex®), mitoxantrone (Novantrone®), mylotarg, paclitaxel (Taxol®), phoenix (Yttrium90/MX-DTPA), pentostatin, polifeprosan 20 with carmustine implant (Gliadel®), tamoxifen citrate (Nolvadex®), teniposide (Vumon®), 6-thioguanine, thiotepa, tirapazamine (Tirazone®), topotecan hydrochloride for injection (Hycamtin®), vinblastine (Velban®), vincristine (Oncovin®), and vinorelbine (Navelbine®).

[00462] Exemplary alkylating agents include, without limitation, nitrogen mustards, ethylenimine derivatives, alkyl sulfonates, nitrosoureas and triazenes): uracil mustard (Aminouracil Mustard®, Chlorethaminacil®, Demethyldopan®, Desmethyldopan®, Haemanthamine®, Nordopan®, Uracil nitrogen mustard®, Uracillost®, Uracilmostaza®, Uramustin®, Uramustine®), chlormethine (Mustargen®), cyclophosphamide (Cytoxan®, Neosar®, Clafen®, Endoxan®, Procytox®, Revimmune™), ifosfamide (Mitoxana®), melphalan (Alkeran®), Chlorambucil (Leukeran®), pipobroman (Amedel®, Vercyte®), triethylenemelamine (Hemel®, Hexalen®, Hexastat®), triethylenethiophosphoramine, Temozolomide (Temodar®), thiotepa (Thioplex®), busulfan (Busilvex®, Myleran®), carmustine (BiCNU®), lomustine (CeeNU®), streptozocin (Zanosar®), and Dacarbazine (DTIC-Dome®). Additional exemplary alkylating agents include, without limitation, Oxaliplatin (Eloxatin®); Temozolomide (Temodar® and Temodal®); Dactinomycin (also known as actinomycin-D, Cosmegen®); Melphalan (also known as L-PAM, L-sarcolysin, and phenylalanine mustard, Alkeran®); Altretamine (also known as hexamethylmelamine (HMM), Hexalen®); Carmustine (BiCNU®); Bendamustine (Treanda®); Busulfan (Busulfex® and

Myleran®); Carboplatin (Paraplatin®); Lomustine (also known as CCNU, CeeNU®); Cisplatin (also known as CDDP, Platinol® and Platinol®-AQ); Chlorambucil (Leukeran®); Cyclophosphamide (Cytoxan® and Neosar®); Dacarbazine (also known as DTIC, DIC and imidazole carboxamide, DTIC-Dome®); Altretamine (also known as hexamethylmelamine (HMM), Hexalen®); Ifosfamide (Ifex®); Prednumustine; Procarbazine (Matulane®); Mechlorethamine (also known as nitrogen mustard, mustine and mechloroethamine hydrochloride, Mustargen®); Streptozocin (Zanosar®); Thiotepa (also known as thiophosphoamide, TESPA and TSPA, Thioplex®); Cyclophosphamide (Endoxan®, Cytoxan®, Neosar®, Procytox®, Revimmune®); and Bendamustine HCl (Treanda®).

[00463] Exemplary mTOR inhibitors include, e.g., temsirolimus; ridaforolimus (formally known as deferolimus, (1*R*,2*R*,4*S*)-4-[(2*R*)-2 [(1*R*,9*S*,12*S*,15*R*,16*E*,18*R*,19*R*,21*R*,23*S*,24*E*,26*E*,28*Z*,30*S*,32*S*,35*R*)-1,18-dihydroxy-19,30-dimethoxy-15,17,21,23, 29,35-hexamethyl-2,3,10,14,20-pentaoxo-11,36-dioxa-4-azatricyclo[30.3.1.0^{4,9}]hexatriaconta-16,24,26,28-tetraen-12-yl]propyl]-2-methoxycyclohexyl dimethylphosphinate, also known as AP23573 and MK8669, and described in PCT Publication No. WO 03/064383); everolimus (Afinitor® or RAD001); rapamycin (AY22989, Sirolimus®); simapimod (CAS 164301-51-3); emsirolimus, (5- {2,4-Bis[(3*S*)-3-methylmorpholin-4-yl]pyrido[2,3-*d*]pyrimidin-7-yl}-2-methoxyphenyl)methanol (AZD8055); 2-Amino-8-[*trans*-4-(2-hydroxyethoxy)cyclohexyl]-6-(6-methoxy-3-pyridinyl)-4-methyl-pyrido[2,3-*d*]pyrimidin-7(8*H*)-one (PF04691502, CAS 1013101-36-4); and *N*²-[1,4-dioxo-4-[[4-(4-oxo-8-phenyl-4*H*-1-benzopyran-2-yl)morpholinium-4-yl]methoxy]butyl]-L-arginylglycyl-L- α -aspartylL-serine-, inner salt (SF1126, CAS 936487-67-1), and XL765.

[00464] Exemplary immunomodulators include, e.g., afutuzumab (available from Roche®); pegfilgrastim (Neulasta®); lenalidomide (CC-5013, Revlimid®); thalidomide (Thalomid®), actimid (CC4047); and IRX-2 (mixture of human cytokines including interleukin 1, interleukin 2, and interferon γ , CAS 951209-71-5, available from IRX Therapeutics).

[00465] Exemplary anthracyclines include, e.g., doxorubicin (Adriamycin® and Rubex®); bleomycin (lenoxane®); daunorubicin (daunorubicin hydrochloride, daunomycin, and rubidomycin hydrochloride, Cerubidine®); daunorubicin liposomal (daunorubicin citrate liposome, DaunoXome®); mitoxantrone (DHAD, Novantrone®); epirubicin (Ellence™);

idarubicin (Idamycin®, Idamycin PFS®); mitomycin C (Mutamycin®); geldanamycin; herbimycin; ravidomycin; and desacetyl ravidomycin.

[00466] Exemplary vinca alkaloids include, e.g., vinorelbine tartrate (Navelbine®), Vincristine (Oncovin®), and Vindesine (Eldisine®)); vinblastine (also known as vinblastine sulfate, vincleukoblastine and VLB, Alkaban-AQ® and Velban®); and vinorelbine (Navelbine®).

[00467] Exemplary proteosome inhibitors include bortezomib (Velcade®); carfilzomib (PX-171-007, (S)-4-Methyl-N-((S)-1-(((S)-4-methyl-1-((R)-2-methyloxiran-2-yl)-1-oxopentan-2-yl)amino)-1-oxo-3-phenylpropan-2-yl)-2-((S)-2-(2-morpholinoacetamido)-4-phenylbutanamido)-pentanamide); marizomib (NPI-0052); ixazomib citrate (MLN-9708); delanzomib (CEP-18770); and *O*-Methyl-*N*-[(2-methyl-5-thiazolyl)carbonyl]-L-seryl-*O*-methyl-*N*-[(1*S*)-2-[(2*R*)-2-methyl-2-oxiranyl]-2-oxo-1-(phenylmethyl)ethyl]- L-serinamide (ONX-0912).

[00468] In one embodiment, a CAR expressing cell described herein is administered to a subject in combination with a molecule targeting GITR and/or modulating GITR functions, such as a GITR agonist and/or a GITR antibody that depletes regulatory T cells (Tregs). In one embodiment, the GITR binding molecules and/or molecules modulating GITR functions (e.g., GITR agonist and/or Treg depleting GITR antibodies) are administered prior to the CAR-expressing cell. For example, in one embodiment, the GITR agonist can be administered prior to apheresis of the cells. Exemplary GITR agonists include, e.g., GITR fusion proteins and anti-GITR antibodies (e.g., bivalent anti-GITR antibodies) such as, e.g., a GITR fusion protein described in U.S. Patent No.: 6,111,090, European Patent No.: 090505B1, U.S Patent No.: 8,586,023, PCT Publication Nos.: WO 2010/003118 and 2011/090754, or an anti-GITR antibody described, e.g., in U.S. Patent No.: 7,025,962, European Patent No.: 1947183B1, U.S. Patent No.: 7,812,135, U.S. Patent No.: 8,388,967, U.S. Patent No.: 8,591,886, European Patent No.: EP 1866339, PCT Publication No.: WO 2011/028683, PCT Publication No.: WO 2013/039954, PCT Publication No.: WO2005/007190, PCT Publication No.: WO 2007/133822, PCT Publication No.: WO2005/055808, PCT Publication No.: WO 99/40196, PCT Publication No.: WO 2001/03720, PCT Publication No.: WO99/20758, PCT Publication No.: WO2006/083289, PCT Publication No.: WO 2005/115451, U.S. Patent No.: 7,618,632, and PCT Publication No.: WO 2011/051726.

[00469] In one embodiment, a CAR expressing cell described herein is administered to a subject in combination with an mTOR inhibitor, e.g., an mTOR inhibitor described herein, e.g., a rapalog such as everolimus. In one embodiment, the mTOR inhibitor is administered prior to the CAR-expressing cell. For example, in one embodiment, the mTOR inhibitor can be administered prior to apheresis of the cells.

[00470] In one embodiment, a CAR expressing cell described herein is administered to a subject in combination with a GITR agonist, e.g., a GITR agonist described herein. In one embodiment, the GITR agonist is administered prior to the CAR-expressing cell. For example, in one embodiment, the GITR agonist can be administered prior to apheresis of the cells.

[00471] In one embodiment, a CAR expressing cell described herein is administered to a subject in combination with a protein tyrosine phosphatase inhibitor, e.g., a protein tyrosine phosphatase inhibitor described herein. In one embodiment, the protein tyrosine phosphatase inhibitor is an SHP-1 inhibitor, e.g., an SHP-1 inhibitor described herein, such as, e.g., sodium stibogluconate. In one embodiment, the protein tyrosine phosphatase inhibitor is an SHP-2 inhibitor, e.g., an SHP-2 inhibitor described herein.

[00472] In one embodiment, a CAR-expressing cell described herein can be used in combination with a kinase inhibitor. In one embodiment, the kinase inhibitor is a CDK4 inhibitor, e.g., a CDK4 inhibitor described herein, e.g., a CDK4/6 inhibitor, such as, e.g., 6-Acetyl-8-cyclopentyl-5-methyl-2-(5-piperazin-1-yl-pyridin-2-ylamino)-8*H*-pyrido[2,3-*d*]pyrimidin-7-one, hydrochloride (also referred to as palbociclib or PD0332991). In one embodiment, the kinase inhibitor is a BTK inhibitor, e.g., a BTK inhibitor described herein, such as, e.g., ibrutinib. In one embodiment, the kinase inhibitor is an mTOR inhibitor, e.g., an mTOR inhibitor described herein, such as, e.g., rapamycin, a rapamycin analog, OSI-027. The mTOR inhibitor can be, e.g., an mTORC1 inhibitor and/or an mTORC2 inhibitor, e.g., an mTORC1 inhibitor and/or mTORC2 inhibitor described herein. In one embodiment, the kinase inhibitor is a MNK inhibitor, e.g., a MNK inhibitor described herein, such as, e.g., 4-amino-5-(4-fluoroanilino)-pyrazolo [3,4-*d*] pyrimidine. The MNK inhibitor can be, e.g., a MNK1a, MNK1b, MNK2a and/or MNK2b inhibitor. In one embodiment, the kinase inhibitor is a dual PI3K/mTOR inhibitor described herein, such as, e.g., PF-04695102. In one embodiment, the

kinase inhibitor is a DGK inhibitor, e.g., a DGK inhibitor described herein, such as, e.g., DGKinh1 (D5919) or DGKinh2 (D5794).

[00473] In one embodiment, the kinase inhibitor is a CDK4 inhibitor selected from aloisine A; flavopiridol or HMR-1275, 2-(2-chlorophenyl)-5,7-dihydroxy-8-[(3S,4R)-3-hydroxy-1-methyl-4-piperidinyl]-4-chromenone; crizotinib (PF-02341066; 2-(2-Chlorophenyl)-5,7-dihydroxy-8-[(2R,3S)-2-(hydroxymethyl)-1-methyl-3-pyrrolidinyl]-4H-1-benzopyran-4-one, hydrochloride (P276-00); 1-methyl-5-[[2-[5-(trifluoromethyl)-1H-imidazol-2-yl]-4-pyridinyl]oxy]-N-[4-(trifluoromethyl)phenyl]-1H-benzimidazol-2-amine (RAF265); indisulam (E7070); roscovitine (CYC202); palbociclib (PD0332991); dinaciclib (SCH727965); N-[5-[[5-*tert*-butyloxazol-2-yl)methyl]thio]thiazol-2-yl]piperidine-4-carboxamide (BMS 387032); 4-[[9-chloro-7-(2,6-difluorophenyl)-5H-pyrimido[5,4-*d*][2]benzazepin-2-yl]amino]-benzoic acid (MLN8054); 5-[3-(4,6-difluoro-1H-benzimidazol-2-yl)-1H-indazol-5-yl]-N-ethyl-4-methyl-3-pyridinemethanamine (AG-024322); 4-(2,6-dichlorobenzoylamino)-1H-pyrazole-3-carboxylic acid N-(piperidin-4-yl)amide (AT7519); 4-[2-methyl-1-(1-methylethyl)-1H-imidazol-5-yl]-N-[4-(methylsulfonyl)phenyl]-2-pyrimidinamine (AZD5438); and XL281 (BMS908662).

[00474] In one embodiment, the kinase inhibitor is a CDK4 inhibitor, e.g., palbociclib (PD0332991), and the palbociclib is administered at a dose of about 50 mg, 60 mg, 70 mg, 75 mg, 80 mg, 90 mg, 100 mg, 105 mg, 110 mg, 115 mg, 120 mg, 125 mg, 130 mg, 135 mg (e.g., 75 mg, 100 mg or 125 mg) daily for a period of time, e.g., daily for 14-21 days of a 28 day cycle, or daily for 7-12 days of a 21 day cycle. In one embodiment, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 or more cycles of palbociclib are administered.

[00475] In one embodiment, the kinase inhibitor is a BTK inhibitor selected from ibrutinib (PCI-32765); GDC-0834; RN-486; CGI-560; CGI-1764; HM-71224; CC-292; ONO-4059; CNX-774; and LFM-A13. In a preferred embodiment, the BTK inhibitor does not reduce or inhibit the kinase activity of interleukin-2-inducible kinase (ITK), and is selected from GDC-0834; RN-486; CGI-560; CGI-1764; HM-71224; CC-292; ONO-4059; CNX-774; and LFM-A13.

[00476] In one embodiment, the kinase inhibitor is a BTK inhibitor, e.g., ibrutinib (PCI-32765), and the ibrutinib is administered at a dose of about 250 mg, 300 mg, 350 mg, 400 mg, 420 mg, 440 mg, 460 mg, 480 mg, 500 mg, 520 mg, 540 mg, 560 mg, 580 mg, 600 mg (e.g., 250 mg, 420 mg or 560 mg) daily for a period of time, e.g., daily for 21 day cycle cycle, or daily for

28 day cycle. In one embodiment, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 or more cycles of ibrutinib are administered.

[00477] In one embodiment, the kinase inhibitor is an mTOR inhibitor selected from temsirolimus; ridaforolimus (1*R*,2*R*,4*S*)-4-[(2*R*)-2 [(1*R*,9*S*,12*S*,15*R*,16*E*,18*R*,19*R*,21*R*,23*S*,24*E*,26*E*,28*Z*,30*S*,32*S*,35*R*)-1,18-dihydroxy-19,30-dimethoxy-15,17,21,23, 29,35-hexamethyl-2,3,10,14,20-pentaoxo-11,36-dioxa-4-azatricyclo[30.3.1.0^{4,9}]hexatriaconta-16,24,26,28-tetraen-12-yl]propyl]-2-methoxycyclohexyl dimethylphosphinate, also known as AP23573 and MK8669; everolimus (RAD001); rapamycin (AY22989); simapimod; (5-{2,4-bis[(3*S*)-3-methylmorpholin-4-yl]pyrido[2,3-*d*]pyrimidin-7-yl}-2-methoxyphenyl)methanol (AZD8055); 2-amino-8-[*trans*-4-(2-hydroxyethoxy)cyclohexyl]-6-(6-methoxy-3-pyridinyl)-4-methyl-pyrido[2,3-*d*]pyrimidin-7(8*H*)-one (PF04691502); and *N*²-[1,4-dioxo-4-[[4-(4-oxo-8-phenyl-4*H*-1-benzopyran-2-yl)morpholinium-4-yl]methoxy]butyl]-L-arginylglycyl-L- α -aspartylL-serine- (SEQ ID NO: 272), inner salt (SF1126); and XL765.

[00478] In one embodiment, the kinase inhibitor is an mTOR inhibitor, e.g., rapamycin, and the rapamycin is administered at a dose of about 3 mg, 4 mg, 5 mg, 6 mg, 7 mg, 8 mg, 9 mg, 10 mg (e.g., 6 mg) daily for a period of time, e.g., daily for 21 day cycle cycle, or daily for 28 day cycle. In one embodiment, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 or more cycles of rapamycin are administered. In one embodiment, the kinase inhibitor is an mTOR inhibitor, e.g., everolimus and the everolimus is administered at a dose of about 2 mg, 2.5 mg, 3 mg, 4 mg, 5 mg, 6 mg, 7 mg, 8 mg, 9 mg, 10 mg, 11 mg, 12 mg, 13 mg, 14 mg, 15 mg (e.g., 10 mg) daily for a period of time, e.g., daily for 28 day cycle. In one embodiment, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 or more cycles of everolimus are administered.

[00479] In one embodiment, the kinase inhibitor is an MNK inhibitor selected from CGP052088; 4-amino-3-(p-fluorophenylamino)-pyrazolo [3,4-*d*] pyrimidine (CGP57380); cercosporamide; ETC-1780445-2; and 4-amino-5-(4-fluoroanilino)-pyrazolo [3,4-*d*] pyrimidine.

[00480] In one embodiment, the kinase inhibitor is a dual phosphatidylinositol 3-kinase (PI3K) and mTOR inhibitor selected from 2-Amino-8-[*trans*-4-(2-hydroxyethoxy)cyclohexyl]-6-(6-methoxy-3-pyridinyl)-4-methyl-pyrido[2,3-*d*]pyrimidin-7(8*H*)-one (PF-04691502); *N*-[4-[[4-(Dimethylamino)-1-piperidinyl]carbonyl]phenyl]-*N*¹-[4-(4,6-di-4-morpholinyl-1,3,5-triazin-2-yl)phenyl]urea (PF-05212384, PKI-587); 2-Methyl-2- {4-[3-methyl-2-oxo-8-(quinolin-3-yl)-2,3-

dihydro-1*H*-imidazo[4,5-*c*]quinolin-1-yl]phenyl} propanenitrile (BEZ-235); apitolisib (GDC-0980, RG7422); 2,4-Difluoro-N-{2-(methyloxy)-5-[4-(4-pyridazinyl)-6-quinolinyl]-3-pyridinyl}benzenesulfonamide (GSK2126458); 8-(6-methoxypyridin-3-yl)-3-methyl-1-(4-piperazin-1-yl)-3-(trifluoromethyl)phenyl)-1*H*-imidazo[4,5-*c*]quinolin-2(3*H*)-one Maleic acid (NVP-BGT226); 3-[4-(4-Morpholinylpyrido[3',2':4,5]furo[3,2-d]pyrimidin-2-yl]phenol (PI-103); 5-(9-isopropyl-8-methyl-2-morpholino-9*H*-purin-6-yl)pyrimidin-2-amine (VS-5584, SB2343); and N-[2-[(3,5-Dimethoxyphenyl)amino]quinoxalin-3-yl]-4-[(4-methyl-3-methoxyphenyl)carbonyl]aminophenylsulfonamide (XL765).

[00481] Drugs that inhibit either the calcium dependent phosphatase calcineurin (cyclosporine and FK506) or inhibit the p70S6 kinase that is important for growth factor induced signaling (rapamycin). (Liu *et al.*, Cell 66:807-815, 1991; Henderson *et al.*, Immun. 73:316-321, 1991; Bierer *et al.*, Curr. Opin. Immun. 5:763-773, 1993) can also be used. In a further aspect, the cell compositions of the present invention may be administered to a patient in conjunction with (e.g., before, simultaneously or following) bone marrow transplantation, T cell ablative therapy using chemotherapy agents such as, fludarabine, external-beam radiation therapy (XRT), cyclophosphamide, and/or antibodies such as OKT3 or CAMPATH. In one aspect, the cell compositions of the present invention are administered following B-cell ablative therapy such as agents that react with CD20, e.g., Rituxan. For example, in one embodiment, subjects may undergo standard treatment with high dose chemotherapy followed by peripheral blood stem cell transplantation. In certain embodiments, following the transplant, subjects receive an infusion of the expanded immune cells of the present invention. In an additional embodiment, expanded cells are administered before or following surgery.

[00482] In one embodiment, the subject can be administered an agent which reduces or ameliorates a side effect associated with the administration of a CAR-expressing cell. Side effects associated with the administration of a CAR-expressing cell include, but are not limited to CRS, and hemophagocytic lymphohistiocytosis (HLH), also termed Macrophage Activation Syndrome (MAS). Symptoms of CRS include high fevers, nausea, transient hypotension, hypoxia, and the like. CRS may include clinical constitutional signs and symptoms such as fever, fatigue, anorexia, myalgias, arthalgias, nausea, vomiting, and headache. CRS may include clinical skin signs and symptoms such as rash. CRS may include clinical gastrointestinal signs and symptoms such as nausea, vomiting and diarrhea. CRS may include clinical respiratory

signs and symptoms such as tachypnea and hypoxemia. CRS may include clinical cardiovascular signs and symptoms such as tachycardia, widened pulse pressure, hypotension, increased cardiac output (early) and potentially diminished cardiac output (late). CRS may include clinical coagulation signs and symptoms such as elevated d-dimer, hypofibrinogenemia with or without bleeding. CRS may include clinical renal signs and symptoms such as azotemia. CRS may include clinical hepatic signs and symptoms such as transaminitis and hyperbilirubinemia. CRS may include clinical neurologic signs and symptoms such as headache, mental status changes, confusion, delirium, word finding difficulty or frank aphasia, hallucinations, tremor, dysemetria, altered gait, and seizures.

[00483] Accordingly, the methods described herein can comprise administering a CAR-expressing cell described herein to a subject and further administering one or more agents to manage elevated levels of a soluble factor resulting from treatment with a CAR-expressing cell. In one embodiment, the soluble factor elevated in the subject is one or more of IFN- γ , TNF α , IL-2 and IL-6. In an embodiment, the factor elevated in the subject is one or more of IL-1, GM-CSF, IL-10, IL-8, IL-5 and fractalkine. Therefore, an agent administered to treat this side effect can be an agent that neutralizes one or more of these soluble factors. In one embodiment, the agent that neutralizes one or more of these soluble forms is an antibody or antigen binding fragment thereof. Examples of such agents include, but are not limited to a steroid (e.g., corticosteroid), an inhibitor of TNF α , and an inhibitor of IL-6. An example of a TNF α inhibitor is an anti-TNF α antibody molecule such as, infliximab, adalimumab, certolizumab pegol, and golimumab. Another example of a TNF α inhibitor is a fusion protein such as entanercept. Small molecule inhibitor of TNF α include, but are not limited to, xanthine derivatives (e.g. pentoxifylline) and bupropion. An example of an IL-6 inhibitor is an anti-IL-6 antibody molecule or an anti-IL-6 receptor antibody molecule such as tocilizumab (toc), sarilumab, elsilimomab, CNTO 328, ALD518/BMS-945429, CNTO 136, CPSI-2364, CDP6038, VX30, ARGX-109, FE301, and FM101. In one embodiment, the anti-IL-6 antibody molecule is tocilizumab. An example of an IL-1R based inhibitor is anakinra.

[00484] In some embodiment, the subject is administered a corticosteroid, such as, e.g., methylprednisolone, hydrocortisone, among others.

[00485] In some embodiments, the subject is administered a vasopressor, such as, e.g., norepinephrine, dopamine, phenylephrine, epinephrine, vasopressin, or a combination thereof.

[00486] In an embodiment, the subject can be administered an antipyretic agent. In an embodiment, the subject can be administered an analgesic agent.

[00487] In one embodiment, the subject can be administered an agent which enhances the activity or fitness of a CAR-expressing cell. For example, in one embodiment, the agent can be an agent which inhibits a molecule that modulates or regulates, e.g., inhibits, T cell function. In some embodiments, the molecule that modulates or regulates T cell function is an inhibitory molecule. Inhibitory molecules, e.g., Programmed Death 1 (PD1), can, in some embodiments, decrease the ability of a CAR-expressing cell to mount an immune effector response. Examples of inhibitory molecules include PD1, PD-L1, CTLA4, TIM3, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), LAG3, VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4 and TGFR beta. Inhibition of a molecule that modulates or regulates, e.g., inhibits, T cell function, e.g., by inhibition at the DNA, RNA or protein level, can optimize a CAR-expressing cell performance. . In embodiments, an agent, e.g., an inhibitory nucleic acid, e.g., a dsRNA, e.g., an siRNA or shRNA; or e.g., an inhibitory protein or system, e.g., a clustered regularly interspaced short palindromic repeats (CRISPR), a transcription-activator like effector nuclease (TALEN), or a zinc finger endonuclease (ZFN), e.g., as described herein, can be used to inhibit expression of a molecule that modulates or regulates, e.g., inhibits, T-cell function in the CAR-expressing cell. In an embodiment the agent is an shRNA. In an embodiment, the agent that modulates or regulates, e.g., inhibits, T-cell function is inhibited within a CAR-expressing cell. In these embodiments, a dsRNA molecule that inhibits expression of a molecule that modulates or regulates, e.g., inhibits, T-cell function is linked to the nucleic acid that encodes a component, e.g., all of the components, of the CAR. In an embodiment, a nucleic acid molecule that encodes a dsRNA molecule that inhibits expression of the molecule that modulates or regulates, e.g., inhibits, T-cell function is operably linked to a promoter, e.g., a H1- or a U6-derived promoter such that the dsRNA molecule that inhibits expression of the molecule that modulates or regulates, e.g., inhibits, T-cell function is expressed, e.g., is expressed within a CAR-expressing cell. See e.g., Tiscornia G., “Development of Lentiviral Vectors Expressing siRNA,” Chapter 3, in *Gene Transfer: Delivery and Expression of DNA and RNA* (eds. Friedmann and Rossi). Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, USA, 2007; Brummelkamp TR, *et al.*

(2002) *Science* 296: 550–553; Miyagishi M, *et al.* (2002) *Nat. Biotechnol.* 19: 497–500. In an embodiment the nucleic acid molecule that encodes a dsRNA molecule that inhibits expression of the molecule that modulates or regulates, e.g., inhibits, T-cell function is present on the same vector, e.g., a lentiviral vector, that comprises a nucleic acid molecule that encodes a component, e.g., all of the components, of the CAR. In such an embodiment, the nucleic acid molecule that encodes a dsRNA molecule that inhibits expression of the molecule that modulates or regulates, e.g., inhibits, T-cell function is located on the vector, e.g., the lentiviral vector, 5'- or 3'- to the nucleic acid that encodes a component, e.g., all of the components, of the CAR. The nucleic acid molecule that encodes a dsRNA molecule that inhibits expression of the molecule that modulates or regulates, e.g., inhibits, T-cell function can be transcribed in the same or different direction as the nucleic acid that encodes a component, e.g., all of the components, of the CAR. In an embodiment the nucleic acid molecule that encodes a dsRNA molecule that inhibits expression of the molecule that modulates or regulates, e.g., inhibits, T-cell function is present on a vector other than the vector that comprises a nucleic acid molecule that encodes a component, e.g., all of the components, of the CAR. In an embodiment, the nucleic acid molecule that encodes a dsRNA molecule that inhibits expression of the molecule that modulates or regulates, e.g., inhibits, T-cell function it transiently expressed within a CAR-expressing cell. In an embodiment, the nucleic acid molecule that encodes a dsRNA molecule that inhibits expression of the molecule that modulates or regulates, e.g., inhibits, T-cell function is stably integrated into the genome of a CAR-expressing cell. Figure 47 depicts examples of vectors for expressing a component, e.g., all of the components, of the CAR with a dsRNA molecule that inhibits expression of the molecule that modulates or regulates, e.g., inhibits, T-cell function.

[00488] Examples of dsRNA molecules useful for inhibiting expression of a molecule that modulates or regulates, e.g., inhibits, T-cell function, wherein the molecule that modulates or regulates, e.g., inhibits, T-cell function is PD-1 are provided below.

[00489] Provided in Table 16 below are the names of PDCD1 (PD1) RNAi agents (derived from their position in the mouse PDCD1 gene sequence NM_008798.2), along with the SEQ ID NOs: 280-327 representing the DNA sequence. Both sense (S) and antisense (AS) sequences are presented as 19mer and 21mer sequences are in this table. Also note that the position (PoS, e.g., 176) is derived from the position number in the mouse PDCD1 gene sequence NM_008798.2. SEQ ID NOs are indicated in groups of 12 that correspond with “sense 19” SEQ ID NOs: 280-

291; “sense 21” SEQ ID NOs: 292-303; “asense 21” SEQ ID NOs: 304-315; “asense 19” SEQ ID NOs: 316-327.

Table 16. Mouse PDCD1 (PD1) shRNA sequences

Position on NM_008798.2	Target region	Sense19	Sense21	Asense21	Asense19
176	CDS	GGAGGTCCCTC ACCTTCTA (SEQ ID NO: 280)	CTGGAGGTCCC TCACCTTCTA (SEQ ID NO: 292)	TAGAAGGTGAG GGACCTCCAG (SEQ ID NO: 304)	TAGAAGGTGAG GGACCTCC (SEQ ID NO: 316)
260	CDS	CGGAGGATCTT ATGCTGAA (SEQ ID NO: 281)	GTCGGAGGATC TTATGCTGAA (SEQ ID NO: 293)	TTCAGCATAAG ATCCTCCGAC (SEQ ID NO: 305)	TTCAGCATAAG ATCCTCCG (SEQ ID NO: 317)
359	CDS	CCCGCTTCCAG ATCATACA (SEQ ID NO: 282)	TGCCCGCTTCC AGATCATACA (SEQ ID NO: 294)	TGTATGATCTG GAAGCGGGCA (SEQ ID NO: 306)	TGTATGATCTG GAAGCGGG (SEQ ID NO: 318)
528	CDS	GGAGACCTCAA CAAGATAT (SEQ ID NO: 283)	CTGGAGACCTC AACAAAGATAT (SEQ ID NO: 295)	ATATCTTGTG AGGTCTCCAG (SEQ ID NO: 307)	ATATCTTGTG AGGTCTCC (SEQ ID NO: 319)
581	CDS	AAGGCATGGTC ATTGGTAT (SEQ ID NO: 284)	TCAAGGCATGG TCATTGGTAT (SEQ ID NO: 296)	ATACCAATGAC CATGCCTTGA (SEQ ID NO: 308)	ATACCAATGAC CATGCCTT (SEQ ID NO: 320)
584	CDS	GCATGGTCATT GGTATCAT (SEQ ID NO: 285)	AGGCATGGTCA TTGGTATCAT (SEQ ID NO: 297)	ATGATACCAAT GACCATGCCT (SEQ ID NO: 309)	ATGATACCAAT GACCATGC (SEQ ID NO: 321)
588	CDS	GGTCATTGGTA TCATGAGT (SEQ ID NO: 286)	ATGGTCATTGG TATCATGAGT (SEQ ID NO: 298)	ATGGTCATTGG TATCATGAGT (SEQ ID NO: 310)	ATGGTCATTGG TATCATGA (SEQ ID NO: 322)
609	CDS	CCTAGTGGGT TCCCTGTA (SEQ ID NO: 287)	GCCCTAGTGG GTATCCCTGTA (SEQ ID NO: 299)	GCCCTAGTGG GTATCCCTGTA (SEQ ID NO: 311)	GCCCTAGTGG GTATCCCTG (SEQ ID NO: 323)
919	CDS	GAGGATGGACA TTGTTCTT (SEQ ID NO: 288)	ATGAGGATGGA CATTGTTCTT (SEQ ID NO: 300)	ATGAGGATGGA CATTGTTCTT (SEQ ID NO: 312)	ATGAGGATGGA CATTGTT (SEQ ID NO: 324)
1021	3'UTR	GCATGCAGGCT ACAGTTCA (SEQ ID NO: 289)	GAGCATGCAG GCTACAGTTCA (SEQ ID NO: 301)	GAGCATGCAG GCTACAGTTCA (SEQ ID NO: 313)	GAGCATGCAG GCTACAGTT (SEQ ID NO: 325)
1097	3'UTR	CCAGCACATGC ACTGTTGA (SEQ ID NO: 290)	TTCCAGCACAT GCACTGTTGA (SEQ ID NO: 302)	TTCCAGCACAT GCACTGTTGA (SEQ ID NO: 314)	TTCCAGCACAT GCACTGTT (SEQ ID NO: 326)
1101	3'UTR	CACATGCACTG	AGCACATGCAC	AGCACATGCAC	AGCACATGCAC

		TTGAGTGA (SEQ ID NO: 291)	TGTTGAGTGA (SEQ ID NO: 303)	TGTTGAGTGA (SEQ ID NO: 315)	TGTTGAGT (SEQ ID NO: 327)
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Provided in Table 17 below are the names of PDCD1 (PD1) shRNA agents (derived from their position in the human PDCD1 gene sequence, along with the SEQ ID NOs. 323-370 representing the DNA sequence. Both sense (S) and antisense (AS) sequences are presented as 19mer and 21mer sequences. SEQ ID NOs are indicated in groups of 12 that correspond with “sense 19” SEQ ID NOs: 328-339; “sense 21” SEQ ID NOs: 340-351; “asense 21” SEQ ID NOs: 352-363; “asense 19” SEQ ID NOs: 364-375.

Table 17. Human PDCD1 (PD1) shRNA sequences

Position on NM_0050 18.2	Target region	Sense19	Asense19	Sense21	Asense21
145	CDS	GGCCAGGATG GTTCTTAGA (SEQ ID NO: 328)	TCTAAGAACCA TCCTGGCC (SEQ ID NO: 340)	GCGGCCAGGA TGGTTCTTAGA (SEQ ID NO: 352)	TCTAAGAACCA TCCTGGCCGC (SEQ ID NO: 364)
271	CDS	GCTTCGTGCTA AACTGGTA (SEQ ID NO: 329)	TACCAAGTTAG CACGAAGC (SEQ ID NO: 341)	GAGCTTCGTGC TAAACTGGTA (SEQ ID NO: 353)	TACCAAGTTAG CACGAAGCTC (SEQ ID NO: 365)
393	CDS	GGCGGTGACTT CCACATGA (SEQ ID NO: 330)	TCATGTGGAAG TCACGCC (SEQ ID NO: 342)	ACGGGCGTGA CTTCCACATGA (SEQ ID NO: 354)	TCATGTGGAAG TCACGCCGT (SEQ ID NO: 366)
1497	3'UTR	CAGGCCTAGAG AAGTTCA (SEQ ID NO: 331)	TGAAACTTCTC TAGGCCTG (SEQ ID NO: 343)	TGCAGGCCTAG AGAAGTTCA (SEQ ID NO: 355)	TGAAACTTCTC TAGGCCTGCA (SEQ ID NO: 367)
1863	3'UTR	CTTGGAACCCA TTCCTGAA (SEQ ID NO: 332)	TTCAAGGAATGG GTTCCAAG (SEQ ID NO: 344)	TCCTTGGAACCC CATTCCTGAA (SEQ ID NO: 356)	TTCAGGAATGG GTTCCAAGGA (SEQ ID NO: 368)
1866	3'UTR	GGAACCCATTTC CTGAAATT (SEQ ID NO: 333)	AATTCAGGAA TGGGTTCC (SEQ ID NO: 345)	TTGGAACCCATT TCCTGAAATT (SEQ ID NO: 357)	AATTCAGGAA TGGGTTCCAA (SEQ ID NO: 369)
1867	3'UTR	GAACCCATTCC TGAAATTAA (SEQ ID NO: 334)	TAATTCAGGA ATGGGTT (SEQ ID NO: 346)	TGGAACCCATT CCTGAAATTAA (SEQ ID NO: 358)	TAATTCAGGA ATGGGTTCCA (SEQ ID NO: 370)
1868	3'UTR	AACCCATTCC GAAATTAT (SEQ ID NO: 335)	ATAATTCAGG AATGGGTT (SEQ ID NO: 347)	GGAACCCATT CTGAAATTAT (SEQ ID NO: 359)	ATAATTCAGG AATGGGTTCC (SEQ ID NO:371)
1869	3'UTR	ACCCATTCC GAAATTAA (SEQ ID NO: 336)	AATAATTCAG GAACCCATTCC (SEQ ID NO: 360)	GAACCCATTCC AATAATTCAG (SEQ ID NO: 372)	AATAATTCAG AATGGGTTCC (SEQ ID NO: 373)

		AAATTATT (SEQ ID NO: 336)	GAATGGGT (SEQ ID NO: 348)	TGAAATTATT (SEQ ID NO: 360)	GAATGGGTTC (SEQ ID NO: 372)
1870	3'UTR	CCCATTCCTGA AATTATTT (SEQ ID NO: 337)	AAATAATTTCA GGAATGGG (SEQ ID NO: 349)	AACCCATTCCCT GAAATTATTT (SEQ ID NO: 361)	AAATAATTTCA GGAATGGGTT (SEQ ID NO: 373)
2079	3'UTR	CTGTGGTTCTA TTATATTA (SEQ ID NO: 338)	TAATATAATAGA ACCACAG (SEQ ID NO: 350)	CCCTGTGGTTC TATTATATTA (SEQ ID NO: 362)	TAATATAATAGA ACCACAGGG (SEQ ID NO: 374)
2109	3'UTR	AAATATGAGAG CATGCTAA (SEQ ID NO: 339)	TTAGCATGCTC TCATATT (SEQ ID NO: 351)	TTAAATATGAG AGCATGCTAA (SEQ ID NO: 363)	TTAGCATGCTC TCATATTAA (SEQ ID NO: 375)

[00490] In one embodiment, the inhibitor of an inhibitory signal can be, e.g., an antibody or antibody fragment that binds to an inhibitory molecule. For example, the agent can be an antibody or antibody fragment that binds to PD1, PD-L1, PD-L2 or CTLA4 (e.g., ipilimumab (also referred to as MDX-010 and MDX-101, and marketed as Yervoy®; Bristol-Myers Squibb; Tremelimumab (IgG2 monoclonal antibody available from Pfizer, formerly known as ticilimumab, CP-675,206)). In an embodiment, the agent is an antibody or antibody fragment that binds to TIM3. In an embodiment, the agent is an antibody or antibody fragment that binds to LAG3.

[00491] PD-1 is an inhibitory member of the CD28 family of receptors that also includes CD28, CTLA-4, ICOS, and BTLA. PD-1 is expressed on activated B cells, T cells and myeloid cells (Agata et al. 1996 *Int. Immunol.* 8:765-75). Two ligands for PD-1, PD-L1 and PD-L2 have been shown to downregulate T cell activation upon binding to PD-1 (Freeman et al. 2000 *J Exp Med* 192:1027-34; Latchman et al. 2001 *Nat Immunol* 2:261-8; Carter et al. 2002 *Eur J Immunol* 32:634-43). PD-L1 is abundant in human cancers (Dong et al. 2003 *J Mol Med* 81:281-7; Blank et al. 2005 *Cancer Immunol. Immunother* 54:307-314; Konishi et al. 2004 *Clin Cancer Res* 10:5094). Immune suppression can be reversed by inhibiting the local interaction of PD-1 with PD-L1. Antibodies, antibody fragments, and other inhibitors of PD-1, PD-L1 and PD-L2 are available in the art and may be used combination with a CAR of the present invention described herein. For example, nivolumab (also referred to as BMS-936558 or MDX1106; Bristol-Myers Squibb) is a fully human IgG4 monoclonal antibody which specifically blocks PD-1. Nivolumab

(clone 5C4) and other human monoclonal antibodies that specifically bind to PD-1 are disclosed in US 8,008,449 and WO2006/121168. Pidilizumab (CT-011; Cure Tech) is a humanized IgG1k monoclonal antibody that binds to PD-1. Pidilizumab and other humanized anti-PD-1 monoclonal antibodies are disclosed in WO2009/101611. Pembrolizumab (formerly known as lambrolizumab, and also referred to as MK03475; Merck) is a humanized IgG4 monoclonal antibody that binds to PD-1. Pembrolizumab and other humanized anti-PD-1 antibodies are disclosed in US 8,354,509 and WO2009/114335. MEDI4736 (Medimmune) is a human monoclonal antibody that binds to PDL1, and inhibits interaction of the ligand with PD1. MDPL3280A (Genentech / Roche) is a human Fc optimized IgG1 monoclonal antibody that binds to PD-L1. MDPL3280A and other human monoclonal antibodies to PD-L1 are disclosed in U.S. Patent No.: 7,943,743 and U.S Publication No.: 20120039906. Other anti-PD-L1 binding agents include YW243.55.S70 (heavy and light chain variable regions are shown in SEQ ID NOs 20 and 21 in WO2010/077634) and MDX-1 105 (also referred to as BMS-936559, and, e.g., anti-PD-L1 binding agents disclosed in WO2007/005874). AMP-224 (B7-DC Ig; Amplimmune; e.g., disclosed in WO2010/027827 and WO2011/066342), is a PD-L2 Fc fusion soluble receptor that blocks the interaction between PD-1 and B7-H1. Other anti-PD-1 antibodies include AMP 514 (Amplimmune), among others, e.g., anti-PD-1 antibodies disclosed in US 8,609,089, US 2010028330, and/or US 20120114649.

[00492] TIM3 (T cell immunoglobulin-3) also negatively regulates T cell function, particularly in IFN- γ -secreting CD4+ T helper 1 and CD8+ T cytotoxic 1 cells, and plays a critical role in T cell exhaustion. Inhibition of the interaction between TIM3 and its ligands, e.g., galectin-9 (Gal9), phosphotidylserine (PS), and HMGB1, can increase immune response. Antibodies, antibody fragments, and other inhibitors of TIM3 and its ligands are available in the art and may be used combination with a CD19 CAR described herein. For example, antibodies, antibody fragments, small molecules, or peptide inhibitors that target TIM3 binds to the IgV domain of TIM3 to inhibit interaction with its ligands. Antibodies and peptides that inhibit TIM3 are disclosed in WO2013/006490 and US20100247521. Other anti-TIM3 antibodies include humanized versions of RMT3-23 (disclosed in Ngiow et al., 2011, Cancer Res, 71:3540-3551), and clone 8B.2C12 (disclosed in Monney et al., 2002, Nature, 415:536-541). Bi-specific antibodies that inhibit TIM3 and PD-1 are disclosed in US20130156774.

[00493] In other embodiments, the agent which enhances the activity of a CAR-expressing cell is a CEACAM inhibitor (e.g., CEACAM-1, CEACAM-3, and/or CEACAM-5 inhibitor). In one embodiment, the inhibitor of CEACAM is an anti-CEACAM antibody molecule. Exemplary anti-CEACAM-1 antibodies are described in WO 2010/125571, WO 2013/082366 WO 2014/059251 and WO 2014/022332, e.g., a monoclonal antibody 34B1, 26H7, and 5F4; or a recombinant form thereof, as described in, e.g., US 2004/0047858, US 7,132,255 and WO 99/052552. In other embodiments, the anti-CEACAM antibody binds to CEACAM-5 as described in, e.g., Zheng et al. *PLoS One*. 2010 Sep 2;5(9). pii: e12529 (DOI:10.1371/journal.pone.0021146), or crossreacts with CEACAM-1 and CEACAM-5 as described in, e.g., WO 2013/054331 and US 2014/0271618.

[00494] Without wishing to be bound by theory, carcinoembryonic antigen cell adhesion molecules (CEACAM), such as CEACAM-1 and CEACAM-5, are believed to mediate, at least in part, inhibition of an anti-tumor immune response (see e.g., Markel et al. *J Immunol*. 2002 Mar 15;168(6):2803-10; Markel et al. *J Immunol*. 2006 Nov 1;177(9):6062-71; Markel et al. *Immunology*. 2009 Feb;126(2):186-200; Markel et al. *Cancer Immunol Immunother*. 2010 Feb;59(2):215-30; Ortenberg et al. *Mol Cancer Ther*. 2012 Jun;11(6):1300-10; Stern et al. *J Immunol*. 2005 Jun 1;174(11):6692-701; Zheng et al. *PLoS One*. 2010 Sep 2;5(9). pii: e12529). For example, CEACAM-1 has been described as a heterophilic ligand for TIM-3 and as playing a role in TIM-3-mediated T cell tolerance and exhaustion (see e.g., WO 2014/022332; Huang, et al. (2014) *Nature* doi:10.1038/nature13848). In embodiments, co-blockade of CEACAM-1 and TIM-3 has been shown to enhance an anti-tumor immune response in xenograft colorectal cancer models (see e.g., WO 2014/022332; Huang, et al. (2014), *supra*). In other embodiments, co-blockade of CEACAM-1 and PD-1 reduce T cell tolerance as described, e.g., in WO 2014/059251. Thus, CEACAM inhibitors can be used with the other immunomodulators described herein (e.g., anti-PD-1 and/or anti-TIM-3 inhibitors) to enhance an immune response against a cancer, e.g., a melanoma, a lung cancer (e.g., NSCLC), a bladder cancer, a colon cancer an ovarian cancer, and other cancers as described herein

[00495] LAG3 (lymphocyte activation gene-3 or CD223) is a cell surface molecule expressed on activated T cells and B cells that has been shown to play a role in CD8+ T cell exhaustion. Antibodies, antibody fragments, and other inhibitors of LAG3 and its ligands are available in the art and may be used combination with a CD19 CAR described herein. For example, BMS-

986016 (Bristol-Myers Squib) is a monoclonal antibody that targets LAG3. IMP701 (Immune) is an antagonist LAG3 antibody and IMP731 (Immune and GlaxoSmithKline) is a depleting LAG3 antibody. Other LAG3 inhibitors include IMP321 (Immune), which is a recombinant fusion protein of a soluble portion of LAG3 and Ig that binds to MHC class II molecules and activates antigen presenting cells (APC). Other antibodies are disclosed, e.g., in WO2010/019570.

[00496] In some embodiments, the agent which enhances the activity of a CAR-expressing cell can be, e.g., a fusion protein comprising a first domain and a second domain, wherein the first domain is an inhibitory molecule, or fragment thereof, and the second domain is a polypeptide that is associated with a positive signal, e.g., a polypeptide comprising an intracellular signaling domain as described herein. In some embodiments, the polypeptide that is associated with a positive signal can include a costimulatory domain of CD28, CD27, ICOS, e.g., an intracellular signaling domain of CD28, CD27 and/or ICOS, and/or a primary signaling domain, e.g., of CD3 zeta, e.g., described herein. In one embodiment, the fusion protein is expressed by the same cell that expressed the CAR. In another embodiment, the fusion protein is expressed by a cell, e.g., a T cell that does not express a mesothelin CAR.

[00497] In one embodiment, the agent which enhances activity of a CAR-expressing cell described herein is miR-17-92.

Combination with a low dose of an mTOR inhibitor

[00498] In one embodiment, the cells expressing a CAR molecule, e.g., a CAR molecule described herein, are administered in combination with a low, immune enhancing dose of an mTOR inhibitor.

[00499] In an embodiment, a dose of an mTOR inhibitor is associated with, or provides, mTOR inhibition of at least 5 but no more than 90%, at least 10 but no more than 90%, at least 15, but no more than 90%, at least 20 but no more than 90%, at least 30 but no more than 90%, at least 40 but no more than 90%, at least 50 but no more than 90%, at least 60 but no more than 90%, or at least 70 but no more than 90%.

[00500] In an embodiment, a dose of an mTOR inhibitor is associated with, or provides, mTOR inhibition of at least 5 but no more than 80%, at least 10 but no more than 80%, at least

15, but no more than 80%, at least 20 but no more than 80%, at least 30 but no more than 80%, at least 40 but no more than 80%, at least 50 but no more than 80%, or at least 60 but no more than 80%.

[00501] In an embodiment, a dose of an mTOR inhibitor is associated with, or provides, mTOR inhibition of at least 5 but no more than 70%, at least 10 but no more than 70%, at least 15, but no more than 70%, at least 20 but no more than 70%, at least 30 but no more than 70%, at least 40 but no more than 70%, or at least 50 but no more than 70%.

[00502] In an embodiment, a dose of an mTOR inhibitor is associated with, or provides, mTOR inhibition of at least 5 but no more than 60%, at least 10 but no more than 60%, at least 15, but no more than 60%, at least 20 but no more than 60%, at least 30 but no more than 60%, or at least 40 but no more than 60%.

[00503] In an embodiment, a dose of an mTOR inhibitor is associated with, or provides, mTOR inhibition of at least 5 but no more than 50%, at least 10 but no more than 50%, at least 15, but no more than 50%, at least 20 but no more than 50%, at least 30 but no more than 50%, or at least 40 but no more than 50%.

[00504] In an embodiment, a dose of an mTOR inhibitor is associated with, or provides, mTOR inhibition of at least 5 but no more than 40%, at least 10 but no more than 40%, at least 15, but no more than 40%, at least 20 but no more than 40%, at least 30 but no more than 40%, or at least 35 but no more than 40%.

[00505] In an embodiment, a dose of an mTOR inhibitor is associated with, or provides, mTOR inhibition of at least 5 but no more than 30%, at least 10 but no more than 30%, at least 15, but no more than 30%, at least 20 but no more than 30%, or at least 25 but no more than 30%.

[00506] In an embodiment, a dose of an mTOR inhibitor is associated with, or provides, mTOR inhibition of at least 1, 2, 3, 4 or 5 but no more than 20%, at least 1, 2, 3, 4 or 5 but no more than 30%, at least 1, 2, 3, 4 or 5, but no more than 35, at least 1, 2, 3, 4 or 5 but no more than 40%, or at least 1, 2, 3, 4 or 5 but no more than 45%.

[00507] In an embodiment, a dose of an mTOR inhibitor is associated with, or provides, mTOR inhibition of at least 1, 2, 3, 4 or 5 but no more than 90%.

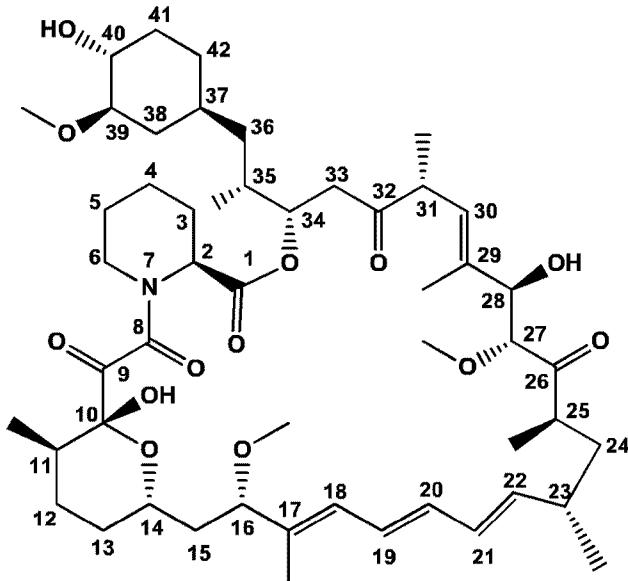
[00508] As is discussed herein, the extent of mTOR inhibition can be expressed as the extent of P70 S6 inhibition, e.g., the extent of mTOR inhibition can be determined by the level of decrease in P70 S6 activity, e.g., by the decrease in phosphorylation of a P70 S6 substrate. The level of mTOR inhibition can be evaluated by a method described herein, e.g. by the Boulay assay.

EXEMPLARY mTOR INHIBITORS

[00509] As used herein, the term “mTOR inhibitor” refers to a compound or ligand, or a pharmaceutically acceptable salt thereof, which inhibits the mTOR kinase in a cell. In an embodiment an mTOR inhibitor is an allosteric inhibitor. In an embodiment an mTOR inhibitor is a catalytic inhibitor.

[00510] Allosteric mTOR inhibitors include the neutral tricyclic compound rapamycin (sirolimus), rapamycin-related compounds, that is compounds having structural and functional similarity to rapamycin including, e.g., rapamycin derivatives, rapamycin analogs (also referred to as rapalogs) and other macrolide compounds that inhibit mTOR activity.

[00511] Rapamycin is a known macrolide antibiotic produced by *Streptomyces hygroscopicus* having the structure shown in Formula A.



[00512]

(A)

[00513] See, e.g., McAlpine, J.B., et al., *J. Antibiotics* (1991) 44: 688; Schreiber, S.L., et al., *J. Am. Chem. Soc.* (1991) 113: 7433; U.S. Patent No. 3,929,992. There are various numbering schemes proposed for rapamycin. To avoid confusion, when specific rapamycin analogs are named herein, the names are given with reference to rapamycin using the numbering scheme of formula A.

[00514] Rapamycin analogs useful in the invention are, for example, O-substituted analogs in which the hydroxyl group on the cyclohexyl ring of rapamycin is replaced by OR₁ in which R₁ is hydroxyalkyl, hydroxyalkoxyalkyl, acylaminoalkyl, or aminoalkyl; e.g. RAD001, also known as, everolimus as described in US 5,665,772 and WO94/09010 the contents of which are incorporated by reference. Other suitable rapamycin analogs include those substituted at the 26- or 28-position. The rapamycin analog may be an epimer of an analog mentioned above, particularly an epimer of an analog substituted in position 40, 28 or 26, and may optionally be further hydrogenated, e.g. as described in US 6,015,815, WO95/14023 and WO99/15530 the contents of which are incorporated by reference, e.g. ABT578 also known as zotarolimus or a rapamycin analog described in US 7,091,213, WO98/02441 and WO01/14387 the contents of which are incorporated by reference, e.g. AP23573 also known as ridaforolimus.

[00515] Examples of rapamycin analogs suitable for use in the present invention from US 5,665,772 include, but are not limited to, 40-O-benzyl-rapamycin, 40-O-(4'-hydroxymethyl)benzyl-rapamycin, 40-O-[4'-(1,2-dihydroxyethyl)]benzyl-rapamycin, 40-O-allyl-rapamycin, 40-O-[3'-(2,2-dimethyl-1,3-dioxolan-4(S)-yl)-prop-2'-en-1'-yl]-rapamycin, (2'E,4'S)-40-O-(4',5'-dihydroxypent-2'-en-1'-yl)-rapamycin, 40-O-(2-hydroxy)ethoxycarbonylmethyl-rapamycin, 40-O-(2-hydroxy)ethyl-rapamycin, 40-O-(3-hydroxy)propyl-rapamycin, 40-O-(6-hydroxy)hexyl-rapamycin, 40-O-[2-(2-hydroxy)ethoxy]ethyl-rapamycin, 40-O-[(3S)-2,2-dimethyldioxolan-3-yl]methyl-rapamycin, 40-O-[(2S)-2,3-dihydroxyprop-1-yl]-rapamycin, 40-O-(2-acetoxy)ethyl-rapamycin, 40-O-(2-nicotinoyloxy)ethyl-rapamycin, 40-O-[2-(N-morpholino)acetoxy]ethyl-rapamycin, 40-O-(2-N-imidazolylacetoxyl)ethyl-rapamycin, 40-O-[2-(N-methyl-N'-piperazinyl)acetoxy]ethyl-rapamycin, 39-O-desmethyl-39,40-O,O-ethylene-rapamycin, (26R)-26-dihydro-40-O-(2-hydroxy)ethyl-rapamycin, 40-O-(2-aminoethyl)-rapamycin, 40-O-(2-acetaminoethyl)-rapamycin, 40-O-(2-nicotinamidoethyl)-rapamycin, 40-O-(2-(N-methyl-imidazo-2'-

ylcarbethoxamido)ethyl)-rapamycin, 40-O-(2-ethoxycarbonylaminoethyl)-rapamycin, 40-O-(2-tolylsulfonamidoethyl)-rapamycin and 40-O-[2-(4',5'-dicarboethoxy-1',2',3'-triazol-1'-yl)-ethyl]-rapamycin.

[00516] Other rapamycin analogs useful in the present invention are analogs where the hydroxyl group on the cyclohexyl ring of rapamycin and/or the hydroxy group at the 28 position is replaced with an hydroxyester group are known, for example, rapamycin analogs found in US RE44,768, e.g. temsirolimus.

[00517] Other rapamycin analogs useful in the present invention include those wherein the methoxy group at the 16 position is replaced with another substituent, preferably (optionally hydroxy-substituted) alkynloxy, benzyl, orthomethoxybenzyl or chlorobenzyl and/or wherein the methoxy group at the 39 position is deleted together with the 39 carbon so that the cyclohexyl ring of rapamycin becomes a cyclopentyl ring lacking the 39 position methoxy group; e.g. as described in WO95/16691 and WO96/41807 the contents of which are incorporated by reference. The analogs can be further modified such that the hydroxy at the 40-position of rapamycin is alkylated and/or the 32-carbonyl is reduced.

[00518] Rapamycin analogs from WO95/16691 include, but are not limited to, 16-demethoxy-16-(pent-2-ynyl)oxy-rapamycin, 16-demethoxy-16-(but-2-ynyl)oxy-rapamycin, 16-demethoxy-16-(propargyl)oxy-rapamycin, 16-demethoxy-16-(4-hydroxy-but-2-ynyl)oxy-rapamycin, 16-demethoxy-16-benzylloxy-40-O-(2-hydroxyethyl)-rapamycin, 16-demethoxy-16-benzylloxy-rapamycin, 16-demethoxy-16-ortho-methoxybenzyl-rapamycin, 16-demethoxy-40-O-(2-methoxyethyl)-16-pent-2-ynyl)oxy-rapamycin, 39-demethoxy-40-desoxy-39-formyl-42-nor-rapamycin, 39-demethoxy-40-desoxy-39-hydroxymethyl-42-nor-rapamycin, 39-demethoxy-40-desoxy-39-carboxy-42-nor-rapamycin, 39-demethoxy-40-desoxy-39-(4-methyl-piperazin-1-yl)carbonyl-42-nor-rapamycin, 39-demethoxy-40-desoxy-39-(morpholin-4-yl)carbonyl-42-nor-rapamycin, 39-demethoxy-40-desoxy-39-[N-methyl, N-(2-pyridin-2-yl-ethyl)]carbamoyl-42-nor-rapamycin and 39-demethoxy-40-desoxy-39-(p-toluenesulfonylhydrazonomethyl)-42-nor-rapamycin.

[00519] Rapamycin analogs from WO96/41807 include, but are not limited to, 32-deoxo-rapamycin, 16-O-pent-2-ynyl-32-deoxo-rapamycin, 16-O-pent-2-ynyl-32-deoxo-40-O-(2-hydroxy-ethyl)-rapamycin, 16-O-pent-2-ynyl-32-(S)-dihydro-40-O-(2-hydroxyethyl)-

rapamycin, 32(S)-dihydro-40-O-(2-methoxy)ethyl-rapamycin and 32(S)-dihydro-40-O-(2-hydroxyethyl)-rapamycin.

[00520] Another suitable rapamycin analog is umirolimus as described in US2005/0101624 the contents of which are incorporated by reference.

[00521] RAD001, otherwise known as everolimus (Afinitor®), has the chemical name (1R,9S,12S,15R,16E,18R,19R,21R,23S,24E,26E,28E,30S,32S,35R)-1,18-dihydroxy-12-((1R)-2-[(1S,3R,4R)-4-(2-hydroxyethoxy)-3-methoxycyclohexyl]-1-methylethyl}-19,30-dimethoxy-15,17,21,23,29,35-hexamethyl-11,36-dioxa-4-aza-tricyclo[30.3.1.04,9]hexatriaconta-16,24,26,28-tetraene-2,3,10,14,20-pentaone

[00522] Further examples of allosteric mTOR inhibitors include sirolimus (rapamycin, AY-22989), 40-[3-hydroxy-2-(hydroxymethyl)-2-methylpropanoate]-rapamycin (also called temsirolimus or CCI-779) and ridaforolimus (AP-23573/MK-8669). Other examples of allosteric mTor inhibtors include zotarolimus (ABT578) and umirolimus.

[00523] Alternatively or additionally, catalytic, ATP-competitive mTOR inhibitors have been found to target the mTOR kinase domain directly and target both mTORC1 and mTORC2. These are also more effective inhibitors of mTORC1 than such allosteric mTOR inhibitors as rapamycin, because they modulate rapamycin-resistant mTORC1 outputs such as 4EBP1-T37/46 phosphorylation and cap-dependent translation.

[00524] Catalytic inhibitors include: BEZ235 or 2-methyl-2-[4-(3-methyl-2-oxo-8-quinolin-3-yl-2,3-dihydro-imidazo[4,5-c]quinolin-1-yl)-phenyl]-propionitrile, or the monotosylate salt form. the synthesis of BEZ235 is described in WO2006/122806; CCG168 (otherwise known as AZD-8055, Chresta, C.M., et al., Cancer Res, 2010, 70(1), 288-298) which has the chemical name {5-[2,4-bis-((S)-3-methyl-morpholin-4-yl)-pyrido[2,3d]pyrimidin-7-yl]-2-methoxy-phenyl}-methanol; 3-[2,4-bis[(3S)-3-methylmorpholin-4-yl]pyrido[2,3-d]pyrimidin-7-yl]-N-methylbenzamide (WO09104019); 3-(2-aminobenzo[d]oxazol-5-yl)-1-isopropyl-1H-pyrazolo[3,4-d]pyrimidin-4-amine (WO10051043 and WO2013023184); A N-(3-(N-(3-((3,5-dimethoxyphenyl)amino)quinoxaline-2-yl)sulfamoyl)phenyl)-3-methoxy-4-methylbenzamide (WO07044729 and WO12006552); PKI-587 (Venkatesan, A.M., J. Med. Chem., 2010, 53, 2636-2645) which has the chemical name 1-[4-[4-(dimethylamino)piperidine-1-carbonyl]phenyl]-3-[4-(4,6-dimorpholino-1,3,5-triazin-2-yl)phenyl]urea; GSK-2126458 (ACS Med. Chem. Lett., 2010, 1, 39-43) which has the chemical name 2,4-difluoro-N-{2-methoxy-5-[4-(4-pyridazinyl)-6-

quinolinyl]-3-pyridinyl}benzenesulfonamide; ; 5-(9-isopropyl-8-methyl-2-morpholino-9H-purin-6-yl)pyrimidin-2-amine (WO10114484); (E)-N-(8-(6-amino-5-(trifluoromethyl)pyridin-3-yl)-1-(6-(2-cyanopropan-2-yl)pyridin-3-yl)-3-methyl-1H-imidazo[4,5-c]quinolin-2(3H)-ylidene)cyanamide (WO12007926).

[00525] Further examples of catalytic mTOR inhibitors include 8-(6-methoxy-pyridin-3-yl)-3-methyl-1-(4-piperazin-1-yl-3-trifluoromethyl-phenyl)-1,3-dihydro-imidazo[4,5-c]quinolin-2-one (WO2006/122806) and Ku-0063794 (Garcia-Martinez JM, et al., Biochem J., 2009, 421(1), 29-42.. Ku-0063794 is a specific inhibitor of the mammalian target of rapamycin (mTOR.) WYE-354 is another example of a catalytic mTor inhibitor (Yu K, et al. (2009). Biochemical, Cellular, and In vivo Activity of Novel ATP-Competitive and Selective Inhibitors of the Mammalian Target of Rapamycin. Cancer Res. 69(15): 6232-6240).

[00526] mTOR inhibitors useful according to the present invention also include prodrugs, derivatives, pharmaceutically acceptable salts, or analogs thereof of any of the foregoing.

[00527] mTOR inhibitors, such as RAD001, may be formulated for delivery based on well-established methods in the art based on the particular dosages described herein. In particular, US Patent 6,004,973 (incorporated herein by reference) provides examples of formulations useable with the mTOR inhibitors described herein.

EVALUATION OF MTOR INHIBITION

[00528] mTOR phosphorylates the kinase P70 S6, thereby activating P70 S6 kinase and allowing it to phosphorylate its substrate. The extent of mTOR inhibition can be expressed as the extent of P70 S6 kinase inhibition, e.g., the extent of mTOR inhibition can be determined by the level of decrease in P70 S6 kinase activity, e.g., by the decrease in phosphorylation of a P70 S6 kinase substrate. One can determine the level of mTOR inhibition, by measuring P70 S6 kinase activity (the ability of P70 S6 kinase to phosphorylate a substrate), in the absence of inhibitor, e.g., prior to administration of inhibitor, and in the presence of inhibitor, or after the administration of inhibitor. The level of inhibition of P70 S6 kinase gives the level of mTOR inhibition. Thus, if P70 S6 kinase is inhibited by 40%, mTOR activity, as measured by P70 S6 kinase activity, is inhibited by 40%. The extent or level of inhibition referred to herein is the average level of inhibition over the dosage interval. By way of example, if the inhibitor is given

once per week, the level of inhibition is given by the average level of inhibition over that interval, namely a week.

[00529] Boulay et al., Cancer Res, 2004, 64:252-61, hereby incorporated by reference, teaches an assay that can be used to assess the level of mTOR inhibition (referred to herein as the Boulay assay). In an embodiment, the assay relies on the measurement of P70 S6 kinase activity from biological samples before and after administration of an mTOR inhibitor, e.g., RAD001.

Samples can be taken at preselected times after treatment with an mTOR inhibitor, e.g., 24, 48, and 72 hours after treatment. Biological samples, e.g., from skin or peripheral blood mononuclear cells (PBMCs) can be used. Total protein extracts are prepared from the samples. P70 S6 kinase is isolated from the protein extracts by immunoprecipitation using an antibody that specifically recognizes the P70 S6 kinase. Activity of the isolated P70 S6 kinase can be measured in an in vitro kinase assay. The isolated kinase can be incubated with 40S ribosomal subunit substrates (which is an endogenous substrate of P70 S6 kinase) and gamma-³²P under conditions that allow phosphorylation of the substrate. Then the reaction mixture can be resolved on an SDS-PAGE gel, and ³²P signal analyzed using a PhosphorImager. A ³²P signal corresponding to the size of the 40S ribosomal subunit indicates phosphorylated substrate and the activity of P70 S6 kinase. Increases and decreases in kinase activity can be calculated by quantifying the area and intensity of the ³²P signal of the phosphorylated substrate (e.g., using ImageQuant, Molecular Dynamics), assigning arbitrary unit values to the quantified signal, and comparing the values from after administration with values from before administration or with a reference value. For example, percent inhibition of kinase activity can be calculated with the following formula: 1-(value obtained after administration/value obtained before administration) X 100. As described above, the extent or level of inhibition referred to herein is the average level of inhibition over the dosage interval.

[00530] Methods for the evaluation of kinase activity, e.g., P70 S6 kinase activity, are also provided in US 7,727,950, hereby incorporated by reference.

[00531] The level of mTOR inhibition can also be evaluated by a change in the ration of PD1 negative to PD1 positive T cells. T cells from peripheral blood can be identified as PD1 negative or positive by art-known methods.

Low-Dose mTOR Inhibitors

[00532] Methods described herein use low, immune enhancing, dose mTOR inhibitors, doses of mTOR inhibitors, e.g., allosteric mTOR inhibitors, including rapalogs such as RAD001. In contrast, levels of inhibitor that fully or near fully inhibit the mTOR pathway are immunosuppressive and are used, e.g., to prevent organ transplant rejection. In addition, high doses of rapalogs that fully inhibit mTOR also inhibit tumor cell growth and are used to treat a variety of cancers (See, e.g., Antineoplastic effects of mammalian target of rapamycin inhibitors.

Salvadori M. World J Transplant. 2012 Oct 24;2(5):74-83; Current and Future Treatment Strategies for Patients with Advanced Hepatocellular Carcinoma: Role of mTOR Inhibition.

Finn RS. Liver Cancer. 2012 Nov;1(3-4):247-256; Emerging Signaling Pathways in Hepatocellular Carcinoma. Moeini A, Cornellà H, Villanueva A. Liver Cancer. 2012

Sep;1(2):83-93; Targeted cancer therapy - Are the days of systemic chemotherapy numbered?

Joo WD, Visintin I, Mor G. Maturitas. 2013 Sep 20.; Role of natural and adaptive immunity in renal cell carcinoma response to VEGFR-TKIs and mTOR inhibitor. Santoni M, Berardi R, Amantini C, Burattini L, Santini D, Santoni G, Cascinu S. Int J Cancer. 2013 Oct 2).

[00533] The present invention is based, at least in part, on the surprising finding that doses of mTOR inhibitors well below those used in current clinical settings had a superior effect in increasing an immune response in a subject and increasing the ratio of PD-1 negative T cells/PD-1 positive T cells. It was surprising that low doses of mTOR inhibitors, producing only partial inhibition of mTOR activity, were able to effectively improve immune responses in human subjects and increase the ratio of PD-1 negative T cells/PD-1 positive T cells.

[00534] Alternatively, or in addition, without wishing to be bound by any theory, it is believed that low, a low, immune enhancing, dose of an mTOR inhibitor can increase naive T cell numbers, e.g., at least transiently, e.g., as compared to a non-treated subject. Alternatively or additionally, again while not wishing to be bound by theory, it is believed that treatment with an mTOR inhibitor after a sufficient amount of time or sufficient dosing results in one or more of the following:

an increase in the expression of one or more of the following markers: CD62L^{high}, CD127^{high}, CD27⁺, and BCL2, e.g., on memory T cells, e.g., memory T cell precursors;

a decrease in the expression of KLRG1, e.g., on memory T cells, e.g., memory T cell precursors; and

an increase in the number of memory T cell precursors, e.g., cells with any one or combination of the following characteristics: increased CD62L^{high}, increased CD127^{high}, increased CD27⁺, decreased KLRG1, and increased BCL2;

and wherein any of the changes described above occurs, e.g., at least transiently, e.g., as compared to a non-treated subject (Araki, K et al. (2009) *Nature* 460:108-112). Memory T cell precursors are memory T cells that are early in the differentiation program. For example, memory T cells have one or more of the following characteristics: increased CD62L^{high}, increased CD127^{high}, increased CD27⁺, decreased KLRG1, and/or increased BCL2.

[00535] In an embodiment, the invention relates to a composition, or dosage form, of an mTOR inhibitor, e.g., an allosteric mTOR inhibitor, e.g., a rapalog, rapamycin, or RAD001, or a catalytic mTOR inhibitor, which, when administered on a selected dosing regimen, e.g., once daily or once weekly, is associated with: a level of mTOR inhibition that is not associated with complete, or significant immune suppression, but is associated with enhancement of the immune response.

[00536] An mTOR inhibitor, e.g., an allosteric mTOR inhibitor, e.g., a rapalog, rapamycin, or RAD001, or a catalytic mTOR inhibitor, can be provided in a sustained release formulation. Any of the compositions or unit dosage forms described herein can be provided in a sustained release formulation. In some embodiments, a sustained release formulation will have lower bioavailability than an immediate release formulation. E.g., in embodiments, to attain a similar therapeutic effect of an immediate release formulation a sustained release formulation will have from about 2 to about 5, about 2.5 to about 3.5, or about 3 times the amount of inhibitor provided in the immediate release formulation.

[00537] In an embodiment, immediate release forms, e.g., of RAD001, typically used for one administration per week, having 0.1 to 20, 0.5 to 10, 2.5 to 7.5, 3 to 6, or about 5, mgs per unit dosage form, are provided. For once per week administrations, these immediate release formulations correspond to sustained release forms, having, respectively, 0.3 to 60, 1.5 to 30, 7.5 to 22.5, 9 to 18, or about 15 mgs of an mTOR inhibitor, e.g., an allosteric mTOR inhibitor, e.g., rapamycin or RAD001. In embodiments both forms are administered on a once/week basis.

[00538] In an embodiment, immediate release forms, e.g., of RAD001, typically used for one administration per day, having having 0.005 to 1.5, 0.01 to 1.5, 0.1 to 1.5, 0.2 to 1.5, 0.3 to 1.5, 0.4 to 1.5, 0.5 to 1.5, 0.6 to 1.5, 0.7 to 1.5, 0.8 to 1.5, 1.0 to 1.5, 0.3 to 0.6, or about 0.5 mgs per

unit dosage form, are provided. For once per day administrations, these immediate release forms correspond to sustained release forms, having, respectively, 0.015 to 4.5, 0.03 to 4.5, 0.3 to 4.5, 0.6 to 4.5, 0.9 to 4.5, 1.2 to 4.5, 1.5 to 4.5, 1.8 to 4.5, 2.1 to 4.5, 2.4 to 4.5, 3.0 to 4.5, 0.9 to 1.8, or about 1.5 mgs of an mTOR inhibitor, e.g., an allosteric mTOR inhibitor, e.g., rapamycin or RAD001. For once per week administrations, these immediate release forms correspond to sustained release forms, having, respectively, 0.1 to 30, 0.2 to 30, 2 to 30, 4 to 30, 6 to 30, 8 to 30, 10 to 30, 1.2 to 30, 14 to 30, 16 to 30, 20 to 30, 6 to 12, or about 10 mgs of an mTOR inhibitor, e.g., an allosteric mTOR inhibitor, e.g., rapamycin or RAD001.

[00539] In an embodiment, immediate release forms, e.g., of RAD001, typically used for one administration per day, having having 0.01 to 1.0 mgs per unit dosage form, are provided. For once per day administrations, these immediate release forms correspond to sustained release forms, having, respectively, 0.03 to 3 mgs of an mTOR inhibitor, e.g., an allosteric mTOR inhibitor, e.g., rapamycin or RAD001. For once per week administrations, these immediate release forms correspond to sustained release forms, having, respectively, 0.2 to 20 mgs of an mTOR inhibitor, e.g., an allosteric mTOR inhibitor, e.g., rapamycin or RAD001.

[00540] In an embodiment, immediate release forms, e.g., of RAD001, typically used for one administration per week, having having 0.5 to 5.0 mgs per unit dosage form, are provided. For once per week administrations, these immediate release forms correspond to sustained release forms, having, respectively, 1.5 to 15 mgs of an mTOR inhibitor, e.g., an allosteric mTOR inhibitor, e.g., rapamycin or RAD001.

[00541] As described above, one target of the mTOR pathway is the P70 S6 kinase. Thus, doses of mTOR inhibitors which are useful in the methods and compositions described herein are those which are sufficient to achieve no greater than 80% inhibition of P70 S6 kinase activity relative to the activity of the P70 S6 kinase in the absence of an mTOR inhibitor, e.g., as measured by an assay described herein, e.g., the Boulay assay. In a further aspect, the invention provides an amount of an mTOR inhibitor sufficient to achieve no greater than 38% inhibition of P70 S6 kinase activity relative to P70 S6 kinase activity in the absence of an mTOR inhibitor.

[00542] In one aspect the dose of mTOR inhibitor useful in the methods and compositions of the invention is sufficient to achieve, e.g., when administered to a human subject, 90 +/- 5 % (i.e., 85-95%), 89+/-5 %, 88+/-5 %, 87+/-5 %, 86+/-5 %, 85+/-5 %, 84+/-5 %, 83+/-5 %, 82+/-5 %, 81+/-5 %, 80+/-5 %, 79+/-5 %, 78+/-5 %, 77+/-5 %, 76+/-5 %, 75+/-5 %, 74+/-5 %, 73+/-5 %,

72 +/-5%, 71 +/-5%, 70 +/-5%, 69 +/-5%, 68 +/-5%, 67 +/-5%, 66 +/-5%, 65 +/-5%, 64 +/-5%, 63 +/-5%, 62 +/-5%, 61 +/-5%, 60 +/-5%, 59 +/-5%, 58 +/-5%, 57 +/-5%, 56 +/-5%, 55 +/-5%, 54 +/-5%, 54 +/-5%, 53 +/-5%, 52 +/-5%, 51 +/-5%, 50 +/-5%, 49 +/-5%, 48 +/-5%, 47 +/-5%, 46 +/-5%, 45 +/-5%, 44 +/-5%, 43 +/-5%, 42 +/-5%, 41 +/-5%, 40 +/-5%, 39 +/-5%, 38 +/-5%, 37 +/-5%, 36 +/-5%, 35 +/-5%, 34 +/-5%, 33 +/-5%, 32 +/-5%, 31 +/-5%, 30 +/-5%, 29 +/-5%, 28 +/-5%, 27 +/-5%, 26 +/-5%, 25 +/-5%, 24 +/-5%, 23 +/-5%, 22 +/-5%, 21 +/-5%, 20 +/-5%, 19 +/-5%, 18 +/-5%, 17 +/-5%, 16 +/-5%, 15 +/-5%, 14 +/-5%, 13 +/-5%, 12 +/-5%, 11 +/-5%, or 10 +/-5%, inhibition of P70 S6 kinase activity, e.g., as measured by an assay described herein, e.g., the Boulay assay.

[00543] P70 S6 kinase activity in a subject may be measured using methods known in the art, such as, for example, according to the methods described in U.S. Pat. 7,727,950, by immunoblot analysis of phosphoP70 S6K levels and/or phosphoP70 S6 levels or by in vitro kinase activity assays.

[00544] As used herein, the term "about" in reference to a dose of mTOR inhibitor refers to up to a +/- 10% variability in the amount of mTOR inhibitor, but can include no variability around the stated dose.

[00545] In some embodiments, the invention provides methods comprising administering to a subject an mTOR inhibitor, e.g., an allosteric inhibitor, e.g., RAD001, at a dosage within a target trough level. In some embodiments, the trough level is significantly lower than trough levels associated with dosing regimens used in organ transplant and cancer patients. In an embodiment mTOR inhibitor, e.g., RAD001, or rapamycin, is administered to result in a trough level that is less than 1/2, 1/4, 1/10, or 1/20 of the trough level that results in immunosuppression or an anticancer effect. In an embodiment mTOR inhibitor, e.g., RAD001, or rapamycin, is administered to result in a trough level that is less than 1/2, 1/4, 1/10, or 1/20 of the trough level provided on the FDA approved packaging insert for use in immunosuppression or an anticancer indications.

[00546] In an embodiment a method disclosed herein comprises administering to a subject an mTOR inhibitor, e.g., an allosteric inhibitor, e.g., RAD001, at a dosage that provides a target trough level of 0.1 to 10 ng/ml, 0.1 to 5 ng/ml, 0.1 to 3 ng/ml, 0.1 to 2 ng/ml, or 0.1 to 1 ng/ml.

[00547] In an embodiment a method disclosed herein comprises administering to a subject an mTOR inhibitor, e.g., an allosteric inhibitor, e.g., RAD001, at a dosage that provides a target trough level of 0.2 to 10 ng/ml, 0.2 to 5 ng/ml, 0.2 to 3ng/ml, 0.2 to 2 ng/ml, or 0.2 to 1 ng/ml.

[00548] In an embodiment a method disclosed herein comprises administering to a subject an mTOR inhibitor, e.g. an, allosteric inhibitor, e.g., RAD001, at a dosage that provides a target trough level of 0.3 to 10 ng/ml, 0.3 to 5 ng/ml, 0.3 to 3ng/ml, 0.3 to 2 ng/ml, or 0.3 to 1 ng/ml.

[00549] In an embodiment a method disclosed herein comprises administering to a subject an mTOR inhibitor, e.g., an allosteric inhibitor, e.g., RAD001, at a dosage that provides a target trough level of 0.4 to 10 ng/ml, 0.4 to 5 ng/ml, 0.4 to 3ng/ml, 0.4 to 2 ng/ml, or 0.4 to 1 ng/ml.

[00550] In an embodiment a method disclosed herein comprises administering to a subject an mTOR inhibitor, e.g., an allosteric inhibitor, e.g., RAD001, at a dosage that provides a target trough level of 0.5 to 10 ng/ml, 0.5 to 5 ng/ml, 0.5 to 3ng/ml, 0.5 to 2 ng/ml, or 0.5 to 1 ng/ml.

[00551] In an embodiment a method disclosed herein comprises administering to a subject an mTOR inhibitor, e.g., an allosteric inhibitor, e.g., RAD001, at a dosage that provides a target trough level of 1 to 10 ng/ml, 1 to 5 ng/ml, 1 to 3ng/ml, or 1 to 2 ng/ml.

[00552] As used herein, the term “trough level” refers to the concentration of a drug in plasma just before the next dose, or the minimum drug concentration between two doses.

[00553] In some embodiments, a target trough level of RAD001 is in a range of between about 0.1 and 4.9 ng/ml. In an embodiment, the target trough level is below 3ng/ml, e.g., is between 0.3 or less and 3 ng/ml. In an embodiment, the target trough level is below 3ng/ml, e.g., is between 0.3 or less and 1 ng/ml.

[00554] In a further aspect, the invention can utilize an mTOR inhibitor other than RAD001 in an amount that is associated with a target trough level that is bioequivalent to the specified target trough level for RAD001. In an embodiment, the target trough level for an mTOR inhibitor other than RAD001, is a level that gives the same level of mTOR inhibition (e.g., as measured by a method described herein, e.g., the inhibition of P70 S6) as does a trough level of RAD001 described herein.

Pharmaceutical compositions: mTOR Inhibitors

[00555] In one aspect, the present invention relates to pharmaceutical compositions comprising an mTOR inhibitor, e.g., an mTOR inhibitor as described herein, formulated for use in combination with CAR cells described herein.

[00556] In some embodiments, the mTOR inhibitor is formulated for administration in combination with an additional, e.g., as described herein.

[00557] In general, compounds of the invention will be administered in therapeutically effective amounts as described above via any of the usual and acceptable modes known in the art, either singly or in combination with one or more therapeutic agents.

[00558] The pharmaceutical formulations may be prepared using conventional dissolution and mixing procedures. For example, the bulk drug substance (e.g., an mTOR inhibitor or stabilized form of the compound (e.g., complex with a cyclodextrin derivative or other known complexation agent) is dissolved in a suitable solvent in the presence of one or more of the excipients described herein. The mTOR inhibitor is typically formulated into pharmaceutical dosage forms to provide an easily controllable dosage of the drug and to give the patient an elegant and easily handleable product.

[00559] Compounds of the invention can be administered as pharmaceutical compositions by any conventional route, in particular enterally, e.g., orally, e.g., in the form of tablets or capsules, or parenterally, e.g., in the form of injectable solutions or suspensions, topically, e.g., in the form of lotions, gels, ointments or creams, or in a nasal or suppository form. Where an mTOR inhibitor is administered in combination with (either simultaneously with or separately from) another agent as described herein, in one aspect, both components can be administered by the same route (e.g., parenterally). Alternatively, another agent may be administered by a different route relative to the mTOR inhibitor. For example, an mTOR inhibitor may be administered orally and the other agent may be administered parenterally.

SUSTAINED RELEASE

[00560] mTOR inhibitors, e.g., allosteric mTOR inhibitors or catalytic mTOR inhibitors, disclosed herein can be provided as pharmaceutical formulations in form of oral solid dosage forms comprising an mTOR inhibitor disclosed herein, e.g., rapamycin or RAD001, which satisfy product stability requirements and/or have favorable pharmacokinetic properties over the immediate release (IR) tablets, such as reduced average plasma peak concentrations, reduced inter- and intra-patient variability in the extent of drug absorption and in the plasma peak

concentration, reduced C_{\max} / C_{\min} ratio and/or reduced food effects. Provided pharmaceutical formulations may allow for more precise dose adjustment and/or reduce frequency of adverse events thus providing safer treatments for patients with an mTOR inhibitor disclosed herein, e.g., rapamycin or RAD001.

[00561] In some embodiments, the present disclosure provides stable extended release formulations of an mTOR inhibitor disclosed herein, e.g., rapamycin or RAD001, which are multi-particulate systems and may have functional layers and coatings.

[00562] The term “extended release, multi-particulate formulation as used herein refers to a formulation which enables release of an mTOR inhibitor disclosed herein, e.g., rapamycin or RAD001, over an extended period of time e.g. over at least 1, 2, 3, 4, 5 or 6 hours. The extended release formulation may contain matrices and coatings made of special excipients, e.g., as described herein, which are formulated in a manner as to make the active ingredient available over an extended period of time following ingestion.

[00563] The term “extended release” can be interchangeably used with the terms “sustained release” (SR) or “prolonged release”. The term “extended release” relates to a pharmaceutical formulation that does not release active drug substance immediately after oral dosing but over an extended in accordance with the definition in the pharmacopoeias Ph. Eur. (7th edition) monograph for tablets and capsules and USP general chapter <1151> for pharmaceutical dosage forms. The term “Immediate Release” (IR) as used herein refers to a pharmaceutical formulation which releases 85% of the active drug substance within less than 60 minutes in accordance with the definition of “Guidance for Industry: “Dissolution Testing of Immediate Release Solid Oral Dosage Forms” (FDA CDER, 1997). In some embodiments, the term “immediate release” means release of everolismus from tablets within the time of 30 minutes, e.g., as measured in the dissolution assay described herein.

[00564] Stable extended release formulations of an mTOR inhibitor disclosed herein, e.g., rapamycin or RAD001, can be characterized by an in-vitro release profile using assays known in the art, such as a dissolution assay as described herein: a dissolution vessel filled with 900 mL phosphate buffer pH 6.8 containing sodium dodecyl sulfate 0.2% at 37°C and the dissolution is performed using a paddle method at 75 rpm according to USP by according to USP testing monograph 711, and Ph.Eur. testing monograph 2.9.3. respectively.

[00565] In some embodiments, stable extended release formulations of an mTOR inhibitor disclosed herein, e.g., rapamycin or RAD001, release the mTOR inhibitor in the in-vitro release assay according to following release specifications:

0.5h: <45%, or <40, e.g., <30%

1h: 20-80%, e.g., 30-60%

2h: >50%, or >70%, e.g., >75%

3h: >60%, or >65%, e.g., >85%, e.g., >90%.

[00566] In some embodiments, stable extended release formulations of an mTOR inhibitor disclosed herein, e.g., rapamycin or RAD001, release 50% of the mTOR inhibitor not earlier than 45, 60, 75, 90, 105 min or 120 min in the in-vitro dissolution assay.

Pharmaceutical compositions and treatments

[00567] Pharmaceutical compositions of the present invention may comprise a CAR-expressing cell, e.g., a plurality of CAR-expressing cells, as described herein, in combination with one or more pharmaceutically or physiologically acceptable carriers, diluents or excipients. Such compositions may comprise buffers such as neutral buffered saline, phosphate buffered saline and the like; carbohydrates such as glucose, mannose, sucrose or dextrans, mannitol; proteins; polypeptides or amino acids such as glycine; antioxidants; chelating agents such as EDTA or glutathione; adjuvants (e.g., aluminum hydroxide); and preservatives. Compositions of the present invention are in one aspect formulated for intravenous administration.

[00568] Pharmaceutical compositions of the present invention may be administered in a manner appropriate to the disease to be treated (or prevented). The quantity and frequency of administration will be determined by such factors as the condition of the patient, and the type and severity of the patient's disease, although appropriate dosages may be determined by clinical trials.

[00569] In one embodiment, the pharmaceutical composition is substantially free of, e.g., there are no detectable levels of a contaminant, e.g., selected from the group consisting of endotoxin, mycoplasma, replication competent lentivirus (RCL), p24, VSV-G nucleic acid, HIV gag, residual anti-CD3/anti-CD28 coated beads, mouse antibodies, pooled human serum, bovine

serum albumin, bovine serum, culture media components, vector packaging cell or plasmid components, a bacterium and a fungus. In one embodiment, the bacterium is at least one selected from the group consisting of *Alcaligenes faecalis*, *Candida albicans*, *Escherichia coli*, *Haemophilus influenza*, *Neisseria meningitidis*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Streptococcus pneumonia*, and *Streptococcus pyogenes* group A.

[00570] When “an immunologically effective amount,” “an anti-cancer effective amount,” “a cancer-inhibiting effective amount,” or “therapeutic amount” is indicated, the precise amount of the compositions of the present invention to be administered can be determined by a physician with consideration of individual differences in age, weight, tumor size, extent of infection or metastasis, and condition of the patient (subject). It can generally be stated that a pharmaceutical composition comprising the immune effector cells described herein may be administered at a dosage of 10^4 to 10^9 cells/kg body weight, in some instances 10^5 to 10^6 cells/kg body weight, including all integer values within those ranges. The immune effector cell compositions may also be administered multiple times at these dosages. The cells can be administered by using infusion techniques that are commonly known in immunotherapy (see, e.g., Rosenberg *et al.*, *New Eng. J. of Med.* 319:1676, 1988).

[00571] In certain aspects, it may be desired to administer activated immune effector cells to a subject and then subsequently redraw blood (or have an apheresis performed), activate the cells therefrom according to the present invention, and reinfuse the patient with these activated and expanded cells. This process can be carried out multiple times every few weeks. In certain aspects, the cells can be activated from blood draws of from 10cc to 400cc. In certain aspects, the cells are activated from blood draws of 20cc, 30cc, 40cc, 50cc, 60cc, 70cc, 80cc, 90cc, or 100cc.

[00572] The administration of the subject compositions may be carried out in any convenient manner, including by aerosol inhalation, injection, ingestion, transfusion, implantation or transplantation. The compositions described herein may be administered to a patient trans arterially, subcutaneously, intradermally, intratumorally, intranodally, intramedullary, intramuscularly, by intravenous (i.v.) injection, or intraperitoneally. In one aspect, the T cell compositions of the present invention are administered to a patient by intradermal or subcutaneous injection. In one aspect, the immune effector cell compositions of the present

invention are administered by i.v. injection. The compositions of immune effector cells may be injected directly into a tumor, lymph node, or site of infection.

[00573] In a particular exemplary aspect, subjects may undergo leukapheresis, wherein leukocytes are collected, enriched, or depleted ex vivo to select and/or isolate the cells of interest, e.g., T cells. These T cell isolates may be expanded by methods known in the art and treated such that one or more CAR constructs of the invention may be introduced, thereby creating a CAR T cell of the invention. Subjects in need thereof may subsequently undergo standard treatment with high dose chemotherapy followed by peripheral blood stem cell transplantation. In certain aspects, following or concurrent with the transplant, subjects receive an infusion of the expanded CAR T cells of the present invention. In an additional aspect, expanded cells are administered before or following surgery.

[00574] The dosage of the above treatments to be administered to a patient will vary with the precise nature of the condition being treated and the recipient of the treatment. The scaling of dosages for human administration can be performed according to art-accepted practices. The dose for CAMPATH, for example, will generally be in the range 1 to about 100 mg for an adult patient, usually administered daily for a period between 1 and 30 days. The preferred daily dose is 1 to 10 mg per day although in some instances larger doses of up to 40 mg per day may be used (described in U.S. Patent No. 6,120,766).

[00575] In one embodiment, the CAR is introduced into immune effector cells, e.g., using in vitro transcription, and the subject (e.g., human) receives an initial administration of CAR-expressing cells of the invention, and one or more subsequent administrations of the CAR-expressing cells of the invention, wherein the one or more subsequent administrations are administered less than 15 days, e.g., 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, or 2 days after the previous administration. In one embodiment, more than one administration of the CAR-expressing cells of the invention are administered to the subject (e.g., human) per week, e.g., 2, 3, or 4 administrations of the CAR-expressing cells of the invention are administered per week. In one embodiment, the subject (e.g., human subject) receives more than one administration of the CAR-expressing cells per week (e.g., 2, 3 or 4 administrations per week) (also referred to herein as a cycle), followed by a week of no CAR-expressing cells administration, and then one or more additional administration of the CAR-expressing cells (e.g., more than one administration of the

CAR-expressing cells per week) is administered to the subject. In another embodiment, the subject (e.g., human subject) receives more than one cycle of CAR-expressing cells, and the time between each cycle is less than 10, 9, 8, 7, 6, 5, 4, or 3 days. In one embodiment, the CAR-expressing cells are administered every other day for 3 administrations per week. In one embodiment, the CAR-expressing cells of the invention are administered for at least two, three, four, five, six, seven, eight or more weeks.

[00576] In one aspect, mesothelin CAR-expressing cells are generated using lentiviral viral vectors, such as lentivirus. CAR-expressing cells generated that way will have stable CAR expression.

[00577] In one aspect, the CAR-expressing celss transiently express CAR vectors for 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 days after transduction. Transient expression of CARs can be effected by RNA CAR vector delivery. In one aspect, the CAR RNA is transduced into the T cell by electroporation.

[00578] In one embodiment, the dose and/or dosing schedule is one provided in Figure 6.

[00579] A potential issue that can arise in patients being treated using transiently expressing CAR-expressing cells (particularly with murine scFv bearing CAR-expressing cells) is anaphylaxis after multiple treatments.

[00580] Without being bound by this theory, it is believed that such an anaphylactic response might be caused by a patient developing humoral anti-CAR response, i.e., anti-CAR antibodies having an anti-IgE isotype. It is thought that a patient's antibody producing cells undergo a class switch from IgG isotype (that does not cause anaphylaxis) to IgE isotype when there is a ten to fourteen day break in exposure to antigen.

[00581] If a patient is at high risk of generating an anti-CAR antibody response during the course of transient CAR therapy (such as those generated by RNA transductions), CAR-expressing cell infusion breaks should not last more than ten to fourteen days.

[00582] Using CARs with human (instead of murine) scFvs can reduce the likelihood and intensity of a patient having an anti-CAR response.

[00583]

[00584] Table 2: Amino Acid Sequences of Human scFvs and CARs (bold underline is the leader sequence and grey box is a linker sequence). In the case of the scFvs, the remaining amino acids are the heavy chain variable region and light chain variable regions, with each of the HC CDRs (HC CDR1, HC CDR2, HC CDR3) and LC CDRs (LC CDR1, LC CDR2, LCCDR3) underlined). In the case of the CARs, the further remaining amino acids are the remaining amino acids of the CARs.)

SEQ ID NO:	Description	Amino Acid Sequence
39	M1 (ScFv domain)	QVQLQQSGAEVKPGASVKVSCKAS <u>GYTFTGYMMHWVRQ</u> APGQGLEWMGR <u>WINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSLRSEDTAVYYCARG</u> <u>RYYGMDVWGQGTMVTVSSGGGGSGGGGGSGGGGGSEIVL</u> <u>TQSPATLSSLSPGERATIS</u> <u>CRASQSVSSNF</u> <u>AWYQQRPGQAPRLLIYDASNRATGIPPRFSGSGSGTDF</u> <u>TLTISSLEPED</u> <u>FAAYYCHQRSNWLYTFGQGTV</u> <u>DIK</u>
63	M1 (full) >ZA53-27BC (M1) ZA53-27BC R001-A11 126161)	<u>MALPVTA</u> <u>LLPLA</u> <u>LLHAA</u> <u>R</u> QVQLQQSGAEVKPGASVKVSCKAS <u>GYTFTGYMMHWVRQ</u> APGQGLEWMGR <u>WINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSLRSEDTAVYYCARG</u> <u>RYYGMDVWGQGTMVTVSSGGGGSGGGGGSGGGGGSEIVL</u> <u>TQSPATLSSLSPGERATIS</u> <u>CRASQSVSSNF</u> <u>AWYQQRPGQAPRLLIYDASNRATGIPPRFSGSGSGTDF</u> <u>TLTISSLEPED</u> <u>FAAYYCHQRSNWLYTFGQGTV</u> <u>DIKTTT</u> <u>PAPRPT</u> <u>PAPTIASQPLSLRPEACRPAAGGAV</u> HTRGLDFACDIYIWAPLAGTCGVLLSLVITLYCKRGRKKLLYIFKQPFMVPVQTTQEE GCSCRFP <small>EE</small> EGGCELRVKFSRSADAPAYKQGQNQLYNELNLRREYDVL DKRRGRDPE MGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKERRGKGDGLYQGLSTATKDTYDAL HMQALPPR
40	M2 (ScFv domain)	QVQLVQSGAEVKPGASVKVSCKAS <u>GYTFTGYMMHWVRQ</u> APGQGLEWMG <u>WINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSLRSEDTAVYYCARG</u> <u>LRRTVVT</u> <u>PRA</u> <u>YYGMDVWGQGTT</u> <u>TVSSGGGGSGGGGGSGGGGGSDIQLTQSPSTLSA</u> <u>SVGDRV</u> <u>TITC</u> <u>QASQDI</u> <u>NSLNWYQQKAGKAPKLLIYDAST</u> <u>LETG</u> <u>VPSRFSGSGSGTDF</u> <u>SF</u> <u>TISSLQ</u> <u>PEDIATYYC</u> <u>QOHDNL</u> <u>PLTFGQGTV</u> <u>KEI</u>
64	M2 (full) >FA56-26RC (M2) FA56-26RC R001-A10 126162)	<u>MALPVTA</u> <u>LLPLA</u> <u>LLHAA</u> <u>R</u> QVQLVQSGAEVKPGASVKVSCKAS <u>GYTFTGYMMHWVRQ</u> APGQGLEWMG <u>WINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSLRSEDTAVYYCARG</u> <u>LRRTVVT</u> <u>PRA</u> <u>YYGMDVWGQGTT</u> <u>TVSSGGGGSGGGGGSGGGGGSDIQLTQSPSTLSA</u> <u>SVGDRV</u> <u>TITC</u> <u>QASQDI</u> <u>NSLNWYQQKAGKAPKLLIYDAST</u> <u>LETG</u> <u>VPSRFSGSGSGTDF</u> <u>SF</u> <u>TISSLQ</u> <u>PEDIATYYC</u> <u>QOHDNL</u> <u>PLTFGQGTV</u> <u>KEI</u> I KTTT PAPRPT PAPTIASQPLSLRPEA CRPAAGGAHTRGLDFACDIYIWAPLAGTCGVLLSLVITLYCKRGRKKLLYIFKQPFM PVQTQEEGCSRF <small>EE</small> EGGCELRVKFSRSADAPAYKQGQNQLYNELNLRREYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKERRGKGDGLYQGLST ATKDTYDALHMQALPPR
41	M3 (ScFv domain)	QVQLVQSGAEVKPGAPVKVSCKAS <u>GYTFTGYMMHWVRQ</u> APGQGLEWMG <u>WINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSLRSEDTAVYYCARG</u> <u>EWDGS</u> <u>YYD</u> <u>WQGT</u> <u>LTV</u> <u>VSSGGGGSGGGGGSGGGGGSDIVL</u> <u>TQTPSSLSASVGDRV</u> <u>TITCRASQ</u> <u>SINTYLNWYQHKPGKAPKLLIY</u> <u>AASSLQSGVPSRFSGSGSGTDF</u> <u>TLTISSLQ</u> <u>PEDFATYYC</u> <u>QOQFS</u> <u>PLTFGGGT</u> <u>KLEIK</u>
65	M3 >VA58-21LC	<u>MALPVTA</u> <u>LLPLA</u> <u>LLHAA</u> <u>R</u> QVQLVQSGAEVKPGAPVKVSCKAS <u>GYTFTGYMMHWVRQ</u> APGQGLEWMG <u>WINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSLRSEDTAVYYCARG</u> <u>EWDGS</u> <u>YYD</u> <u>WQGT</u> <u>LTV</u> <u>VSSGGGGSGGGGGSGGGGGSDIVL</u> <u>TQTPSSLSASVGDRV</u> <u>TITCRASQ</u> <u>SINTYLNWYQHKPGKAPKLLIY</u> <u>AASSLQSGVPSRFSGSGSGTDF</u> <u>TLTISSLQ</u>

	126166)	ATKDTYDALHMQALPPR
45	M7 (ScFv domain)	QVQLVQSGGGVVQPGRSLRLSCAAS <u>GFTFSSYAMHWVRQ</u> APGKGLEWVA <u>VISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARW</u> <u>KVSSSSPAFDYWGQGTIVT</u> VSSGGGGSGGGGGSGGGGGSEIVLTQS <u>PATLSLSPGER</u> <u>AILSCRASQS</u> VT <u>YTKYL</u> GWYQQKPGQAPRLLIY <u>DASTRATGIPDRFSGSGSGTDF</u> LTINR LE PEDFAVYYC <u>QHYGGSP</u> LIT <u>FGQGTR</u> LEIK
69	M7 >VE12-01CD (M7) VE12-01CD R001-A5 126167)	<u>MALPVTALLPLALLHAARP</u> QVQLVQSGGGVVQPGRSLRLSCAAS <u>GFTFSSYAMHWVRQ</u> APGKGLEWVA <u>VISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARW</u> <u>KVSSSSPAFDYWGQGTIVT</u> VSSGGGGSGGGGGSGGGGGSEIVLTQS <u>PATLSLSPGER</u> <u>AILSCRASQS</u> VT <u>YTKYL</u> GWYQQKPGQAPRLLIY <u>DASTRATGIPDRFSGSGSGTDF</u> LTINR LE PEDFAVYYC <u>QHYGGSP</u> LIT <u>FGQGTR</u> LEIKTTPA <u>PRPPT</u> PARTIASQPLSLRPEACRP AAGGA <u>VHTRGLDFACDIYIWAPLAGTCGV</u> LLS <u>LIVITLYCKRGRK</u> LLYIFKQPFMRPVQ TTQEDGC <u>SCRFPEEEEGG</u> CELRVKFSRSADAPAY <u>KQGQNQLYNE</u> LNLRREEYDVL <u>DKR</u> RGRDPEMGGKPRRKNP <u>QEGLYN</u> E <u>LQDKM</u> AEAYSEIGMKGER <u>RRGKGD</u> GLY <u>QGL</u> STATK DTYDALHMQALPPR
46	M8 (ScFv domain)	QVQLQSGAEVKKPGASVKVSCKTSGY <u>PFTGYS</u> LHWVRQ APGQGLEWMG <u>WINPNSSGT</u> NYA <u>QKFOGRVTMTRDTS</u> ISTAYMEL <u>SLRSDDTAVYYCARD</u> <u>HYGGNSL</u> FYWG <u>QGTIVT</u> VSSGGGGSGGGGGSGGGGGSDIQLTQS <u>PSSISASVGDTVS</u> <u>ITCRASQ</u> DS <u>GTWLA</u> YQQKPGKAPNLL <u>MYDASTLED</u> G <u>VPSRFSGS</u> AS <u>GTEFTL</u> TVNRLQ <u>P</u> EDSATYYC <u>QOYNSYPL</u> TFGGGT <u>KVDI</u> KTTPA <u>PRPPT</u> PARTIASQPLSLRPEACR <u>PAA</u> AVH <u>TRGLDFACDIYIWAPLAGTCGV</u> LLS <u>LIVITLYCKRGRK</u> LLYIFKQPFMRPVQ <u>TTQ</u> EDGC <u>SCRFPEEEEGG</u> CELRVKFSRSADAPAY <u>KQGQNQLYNE</u> LNLRREEYDVL <u>DKR</u> PEMGGKPRRKNP <u>QEGLYN</u> E <u>LQDKM</u> AEAYSEIGMKGER <u>RRGKGD</u> GLY <u>QGL</u> STATK <u>DTYD</u> ALHMQALPPR
70	M8 >LE13-05XD (M8) LE13-05XD R001-E5 126168)	<u>MALPVTALLPLALLHAARP</u> QVQLQSGAEVKKPGASVKVSCKTSGY <u>PFTGYS</u> LHWVRQ APGQGLEWMG <u>WINPNSSGT</u> NYA <u>QKFOGRVTMTRDTS</u> ISTAYMEL <u>SLRSDDTAVYYCARD</u> <u>HYGGNSL</u> FYWG <u>QGTIVT</u> VSSGGGGSGGGGGSGGGGGSDIQLTQS <u>PSSISASVGDTVS</u> <u>ITCRASQ</u> DS <u>GTWLA</u> YQQKPGKAPNLL <u>MYDASTLED</u> G <u>VPSRFSGS</u> AS <u>GTEFTL</u> TVNRLQ <u>P</u> EDSATYYC <u>QOYNSYPL</u> TFGGGT <u>KVDI</u> KTTPA <u>PRPPT</u> PARTIASQPLSLRPEACR <u>PAA</u> AVH <u>TRGLDFACDIYIWAPLAGTCGV</u> LLS <u>LIVITLYCKRGRK</u> LLYIFKQPFMRPVQ <u>TTQ</u> EDGC <u>SCRFPEEEEGG</u> CELRVKFSRSADAPAY <u>KQGQNQLYNE</u> LNLRREEYDVL <u>DKR</u> PEMGGKPRRKNP <u>QEGLYN</u> E <u>LQDKM</u> AEAYSEIGMKGER <u>RRGKGD</u> GLY <u>QGL</u> STATK <u>DTYD</u> ALHMQALPPR
47	M9 (ScFv domain)	QVQLVQSGAEVKKPGASVE <u>SCKASGY</u> TFTSY <u>MHWVRQ</u> APGQGLEWMG <u>INPSGGST</u> GYA <u>QKFOGRVTMTRDTS</u> IST <u>TVH</u> MEL <u>SLRSDDTAVYYCARG</u> <u>GYSSSSDAFDI</u> WG <u>QGTIVT</u> VSSGGGGSGGGGGSGGGGGSDI <u>QMTQSPPSLSASVGDR</u> <u>VTITCRASQ</u> DISSAL <u>AWYQKPGTPPKLLIYDASSLES</u> G <u>VPSRFSGSGSGTDF</u> LT <u>TISSL</u> Q <u>PEDFATYYCQOYNSYPL</u> TFGGTR <u>LEIKTTPA</u> <u>PRPPT</u> PARTIASQPLSLRPEACR <u>PAA</u> GGAVH <u>TRGLDFACDIYIWAPLAGTCGV</u> LLS <u>LIVITLYCKRGRK</u> LLYIFKQPFMRPVQ <u>TTQ</u> QEDGC <u>SCRFPEEEEGG</u> CELRVKFSRSADAPAY <u>KQGQNQLYNE</u> LNLRREEYDVL <u>DKR</u> RDPEMGGKPRRKNP <u>QEGLYN</u> E <u>LQDKM</u> AEAYSEIGMKGER <u>RRGKGD</u> GLY <u>QGL</u> STATK <u>DT</u> YDALHMQALPPR
71	M9 >BE15-00SD (M9) BE15-00SD R001-A3 126169)	<u>MALPVTALLPLALLHAARP</u> QVQLVQSGAEVKKPGASVE <u>SCKASGY</u> TFTSY <u>MHWVRQ</u> APGQGLEWMG <u>INPSGGST</u> GYA <u>QKFOGRVTMTRDTS</u> IST <u>TVH</u> MEL <u>SLRSDDTAVYYCARG</u> <u>GYSSSSDAFDI</u> WG <u>QGTIVT</u> VSSGGGGSGGGGGSGGGGGSDI <u>QMTQSPPSLSASVGDR</u> <u>VTITCRASQ</u> DISSAL <u>AWYQKPGTPPKLLIYDASSLES</u> G <u>VPSRFSGSGSGTDF</u> LT <u>TISSL</u> Q <u>PEDFATYYCQOYNSYPL</u> TFGGTR <u>LEIKTTPA</u> <u>PRPPT</u> PARTIASQPLSLRPEACR <u>PAA</u> GGAVH <u>TRGLDFACDIYIWAPLAGTCGV</u> LLS <u>LIVITLYCKRGRK</u> LLYIFKQPFMRPVQ <u>TTQ</u> QEDGC <u>SCRFPEEEEGG</u> CELRVKFSRSADAPAY <u>KQGQNQLYNE</u> LNLRREEYDVL <u>DKR</u> RDPEMGGKPRRKNP <u>QEGLYN</u> E <u>LQDKM</u> AEAYSEIGMKGER <u>RRGKGD</u> GLY <u>QGL</u> STATK <u>DT</u> YDALHMQALPPR
48	M10 (ScFv domain)	QVQLVQSGAEVKKPGASVKVSCKAS <u>GYTFTSY</u> GISWVRQ APGQGLEWMG <u>WISAYNGNT</u> NYA <u>QKLOGRVTMTRDTS</u> IST <u>ME</u> L <u>SLRSDDTAVYYCARW</u> <u>AGGI</u> YYYYGMD <u>VWGQTT</u> IV <u>SSGGGGSGGGGGSGGGGGSDIVMTQTPDSLAVSLGE</u>

		RATISCKSSHSLVLYNRNNKNYLAWYQQKPGQPPKLLFYWASTRKSGVPDRFSGSGSGTDF TLTISSLQPEDFATYFCQQTQTFPLTFQGQGTRLEIN
72	M10 >RE16-05MD (M10 RE16-05MD R001-D10 126170)	MALEPVTA LLPLA LLHAARP QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISMHWVRQ APGQGLEWMGWIISAYNGNTNYAQKLOGRVTMTTDSTSTSTAYMELRSLSRSDDTAVYYCARV AGGIYYYYGMDVWGQGTTITVSSGGGGSGGGGGSGGGGGSDIVMTQTPDSLAVSLGE RATISCKSSHSLVLYNRNNKNYLAWYQQKPGQPPKLLFYWASTRKSGVPDRFSGSGSGTDF TLTISSLQPEDFATYFCQQTQTFPLTFQGQGTRLEINTTPAPRPPPTAPTIASQPLSLRP EACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLSLVITLYCKRGRKKLLYIFKQPF MRPVQTTQEEGCSRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLRREYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGL STATKDTYDALHMQALPPR
49	M11 (ScFv domain)	QVQLQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQ APGQGLEWMGWINPNSSGTNYAQNFQGRVTMTRDTSISTAYMELRRLRSDDTAVYYCASG WDFDYWGQGTLTVTSSGGGGSGGGGGSGGGGGSDIRMTQSPSSLSASVGDRVITITCR ASQSIRYYLSWYQQKPGKAPKLLIYTASILQNGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCLQTYTTPDFGPGTKVEIK
73	M11 >NE10-19WD (M11 NE10-19WD R001-G2 126171)	MALEPVTA LLPLA LLHAARP QVQLQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQ APGQGLEWMGWINPNSSGTNYAQNFQGRVTMTRDTSISTAYMELRRLRSDDTAVYYCASG WDFDYWGQGTLTVTSSGGGGSGGGGGSGGGGGSDIRMTQSPSSLSASVGDRVITITCR ASQSIRYYLSWYQQKPGKAPKLLIYTASILQNGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCLQTYTTPDFGPGTKVEIKTTTPAPRPPPTAPTIASQPLSLRPEACRPAAGGAVHTR GLDFACDIYIWAPLAGTCGVLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEGCS CRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLRREYDVLDRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQ ALPPR
50	M12 (ScFv domain)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQ APGQGLEWMGRINPNSSGTNYAQKFQGRVTMTTDSTSTAYMELRSLSRSDDTAVYYCART TTSYAFDIWGQGTMVTVSSGGGGSGGGGGSGGGGGSDIQLTQSPSTLSASVGDRVITI TCRASQSISTWLAWYQQKPGKAPNLLIYKASTLESGVPSRFSGSGSGTEFTLTISLQPD DFATYYCQQYNTYSPYTFQGQGKLEIK
74	M12 >DE12-14RD (M12 DE12-14RD R001-G9 126172)	MALEPVTA LLPLA LLHAARP QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQ APGQGLEWMGRINPNSSGTNYAQKFQGRVTMTTDSTSTAYMELRSLSRSDDTAVYYCART TTSYAFDIWGQGTMVTVSSGGGGSGGGGGSGGGGGSDIQLTQSPSTLSASVGDRVITI TCRASQSISTWLAWYQQKPGKAPNLLIYKASTLESGVPSRFSGSGSGTEFTLTISLQPD DFATYYCQQYNTYSPYTFQGQGKLEIKTTTPAPRPPPTAPTIASQPLSLRPEACRPAAGG AVHTRGLDFACDIYIWAPLAGTCGVLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQE EDGCSRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLRREYDVLDRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
51	M13 (ScFv domain)	QVQLVQSGGGLVKPGGLRLSCEASGFIFSDYYMGWIRQ APGKGLEWVSYIGRSGSSMYYADSVKGRFTFSRDNAKNSLYLQMNSLRAEDTAVYYCAAS PVVAATEDFQHWGQGTLTVTSSGGGGSGGGGGSGGGGGSDIVMTQTPATLSLSPGER ATLSCRASQSVTSNYLAWYQQKPGQAPRLLLFGASTRATGIPDRFSGSGSGTDFTLTINR LEPEDFAMYYCQQYGSAPVTFGQGKLEIK
75	M13 >TE13-19LD	MALEPVTA LLPLA LLHAARP QVQLVQSGGGLVKPGGLRLSCEASGFIFSDYYMGWIRQ APGKGLEWVSYIGRSGSSMYYADSVKGRFTFSRDNAKNSLYLQMNSLRAEDTAVYYCAAS PVVAATEDFQHWGQGTLTVTSSGGGGSGGGGGSGGGGGSDIVMTQTPATLSLSPGER

		CGDSLRSYYASWYQQKPGQAPVVLVIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRGSSGNHVFGTGTVT
79	M17 >NS89-94MD (M17) NS89-94MD NT 127555)	MALPVTA LLPLA LLHAARP EVQLVESGGGLVQPGSRLSCAASGFTFSSYWMHWVRQAPGKLEWVSGIWSNSGSGTGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAKDSSSWYGGGSADF _I WGQGTMVTVSSGGGGSGGGGGSSSELTQDPAVSVALGQTVRITCQDSLRSYYASWYQQKPGQAPVVLVIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRGSSGNHVFGTGTVTLLTTPAPRPPPTAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLSLVITLYCGRKRLLYIFKQPFMRFVQTTQEEDGCSRFPEEEQEGGCELRVKFSRSADAPAYKQGQNQLYNELNLRREYDVLDRGRDPEMGGKPRRKNPQEGLYNEQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
56	M18 (ScFv domain)	QVQLVQSGGGLVQPGSRLSCAASGFTFSSYWMHWVRQAPGKLVWVSRINS _I SDGSSTSYADSVKGRFTISRDNAKNTLYLQMN _I SLRAEDTAVYYCVR _I GWVG _Y Y _Y MDVWGKTTVTVSSGGGGSGGGGGSGGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSNYLAWYQQKPGQPPRLLIYD _I VSTRATGIPARFSGGGSGDFTLTISLEPEDFAVYYCQQRSNWPPWTFGQGTKEIK
80	M18 >DS90-09HD (M18) DS90-09HD R003-A05 127556)	MALPVTA LLPLA LLHAARP QVQLVQSGGGLVQPGSRLSCAASGFTFSSYWMHWVRQAPGKLVWVSRINS _I SDGSSTSYADSVKGRFTISRDNAKNTLYLQMN _I SLRAEDTAVYYCVR _I GWVG _Y Y _Y MDVWGKTTVTVSSGGGGSGGGGGSGGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSNYLAWYQQKPGQPPRLLIYD _I VSTRATGIPARFSGGGSGDFTLTISLEPEDFAVYYCQQRSNWPPWTFGQGTKEIKTTTPAPRPPPTAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLSLVITLYCGRKRLLYIFKQPFMRFVQTTQEEDGCSRFPEEEQEGGCELRVKFSRSADAPAYKQGQNQLYNELNLRREYDVLDRGRDPEMGGKPRRKNPQEGLYNEQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
57	M19 (ScFv domain)	QVQLVQSGGGVVQPGSRLSCAASGFTFSSYGMHWVRQAPGKLEWVAV _I SYDGSN _Y YADSVKGRFTISRDNSKNTLYLQMN _I SLRAEDTAVYYCAKG _I YSR _Y Y _Y Y _Y YMDVWGQGTTVTVSSGGGGSGGGGGSGGGGGSEIVMTQSPATLSLSPGERA _I ILSCRASQSVYTKYLWYQQKPGQAPRLLIYD _I ASTRATGIPDRFSGSGSGDFTLTINRLEPEDFAVYYCQHYGGSP _I TFGQGTKVDIK
81	M19 >TS92-04BD (M19) TS92-04BD R003-C06 127557)	MALPVTA LLPLA LLHAARP QVQLVQSGGGVVQPGSRLSCAASGFTFSSYGMHWVRQAPGKLEWVAV _I SYDGSN _Y YADSVKGRFTISRDNSKNTLYLQMN _I SLRAEDTAVYYCAKG _I YSR _Y Y _Y Y _Y YMDVWGQGTTVTVSSGGGGSGGGGGSGGGGGSEIVMTQSPATLSLSPGERA _I ILSCRASQSVYTKYLWYQQKPGQAPRLLIYD _I ASTRATGIPDRFSGSGSGDFTLTINRLEPEDFAVYYCQHYGGSP _I TFGQGTKVDIKTTTPAPRPPPTAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLSLVITLYCGRKRLLYIFKQPFMRFVQTTQEEDGCSRFPEEEQEGGCELRVKFSRSADAPAYKQGQNQLYNELNLRREYDVLDRGRDPEMGGKPRRKNPQEGLYNEQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
58	M20 (ScFv domain)	QVQLVQSGGGLVQPGSRLSCAASGFTFSSYAMSWVRQAPGKLEWVSAISGSGG _I YYADSVKGRFTISRDNSKNTLYLQMN _I SLRAEDTAVYYCAKR _I EAAAGHDWYFDLWGRGTLTVSSGGGGSGGGGGSGGGGGSDIRVTQSPSSLSASVGD _I RV _I ITCRASQSISSYLNWYQQKPGKAPKLLIY _I AASSLQSGVPSRFSGSGSGDFTLT _I SSLEPEDFATYYCQ _I QSYSIPLTFGQGTKVIEK
82	M20	MALPVTA LLPLA LLHAARP QVQLVQSGGGLVQPGSRLSCAASGFTFSSYAMSWVRQAPGKLEWVSAISGSGG _I YYADSVKGRFTISRDNSKNTLYLQMN _I SLRAEDTAVYYCAKR _I

	>JS93-08WD (M20) JS 93-08WD R003-E07 127558)	<u>EAAAGHDWYFDLWGRGTLVTVSSGGGGSGGGGSGGGGSDIRVTQSPSSLSASVGD</u> RVTITCRASOSISSYLNWYQQKPGKAKPLLIYAASSLQSGVPSRFSGSGSTDFTLTISS LQPEDFATYYCQQSYSIPLTFGQGKVEIKTTTPAPRPPPTAPTIASQPLSLRPEACRPA AGGAHVTRGLDFACDIYIWIWAPLAGTCGVLLSLVITLYCKRGRKKLLYIFKQPFMRPVQT TQEEDGCSCRFPEEEEGGCERVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLKRR GRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRGKGHDGLYQGLSTATKD TYDALHMQALPPR
275	Ss1 (scFv domain)	QVQLQQSGPELEKPGASVKISCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASS YNQKFRGKATLTVDKSSSTAYMDLLSITSEDSAVYFCARGGYDGRGFDYWGQGTTVTVS SGGGGGGGGGGGGGGGSDIELTQSPAIMSAPEKEVMTCSASSSVSYMHWYQQKSGTSP KRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSEVAEDDATYYCQQWSGYPLTFGAGTK LEI
278	Ss1 (full)	<u>MALPVTALLPLIALLHAARP</u> QVQLQQSGPELEKPGASVKISCKASGYSFTGYTMNWVK QSHGKSLEWIGLITPYNGASSYNQKFRGKATLTVDKSSSTAYMDLLSITSEDSAVYFCA RGGYDGRGFDYWGQGTTVTVSSGGGGGGGGGGGGSDIELTQSPAIMSAPEKEVMT CSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSEVAED DATYYCQQWSGYPLTFGAGTKLEITTPAPRPPPTAPTIASQPLSLRPEACRPAAGGAV HTRGLDFACDIYIWIWAPLAGTCGVLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTQEE DGCSCRFPEEEEGGCERVKFSRSADAP

Table 3: Nucleic Acid Sequences encoding CAR molecules (underlined is the leader sequence)

SEQ ID NO:	Desc.	Nucleic Acid Sequence
87	M1 (ScFv domain) >ZA53-27BC (M1)	CAAGTCCAACTGCAGCAGTCAGGAGCGGAAGTGAAGAAACCAAGGAGCCTCAGTCAAAGTGTCTGTGCAAGGCTAGCGGCCTA CACCTTCACCGGCTACTA CATGCACTGGTTCGACAGGCTCCAGGGCAGGGCTGGAGTGGATGGCCGCATCAACCGAATTCCGGTGGGACTAACT ACGCCCCAGAAGTTCAGGGAAAGAGTGACCATGACTAGGGACACGTCGATCAGCACTGGTACATGAACTGAGCCGCTG CGGTCGAGGATACTGCCGTCTACTACTGCGCACGCGAAGGTAATGGAATGGACGTGTTGGGCCAAGGGACTATGGT GACTGTGAGCTGGGAGGGGGAGGCTCGGGTGGCGGGGATCAGGAGGAGGATCAGGGGGAGGGAGTTCGGAATTG TCCCTACCCAGAGCCCCGGCAACCCCTCACTTTCCGGGAGAGCGCAGCAACCATCTCTGGCGGGTAGCCAATCCGTG TCGTCCTAACATTGCGCTGGTACAGCAACGGCGGGAGAACAGCCCTAGACTCTGATCTACGACGCCAACAGAGCGAC TGGAAATTCCCTCACCGTTTCGGGATCAGGCTCCGGTACCGACTTCACCTGACTATCTGTCGCTCGAACCCGAGGATT TCGCCGCCTACTACTGTACAGCGGTCAACTGGTTGATACGTTGGCCAGGGACCAAGGTGGATATCAAG
111	M1 (Full) >ZA53-27BC (M1)	ATGGCCCTCCCTGTACCGCCCTGCTGTTCCGCTGGCTCTCTGCTCACAGCGGCTCGGCCCAACTCCAACTCAGCACAG G TCAGGAGCGGAAGTGAAGAAACCAAGGAGCGTCAGTCAAAGTGTCTGTGCAAGGCTAGCGGCTACACCTTCACCGGCTACTA CATGCACTGGTTCGACAGGCTCCAGGGCAGGGCTGGAGTGGATGGCCGCATCAACCGAATTCCGGTGGGACTAACT ACGCCCCAGAAGTTCAGGGAAAGAGTGACCATGACTAGGGACACGTCGATCAGCACTGGTACATGAACTGAGCCGCTG CGGTCGAGGATACTGCGCTACTACTGCGCACGGGAAGGTAATGGAATGGACGTGTTGGGCCAAGGGACTATGGT GACTGTGAGCTGGGAGGGGGAGGCTCGGGTGGGGGGATCAGGAGGAGGATCAGGGGGAGGGAGGTTCCGAATTG TCCCTACCCAGAGCCCCGGCAACCCCTCACTTTCCGGGAGAGCGCCCAACCATCTCTGGCGGGTAGCCAATCCGTG TCGTCCTAACATTGCGCTGGTACAGCAACGGCGGGAGAACAGCCCTAGACTCTGATCTACGACGCCAACAGAGCGAC TGGAAATTCCCTCACCGTTTCGGGATCAGGCTCCGGTACCGACTTCACCTGACTATCTGTCGCTCGAACCCGAGGATT TCGCCGCCTACTACTGTACAGCGGTCAACTGGTTGATACGTTGGCCAGGGACCAAGGTGGATATCAAGAAC ACCCAGCACGGGACCCACCCACCCGGCTCTTACCATCGCCCTTCCAGGCTCTGCTCCCTCGCGTCCGGAGGCTATGAGACC CGCAGCTGGTGGGGCGTGCATACCCGGGGTCTTGAATCTGCTGCGATATCTACATTGGGCCCTCTGGCTGGTACTT GCGGGGTCTGCTGTTCACTCGTGAATCTTACTGTAAGCGCGTCCGAAGAAGCTGCTGATCATCTTAAGCAA CCCTTCACTGAGGGCTGTGCAAGACTACTAAGAGGAGGACGGCTGTTCACTGCGGTTTCCAGGAGGAGGAGGAGGCTG CGAAGTCGGCGTGAATTCCAGGGCAGCGGAGATCTGCTCCAGCTTACAGGAGGAGGAGGAGGAGGAGGAGGCTG ATCTTGGTGGAGAGGAGGAGTACGACGTGCTGGCAAGCGGAGAGGAGGGACCCAGCTCTACAGAAC AAGAATCCCCAAGAGGGCTGATCAACAGGCTCCAAAAGGATAAGATGGCAGAAGGCTATAGCGAGATTGGTATGAAAGG

		GGAAACGCAGAAGAGGCCAAGGCCACGACGGACTGTACCAGGGACTCAGCACCGCCACCAAGGACACCTATGACGCTCTTC ACATGCAGGCCCTGCCGCCTCGG
88	M2 (ScFv domain) >FA56- 26RC (M2)	CAAGTCCAACACTCGTCCACTCAGGAGCAGAAGTCAAGAAACCAGGTGCTAGCGTAAAGTGTCTGCAAGGCGTCGGGATA CACTTTCACCGGATACTAC ATGCACTGGGTCCGCCAGGCCAGGGGGACAAGGGACTGGAATGGATGGGCTGGATCAACCCGAATAGGGGGAACTAATTA CGCCCAGAAGTTTCAGGGACGAGTGACCATGACCCCGGATACTCTATCTGACCGCCTACATGGAGCTCTCCAGACTGC GCTCGACGATACTGCACTGTACTACTGCGCCCGGACTCTGAGCGGACTGTGGTTACTCTCTCGCCCTATTATGGCATG GACGTGTGGGGCAAGGAACTACTGTGACTGTGAGCTCGGGAGGCGTGGGTAGCGGGAGGGCTGGGGCTGGTGG CTCGGGAGGGGGAGGAAGCAGACATTCAACTTACGAGGCCGTCACCCCTGTAGCGTCACTGGGGAGATCGGTGACCA TCACGTGTCAAGGCCAGGGATATCTCAACTCGTCAACTGGTACCGAGAAAGGGGGTAAAGCTCCGAAGCTGCTG ATCTACGACGCTTCCACCCCTCGAGACTGGAGTCCCATTCAGATTTCCGGTCAAGGAGCGGCCACCGATTCTCCTC CATTTCGTCTTGCACCGGAGGACATCCAACTACTGCGAGCTGGGGCCGCTGATACCCGGTCTGGGAGTCTGGCATATCTA GCACCAAGGTGGAAATCAAGACCACGATACCGCAGCCAGGCCACCCCGGCTCACCCTCGGCTGGGAGTCTGGCATATCTA TCCCTCGTCCCGAGGAGTGTAGACCGCAGCTGGGGCCGCTGATACCCGGTCTGGGAGTCTGGCATATCTG CATTGGGCCCTCTGGTGTACTTGGGGCTCTGTGCTTTCACTCGTGTACTCTTACTGTAAGCGCGTC AGAAGCTGTACATTTAACCGAACCTTCATGAGGGCTGTGAGACTACTCAAGAGGAGGACGCCGTGTTCATGCCGG TTCCAGAGGAGGAGGAAGGCCGCTGCAACTGCGCAGGAGATCTGGAGGAGGAGTCTCCACCCCTAACAGCAGGG GCAGAACAGCTTACAAACGAAACTCAATTGGTGGAGAGGAGTACGAGCTGCTGGAGAACCGAGGAGGGACC CAGAATGGCGGAAAGCCGAGAAAGAATCCCAAGAGGGCTGTACAACGAGCTCCAAAAGGATAAGATGCG GCCTATAGCGAGATTGGTATGAAAGGGGAACGAGAAGAGGCCACGAGCAGACTGTACCAGGGACTCAGCACCGC CACCAAGGACACCTATGACGCTTTCACATGCAGGCCCTGCCGCCTCGG
112	M2 (Full) >FA56- 26RC (M2)	ATGGCCCTCCCTGTACCGCCCTGCTGCTTCCGCTGGCTCTCTGCTCCACGCCGCTCGGCCCAAGTCCAACCTCGTCCA GTCAAGGAGCAGAAGTCAAGAAACCAGGTGCTAGCGTAAAGTGTCTGCAAGGCGTCGGGATAACACTTACCGGATACT AC ATGCACTGGGTCCGCCAGGCCAGGGGGACAAGGGACTGGAATGGATGGGCTGGATCAACCCGAATAGGGGGAACTAATTA CGCCCAGAAGTTTCAGGGACGAGTGACCATGACCCCGGATACTCTATCTGACCGCCTACATGGAGCTCTCCAGACTGC GCTCGACGATACTGCACTGTACTACTGCGCCCGGACTCTGAGCGGACTGTGGTTACTCTCTCGCCCTATTATGGCATG GACGTGTGGGGCAAGGAACATTCAACTTACGAGGCCGTCACCCCTGTAGCGTCACTGGGGAGATCGGTGACCA TCACGTGTCAAGGCCAGGGATATCTCAACTCGTCAACTGGTACCGAGAAAGGGGGTAAAGCTCCGAAGCTGCTG ATCTACGACGCTTCCACCCCTCGAGACTGGAGTCCCATTCAGATTTCCGGTCAAGGAGCGGCCACCGATTCTCCTC CATTTCGTCTTGCACCGGAGGACATCCAACTACTGCGAGCTGGGGCCGCTGATACCCGGTCTGGGAGTCTGGCATATCTA GCACCAAGGTGGAAATCAAGACCACGATACCGCAGCCAGGCCACCCCGGCTCACCCTCGGCTGGGAGTCTGGCATATCTA TCCCTCGTCCCGAGGAGTGTAGACCGCAGCTGGGGCCGCTGATACCCGGTCTGGGAGTCTGGCATATCTG CATTGGGCCCTCTGGTGTACTTGGGGCTCTGTGCTTTCACTCGTGTACTCTTACTGTAAGCGCGTC AGAAGCTGTACATTTAACCGAACCTTCATGAGGGCTGTGAGACTACTCAAGAGGAGGACGCCGTGTTCATGCCGG TTCCAGAGGAGGAGGAAGGCCGCTGCAACTGCGCAGGAGATCTGGAGGAGGAGTCTCCACCCCTAACAGCAGGG GCAGAACAGCTTACAAACGAAACTCAATTGGTGGAGAGGAGTACGAGCTGCTGGAGAACCGAGGAGGGACC CAGAATGGCGGAAAGCCGAGAAAGAATCCCAAGAGGGCTGTACAACGAGCTCCAAAAGGATAAGATGCG GCCTATAGCGAGATTGGTATGAAAGGGGAACGAGAAGAGGCCACGAGCAGACTGTACCAGGGACTCAGCACCGC CACCAAGGACACCTATGACGCTTTCACATGCAGGCCCTGCCGCCTCGG
89	M3 (ScFv domain) >VA58- 21LC (M3)	CAAGTCCAACACTCGTCCAA TCAGGAGCGAAGTCAAAGGCCGGAGCTCAGTAAAGTGTATGCAAGGCCCTCCGGTACACCTCACCGGTTACTA TATGCACTGGGTGCGGCAGGCCGGGCCAGGGTTGGAATGGATGGATGGATGGATCAATCCAAACTCGGTGGACTAACT ACGCCAGAAGTTCCAAGGACGGTGACCATGACTAGGGACACCTCGATCTCCACCGCATACATGGAGCTTAGCAGACTC CGCTCGACGATACCGCACTACTATTGCGCGGGAGATGGGACCGATCTACTACGATTACTGGGGCCAGGG AACTCTGGTACTGTTTCGGGTGGAGGAGTTCAGGGAGGCCGCTGGGGAGGAGTCTGGAGGAGGAGGGT CCGACATTGTGCTGACCCAAACTCTTCGCTCGGCGACCGCTGGGGAGGAGTCTGGAGGAGGAGGGT CAATCCATCAAACTACTACCTCAACTGGTACCGACATAAGCCGGGAAAGCACCAAAGCTGCTGATCTACGCCCTCATC CTTGCAGAGCGGTGTGCTTCACGTTAGGGATCGGGATCGGGATCGGGATTTCACCCCTGACTATCAGCTCCCTCAGC CGGAGGATTTCGCGACCTACTGTACGAGAGCTTCACCGCTGACTTCCGGCGCCGGACCAAGCTGGAAATCAAG ACCACATACCCCGACCGAGGCCACCCACCCGGCTTACCATCGCTCCCGACCTCTGCTCCCTGCTCCGGAGGCATG TAGACCCGACGTGGTGGGGCCGTCACCGGGGTTCTGACTTCGCTGCGATATCTACATTTGGGGCCCTGCTG GTACTTGCAGGGTCTCTGCTGCTTTACTCGTGTACTCTTACTGTAAGCGCGGTGCGAAGAAGCTGCTGTAACATCTT AAAGCAACCCCTCATGAGGCCGCTGCGAGACTACTCAAGAGGAGGAGCAGGCTGTTACGCGGGTTCCAGGGAGGAGG CGGCTGCGAAGTGCAGCTGAAATTCAAGGCCGAGCGCAGATGCTCCAGGCTACAAGCGGGAGGAGGAGGAG AACTCAATTGGTGGAGAGGAGTACGAGCTGCTGGACAAGCGGGAGGAGCAGGACCCAGAAATGGGGAGGAGCG CGCAGAAAGAATCCCAAGAGGGCTGTACAACGAGCTCCAAAAGGATAAGATGGCAGAAGCCTATAGCGAGATTGGT GAAAGGGGAACGAGAAGAGGCCACGACGGACTGTACCAGGGACTCAGCACCGCCACCAAGGACACCTATGACG CTCTCACATGCAGGCCCTGCCGCCTCGG
113	M3 (Full) >VA58- 21LC (M3)	ATGGCCCTCCCTGTACCGCCCTGCTGCTTCCGCTGGCTCTCTGCTCCACGCCGCTCGGCCCAAGTCCAACCTCGTCCA A TCAGGAGCGAAGTCAAAGGCCGGAGCTCAGTAAAGTGTATGCAAGGCCCTCCGGTACACCTCACCGGTTACTA TATGCACTGGGTGCGGCAGGCCGGGCCAGGGTTGGAATGGATGGATGGATGGATCAATCCAAACTCGGTGGACTAACT ACGCCAGAAGTTCCAAGGACGGTGACCATGACTAGGGACACCTCGATCTCCACCGCATACATGGAGCTTAGCAGACTC CGCTCGACGATACCGCACTACTATTGCGCGGGAGATGGGACCGATCTACTACGATTACTGGGGCCAGGG AACTCTGGTACTGTTTCGGGTGGAGGAGTTCAGGGAGGCCGCTGGGGAGGAGTCTGGAGGAGGAGGGT CCGACATTGTGCTGACCCAAACTCTTCGCTCGGCGACCGCTGGGGAGGAGTCTGGAGGAGGAGGGT CAATCCATCAAACTACTACCTCAACTGGTACCGACATAAGCCGGGAAAGCACCAAAGCTGCTGATCTACGCCCTCATC CTTGCAGAGCGGTGTGCTTCACGTTAGGGATCGGGATCGGGAACTGGGATTTCACCCCTGACTATCAGCTCCCTCAGC CGGAGGATTTCGCGACCTACTGTACGAGAGCTTCACCGCTGACTTCCGGCGCCGGACCAAGCTGGAAATCAAG ACCACATACCCCGACCGAGGCCACCCACCCGGCTTACCATCGCTCCCGACCTCTGCTCCCTGCTCCGGAGGCATG TAGACCCGACGTGGTGGGGCCGTCACCGGGGTTCTGACTTCGCTGCGATATCTACATTTGGGGCCCTGCTG GTACTTGCAGGGTCTCTGCTGCTTTACTCGTGTACTCTTACTGTAAGCGCGGTGCGAAGAAGCTGCTGTAACATCTT AAAGCAACCCCTCATGAGGCCGCTGCGAGACTACTCAAGAGGAGGAGCAGGCTGTTACGCGGGTTCCAGGGAGGAGG CGGCTGCGAAGTGCAGCTGAAATTCAAGGCCGAGCGCAGATGCTCCAGGCTACAAGCGGGAGGAGGAGGAGG AACTCAATTGGTGGAGAGGAGTACGAGCTGCTGGACAAGCGGGAGGAGCAGGACCCAGAAATGGGGAGGAGCG CGCAGAAAGAATCCCAAGAGGGCTGTACAACGAGCTCCAAAAGGATAAGATGGCAGAAGCCTATAGCGAGATTGGT GAAAGGGGAACGAGAAGAGGCCACGACGGACTGTACCAGGGACTCAGCACCGCCACCAAGGACACCTATGACG CTCTCACATGCAGGCCCTGCCGCCTCGG
90	M4	CAAGTGAACACTCGTTGAA TCAGGTGGAGGTTGGTCAACCCGGAGGATCTCTCAGACTGTGCTGCGGCGTCGGGGTTACCTTCTGCTACTG

		GCACTCGCCTGGAAATCAAG
116	M6 (Full) >FE10-06ID (M6)	<p>ATGGCCCTCCCTGTCAACGCCCTGCTGCCCTCGCTCCACGCCCTCGGCCCAAGTCAACTCGTCCA GTCAGGTGCAAAGTGAAGAAACCGGAGCGTCAGTCAGTCATGCAAGCGTCAGGCTACACCTCACCAAGCTACT AC</p> <p>ATGCACTGGGTGCGCAGGCCAGGCTTGGAGTGGATGGAAATCATTAACCGTCAAGGAGGCTCCACCTCCTA CGCCAGAAGTTCAGGGAGAGTGCAGTCAGTCGGGATACGTCGACCTCGACCGTGTACATGGAAACTGAGCTCGTGC GCTCGAGGACACTGCTGTACTACTGCCACGGTACAGACTCATTCGGTGGCAGGAGACTACTACTATGGCATG GACGCTGGGGGAGGGCACTATGGTCACTGTGTCGCGGAGGGCTCGGGTGGAGGAGTAGCGGAGGAGGGGG AAGCGGAGGGGGGGCTCGATATCCAGATGACTCAAGTCAGTCGCGCTCCCTCGTGTGCCCTCGTTGGAGATCGGTACCA TCACCTGTGAGCTCCCAAGGGTGCAGTGGCTGGGAGGAGCTGGGAAACTGCCCGAAGCTCC ATCTACGCGTAGCAGCACCTCGAGTCGGAGTGCACATCCGGTCAAGGGATCTGGGTCAAGGACTTCACCCCTAC GATAACAATCTCCAGCGGAGGACTTGGCACCTATTACTGCCAACAGCAACAGCTCCCTCACTTTGGAGGG GCACTCGCTGGAAATCAAGACCACTACCCAGCACCGAGGCCACCCACCCGGCTCTACCATCGCCCTCCAGCCTCTG TCCCTGCGTCGGAGGACTGAGACCCGAGCTGGTGGGGCTGCAACCCGGGCTTGAACCTGGGATCTGACTTCGCGATATCTA CATTTGGGCCCCCTGGCTGGTACTTGGGGGCTCTGCTGCTTCACTGTGATCCTTACTGTAAGCGGGTCCGGA AGAAGCTGCTGATCATCTTAAGAACCCCTCATGAGGGCTCGAGACTACTCAAGAGGAGGACGGCTTGCATGCCGG TTCAGAGG GCAAGAACAGCTCTAACAGAACTCAATTTGGTGGAGAGAGGAGTAGCAGCTGGAGAAGCGGAGGAGGAGGAGG CAGAAATGGCGGAAGCGCGAGAAAGAATCCCAAGAGGGCTGTACAACGAGCTCCAAAGGATAAGATGGCAGAA GCCTATAGCGAGATTGGTATGAAAGGGGAACGCGAGAAGAGGAAAGGCCACGAGGACTGTACCGGGACTCAGCACCG CACCAAGGACACCTATGACGCTTTCACATGCAAGGCCCTGCCGCTCGG</p>
93	M7 (ScFv domain) >VE12-01CD (M7)	<p>CAAGTGCACATTGGTTCAA</p> <p>TCAGGAGGAGGAGTGGTGCACACCTGGAAGATCTCTAGACTGCGTGTGGCATCGGATTCACTTCTCATCATACGC AATGCACTGGTCCGCCAGGCCGGCAAGGCTTGGATGGTGGCGTCATTCATACGACGGCTCGAACAGTACT ACGCTGACAGCGTGAAGGGACGCTTACTATTCGGGACAATTGAGAACACTCTGTACCTCCAGATGAACCTCCTT AGGGCTGAGGACACCGCGCTACTACTGCCACGCTGGAAAGTGTGTCAGCTCCAGCTCCAGCTTTGACTACTGGGACA GGGAAACCTTGTGACCGTGTGTCGCGTGGAGGGGGAGCGGGGAGGGGATCAGGTGGGGCGGATCGGGAGGCGGG GATCAGAAATCGTGTGACTCGACTCCCGGACCGCTGTCTCTCAGCCGGAGAGAGAGCGATCCTGCTGCCGCGCC TCGAGAGCGTGTACACTAAGTACCTGGGTGGTACCCAGCAAAACGGGCTCAAGCGCCCTGGCTGTGATCTACGATGC CTCCACCCGGGACCCGGATCCCGATCGGTTCTCCGGCAGCGGCTGGGAACTGATTTCACGCTGACCACATCAATGCC TGGAGCGGAAGATTCCCGTCTATTACTGCCAGTACGCCGGGAGCCACTCATCCTTCGCTCAAGGAACCGGA CTCGAAATCAAGACCACTACCCAGCACCGAGGACCCACCCGGCTCTACCCAGCTCTGCCCCGCGCC TCCGGAGGAGTGTAGACCCGAGCTGGTGGGGCGTGCATACCCGGGCTTGAACCTCGCTGCGATATCTACATTGG CCCCCTGGCTGGTACTTGGGGGCTCTGCTTCACTCGTGTACTCTTACTGTAAGCGCGCTGGAGAAGCTG CTGTACATCTTAAGCAACCTCATGAGGCTGTGAGACTACTCAAGAGGAGGAGGAGGCTGTTCATGCCGGTCCAGA GGAG AGCTCTACACGAACTCAATTTGGTGGAGAGAGGAGTAGCAGCTGGAGAAGCGGAGGAGGAGGAGGAGGAGGAGGAG GGCGGGAGGCCCCGAGAAAGAATCCCAAGAGGGCTGTACAACGACTCTCAAAGGATAAGATGCCAGAAGCTATAG CGAGATTGGTATGAAAGGGGAACGCGAGAAGAGGCAAGGCCACGACGGACTGTACCGGGACTCAGCACCGCAGCAAG ACACATATGACGCTTTCACATGCAAGGCCCTGCCGCTCGG</p>
117	M7 (Full) >VE12-01CD (M7)	<p>ATGGCCCTCCCTGTCAACGCCCTGCTGCCCTGGCTCTCTGCTCCACGCCCTCGGCCCAAGTCAATTGGTCA A</p> <p>TCAGGAGGAGGAGTGGTGCACACCTGGAAGATCTCTAGACTGCGTGTGGCATCGGATTCACTTCTCATCATACGC AATGCACTGGTCCGCCAGGCCGGCAAGGCTTGGATGGTGGCGTCATTCATACGACGGCTCGAACAGTACT ACGCTGACAGCGTGAAGGGACGCTTACTATTCGGGACAATTGAGAACACTCTGTACCTCCAGATGAACCTCCTT AGGGCTGAGGACACCGCGCTACTACTGCCACGCTGGAAAGTGTGTCAGCTCCAGCTCCAGCTTTGACTACTGGGACA GGGAAACCTTGTGACCGTGTGTCGCGTGGAGGGGGAGCGGGGAGGGGATCAGGTGGGGCGGATCGGGAGGCGGG GATCAGAAATCGTGTGACTCGACTCCCGGACCGCTGTCTCTCAGCCGGAGAGAGAGCGATCCTGCTGCCGCGCC TCGAGAGCGTGTACACTAAGTACCTGGGTGGTACCCAGCAAAACGGGCTCAAGCGCCCTGGCTGTGATCTACGATGC CTCCACCCGGGACCCGGATCCCGATCGGTTCTCCGGCAGCGGCTGGGAACTGATTTCACGCTGACCACATCAATGCC TGGAGCGGAAGATTCCCGTCTATTACTGCCAGTACGCCGGGAGCCACTCATCCTTCGCTCAAGGAACCGGA CTCGAAATCAAGACCACTACCCAGCACCGAGGACCCACCCGGCTCTACCCAGCTCTGCCCCGCGCC TCCGGAGGAGTGTAGACCCGAGCTGGTGGGGCGTGCATACCCGGGCTTGAACCTCGCTGCGATATCTACATTGG CCCCCTGGCTGGTACTTGGGGGCTCTGCTTCACTCGTGTACTCTTACTGTAAGCGCGCTGGAGAAGCTG CTGTACATCTTAAGCAACCTCATGAGGCTGTGAGACTACTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG GGAG AGCTCTACACGAACTCAATTTGGTGGAGAGAGGAGTAGCAGCTGGAGAAGCGGAGGAGGAGGAGGAGGAGGAGGAG GGCGGGAGGCCCCGAGAAAGAATCCCAAGAGGGCTGTACAACGACTCTCAAAGGATAAGATGCCAGAAGCTATAG CGAGATTGGTATGAAAGGGGAACGCGAGAAGAGGCAAGGCCACGACGGACTGTACCGGGACTCAGCACCGCAGCAAG ACACATATGACGCTTTCACATGCAAGGCCCTGCCGCTCGG</p>
94	M8 (ScFv domain) >LE13-05XD (M8)	<p>CAAGTCCAACCTCCAGCAG</p> <p>TCAGGTGCAAAGTCAAAGGCCAGGAGCATCCGTGAAGGTTTGTGCAAGACTTCCGGTACCCCTTTACGGGTACTC CCTCCATTGGTGGAGACAAGCACGGGCCAGGGACTGGAGTGGATGGATGCAACCCAAATTCCGGCGGCCACCAACT ATCGCGAGAAATTCCAGGGACGGGTGACCATGACTCGGACACTTCGATCTCCACTGCCATCGGACTGTCCCGCTTG AGATCTGACGACACGGCGCTACTACTGCCGGGACTGGAGTGGATGGATGCAACCCAAATTCCGGCGGCCACCAACT CCTCTGACTGTGTCCTCGGGTGGAGGGCTAGGGAGGAGGAGGCTAGGGAGGAGGAGGAGGAGGAGGAGGAGGAG ACATCCAACGACCCAGTCACCATCTCCATCTGGCTAGCGTGGAGAGACCCGGTGTGATTAATTGTAAGGGCTCCCAA GACTCAGGGACGTGGCTGGCTGGTATCAGCAAAACCCGGCAAGCTCGGAACTCTGCAACCGTGTGATGTCAGCGCAGCAC CGAAGATGGAGTGCCTAGCCGTTAGCGGAAGCGCCTGGGACTGAATTCACTGCACTGTGAACTCGGCTCCAGCG AGGATTGGCGACCTACTACTGCCAGCAGTACAACAGCTACCCCTGACCTTTGGAGGCGGGACCAAGGTGGATATCAAG</p>
118	M8 (Full)	<p>ATGGCCCTCCCTGTCAACGCCCTGCTGCCCTGGCTCTCTGCTCCACGCCCTCGGCCCAAGTCAACTCCAGCA G</p> <p>TCAGGTGCAAAGTCAAAGGCCAGGAGCATCCGTGAAGGTTTGTGCAAGACTTCCGGTACCCCTTTACGGGTACTC</p>

	(ScFv domain) >TE13-19LD (M13)	TATCTTCTCCGATTACATAT ATGGGATGGATTCCGGCAGGCCCGGAAAGGGACTCGAATGGGTGTATACATCGAAGGTCAGGCTGTCATGACTA CGCAGACTCGGTGAAAGGCGATTACCTTTAGCCGGACAACGCCAAAGATTCCCTACTTGCAGATGAACAGCCTGC GAGCCGAGGAACTCTGCTACTACTGTGCGCGTCGCCGGTGGCAGCTACTGAAGATTTCAGCACTGGGACAG GGAACACTGGTGTACGGCTGAGCCGAGGGCGGAAGCGGAGGCGGAGGATCGGGCGCGAGGTTGGGGGGGGGG GTCTGACATCGTGTACGGCTACGGCCACGGGAGGGCGGAAGCGGAGGCGGAGGATCGGGCGCGAGGTTGGGGGGGG CCCAGTCAGTGACCAAGGAACTTCTGGCTTGGTACCAACAGAAGGCCGACAGGCCACGGCTGCTGCTTTGGTGC AGCAACTCGGCCACCGGAATCCGGATCGCTCTCGGGCTCAGGGTCCGGGACGGACTTCACCCGACTATCACCGGCT GGAACCTGAGGACTTCCGATGACTACTGCGAGTCAGGCTCCGACCAAGGACAGCTGGTCACTTCGGACAGGAC ATAGATCAAGACCACATACCCAGCAGGCCACCCACCCCGCTTACCATCGCCCTCCGCTGCTGCGTCC GAGGCTGTAGACCCGAGCTGGTGGGGCGTGCATACCCGGTCTTACTGACTTCGCTGCGTGCATATCTACATTGGGG TCTGGCTGTACTTGGGGGTCTGCTGCTTCACTCGTGTACTTACTGTAAGCGGGTCAAGAAGCTGCTG ACATCTTAAGCAACCCCTCATGAGGCCCTGTGCAAGACTACTCAAGAGGAGGACGGTGTTCATGCCGGTCCAGAGGAG GAGGAAGGCCGCTGCAACTGCCGTGAATTACCGCAGGCCAGGAGGAGTACGACGTGCTGGACAAGCGGAGGAGACGGGACCCAGAAATGGGG GGAAGGCCGCGAGAAAGATCCCAAGAGGGCTGTACACAGAGCTCCAAAGGATAAGATGCCAGAAGCCTATAGCGAG ATTGGTATGAAGGGGAACCGCGAAGAGGCAAGGCCACGAGGACTTACCAAGGGACTCAGCACCCACCAAGGACAC CTATGACGCTTCTCATGCAAGGCCCTGCCGCTCGG
123	M13 (Full) >TE13-19LD (M13)	ATGGGCTCCCTGTACCGCCCTGCTCTCCGCTGGCTCTCTGCTCCACGCCCTCGGCCCAAGTCAACTCGTGCA ATCAGGGTGGAGGACTCGTCAAACCCGGAGGATCATGGAGACTGTATCGAAGGCGAGCGGTTTATCTCTCGGATTACT AT ATGGGATGGATTCCGGCAGGCCCGGAAAGGGACTCGAATGGGTGTATACATCGAAGGTCAGGCTGTCATGACTA CGCAGACTCGGTGAAAGGCGATTACCTTAGCCGGACAACGCCAAAGATTCCCTACTTGCAGATGAACAGCCTGC GAGCCGAGGAACTCTGCTACTACTGTGCGCGTCGCCGGTGGTGGCAGCTACTGAAGATTTCAGCACTGGGACAG GGAACACTCTGTCAGCTGGTGGGGCGGAAGCGGAGGCGGAGGATCGGGCGGGAGGTTGGGGGGGGGGAGG GTCTGACATCGTGTACGGCTACCCGGACGGGAGGGCGGAGGATCGGGCTGCTGCTTGGGGGGGGGGGGAGG CCCAGTCAGTGACCAAGGAACTTCTGGCTTGGTACCAACAGAAGGCCGACAGGCCACGGCTGCTGCTTTGGTGC AGCACTCGGCCACCGGAATCCGGATCGCTCTCGGGCTCAGGGTCCGGGACGGACTTCACCCGACTATCACCGGCT GGAACCTGAGGACTTCCGATGACTACTGCGAGTCAGGCTCCGACCAAGGACAGCTGGTCACTTCGGACAGGAC AGATCAAGACCACATACCCAGCAGGCCACCCACCCCGCTTACCATCGCCCTCCGCTGCTGCGTCC GAGGCTGTAGACCCGAGCTGGTGGGGCGTGCATACCCGGTCTTACTGACTTCGCTGCGTGCATATCTACATTGGGG TCTGGCTGTACTTGGGGGTCTGCTGCTTCACTCGTGTACTTACTGTAAGCGGGTCAAGAAGCTGCTG ACATCTTAAGCAACCCCTCATGAGGCCCTGTGCAAGACTACTCAAGAGGAGGACGGTGTTCATGCCGGTCCAGAGGAG GAGGAAGGCCGCTGCAACTGCCGTGAATTACCGCAGCGCAGATGCTCCAGCTACAGCAGGGCAGAACAG CTACAAACGAACTATCTGGTCCGAGAGGAGTACGACGTGCTGGACAAGCGGAGGAGACGGGACCCAGAAATGGGG GGAAGGCCGCGAGAAAGATCCCAAGAGGGCTGTACACAGAGCTCCAAAGGATAAGATGCCAGAAGCCTATAGCGAG ATTGGTATGAAGGGGAACCGCGAAGAGGCAAGGCCACGAGGACTTACCAAGGGACTCAGCACCCACCAAGGACAC CTATGACGCTTCTCATGCAAGGCCCTGCCGCTCGG
100	M14 (ScFv domain) >BS83-951D (M14)	CAAGTCCAACCTCGTCAGTCGGGAGCAGAAGTTAGAGCACCAGGAGCGTCAGTGAATTCATGCAAGGCCCTGGGCTT CACCTTCCGGGATACTAC ATCCACTGGGTGCGCAAGGCCCGGGTCAGGGATTGGAGTGGATGGGAATCATTAACCCATCAGGAGGGAGCCGGCTTA CGCCAGAGAACTTCCAGGAGCGCTCACTATGACCCGAGATACTTCCACCTGACTGTGTACATGGAACTCTGCTCCCTGA GGTCCGACGACACTCGCAGTGTATTACTGTGCTCGACTGCCAGCTGCCGTGGGACTGTACTACCTGATTACTGGGG CAGGGAACTCTGGTGGACCGCTGCTCAGCGAGGTGGGGGTGCGGAAGCGGAGGCCGGCTTCAAGGCCGAGG AGGCTCGGACATCCAAATGACCGAAATCGCCGCTACCCGCTACCGTGGAGCTTGGGGAGATCGGGTGACCAATTACTGCAAGAG CATCGAGAACGCTAATATCTGGCTGGCTGGTACCAACAGAAGGCCGGAGGGCTTACACTGCTGATCTACAGTGC AGCAGCCTGGCTCTGGAGTGGCCCTCCCGCTCTCGGGCTGGGATCAGGAGGGAACTTACCCCTACCATCTCTCC GCAGGCGAGACATGACTTGGCCACCTACTACTGCCAGCAGTACCCAGAGCTTCCGGTGACCTTGGGGGGAGCAAAAGTGG ACATCAAGACCACATACCCAGCAGGCCACCCACCCCGCTTACCATCGCCCTCCAGGCTCTGCTCCCTGCC GAGGCTGTAGACCCGAGCTGGTGGGGCGTGCATACCCGGGTCTTACTGACTTCGCTGCGTGCATATCTACATTGGGG TCTGGCTGTACTTGGGGGTCTGCTGCTTCACTCGTGTACTTACTGTAAGCGGGTCAAGAAGCTGCTG ACATCTTAAGCAACCCCTCATGAGGCCCTGTGCAAGACTACTCAAGAGGAGGACGGTGTTCATGCCGGTCTCCAGAGGAG GAGGAAGGCCGCTGCAACTGCCGTGAATTACCGCAGCGCAGATGCTCCAGCTACAGCAGGGCAGAACAG CTACAAACGAACTATCTGGTCCGAGAGGAGTACGACGTGCTGGACAAGCGGAGGAGACGGGACCCAGAAATGGGG GGAAGGCCGCGAGAAAGATCCCAAGAGGGCTGTACACAGAGCTCCAAAGGATAAGATGCCAGAAGCCTATAGCGAG ATTGGTATGAAGGGGAACCGCGAAGAGGCAAGGCCACGAGGACTTACCAAGGGACTCAGCACCCACCAAGGACAC CTATGACGCTTCTCATGCAAGGCCCTGCCGCTCGG
124	M14 (Full) >BS83-951D (M14)	ATGGGCTCCCTGTACCGCCCTGCTCTCCGCTGGCTCTCTGCTCCACGCCCTCGGCCCAAGTCAACTCGTCCA GTGGGGAGCAGAAGTTAGAGCACCAGGAGCGTCAGTGAATTCATGCAAGGCCCTGGGCTTCACGTTCCCGGGATACT AC ATCCACTGGGTGCGCAAGGCCCGGGTCAGGGATTGGAGTGGATGGGAATCATTAACCCATCAGGAGGGAGCCGGCTTA CGCCAGAGAACTTCCAGGAGCGCTCACTATGACCCGAGATACTTCCACCTGACTGTGTACATGGAACTCTGCTCCCTGA GGTCCGACGACACTCGCAGTGTATTACTGTGCTCGACTGCCAGCTGCCGTGGGACTGTACTACCTGATTACTGGGG CAGGGAACTCTGGTGGACCGCTGCTCAGCGAGGTGGGGGTGCGGAAGCGGAGGCCGGCTTCAAGGCCGAGG AGGCTCGGACATCCAAATGACCGAAATCGCCGCTACCCGCTACCGTGGAGCTTGGGGAGATCGGGTGACCAATTACTGCAAGAG CATCGAGAACGCTAATATCTGGCTGGCTGGTACCAACAGAAGGCCGGAGGGCTTACACTGCTGATCTACAGTGC AGCAGCCTGGCTCTGGAGTGGCCCTCCCGCTCTCGGGCTGGGATCAGGAGGGAACTTACCCCTACCATCTCTCC GCAGGCGAGATGACTTGGCCACCTACTACTGCCAGCAGTACCCAGAGCTTCCGGTGACCTTGGGGGGAGCAAAAGTGG ACATCAAGACCACATACCCAGCAGGCCACCCACCCCGCTTACCATCGCCCTCCAGGCTCTGCTCCCTGCC GAGGCTGTAGACCCGAGCTGGTGGGGCGTGCATACCCGGGTCTTACTGACTTCGCTGCGTGCATATCTACATTGGGG TCTGGCTGTACTTGGGGGTCTGCTGCTTCACTCGTGTACTTACTGTAAGCGGGTCAAGAAGCTGCTG ACATCTTAAGCAACCCCTCATGAGGCCCTGTGCAAGACTACTCAAGAGGAGGACGGTGTTCATGCCGGTCTCCAGAGGAG GAGGAAGGCCGCTGCAACTGCCGTGAATTACCGCAGCGCAGATGCTCCAGCTACAGCAGGGCAGAACAG CTACAAACGAACTATCTGGTCCGAGAGGAGTACGACGTGCTGGACAAGCGGAGGAGACGGGACCCAGAAATGGGG GGAAGGCCGCGAGAAAGATCCCAAGAGGGCTGTACACAGAGCTCCAAAGGATAAGATGCCAGAAGCCTATAGCGAG ATTGGTATGAAGGGGAACCGCGAAGAGGCAAGGCCACGAGGACTTACCAAGGGACTCAGCACCCACCAAGGACAC CTATGACGCTTCTCATGCAAGGCCCTGCCGCTCGG
101	M15 (ScFv domain) >HS86-94XD	CAAGTCCAACCTCGTTCAA TCAGGTGGAGGACTCTGTCACCGAGGAAAGATCACTCAGACTCAGCTGCCCGCGTCGGGATTCACTTCGATGACTACCG AATGCACTGGGTGCGCAGGCCCGGGCAAGGAGCTGGAAATGGGTGAGCGGAATTAGCTGGAACCTGGGGTCCATCGGG ACGCCGACTCTGGTGAAGGGAGCTTACGATCTCCGGGACAATGCCAAAGAACCTCCCTGATTTCAGATGAACCTCTTG AGGGCTGAGGACACCGCCGCGTACTACTGCCGTTAACAGATGGATCATCGCTCCGGTCTGGGGAGACTTCGAGTACTGGGG CAAGGCCACTCTGGTGGCGCTGCAAGGAGCTTACCGCAGCGCAGATGCTCCAGCTACAGCAGGGCAGAACAG AACTGACCCAGAGGCCCGCGTCTCGTGTCCCGCTTGGTCACTGAGCTGCTGGACAAGCGGAGGAGACGGGACCCAGAAATGGGG GGAAGGCCGCGAGAAAGATCCCAAGAGGGCTGTACACAGAGCTCCAAAGGATAAGATGCCAGAAGCCTATAGCGAG ATTGGTATGAAGGGGAACCGCGAAGAGGCAAGGCCACGAGGACTTACCAAGGGACTCAGCACCCACCAAGGACAC CTATGACGCTTCTCATGCAAGGCCCTGCCGCTCGG

	(M15)	TACTACGCTTCATGGTACCAAGCAGAAAGCCGGACAGGCACCTATGCTGTATCTACGGAAAGAATAACCGCCATCCGGCATCCGGATCGCTTCGGACAGCGCGACACCGCATCCCTGACGATCACTGGAGCGCAGGCCGAGGATGAAGCCGACTACTGCAATTCCCGAGATTCAAGCGGCTACCCGTGTTGGGACCGGAACTAAGGTACCCGCTCTG
125	M15 (Full) >HS86- 94XD (M15)	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTCTGCTCCACGCCGCTCGGCCCAAGTCAACTCGTTCA A TCAGGTGGAGGACTCGTCAACCAAGGAAGATCACTCAGACTCAGCTGCCCGCGCTCGGGATTCACTTCGATGACTACGC AATGCACTGGTGCAGCAGGCCCGGGCAAAAGGACTGGAATGGGTGAGCGGAATTAGCTGGAACTCGGGTCCATCGGGT ACGCCGACTCTGGTCAAGGAGCTTACGATCTCCGGACAATGCCAGAAACTCCCTGATTTGAGATGAACCTCTTG AGGGTCAAGGAGACCCGGCGTGTACTACTGCGCTAAAGATGGATCATCGTCTGGGGACTACTCGATTACTGGG CCAGGGCACTCTGGTACCGTGTGTCAAGGGTGTGGAGGGTCCGGGAGGAGTAGCGGAGGCCGAGGGAGCAGCTG AACTGACCCAAGACCCGGCGGTGTGGTCCGGCTTGGTCAAGACTGTGCGGACTACCTGTCAAGGGGACGCCGCTGCC TACTACGCTTCATGGTACCAAGCAGAAAGCCGGACAGGCACCTATGCTGTTCACTACGGAAAGAATAACCGCCATCCGG CATCCGGATCGCTTCCTGGGTCAGCGGACACCGCATCCCTGACGATCACTGGAGCGCAGGCCGAGGATGAAG CCGACTACTGCAATTCCCGAGATTCAAGCGCCAGTACCCGGTACCTTACCATCGCTTCCACCGCTCTGCTCC ACCCAGCAGGCCGAGGCCACCCGGCTCTACCATCGCTTCCACCGCTCTGCTCCGGAGGGCATGTAGACC CGCAGCTGGTGGGGCGTGATACCCGGGCTTGTGACTCTGCTGCAATCTACATTGGGCCCTCTGGTGGTACTT GCGGGGCTCTGTGCTTCACTCGTGTACTTACTGTAAGCGCCGTGGAAAGAAGCTGCTGTACATCTTAAGCAA CCCTCATGAGGGCTGTGAGAGACTCAAGAGGGAGGGCTGTTCATGCCCTCCAGGAGGAGGAGGAGGAGGAGGCGT CGAAGTGCCTGCGTGAAGATTCAAGCCGAGCGCTCAGCTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG ATCTGGTCGGAGAGGGAGTACGACGTGCTGGACAAGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG AAGAATCCCCAAGAGGGCTGTACAACGAGCTCCAAAGGATAAGATGGCAGAAGCCTATAGCGAGATTGGTATGAAAGG GGAACGCGAGAAGAGGAAAGGCCACGACGGACTGTACCAAGGACTCACGACCGCCACCAAGGACACCTATGACGCTCTG ACATGCAAGCCCTGCCCGCTCG
102	M16 (ScFv domain) >XS87- 99RD (M16)	GAAGTGAACCTCGTGGAA TCTGGTGGAGGACTTGTCAACCTGGAAGATCGTTGAGACTCTCATGTGCTGCCCTCCGGGTTACCTTGACGACTACGC CATGCACTGGTGCAGCAGGCCACAGGAAAGGGTCTGGAGTGGGTTCCGGTATCTCGTGAACCTCGGGAGCACTGGCT ACGCTGATTGGTGAAGGGCGTTTACCATCTCCGAGACAATGCGAAGAAATTCCCTCATCTCGAGATGAACAGCCTC CGGGCGAGGATACTGCCCTGTACTACTGCGCCAAGGATAGCTCATCGTGTACGGGGTGGATCGCTTTCGATATCTG GGGCCAGGGCAGATGGTACCGTGTCTCGGGGGCGAGGCTCCGGGGGGAGGGTAGCGGAGGAGGAGGATCGAGCT CAGAGTTGACTCAAGAACCCGAGTGTCCGTGGACTGGGAAACCCCTCAGGATCAGTCCAGGGAGACGCTGAGG TCGTAACCGCTCTGTGACCGAGAACGGGAGGAGGGCTCTGTGATTTGGAGCCTCAAGAACGCCATC GGGCATCCGGGACCGTTCAAGCGGAAGCTCTCGGAAACACCGCGTCACTTATACCGCGCACAGGCTGAGGAG AAGCGGATTACTACTGCAACTCCCGCACAATACTGCCAACCATACGTGTTCCGGACCGGAAACGAAACTGACTGCTCTG ACCACTACCC ACGACCCGAGGCCACCCACCCGGCTCTACCATCGCTTCCAGGCTCTGCTCCGGAGGAGCATG TAGACCGCAGCTGGTGGGGCGCTGACATCCGGGGCTCTGTGACTTCCGGCTGGGATATCACATTGGGCCCTCTGGCTG GTACTTGGGGCTCTGTGCTTCACTCGTGTACTTACTGTAAGCGGCTGGAAAGAAGCTGCTGTACATCTT AAGCAACCCCTCATGAGGCTGTGAGACTACTCAAGAGGGAGGAGGGCTGTTCATGCCGTTCCCAAGGAGGAGGAGG CGGCTGCGAAGTGCCTGCAAACTCAGCCGAGCGCAGATGCTCCAGGCTACAAGCAGGGCAGAACAGCTCTAACACG AACTCAATCTGGTCGGAGAGGGAGTACGACGTGCTGGACAAGCGGAGAGGAGCAGGAGGAGGAGGAGGAGGAGG CGCAGAAAGATCCCAAGAGGGCTGTACAACGAGCTCCAAAGGATAAGATGGCAGAAGCCTATAGCGAGATTGGTAT GAAAGGGAAACCGAGAAGGCCAGACGGACTGTACCAAGGAGGACTCACGACCCACCAAGGACACCTATGACG CTCTCACATGCAAGCCCTGCCCGCTCG
126	M16 (Full) >XS87- 99RD (M16)	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTCTGCTCCACGCCGCTCGGCCGAAGTGAACCTCGTGGAA A TCTGGTGGAGGACTTGTCAACCTGGAAGATCGTTGAGACTCTCATGTGCTGCCCTCCGGGTTACCTTGACGACTACGC CATGCACTGGTGCAGCAGGCCACAGGAAAGGGTCTGGAGTGGGTTCCGGTATCTCGTGAACCTCGGGAGCACTGGCT ACGCTGATTGGTGAAGGGCGTTTACCATCTCCGAGACAATGCGAAGAAATTCCCTCATCTCGAGATGAACAGCCTC CGGGCCAGGGAGGATACTGCCCTGTACTACTGCGCCAAGGATAGCTCATCGTGTACGGGGTGGATCGCTTTCGATATCTG GGGCCAGGGCAGATGGTACCGTGTCTCGGGGGCGAGGCTCCGGGGGGAGGGTAGCGGAGGAGGAGGATCGAGCT CAGAGTTGACTCAAGAACCCGAGTGTCCGTGGACTGGGAAACCCCTCAGGATCAGTCCAGGGAGACGCTGAGG TCGTAACCGCTCTGTGACCGAGAACGGGAGGAGGGCTCTGTGATTTGGAGCCTCAAGAACGCCATC GGGCATCCGGGACCGTTCAAGCGGAAGCTCTCGGAAACACCGCGTCACTTATACCGCGCACAGGCTGAGGAG AAGCGGATTACTACTGCAACTCCCGCACAATACTGCCAACCATACGTGTTCCGGACCGGAAACGAAACTGACTGCTCTG ACCACTACCC ACGACCCGAGGCCACCCACCCGGCTCTACCATCGCTTCCAGGCTCTGCTCCGGAGGAGCATG TAGACCGCAGCTGGTGGGGCGCTGACATCCGGGGCTCTGTGACTTCCGGCTGGGATATCACATTGGGCCCTCTGGCTG GTACTTGGGGCTCTGTGCTTCACTCGTGTACTTACTGTAAGCGGCTGGAAAGAAGCTGCTGTACATCTT AAGCAACCCCTCATGAGGCTGTGAGACTACTCAAGAGGGAGGAGGGCTGTTCATGCCGTTCCCAAGGAGGAGGAGG CGGCTGCGAAGTGCCTGCAAACTCAGCCGAGCGCAGATGCTCCAGGCTACAAGCAGGGCAGAACAGCTCTAACACG AACTCAATCTGGTCGGAGAGGGAGTACGACGTGCTGGACAAGCGGAGAGGAGCAGGAGGAGGAGGAGGAGGAGG CGCAGAAAGATCCCAAGAGGGCTGTACAACGAGCTCCAAAGGATAAGATGGCAGAAGCCTATAGCGAGATTGGTAT GAAAGGGAAACCGAGAAGGCCAGACGGACTGTACCAAGGAGGACTCACGACCCACCAAGGACACCTATGACG CTCTCACATGCAAGCCCTGCCCGCTCG
103	M17 (ScFv domain) >NS89- 94MD (M17)	GAAGTTCAATTGGTGGAA TCTGGAGGAGGACTTGTCAACCCGTAGATCTCTGAGACTGTCCGTGCGGCATCGGGATTACCTCGACGACTACGC TATGCACTGGTGAAGACAAGCCCTGGAAAGGACTGGAGTGGGTGTCAGGCATCTCTGGAATAGGGGTTCACTGGAT ACGCCGATTGGTCAAGGGTCCATCCCTCACATTCCGGACAATGCCAGAAACTCCCTGTAACCTTCAAAATGAACCTCC CGGGCCAGGGAGTACCGCCCTCTACTACTGCGCCAAGAACAGCTCGTATGGTATGCCGGAGGGTCCGCAATTGACATCTG GGGACAGGGAAACTATGGTACTGTGTACAGGAGGCCAGACCCCTCAGGATCACGTCAGGGAGGAGGAGGAGGAGGAGG GCGAACACTACCCAAAGATCCAGCAAGTGGCTCGCAGGCCAGGGCCAGGGCCGGTCTCGTGTACCTGCACTGCGC TCATFACTACCGCTCTGTGACCGAGCAGAACGCCGGGGCAGGCCGGGCTCTGTGATCTACGGAAAGAACACAACGCCGTC GGGTATCCCAAGACCGTTTCGGGTAGCTCCAGCGGAATACGGCTAGCGTACCATACTGGAGCACAGGCTGAGGATG AAGCGGACTACTACTGCAATTCCGGGGCTCATGGGAACCATACGTGTTCCGGAACTGGTACCAAGGTGACTGTCCTG
127	M17	ATGGCCCTCCCTGTCACCGCCCTGCTGCTTCCGCTGGCTCTCTGCTCCACGCCGCTCGGCCGAAGTCAATTGGTGGAA A

DEMANDE OU BREVET VOLUMINEUX

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

CECI EST LE TOME 1 DE 2
CONTENANT LES PAGES 1 À 182

NOTE : Pour les tomes additionnels, veuillez contacter le Bureau canadien des brevets

JUMBO APPLICATIONS/PATENTS

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VOLUME

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NOTE: For additional volumes, please contact the Canadian Patent Office

NOM DU FICHIER / FILE NAME :

NOTE POUR LE TOME / VOLUME NOTE:

What is claimed is:

1. An isolated nucleic acid molecule encoding a chimeric antigen receptor (CAR), wherein the CAR comprises: i) an antibody or antibody fragment comprising a human anti-mesothelin binding domain, ii) a transmembrane domain, and iii) an intracellular signaling domain comprising a stimulatory domain, and wherein said anti-mesothelin binding domain comprises one or more of 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) comprising an amino acid sequence listed in Table 5 and one or more of 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) comprising an amino acid sequence listed in Table 4.
2. The isolated nucleic acid molecule of claim 1, comprising a LC CDR1, LC CDR2 and LC CDR3, wherein LC CDR1, LC CDR2 and LC CDR3 comprise an amino acid sequence listed in Table 5.
3. The isolated nucleic acid molecule of claim 1, comprising a HC CDR1, HC CDR2 and HC CDR3, wherein HC CDR1, HC CDR2 and HC CDR3 comprise an amino acid sequence listed in Table 4.
4. The isolated nucleic acid molecule of claim 1, comprising LC CDR1, LC CDR2 and LC CDR3, wherein LC CDR1, LC CDR2 and LC CDR3 comprise an amino acid sequence listed in Table 5, and HC CDR1, HC CDR2, and HC CDR3, wherein HC CDR1, HC CDR2 and HC CDR3 comprise an amino acid sequence listed in Table 4.

5. The isolated nucleic acid molecule of claim 1, wherein the anti-mesothelin binding domain comprises an amino acid sequence of any one of the light chain variable regions listed in Table 2.
6. The isolated nucleic acid molecule of claim 1, wherein the anti-mesothelin binding domain comprises an amino acid sequence of any one of the heavy chain variable region listed in Table 2.
7. The isolated nucleic acid molecule of claim 1, wherein the anti-mesothelin binding domain comprises an amino acid sequence of any light chain variable region listed in Table 2 and any heavy chain variable region listed Table 2.
8. The isolated nucleic acid molecule of any of the preceding claims, wherein the anti-mesothelin binding domain is a scFv.
9. The isolated nucleic acid molecule of any of the preceding claims, wherein the anti-mesothelin binding domain comprises a light chain variable region comprising an amino acid sequence having at least one, two or three modifications but not more than 30, 20 or 10 modifications of an amino acid sequence of a light chain variable region provided in Table 2, or a sequence with 95-99% identity to an amino acid sequence provided in Table 2.
10. The isolated nucleic acid molecule of any of the preceding claims, wherein the anti-mesothelin binding domain comprises a heavy chain variable region comprising an amino acid sequence having at least one, two or three modifications but not more than 30, 20 or 10 modifications 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.

11. The isolated nucleic acid molecule of any of the preceding claims, wherein the encoded anti-mesothelin binding domain comprises a sequence selected from a group consisting of SEQ ID NO: 39; SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, 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, and SEQ ID NO: 62, or a sequence with 95-99% identify thereof.
12. The isolated nucleic acid molecule of any of the preceding claims, wherein the nucleic acid sequence encoding the anti-mesothelin binding domain comprises a sequence selected from a group consisting of 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, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, and SEQ ID NO: 110, or a sequence with 95-99% identify thereof.
13. The isolated nucleic acid molecule of any of the preceding claims, wherein the encoded CAR includes a transmembrane domain that comprises a transmembrane domain of a protein selected from the group consisting of the alpha, beta or zeta chain of the T-cell receptor, CD28, CD3 epsilon, CD45, CD4, CD5, CD8, CD9, CD16, CD22, CD33, CD37, CD64, CD80, CD86, CD134, CD137 and CD154.
14. The isolated nucleic acid molecule of any of the preceding claims, wherein the encoded transmembrane domain comprises a sequence of SEQ ID NO: 6.
15. The isolated nucleic acid molecule of any of the preceding claims, wherein the encoded transmembrane domain comprises an amino acid sequence that comprises at least one, two or

three modifications but not more than 20, 10 or 5 modifications of an amino acid sequence of SEQ ID NO:6, or a sequence with 95-99% identity to an amino acid sequence of SEQ ID NO:6.

16. The isolated nucleic acid molecule of any of the preceding claims, wherein the nucleic acid sequence encoding the transmembrane domain comprises a sequence of SEQ ID NO:17, or a sequence with 95-99% identify thereof.

17. The isolated nucleic acid molecule of any of the preceding claims, wherein the encoded anti-mesothelin binding domain is connected to the transmembrane domain by a hinge region.

18. The isolated nucleic acid molecule of claim 17, wherein the encoded hinge region comprises SEQ ID NO:2, or a sequence with 95-99% identity thereof.

19. The isolated nucleic acid molecule of claim 17, wherein the nucleic acid sequence encoding the hinge region comprises a sequence of SEQ ID NO: 13, or a sequence with 95-99% identify thereof.

20. The isolated nucleic acid molecule of any of the preceding claims, further comprising a sequence encoding a costimulatory domain.

21. The isolated nucleic acid molecule of claim 20, wherein the costimulatory domain is a functional signaling domain obtained from a protein selected from the group consisting of OX40, CD2, CD27, CD28, CDS, ICAM-1, LFA-1 (CD11a/CD18), ICOS (CD278), and 4-1BB (CD137).

22. The isolated nucleic acid molecule of claim 20 or 21, wherein the encoded costimulatory domain comprises a sequence of SEQ ID NO:7.
23. The isolated nucleic acid molecule of claim 20 or claim 21, wherein the encoded costimulatory domain comprises an amino acid sequence having at least one, two or three modifications but not more than 20, 10 or 5 modifications of an amino acid sequence of SEQ ID NO:7, or a sequence with 95-99% identity to an amino acid sequence of SEQ ID NO:7.
24. The isolated nucleic acid molecule of claim 20 or 21, wherein the nucleic acid sequence encoding the costimulatory domain comprises a sequence of SEQ ID NO:18, or a sequence with 95-99% identify thereof.
25. The isolated nucleic acid molecule of any of the preceding claims, wherein the encoded intracellular signaling domain comprises a functional signaling domain of 4-1BB and/or a functional signaling domain of CD3 zeta.
26. The isolated nucleic acid molecule of any of the preceding claims, wherein the encoded intracellular signaling domain comprises the sequence of SEQ ID NO: 7 and/or the sequence of SEQ ID NO:9 or SEQ ID NO:10.
27. The isolated nucleic acid molecule of any of the preceding claims, wherein the intracellular signaling domain comprises an amino acid sequence having at least one, two or three modifications but not more than 20, 10 or 5 modifications of an amino acid sequence of SEQ ID NO:7 and/or an amino acid sequence of SEQ ID NO:9 or SEQ ID NO:10, or a sequence with 95-99% identity to an amino acid sequence of SEQ ID NO:7 and/or an amino acid sequence of SEQ ID NO:9 or SEQ ID NO:10.

28. The isolated nucleic acid molecule of any of the preceding claims, wherein the encoded intracellular signaling domain comprises the sequence of SEQ ID NO:7 and the sequence of SEQ ID NO:9 or SEQ ID NO:10, wherein the sequences comprising the intracellular signaling domain are expressed in the same frame and as a single polypeptide chain.
29. The isolated nucleic acid molecule of any of the preceding claims, wherein the nucleic acid sequence encoding the intracellular signaling domain comprises a sequence of SEQ ID NO:18, or a sequence with 95-99% identity thereof, and/or a sequence of SEQ ID NO:20 or SEQ ID NO:21, or a sequence with 95-99% identity thereof.
30. The isolated nucleic acid molecule of any of the preceding claims, further comprising a leader sequence.
31. The isolated nucleic acid molecule of claim 32, wherein the leader sequence comprises SEQ ID NO: 1.
32. An isolated polypeptide molecule encoded by the nucleic acid molecule of any one of claims 1-32.
33. The isolated polypeptide of claim 32, comprising a sequence selected from the group consisting of 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, SEQ ID NO: 70, 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, SEQ ID NO: 79, SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 83, SEQ ID NO: 84, SEQ ID NO: 85, and SEQ ID NO: 86.
34. An isolated chimeric antigen receptor (CAR) molecule comprising a human anti-mesothelin binding domain, a transmembrane domain, and an intracellular signaling domain.

35. The isolated CAR molecule of claim 34, comprising i) an antibody or antibody fragment which includes a human anti-mesothelin binding domain, ii) a transmembrane domain, and iii) an intracellular signaling domain.

36. The isolated CAR molecule of any of claims 34 or 35, wherein the anti-mesothelin binding domain does not compete for binding to human mesothelin with an antigen binding domain comprising a sequence comprising SEQ ID NO: 279.

37. The isolated CAR molecule of any of claims 34-36, wherein the anti-mesothelin binding domain competes with an antigen binding domain comprising:

a) one or more 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 anti-mesothelin binding domain sequence selected from SEQ ID NO: 43 and SEQ ID NO: 49, and one or more 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 anti-mesothelin binding domain sequence selected from SEQ ID NO: 43 and SEQ ID NO: 49;

b) a LC CDR1, LC CDR2 and LC CDR3 of an anti-mesothelin light chain amino acid sequence selected from SEQ ID NO: 43 and SEQ ID NO: 49, and an HC CDR1, HC CDR2, and HC CDR3 of an anti-mesothelin heavy chain amino acid sequence selected from SEQ ID NO: 43 and SEQ ID NO: 49; or

c) a sequence selected from SEQ ID NO: 43 and SEQ ID NO: 49.

38. The isolated CAR molecule of any of claims 34-37, wherein the anti-mesothelin binding domain binds to a different epitope of human mesothelin than the epitope of human mesothelin targeted by the antigen binding domain comprising a sequence comprising SEQ ID NO: 279.

39. The isolated CAR molecule of any of claims 34-38, wherein the anti-mesothelin binding domain binds to the C-terminus of human mesothelin.
40. The isolated CAR molecule of claim 39, wherein the anti-mesothelin binding domain binds an epitope within amino acids 450-588 of SEQ ID NO: 278.
41. The isolated CAR molecule of claim 40, wherein the epitope comprises amino acids 485-490, 498-507, 532-537, or 545-572 of SEQ ID NO: 278, or any subset or a combination thereof.
42. The isolated CAR molecule of any of claims 34-41, wherein the human anti-mesothelin binding domain comprises one or more 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) comprising an amino acid sequence listed in Table 5, and one or more 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) comprising an amino acid sequence listed in Table 4.
43. The isolated CAR molecule of any of claims 34-42, comprising LC CDR1, LC CDR2 and LC CDR3 comprising an amino acid sequence listed in Table 5.
44. The isolated CAR molecule of any of claims 34-43, comprising HC CDR1, HC CDR2, and HC CDR3 comprising an amino acid sequence listed in Table 4.
45. The isolated CAR molecule of any of claims 34-44, comprising LC CDR1, LC CDR2 and LC CDR3 comprising an amino acid sequence listed in Table 5, and HC CDR1, HC CDR2, and HC CDR3 comprising an amino acid sequence listed in Table 4.

46. The isolated CAR molecule of any of claims 59-45, wherein the anti-mesothelin binding domain is a scFv.

47. The isolated CAR molecule of any of claims 34-46, wherein the anti-mesothelin binding domain comprises a light chain and a heavy chain of an amino acid sequence listed in Table 2.

48. The isolated CAR molecule of any of claims 34-47, wherein the anti-mesothelin binding domain comprises: a light chain variable region comprising an amino acid sequence having at least one, two or three modifications but not more than 30, 20 or 10 modifications 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.

49. The isolated CAR molecule of any of claims 34-48, wherein the anti-mesothelin binding domain comprises a heavy chain variable region comprising an amino acid sequence having at least one, two or three modifications but not more than 30, 20 or 10 modifications 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.

50. The isolated CAR molecule of any of claims 34-49, wherein the anti-mesothelin binding domain comprises a sequence selected from a group consisting of SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, 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, and SEQ ID NO: 62, or a sequence with 95-99% identity thereof.

51. The isolated CAR molecule of any of claims 34-50, wherein the transmembrane comprises a transmembrane domain of a protein selected from the group consisting of the alpha, beta or zeta chain of the T-cell receptor, CD28, CD3 epsilon, CD45, CD4, CD5, CD8, CD9, CD16, CD22, CD33, CD37, CD64, CD80, CD86, CD134, CD137 and CD154.
52. The isolated CAR molecule of claim 51, wherein the transmembrane domain comprises a sequence of SEQ ID NO: 6.
53. The isolated CAR molecule of claim 51, wherein the transmembrane domain comprises an amino acid sequence having at least one, two or three modifications but not more than 20, 10 or 5 modifications of an amino acid sequence of SEQ ID NO: 6, or a sequence with 95-99% identity to an amino acid sequence of SEQ ID NO: 6.
54. The isolated CAR molecule of any one of claims 34-53, wherein the human anti-mesothelin binding domain is connected to the transmembrane domain by a hinge region.
55. The isolated CAR molecule of claim 54, wherein the hinge region comprises SEQ ID NO:2 or SEQ ID NO:36, or a sequence with 95-99% identity thereof.
56. The isolated CAR molecule of any of claims 34-55, wherein the intracellular signaling domain comprises a sequence encoding a costimulatory domain.
57. The isolated CAR molecule of claim 56, wherein the costimulatory domain comprises a functional signaling domain of a protein selected from the group consisting of OX40, CD2, CD27, CD28, CDS, ICAM-1, LFA-1 (CD11a/CD18), CD278 (also known as “ICOS”) and 4-1BB (CD137).

58. The isolated CAR molecule of claim 56 or 57, wherein the costimulatory domain comprises a sequence of SEQ ID NO: 7.

59. The isolated CAR molecule of claim 56 or 57, wherein the costimulatory domain comprises an amino acid sequence having at least one, two or three modifications but not more than 20, 10 or 5 modifications of an amino acid sequence of SEQ ID NO: 7, or a sequence with 95-99% identity to an amino acid sequence of SEQ ID NO: 7.

60. The isolated CAR molecule of claim 34-59, wherein the intracellular signaling domain comprises a functional signaling domain of 4-1BB and/or a functional signaling domain of CD3 zeta.

61. The isolated CAR molecule of claim 60, wherein the intracellular signaling domain comprises the sequence of SEQ ID NO: 7 and/or the sequence of SEQ ID NO:9.

62. The isolated CAR molecule of claim 60, wherein the intracellular signaling domain comprises the sequence of SEQ ID NO:7 and/or the sequence of SEQ ID NO:10.

63. The isolated CAR molecule of any of claims 34-55, wherein the intracellular signaling domain comprises an amino acid sequence having at least one, two or three modifications but not more than 20, 10 or 5 modifications of an amino acid sequence of SEQ ID NO: 7 and/or an amino acid sequence of SEQ ID NO:9 or SEQ ID NO:10, or a sequence with 95-99% identity to an amino acid sequence of SEQ ID NO:7 and/or an amino acid sequence of SEQ ID NO:9 or SEQ ID NO:10.

64. The isolated CAR molecule of any of claims 34-55, wherein the intracellular signaling domain comprises the sequence of SEQ ID NO: 7 and the sequence of SEQ ID NO: 9 or SEQ

ID NO:10, wherein the sequences comprising the intracellular signaling domain are expressed in the same frame and as a single polypeptide chain.

65. The isolated CAR molecule of any of claims 59-64, further comprising a leader sequence.

66. The isolated CAR molecule of claim 65, wherein the leader sequence comprises an amino acid sequence of SEQ ID NO: 1, or a sequence with 95-99% identity to an amino acid sequence of SEQ ID NO:1.

67. A human anti-mesothelin binding domain comprising one or more 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 any anti-mesothelin binding domain in SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, 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, and SEQ ID NO: 62, and one or more 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 any human anti-mesothelin binding domain in SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, 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, and SEQ ID NO: 62.

68. The human anti-mesothelin binding domain of claim 67, wherein the human anti-mesothelin binding domain is a scFv comprising a light chain and a heavy chain of an amino acid sequence of SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ

ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, 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, and SEQ ID NO: 62.

56, SEQ ID NO: 57, SEQ ID NO: 58, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, or SEQ ID NO: 62.

70. An human anti-mesothelin binding domain, wherein the anti-mesothelin binding domain does not compete for binding to human mesothelin with an antigen binding domain comprising a sequence comprising SEQ ID NO: 279.

71. The human anti-mesothelin binding domain of claim 70, wherein the anti-mesothelin binding domain competes with an antigen binding domain comprising:

- a) one or more 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 anti-mesothelin binding domain sequence selected from SEQ ID NO: 43 and SEQ ID NO: 49 and one or more 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 anti-mesothelin binding domain sequence selected from SEQ ID NO: 43 and SEQ ID NO: 49
- b) a LC CDR1, LC CDR2 and LC CDR3 of an anti-mesothelin light chain amino acid sequence selected from SEQ ID NO: 43 and SEQ ID NO: 49 and an HC CDR1, HC CDR2, and HC CDR3 of an anti-mesothelin heavy chain amino acid sequence selected from SEQ ID NO: 43 and SEQ ID NO: 49; or
- c) a sequence selected from SEQ ID NO: 43 and SEQ ID NO: 49.

72. The human anti-mesothelin binding domain any of claims 70 or 71, wherein the anti-mesothelin binding domain binds to a different epitope of human mesothelin than the epitope of human mesothelin targeted by an antigen binding domain comprising a sequence comprising SEQ ID NO: 279.

73. The human anti-mesothelin binding domain of any of claims 70-72, wherein the anti-mesothelin binding domain binds to the C-terminus of human mesothelin.
74. The human anti-mesothelin binding domain of claim 73, wherein the anti-mesothelin binding domain binds an epitope within amino acids 450-588 of SEQ ID NO: 278.
75. The human anti-mesothelin binding domain of claim 74, wherein the epitope comprises amino acids 485-490, 498-507, 532-537, or 545-572 of SEQ ID NO: 278, or any subset or a combination thereof.
76. A vector comprising a nucleic acid molecule encoding a CAR of any of the preceding claims.
77. The vector of claim 76, wherein the vector is selected from the group consisting of a DNA, a RNA, a plasmid, a lentivirus vector, adenoviral vector, or a retrovirus vector.
78. The vector of claim 76 or 77, further comprising a promoter.
79. The vector of claim 78, wherein the promoter is an EF-1 promoter.
80. The vector of claim 79, wherein the EF-1 promoter comprises a sequence of SEQ ID NO: 11.
81. The vector of any of claims 76-78, wherein the vector is an in vitro transcribed vector.

82. The vector of claim 81, wherein the nucleic acid sequence in the vector further comprises a poly(A) tail.
83. The vector of any of claims 81, wherein the nucleic acid sequence in the vector further comprises a 3'UTR.
84. A cell comprising the vector of any of claims 76-83.
85. The cell of claim 84, wherein the cell is a human T cell.
86. The cell of claim 85, wherein the T cell is a CD8+ T cell.
87. A method of making a cell comprising transducing a T cell with a vector of any of claims 76-83.
88. A method of generating a population of RNA-engineered cells comprising introducing an in vitro transcribed RNA or synthetic RNA into a cell, where the RNA comprises a nucleic acid encoding a CAR molecule of any of the preceding claims.
89. A method of providing an anti-cancer immunity in a mammal comprising administering to the mammal an effective amount of a cell expressing a CAR molecule of any of the preceding claims.
90. The method of claim 89, wherein the cell is an autologous T cell.
91. The method of claim 89 or 90, wherein the cell is an allogeneic T cell.

92. The method of any of claims 89-91, wherein the mammal is a human.
93. A method of treating a mammal having a disease associated with expression of mesothelin comprising administering to the mammal an effective amount of a cell comprising a CAR molecule of any of the preceding claims.
94. The method of claim 93, wherein the disease associated with mesothelin expression is selected from a proliferative disease such as a cancer or malignancy or a precancerous condition, or is a non-cancer related indication associated with expression of mesothelin.
95. The method of claim 93-94, wherein the disease is a cancer associated with mesothelin selected from the group consisting of mesothelioma, malignant pleural mesothelioma, non-small cell lung cancer, small cell lung cancer, squamous cell lung cancer, or large cell lung cancer, pancreatic cancer, pancreatic ductal adenocarcinoma, pancreatic metatstatic, ovarian cancer, colorectal cancer and bladder cancer, or any combination thereof.
96. The method of any of claims 93-95, wherein the cells expressing a CAR molecule are administered in combination with an agent that increases the efficacy of a cell expressing a CAR molecule.
97. The method of any of claims 93-96, wherein the cells expressing a CAR molecule are administered in combination with an agent that ameliorates one or more side effects associated with administration of a cell expressing a CAR molecule.
98. The method of any of claims 93-97, wherein the cells expressing a CAR molecule are administered in combination with an agent that treats the disease associated with mesothelin

99. The isolated nucleic acid molecule of any of claims 1-31, the isolated polypeptide molecule of any of claims 32-33, the isolated CAR of any of claims 34-66, the anti-mesothelin binding domain of any of claims 67-75, the vector of any of claims 76-83 or the cell of any of claims 84-86 for use as a medicament.

100. The isolated nucleic acid molecule of any of claims 1-31, the isolated polypeptide molecule of any of claims 32-33, the isolated CAR of any of claims 34-66, the anti-mesothelin binding domain of any of claims 67-75, the vector of any of claims 76-83 or the cell of any of claims 84-86 for use in the treatment of a disease expressing mesothelin.

101. A cell of any of claims 84-86, further expressing an inhibitory molecule that comprises a first polypeptide that comprises at least a portion of an inhibitory molecule, associated with a second polypeptide that comprises a positive signal from an intracellular signaling domain.

102. The cell of claim 101, wherein the first polypeptide comprises at least a portion of PD1 and the second polypeptide comprises a costimulatory domain and a intracellular signaling domain.

103. The method of claim 96, wherein the agent is an mTOR inhibitor and the subject is administered a low, immune enhancing, dose of an mTOR inhibitor, e.g., RAD001 or rapamycin.

104. The method of claim 103, wherein the mTOR inhibitor is a RAD001.

105. The method of claim 103, wherein the dose comprises an allosteric and a catalytic mTOR inhibitor.

106. The method of 103, wherein the mTOR inhibitor is administered for an amount of time sufficient to decrease the proportion of PD-1 positive T cells, increase the proportion of PD-

1 negative T cells, or increase the ratio of PD-1 negative T cells/ PD-1 positive T cells, in the peripheral blood of the subject, or in a preparation of T cells isolated from the subject.

107. The method of claim 103, wherein the immune effector cell, e.g., T cell, to be engineered to express a CAR, is harvested after a sufficient time, or after sufficient dosing of the low, immune enhancing, dose of an mTOR inhibitor, such that the level of PD1 negative immune effector cells, e.g., T cells, or the ratio of PD1 negative immune effector cells, e.g., T cells/ PD1 positive immune effector cells, e.g., T cells, in the subject or harvested from the subject has been, at least transiently, increased.

108. The method of claim 103, wherein the dose of an mTOR inhibitor is associated with mTOR inhibition of at least 5 but no more than 90%, e.g., as measured by p70 S6 kinase inhibition.

109. The method of claim 103, wherein the dose of an mTOR inhibitor is associated with mTOR inhibition of at least 10% but no more than 40%, e.g., as measured by p70 S6 kinase inhibition.

110. A method of treating a subject having a disease associated with expression of mesothelin comprising administering to the subject an effective amount of cells comprising a nucleic acid of any of claims 1-31, wherein the nucleic acid is introduced into T cells or NK cells using in vitro transcription, and the subject receives an initial administration of the cells comprising the nucleic acid, and one or more subsequent administrations of cells comprising the nucleic acid, wherein the one or more subsequent administrations are administered less than 15 days, e.g., 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, or 2 days after the previous administration.

FIG. 1

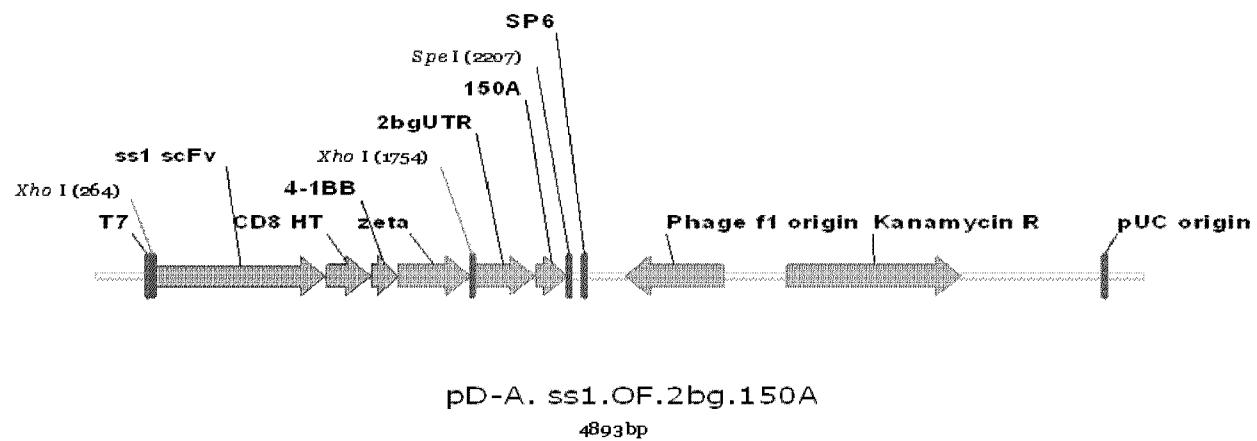
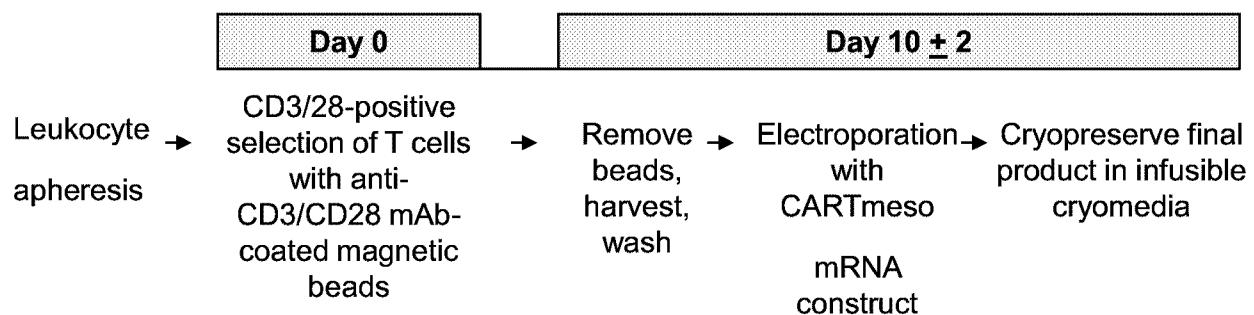
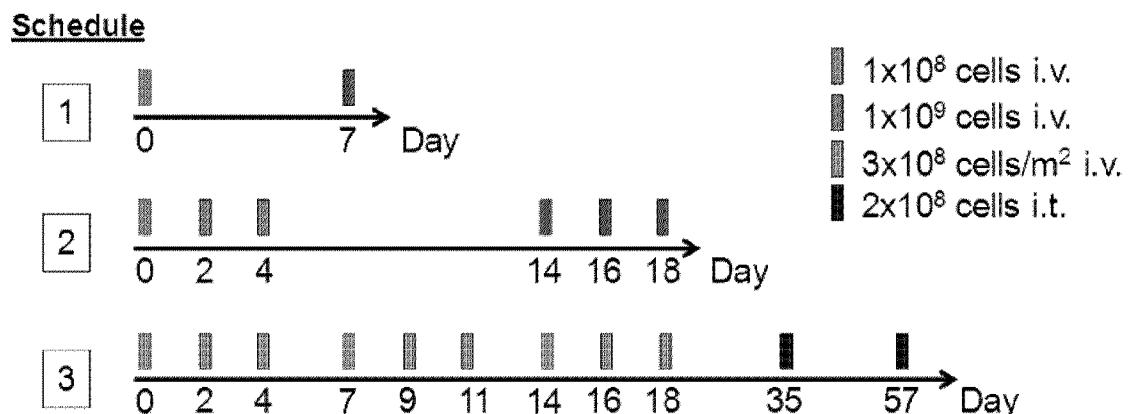
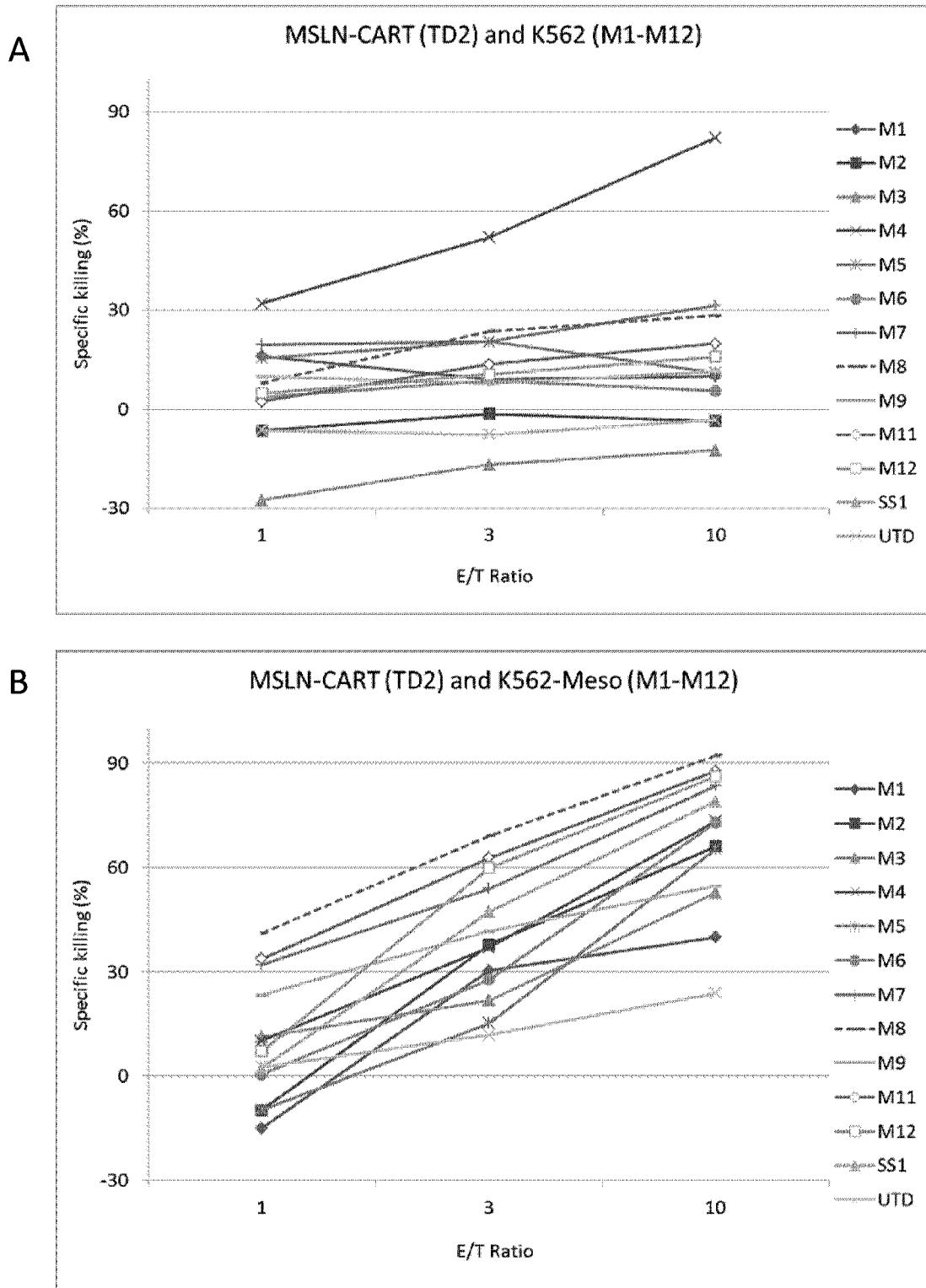


FIG. 2

A**B**

3/53
FIG. 3

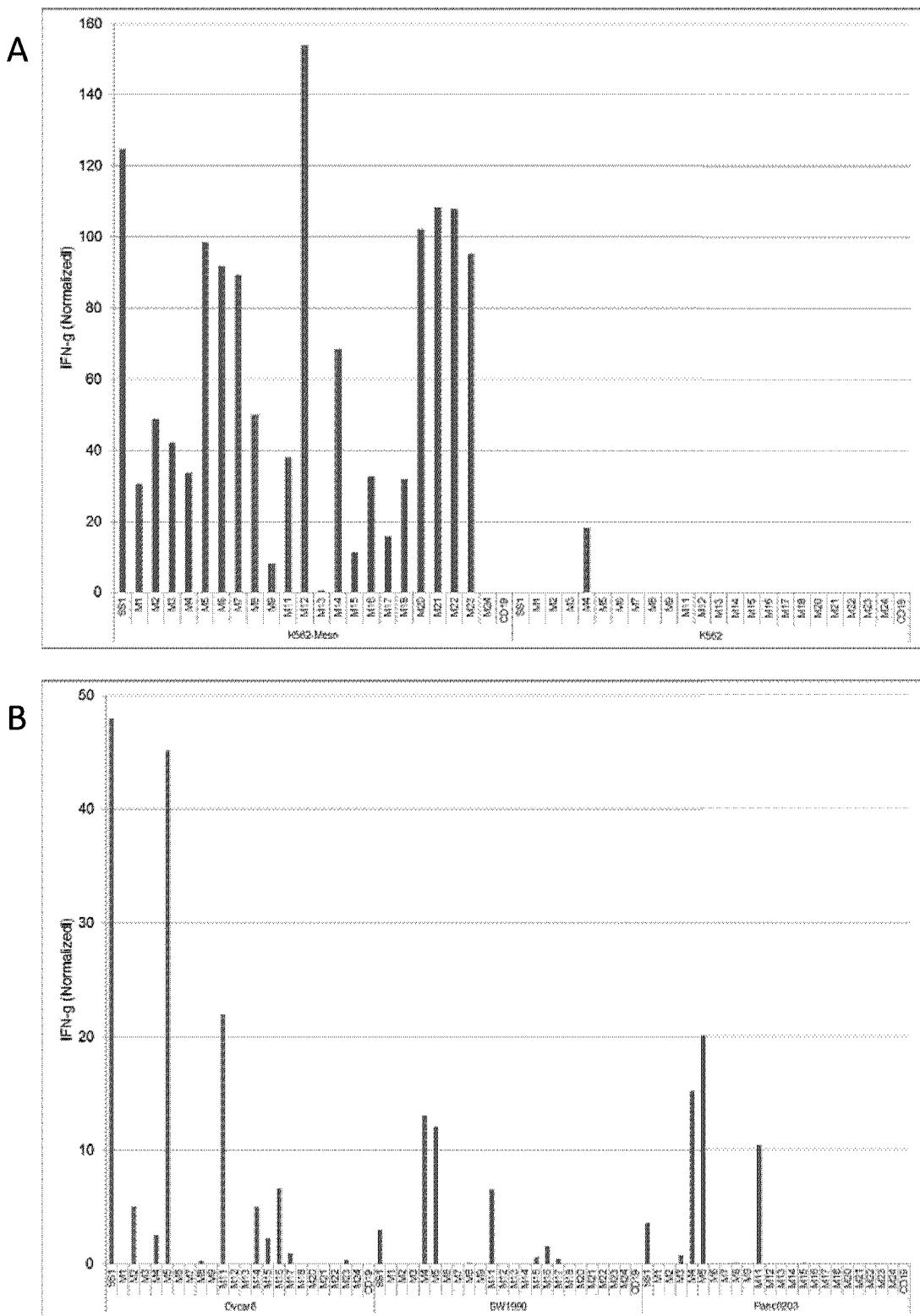
4/53
FIG. 4

FIG. 5

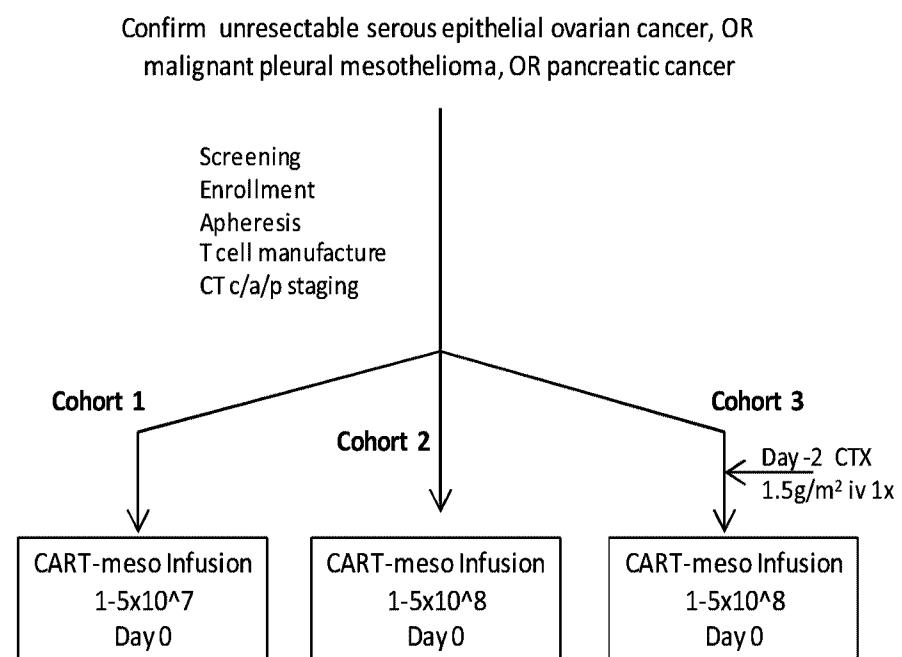


FIG. 6

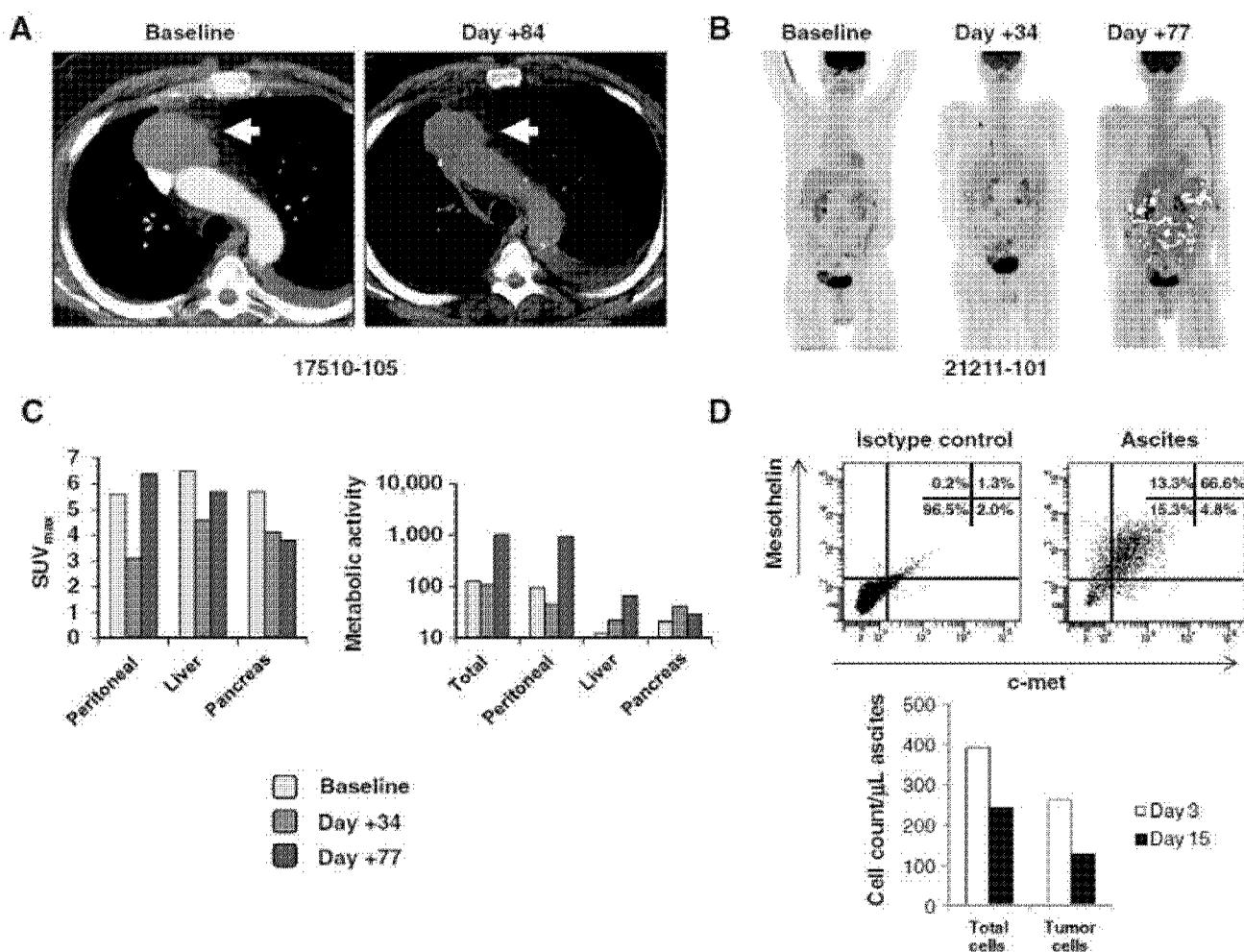


FIG. 7

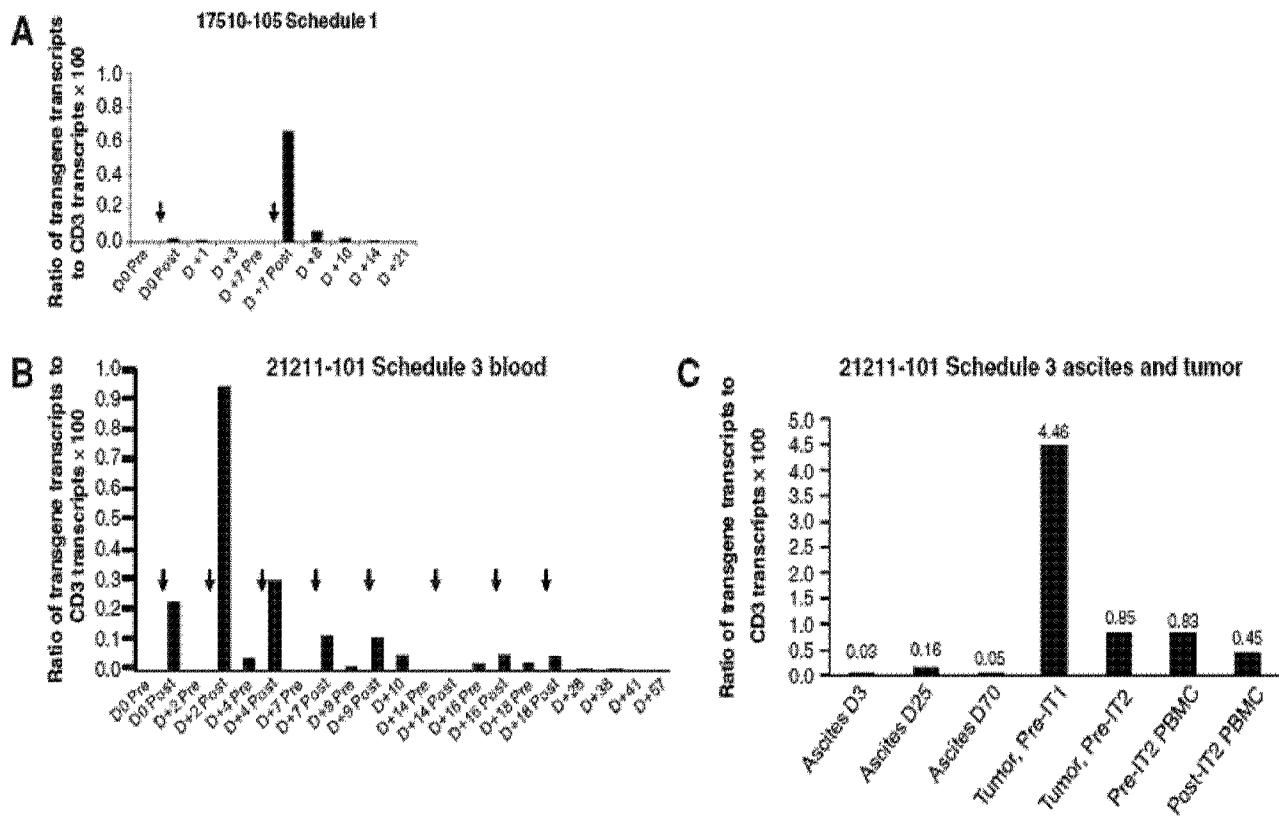


FIG. 8

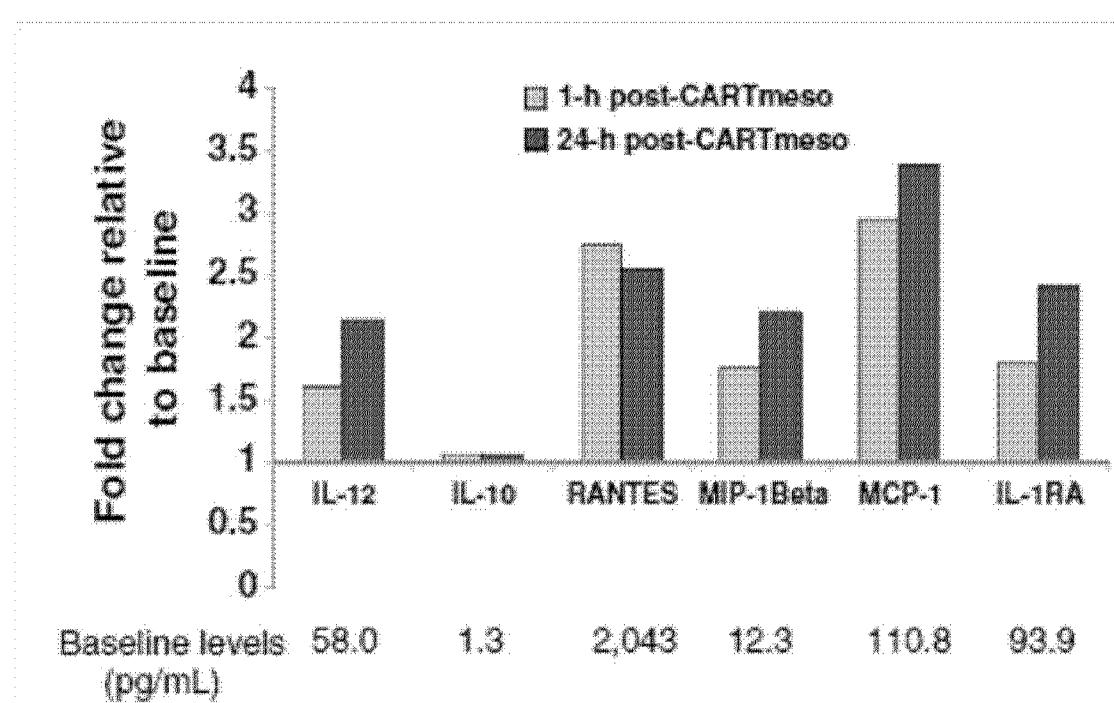


FIG. 9

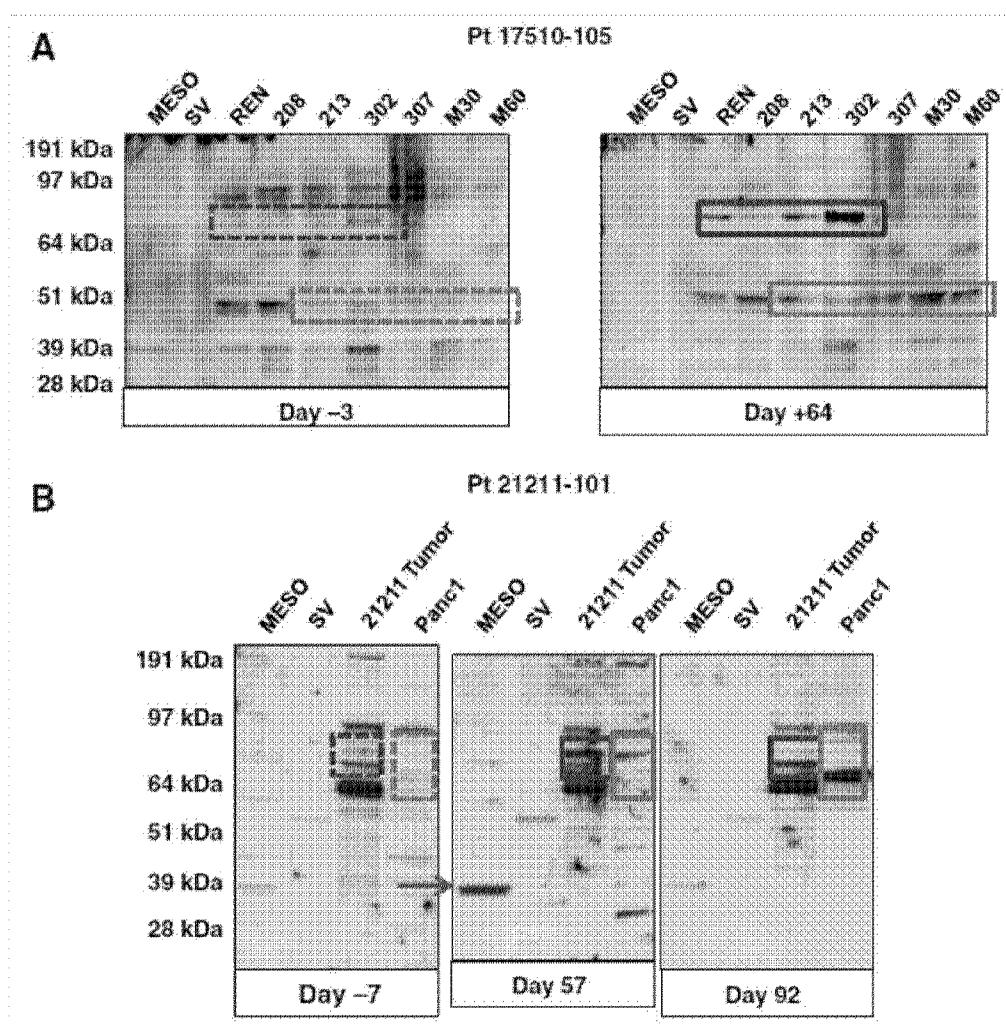


FIG. 10

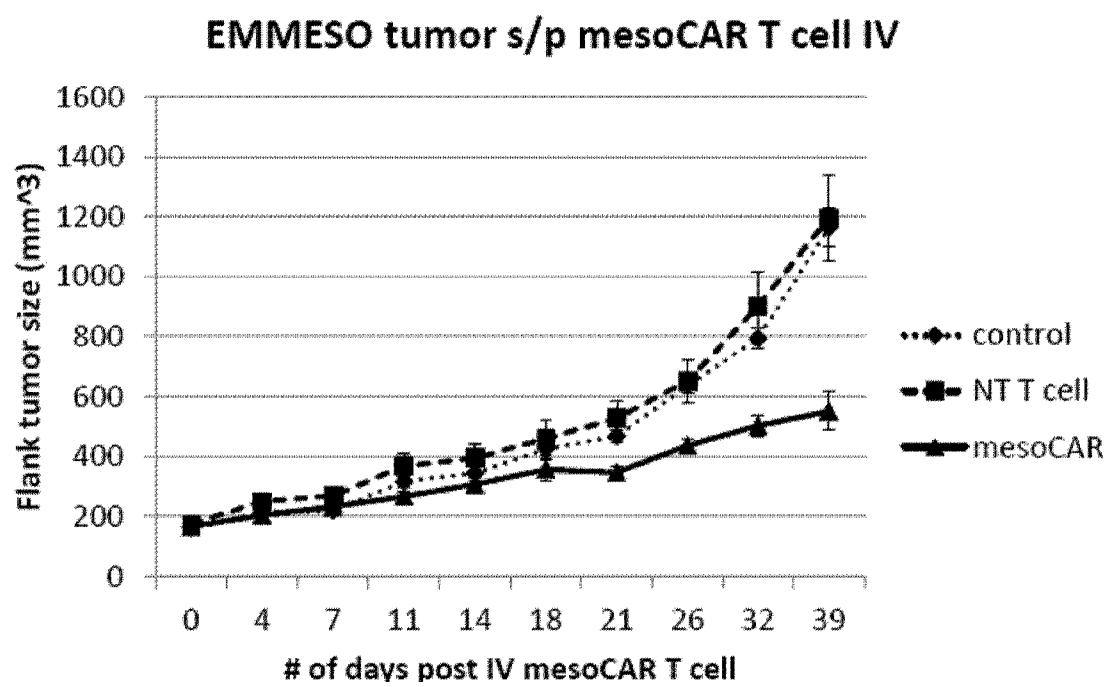


FIG. 11

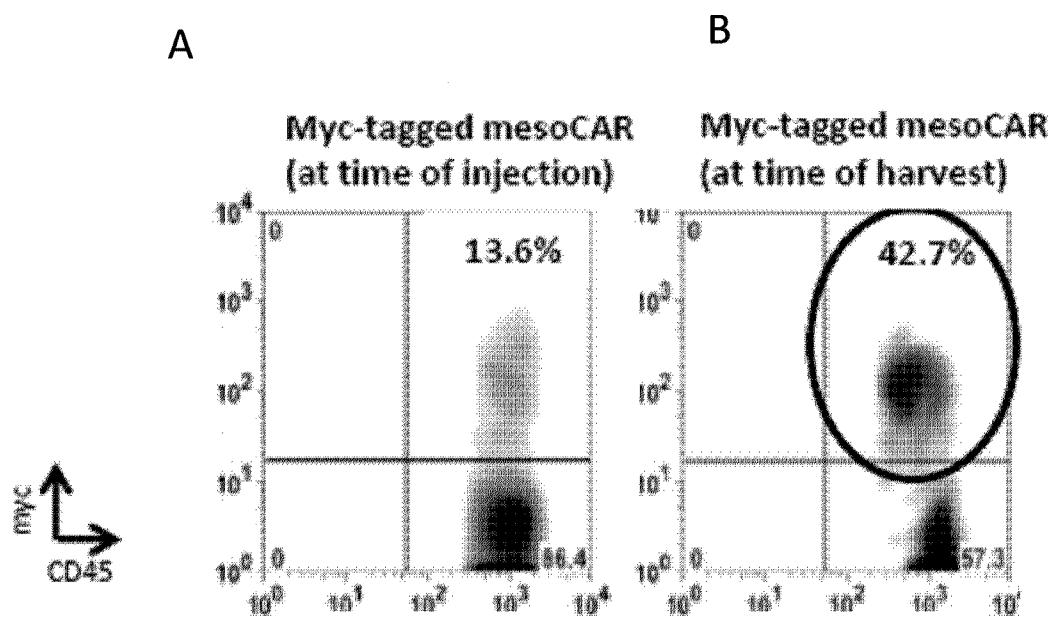


FIG. 12

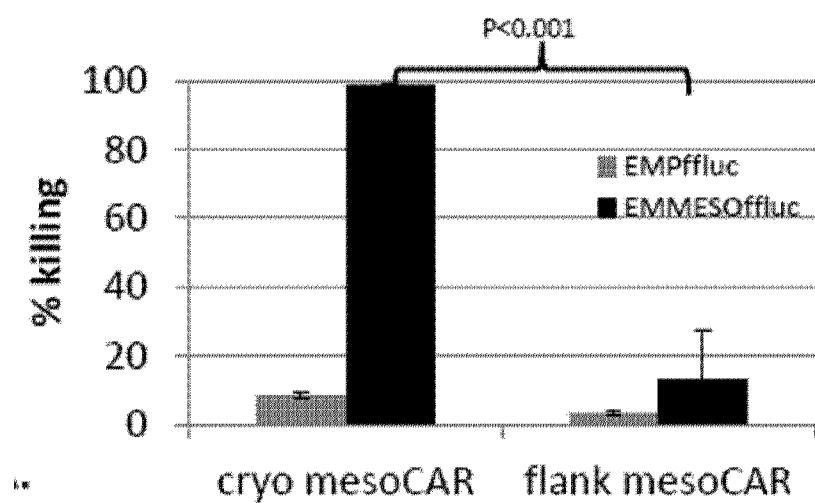


FIG. 13

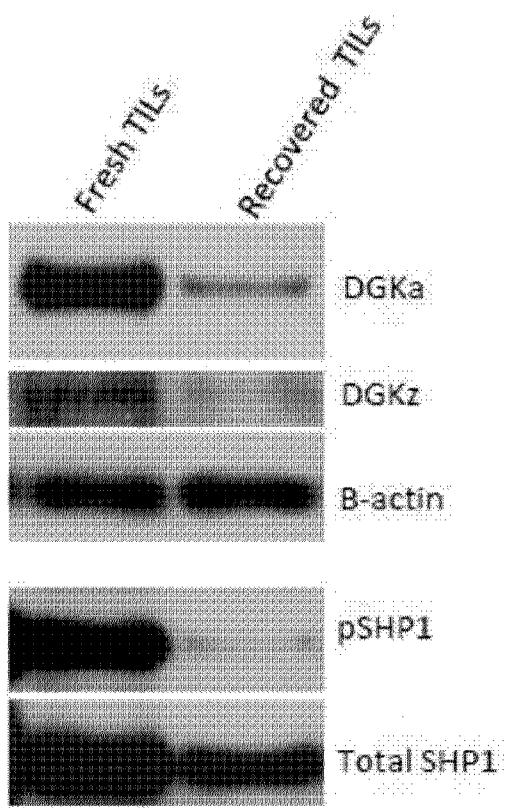


FIG. 14

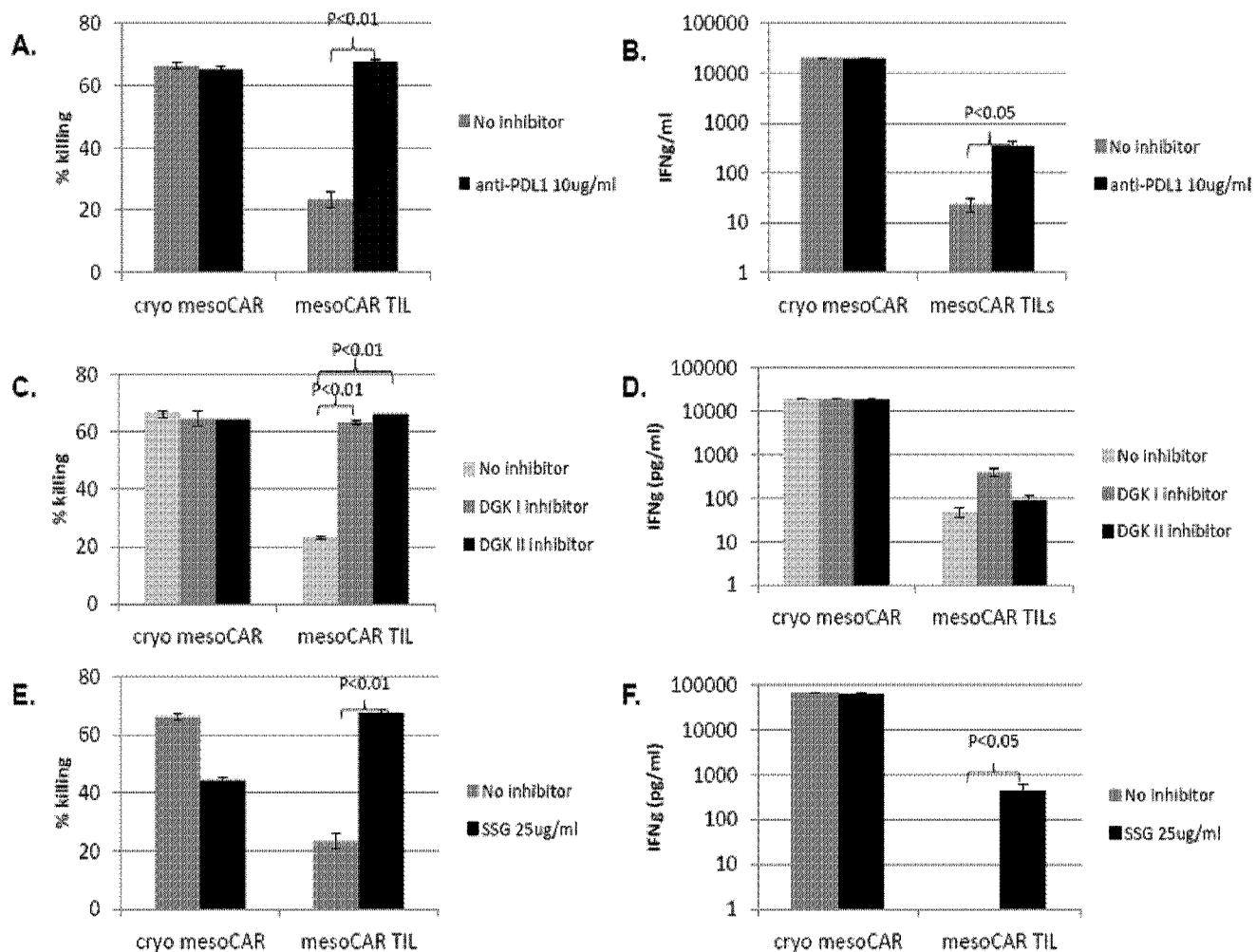


FIG. 15

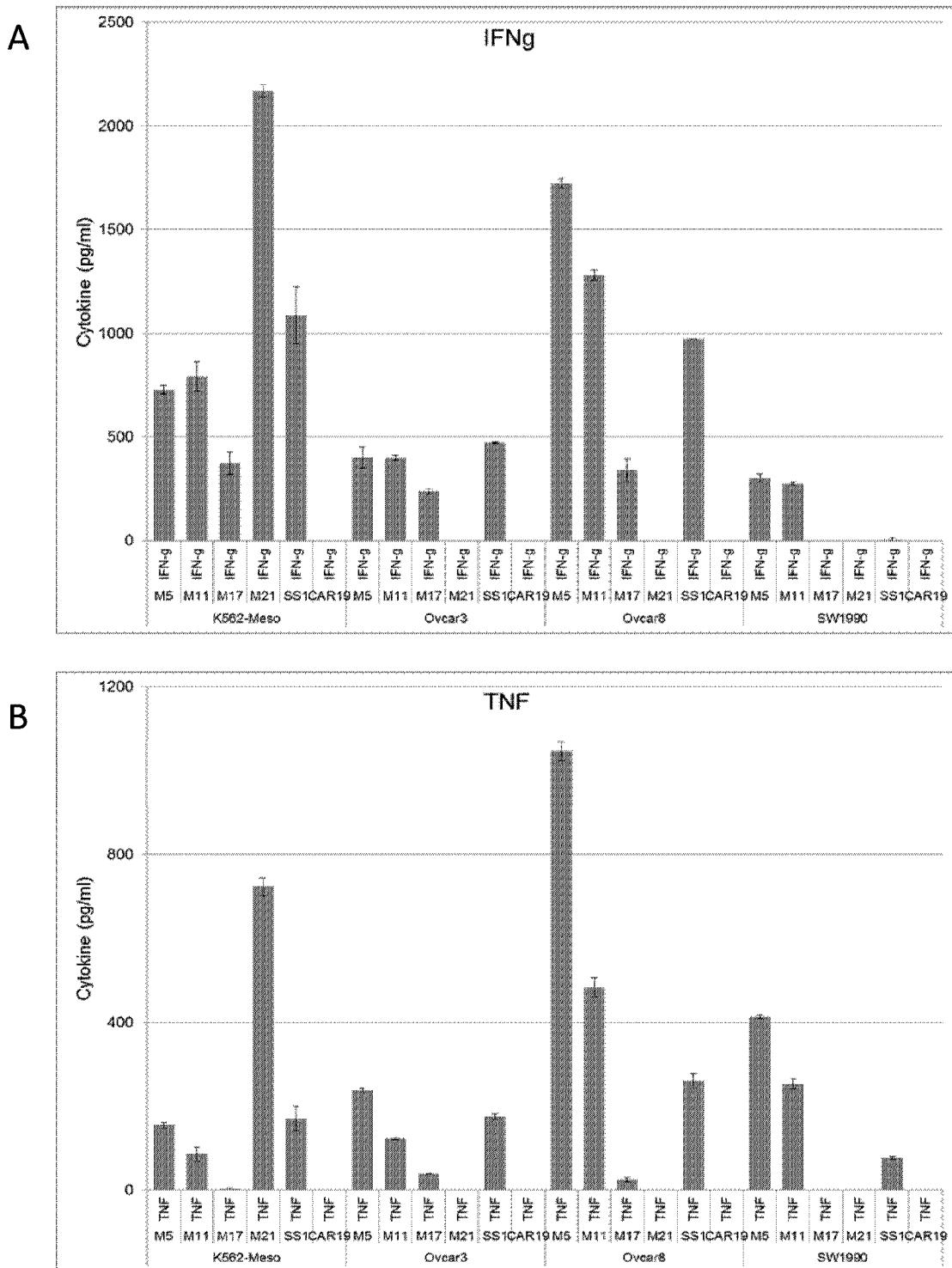


FIG. 15

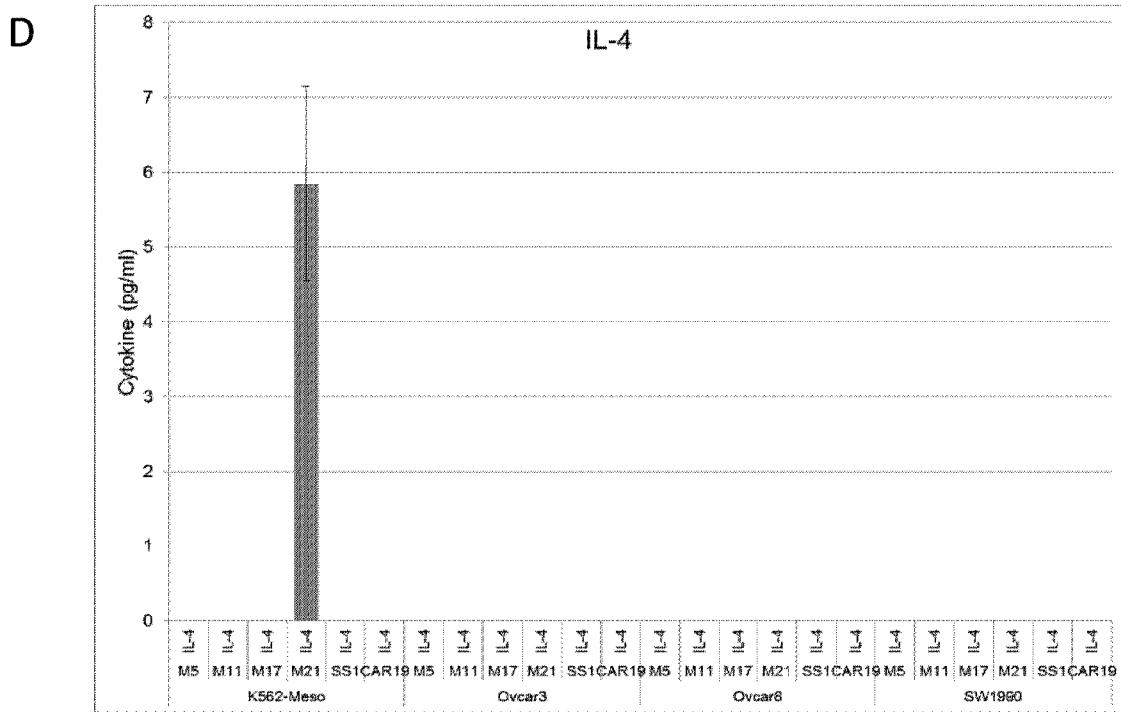
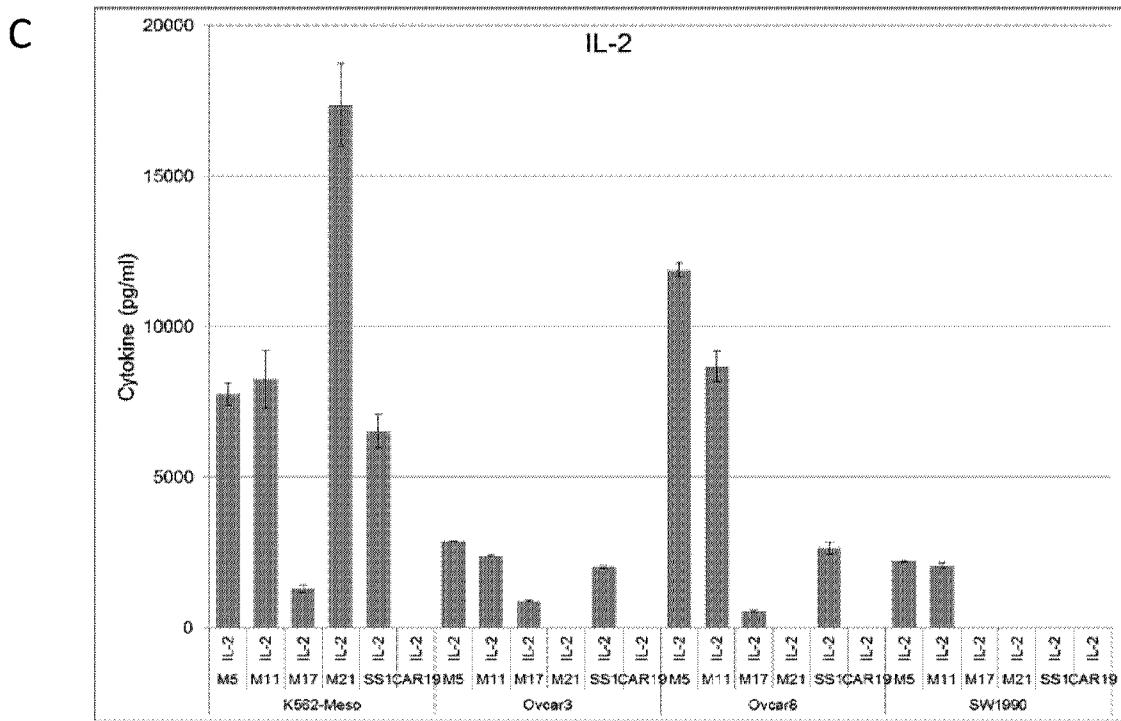


FIG. 16

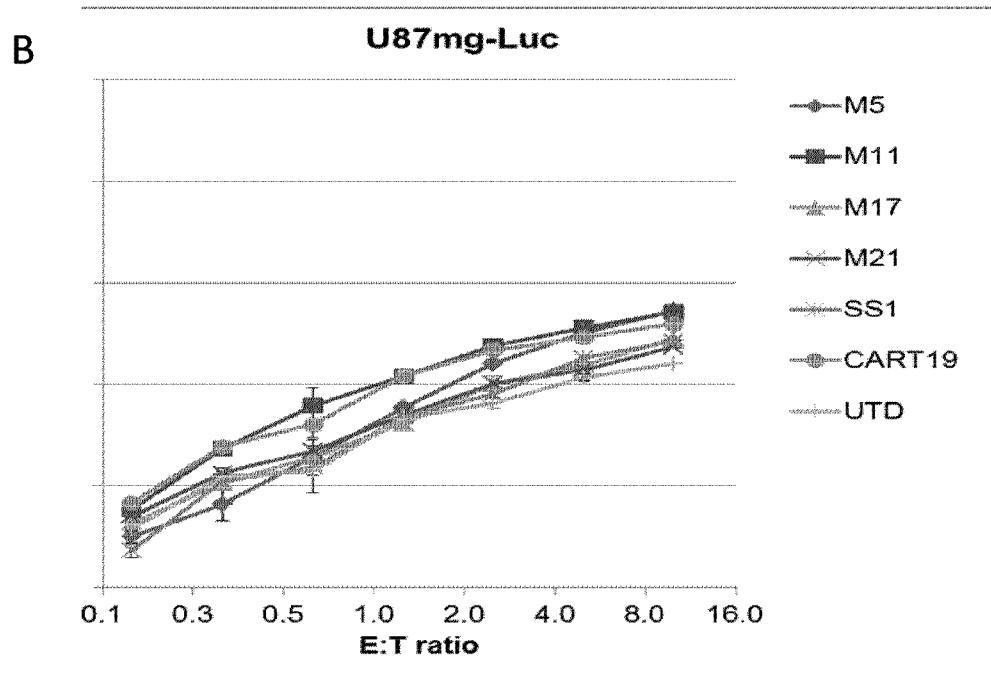
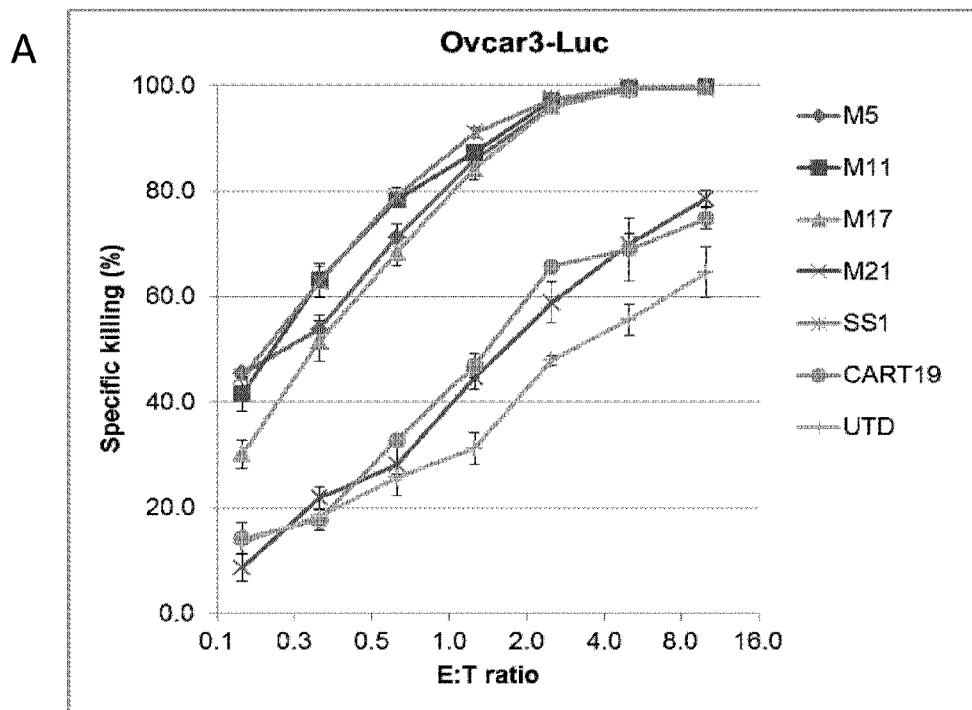


FIG. 17

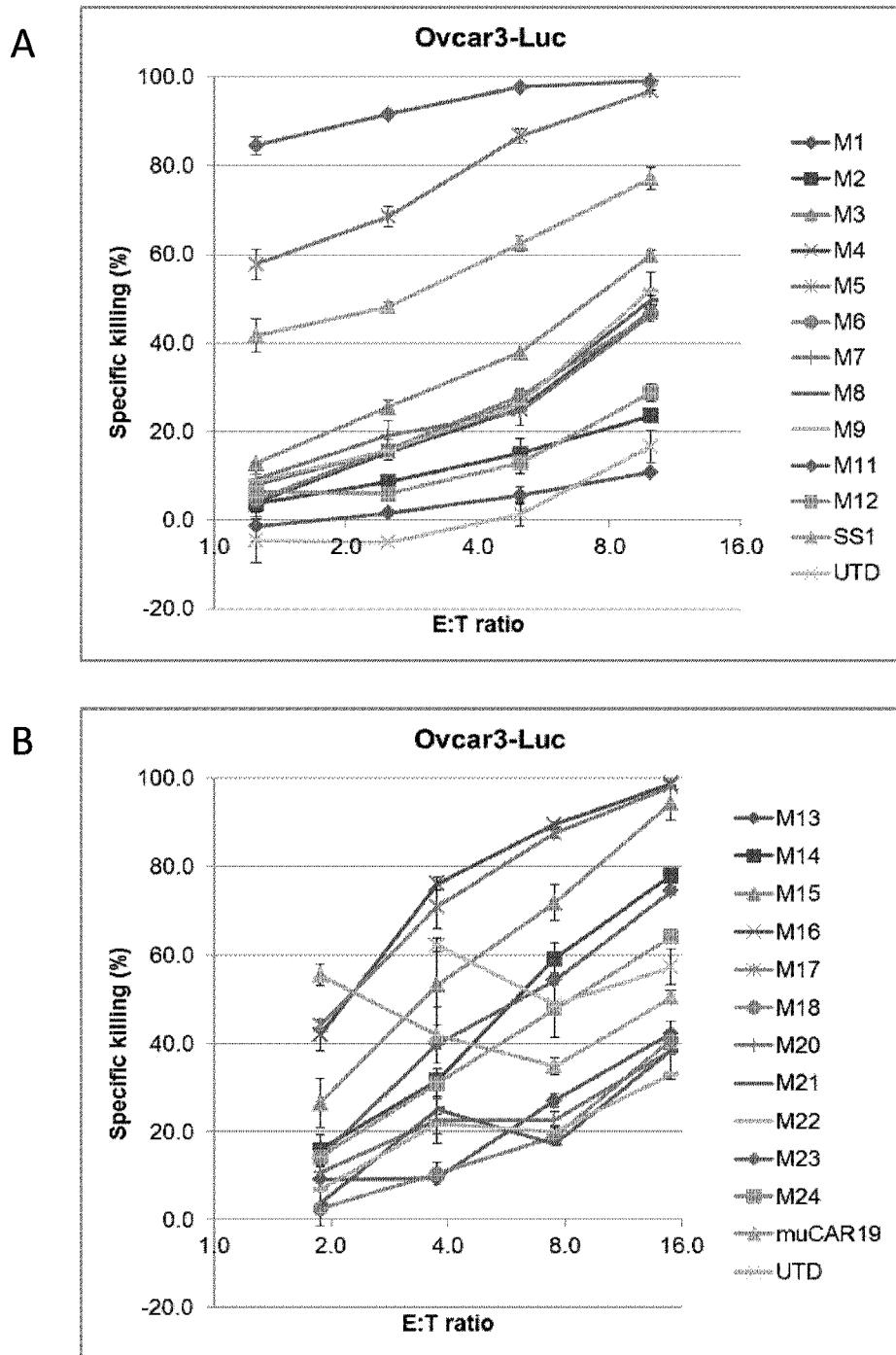


FIG. 18

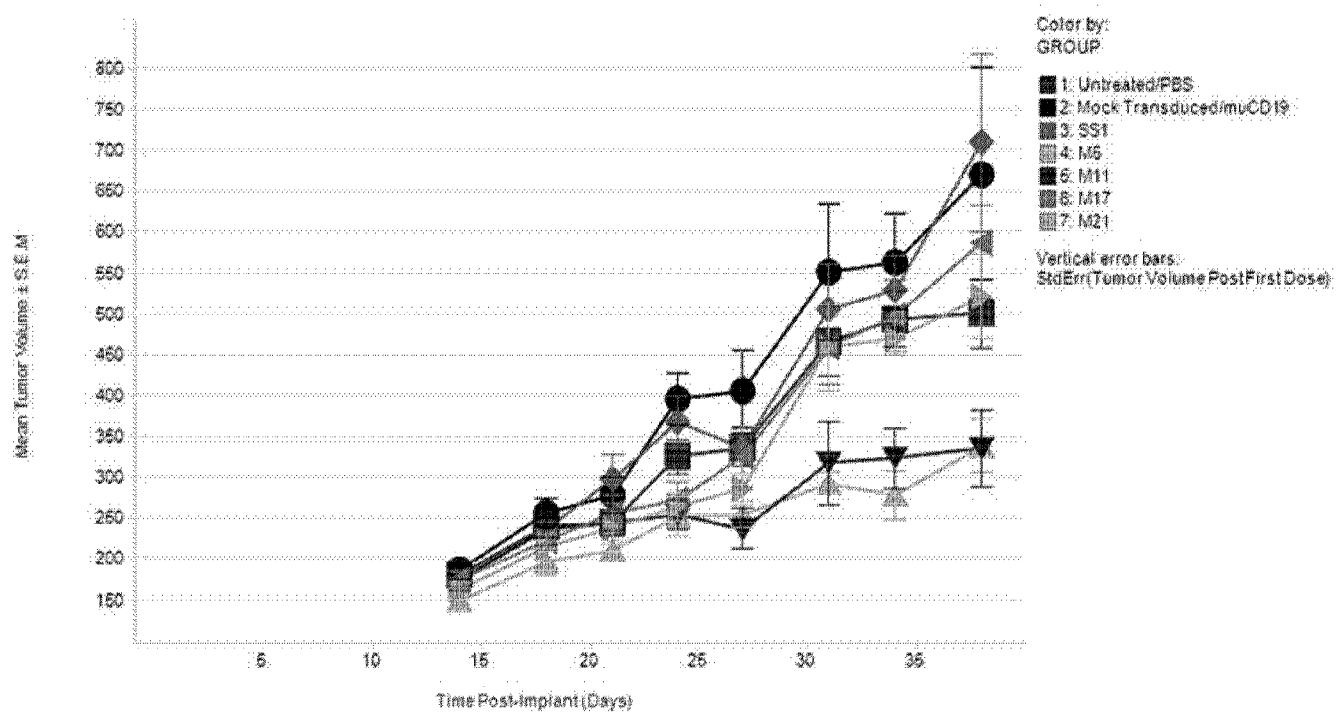
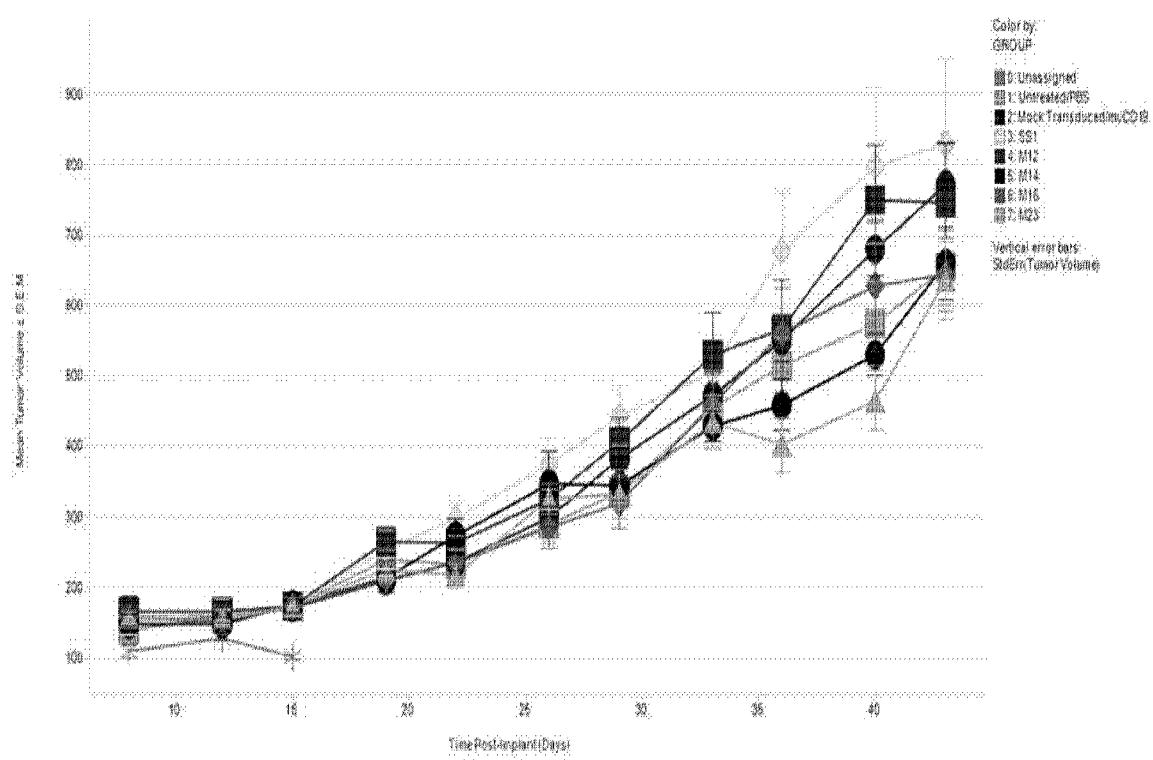


FIG. 19



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FIG. 20A

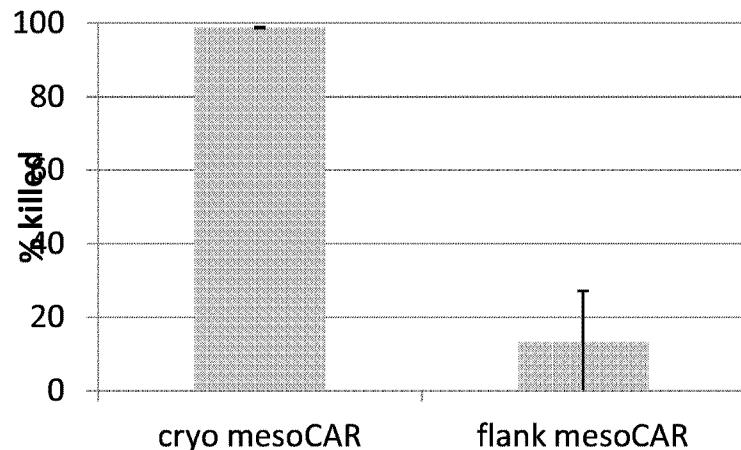
**EMMESO TIL ex vivo killing assay
(immediate harvest)**

FIG. 20B

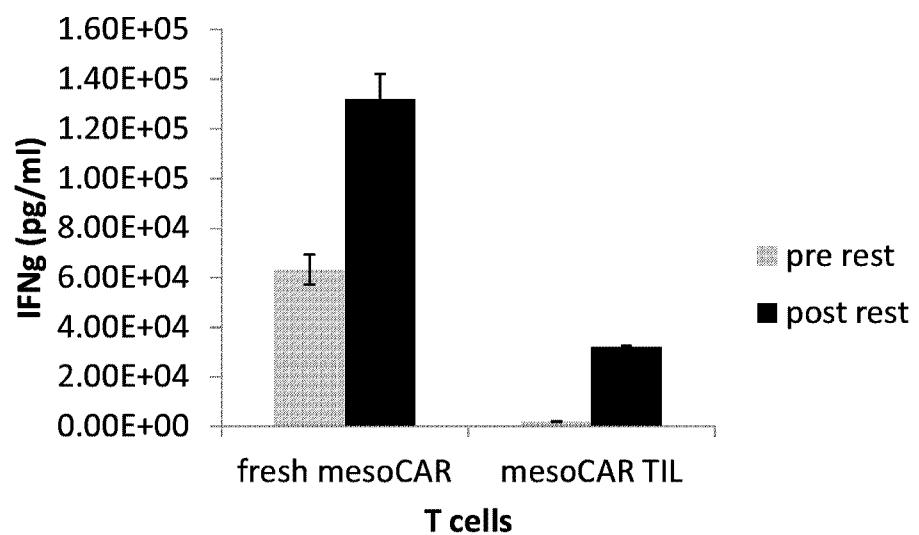
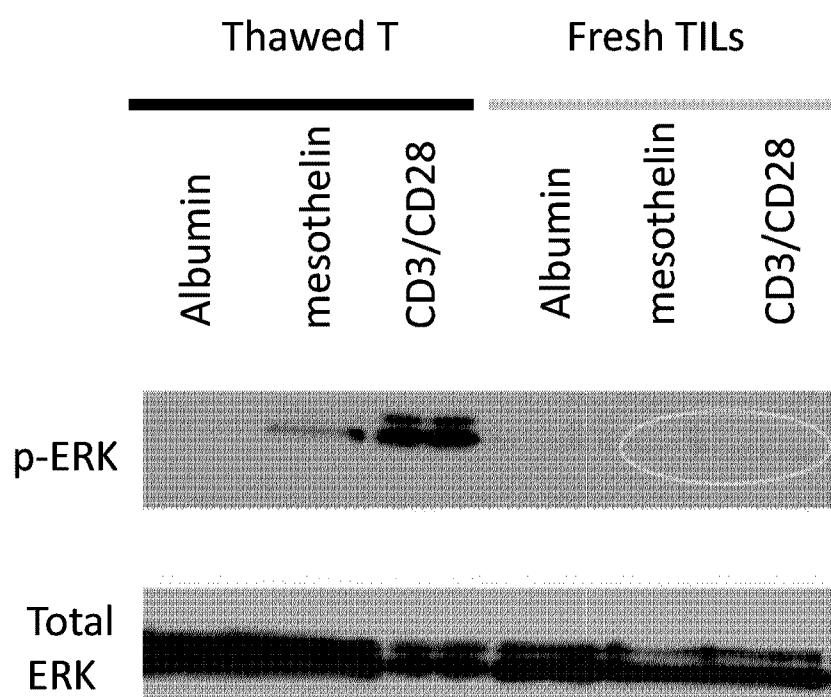
**IFNg level after 20hr 50:1 coculture with
5K EMMESO/ffluc cells pre/post
30IU/ml IL2 overnight rest**

FIG. 20C



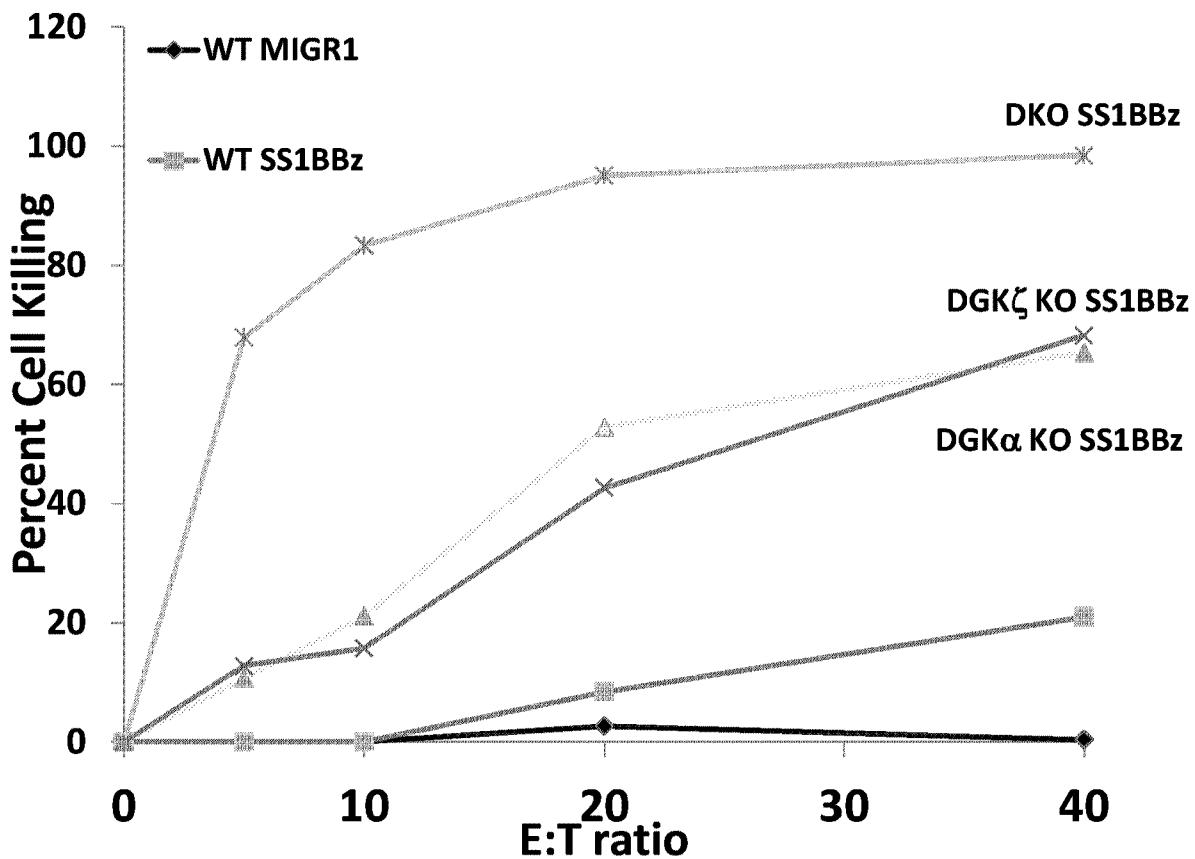
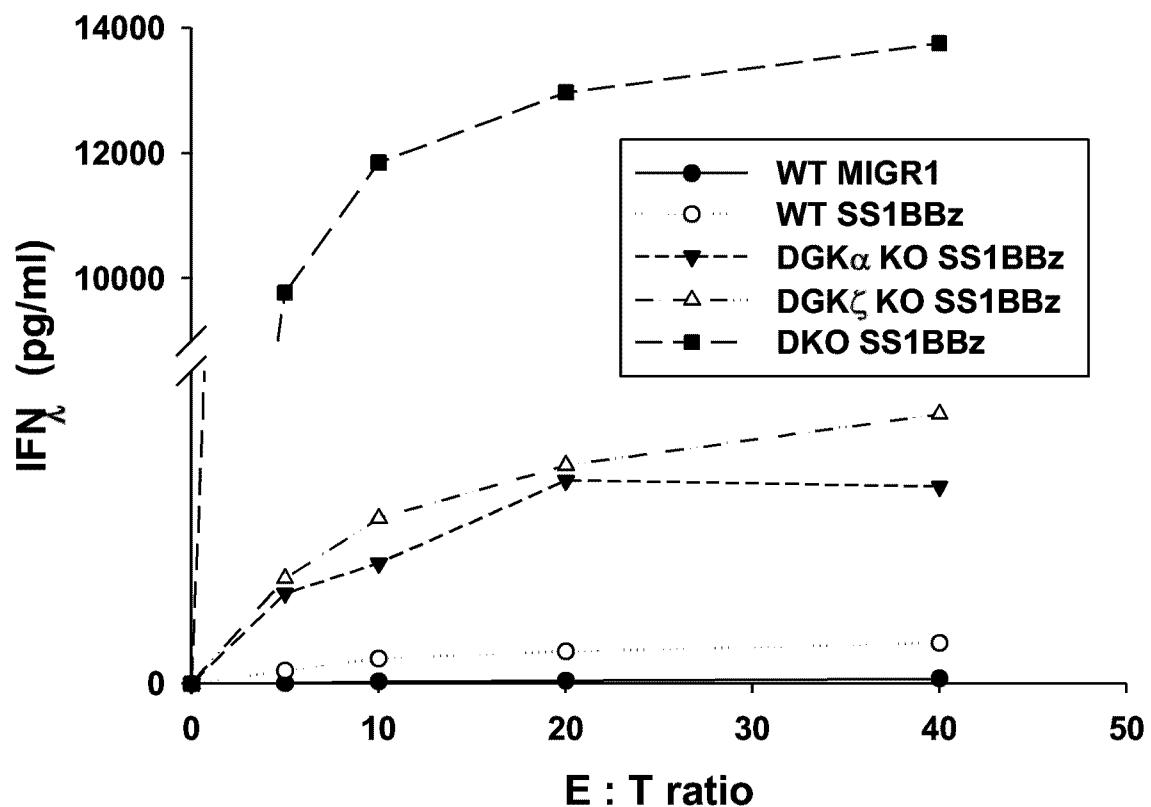
23/53
FIG. 21

FIG. 22



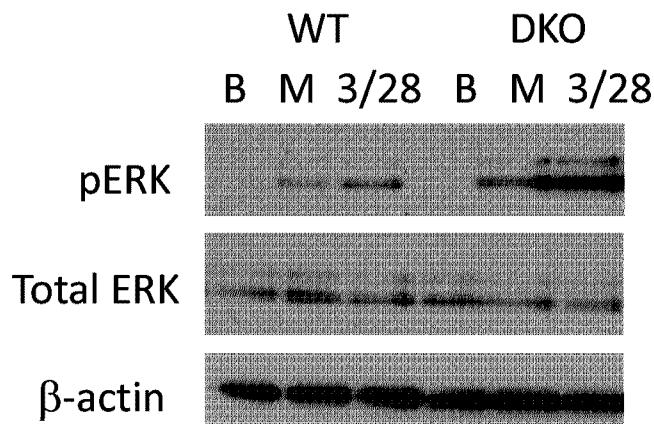
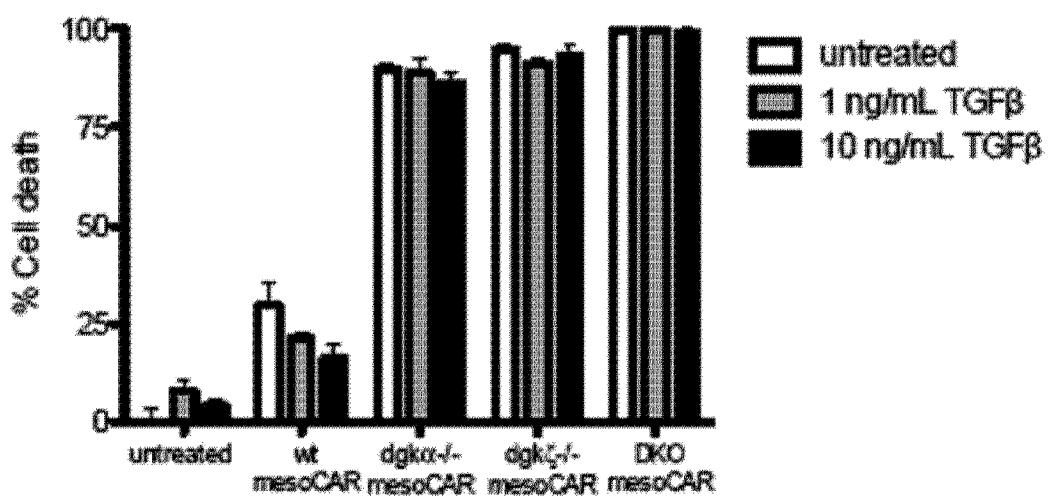
25/53
FIG. 23

FIG. 24



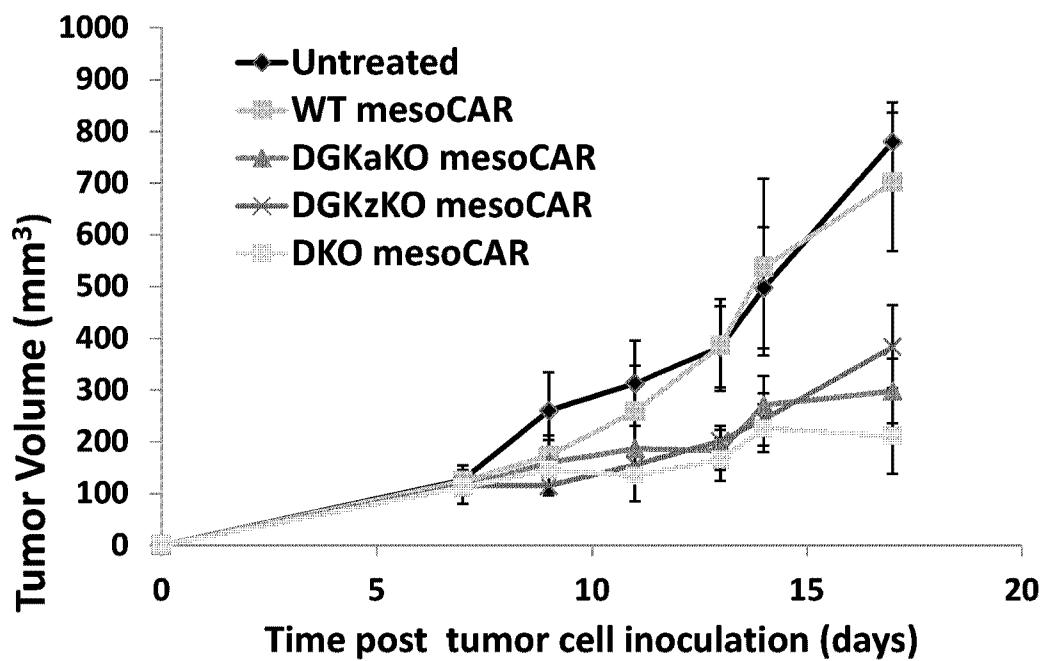
26/53
FIG. 25A

FIG. 25B

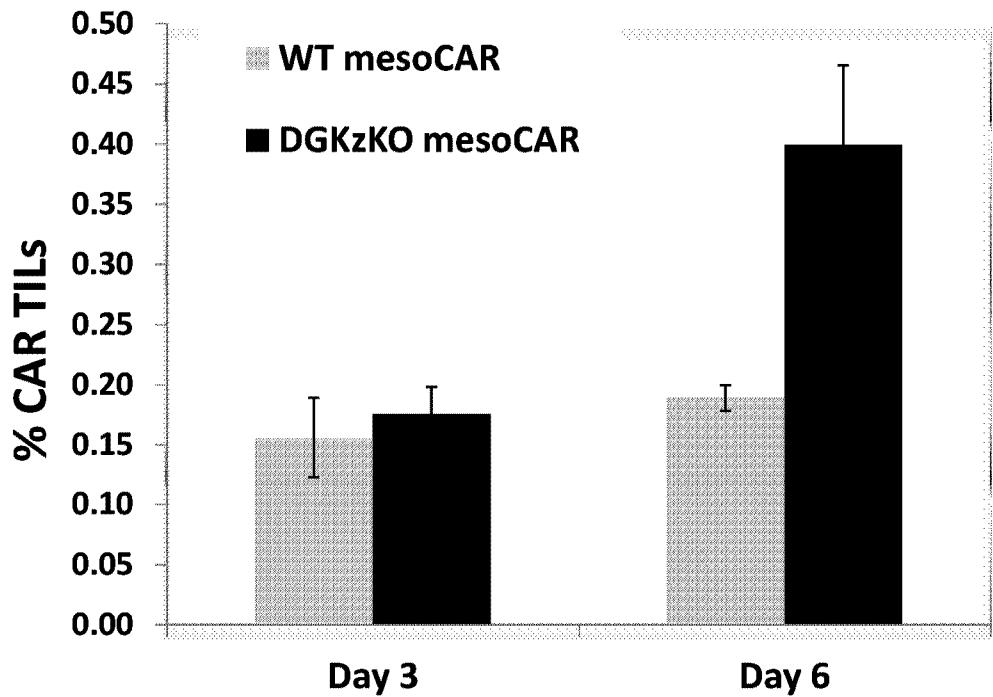


FIG. 26

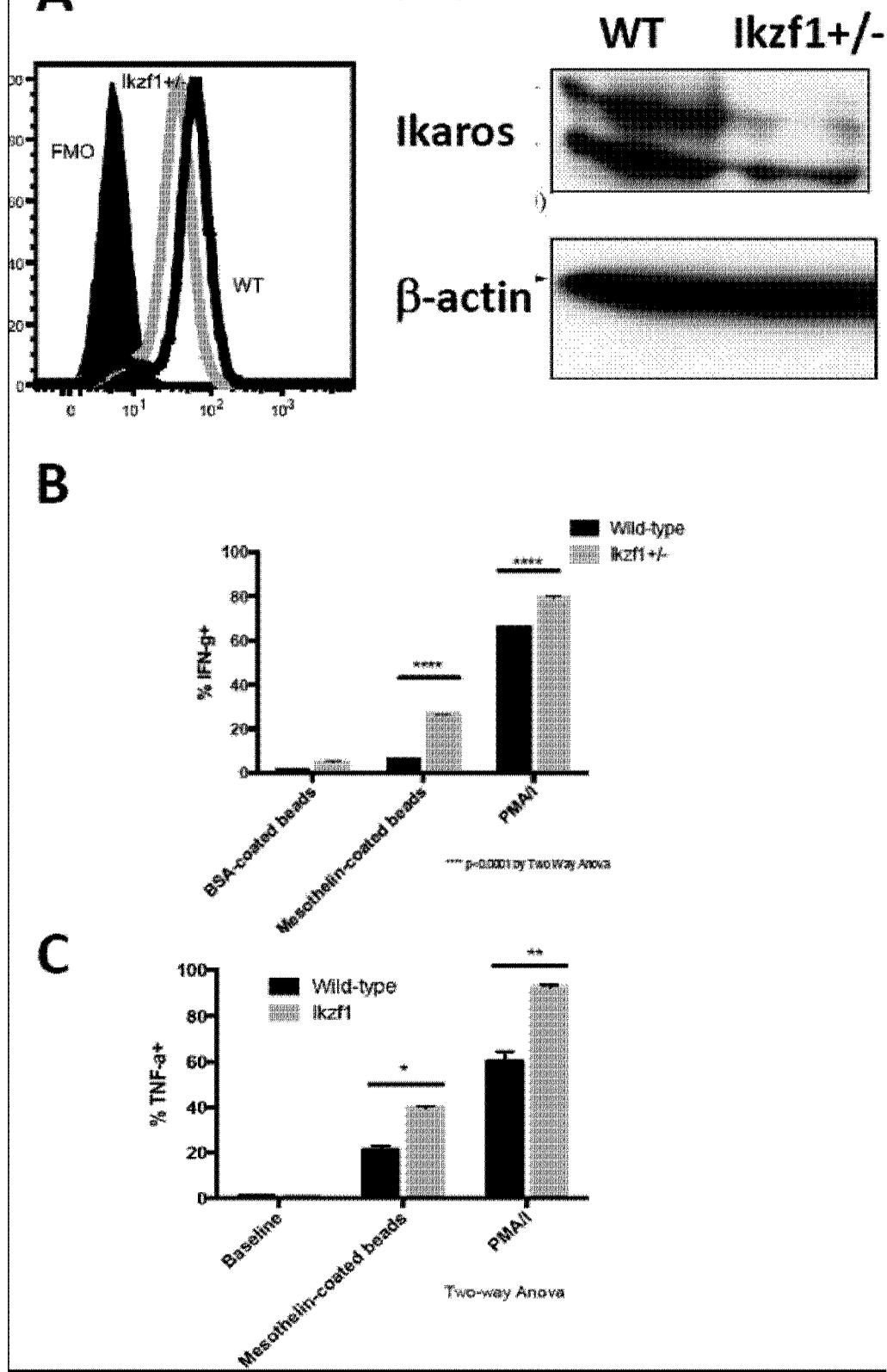


FIG. 26

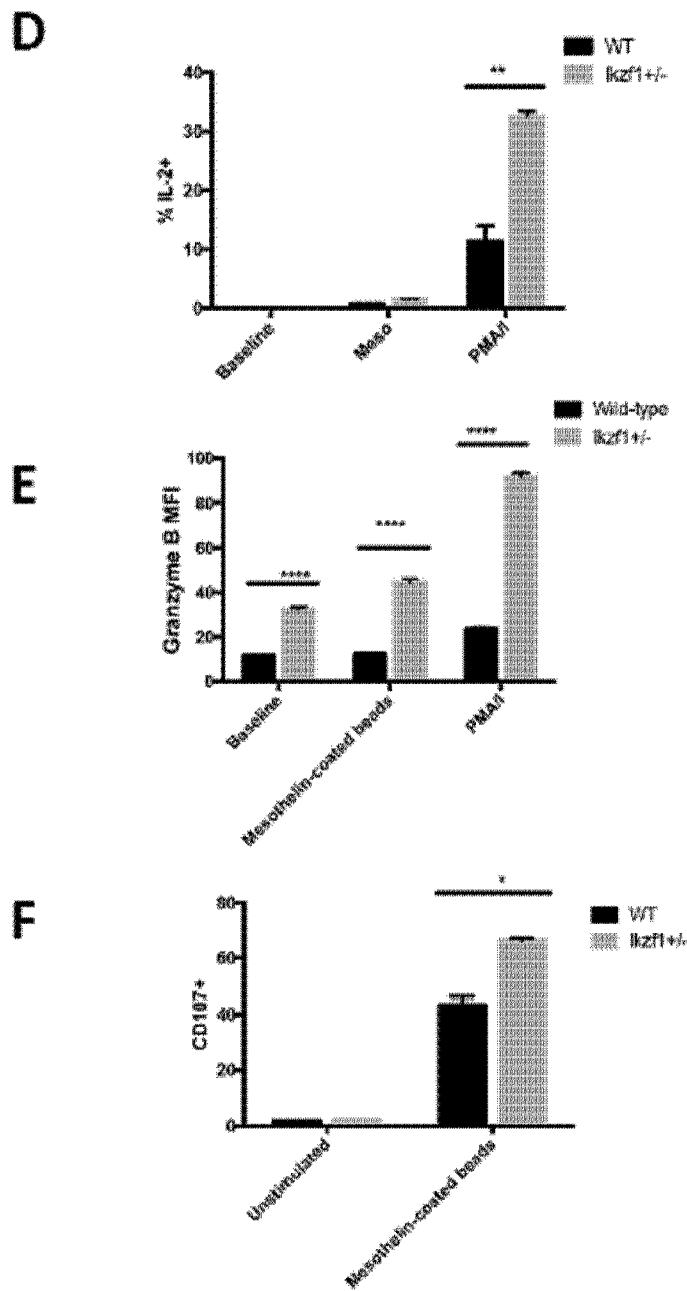
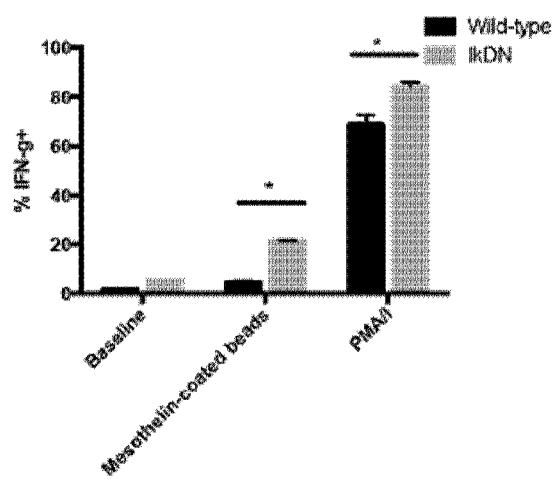
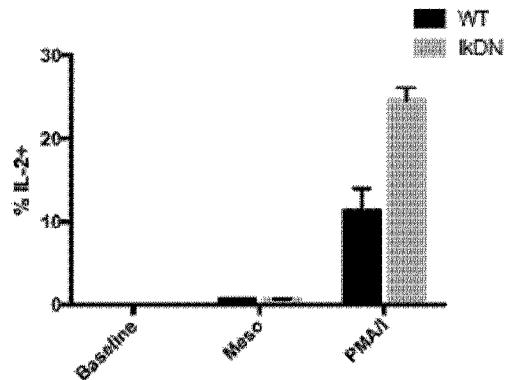


FIG. 27
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A



B



C

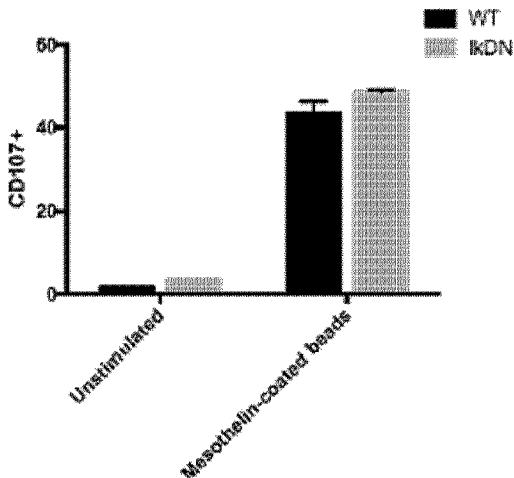


FIG. 28

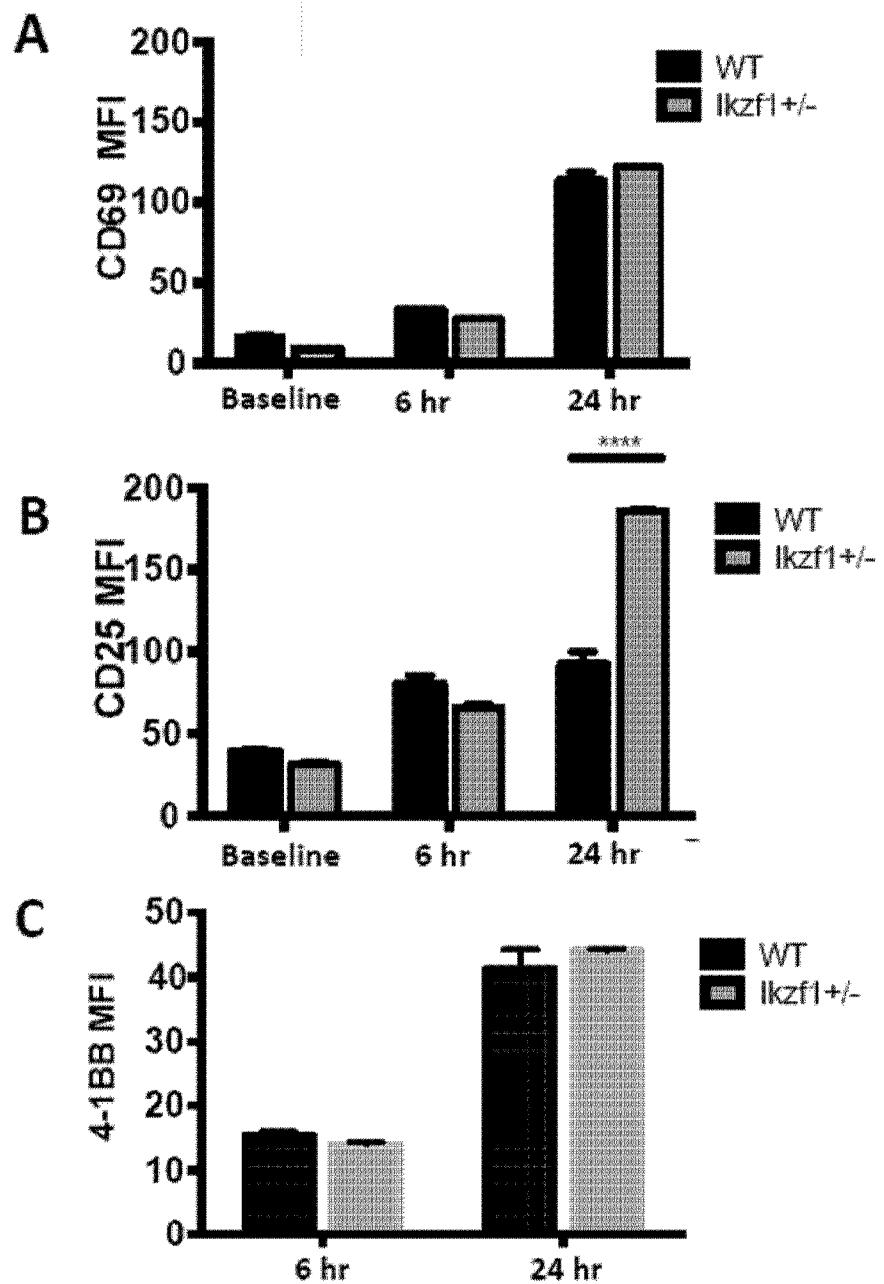
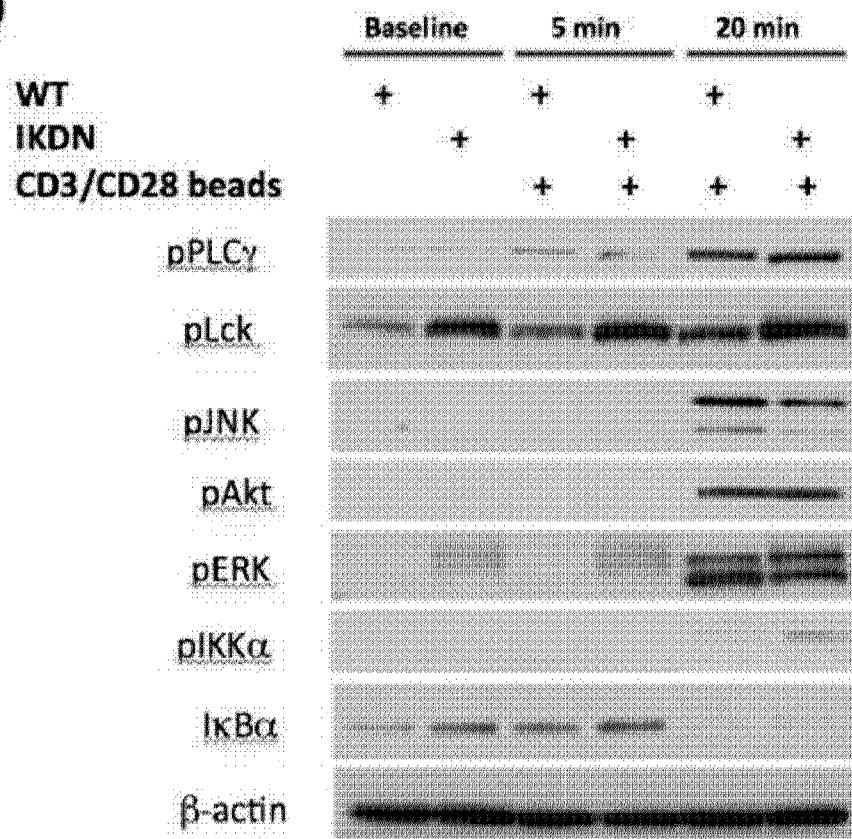
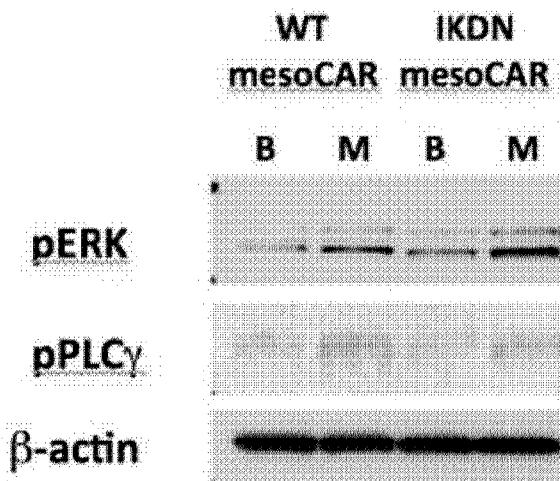


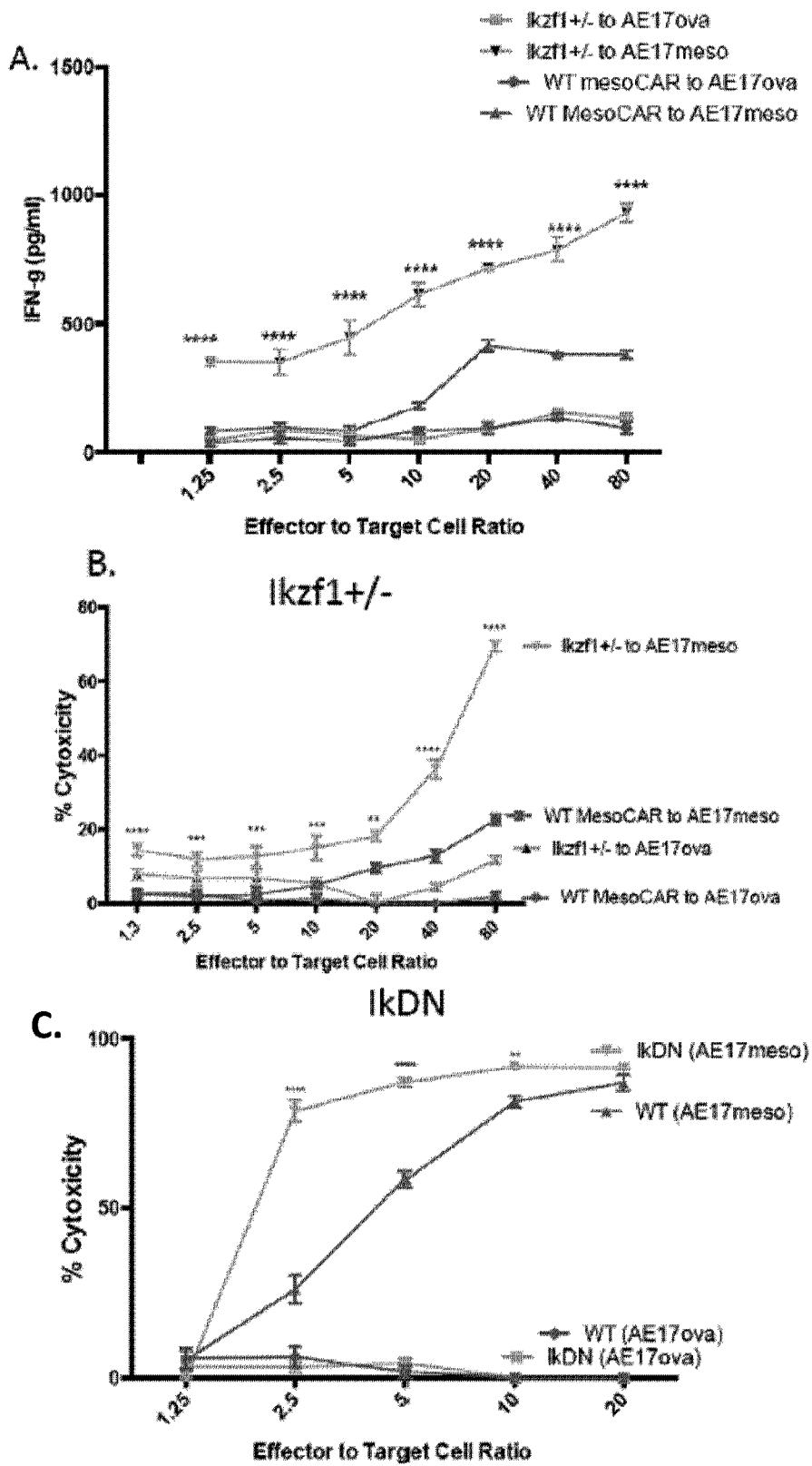
FIG. 28

D



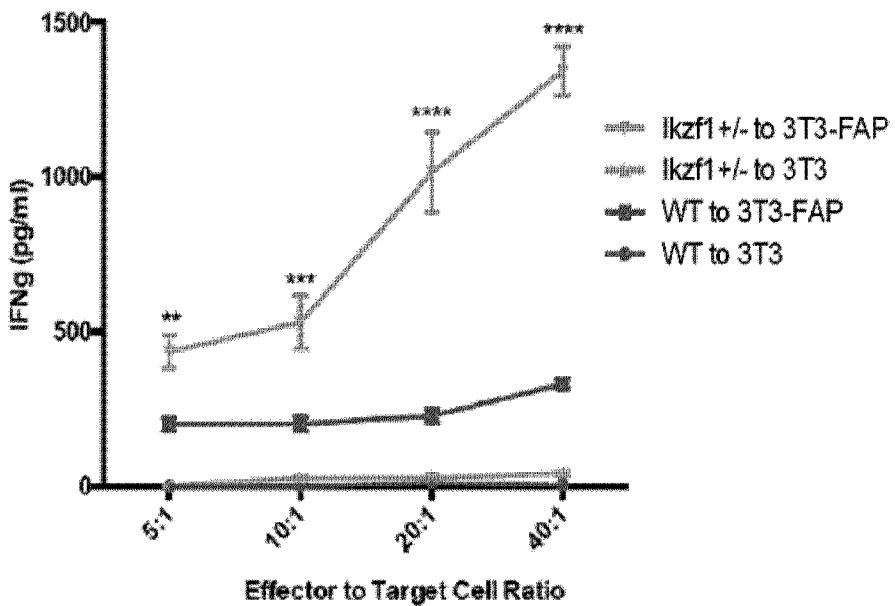
E



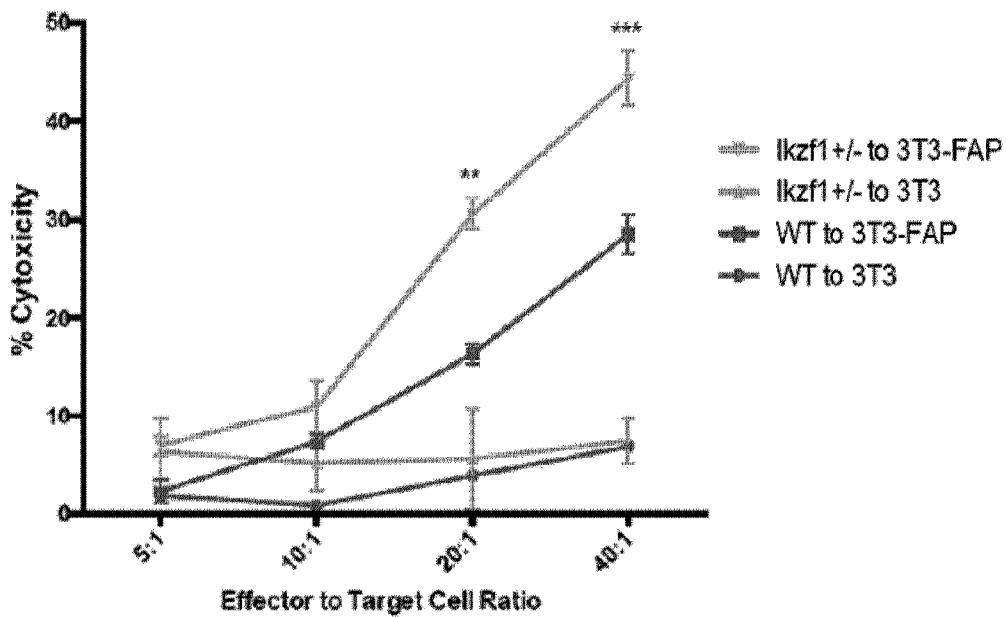
32/53
FIG. 29

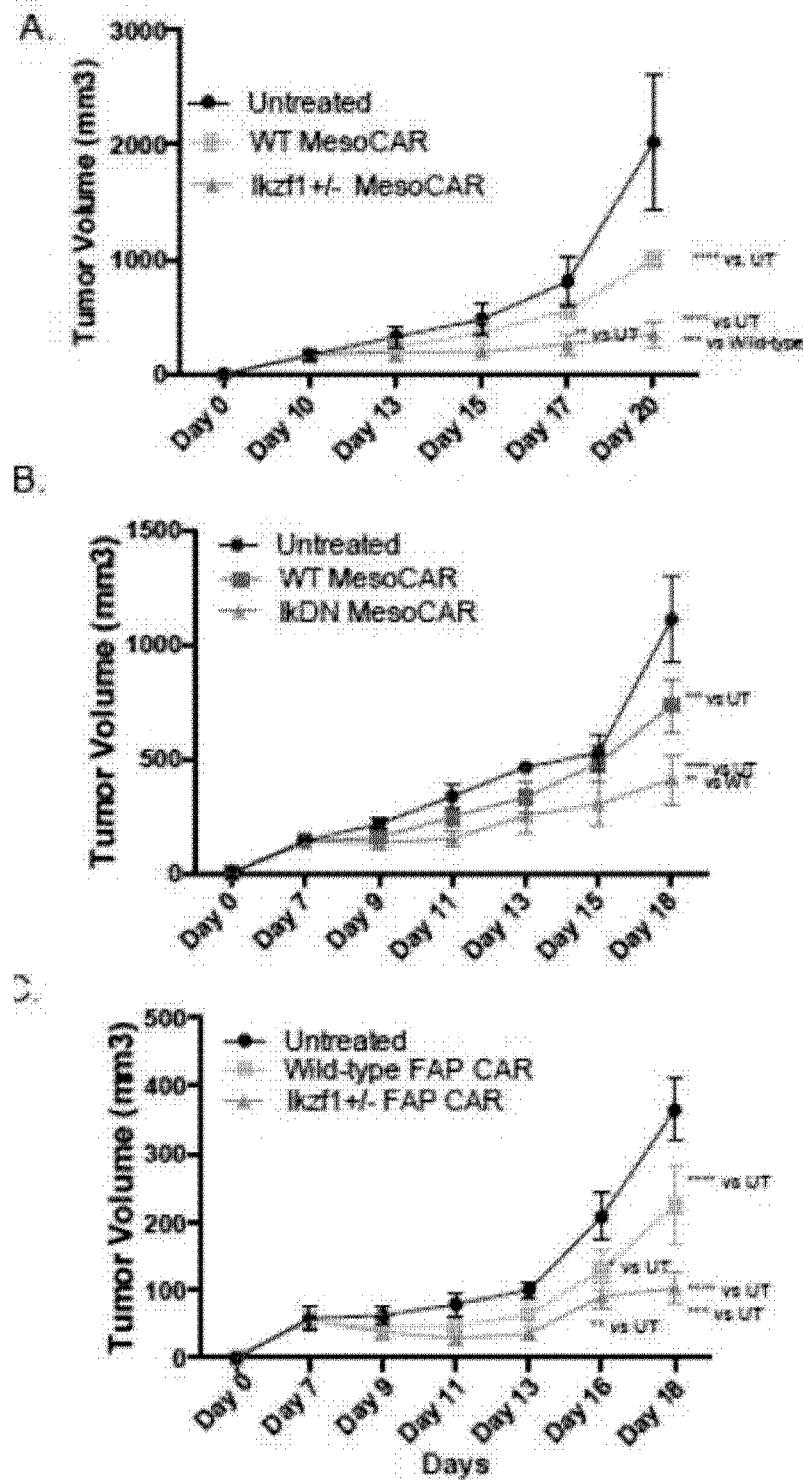
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FIG. 29

D.

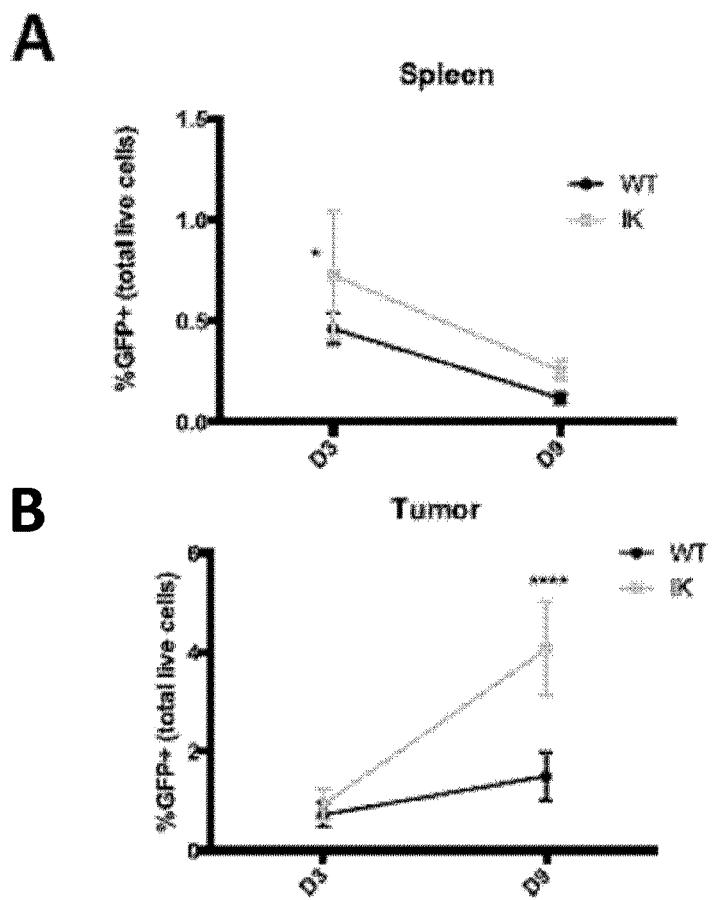


E.

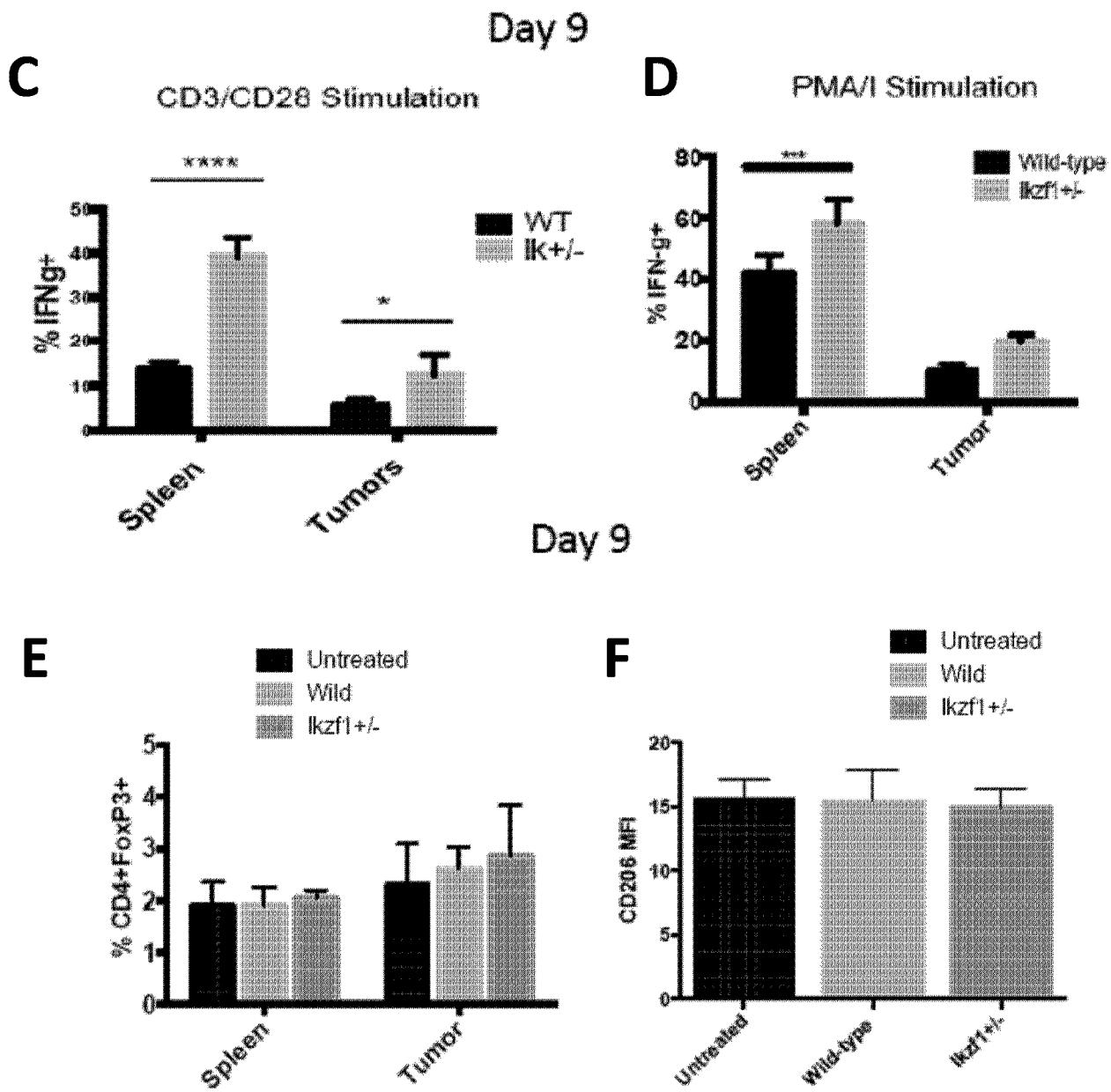


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FIG. 30

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FIG. 31

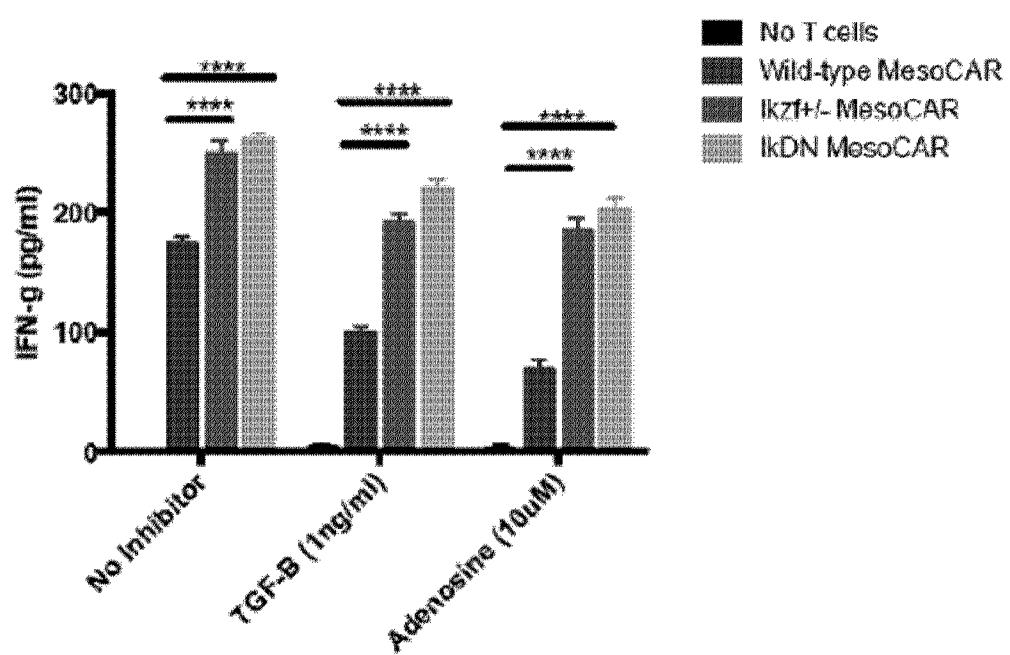


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FIG. 31



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FIG. 32

A



B

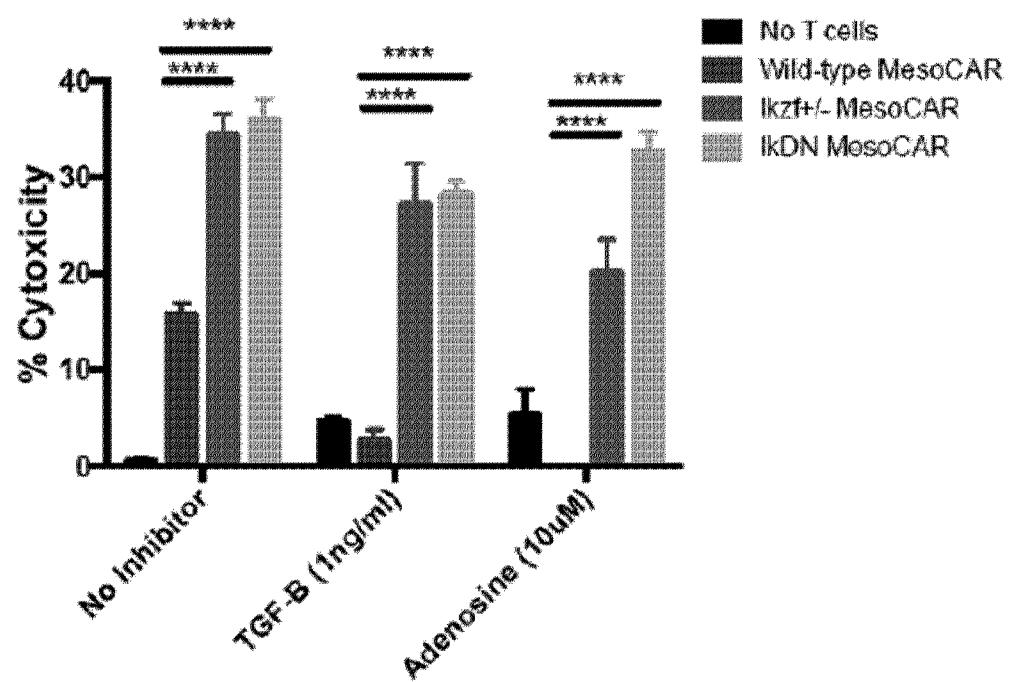
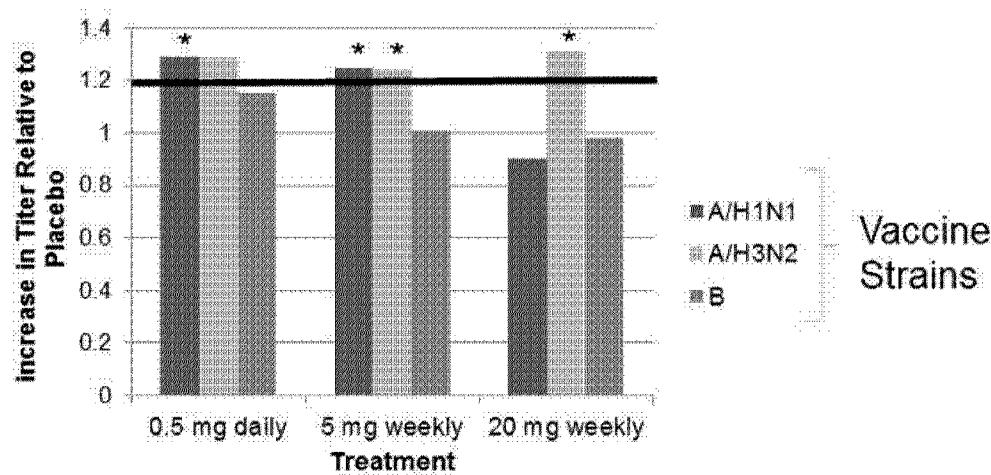


FIG. 33

A.



B.

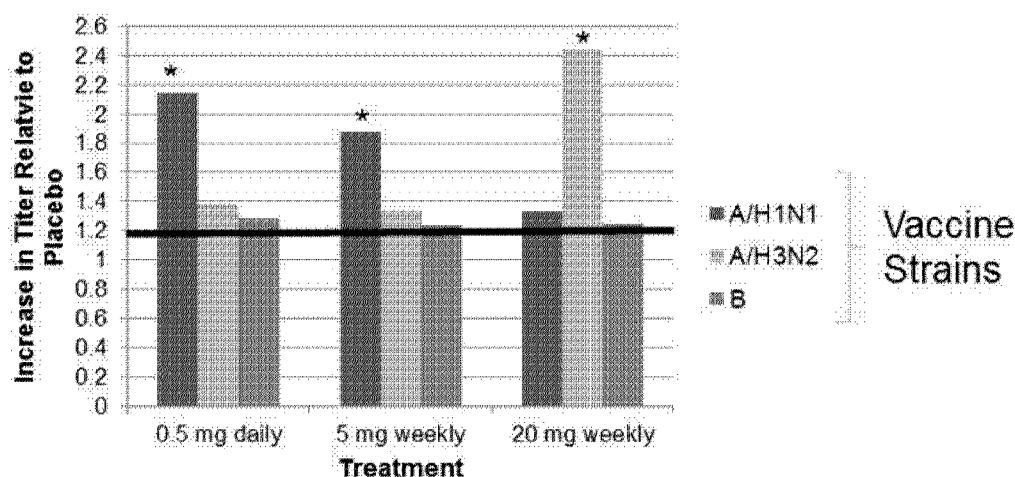


FIG. 34

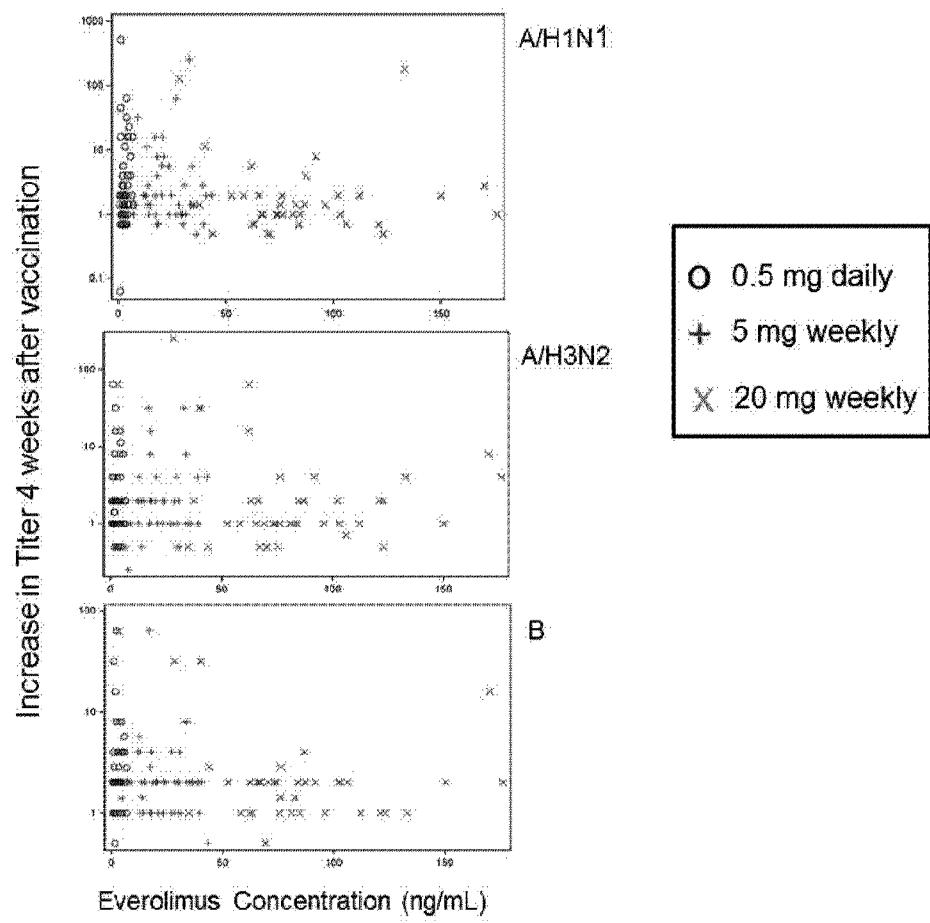
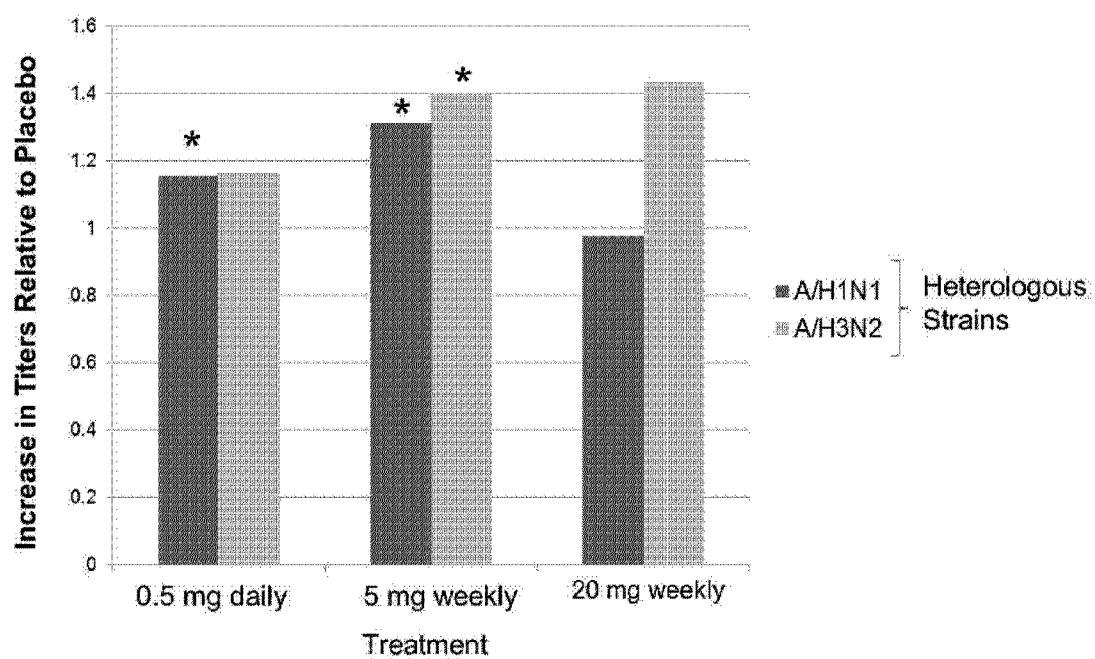


FIG. 35



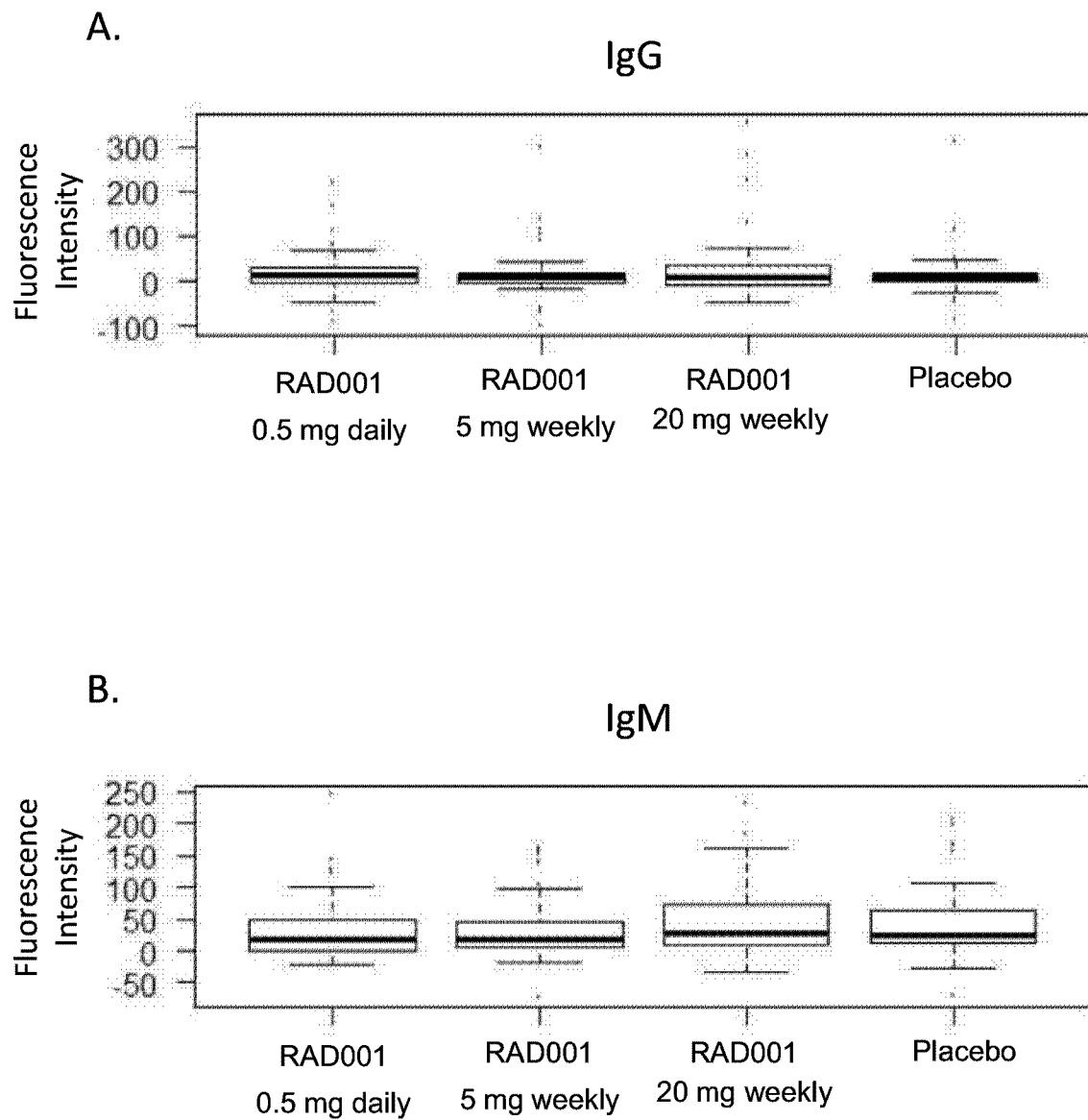
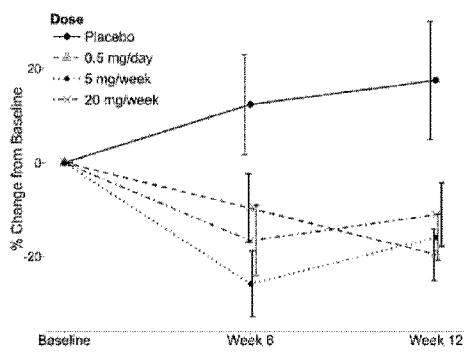
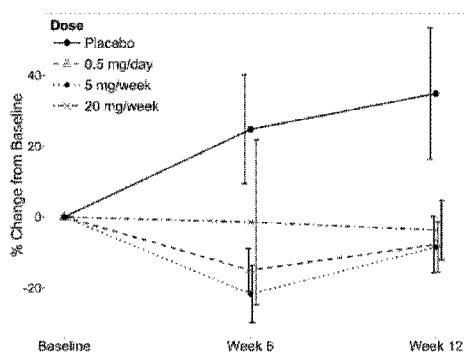
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FIG. 36

FIG. 37

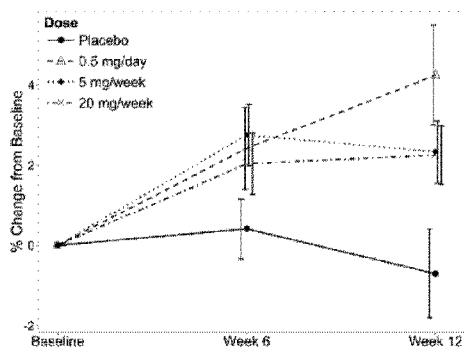
A.



B.



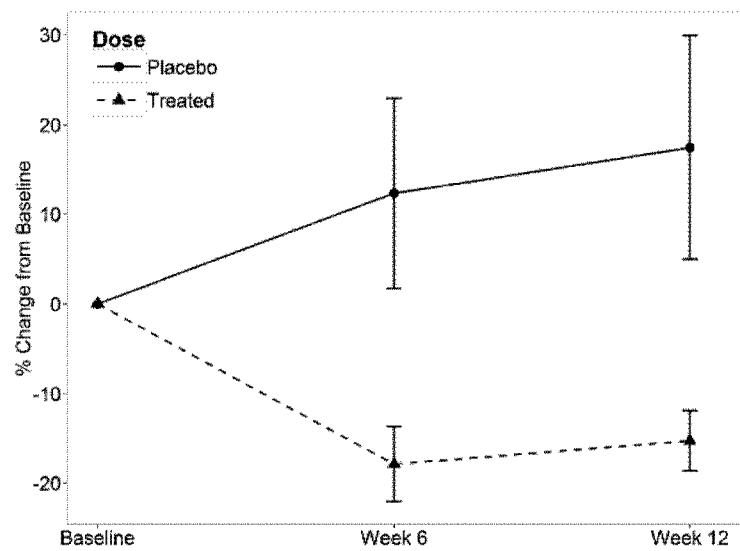
C.



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FIG. 38

A.



B.

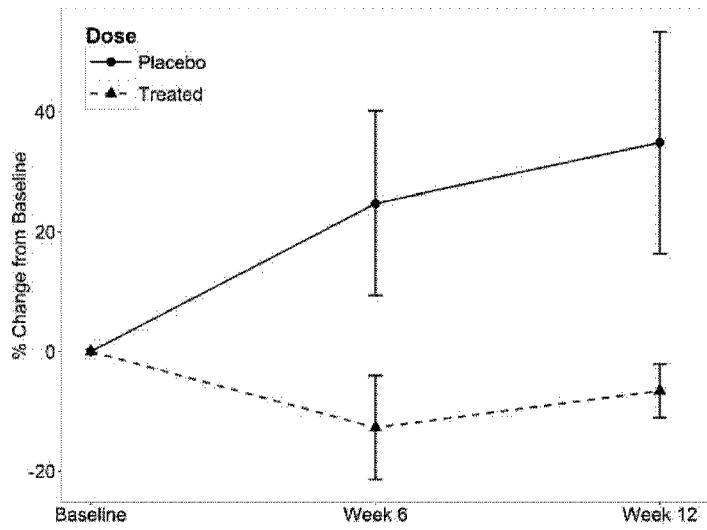


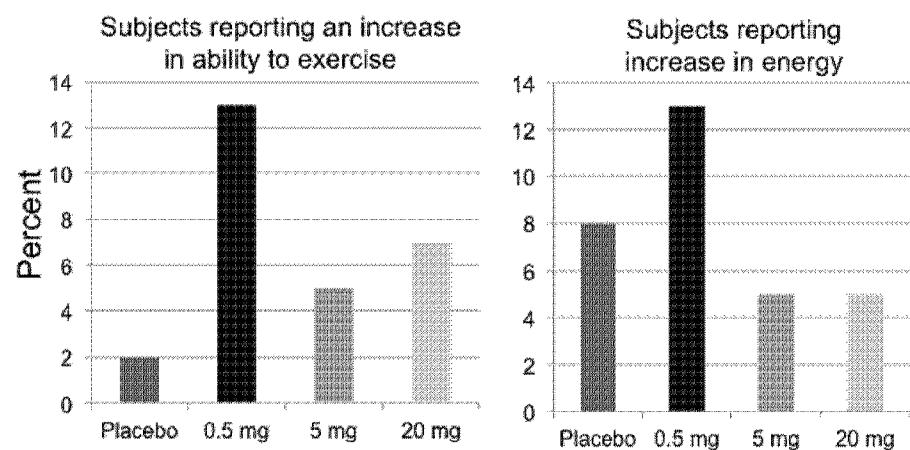
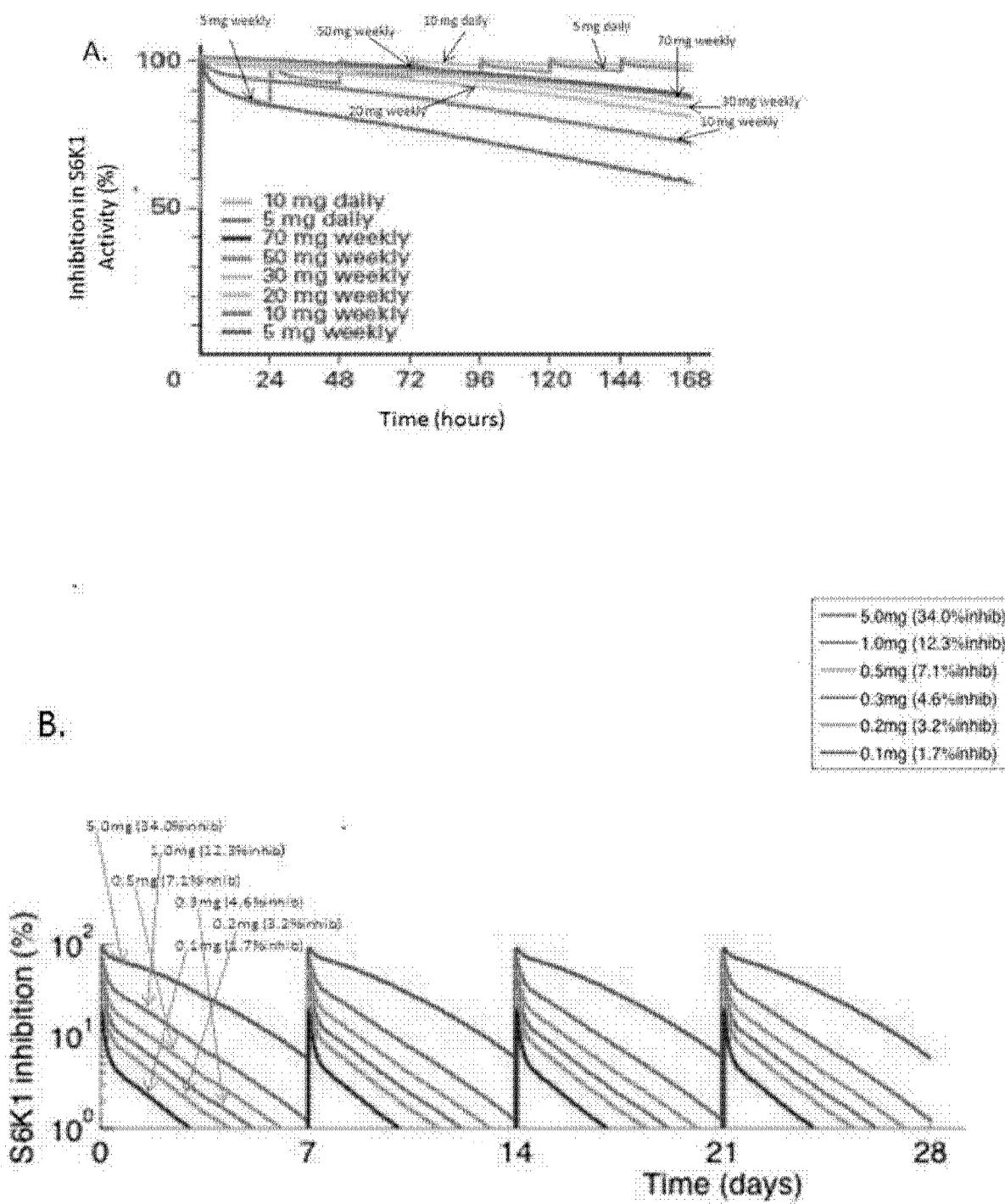
FIG. 39

FIG. 40



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FIG. 41A

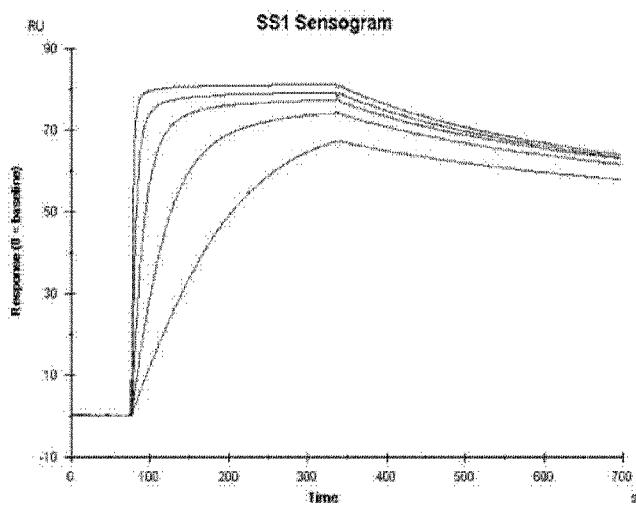


FIG. 41B

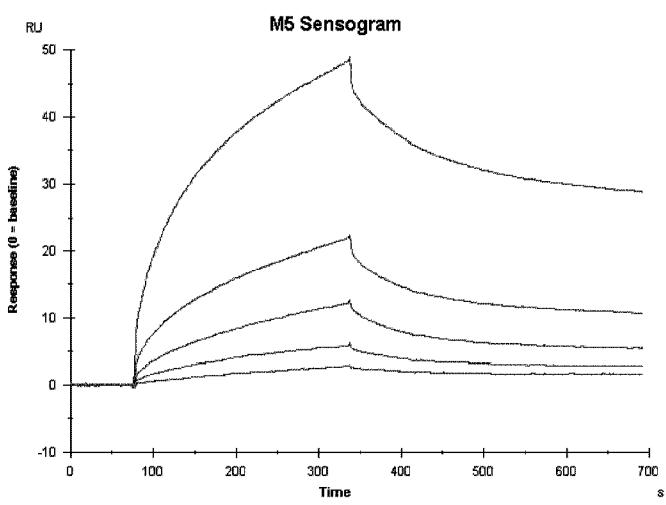


FIG. 41C

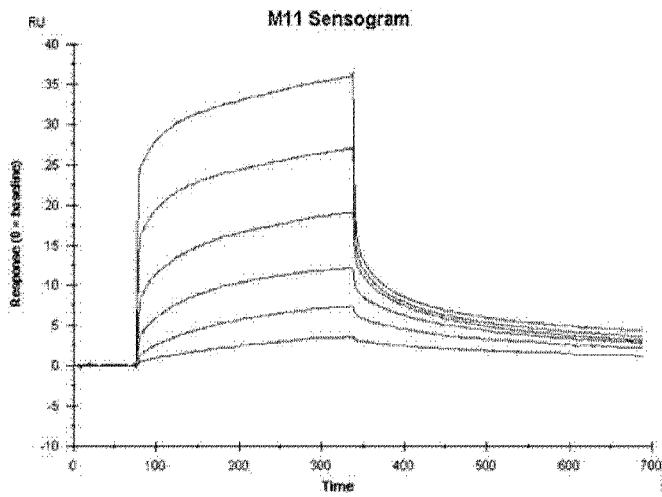


FIG. 42A

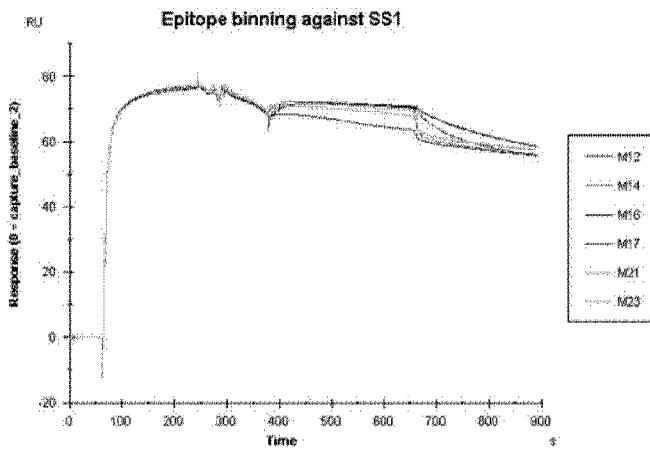


FIG. 42B

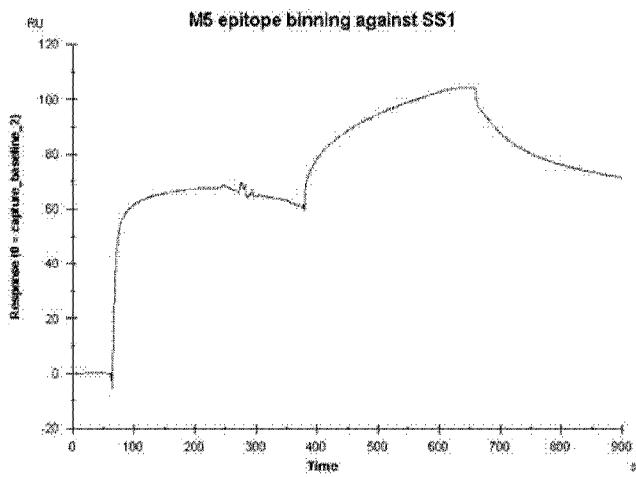


FIG. 42C

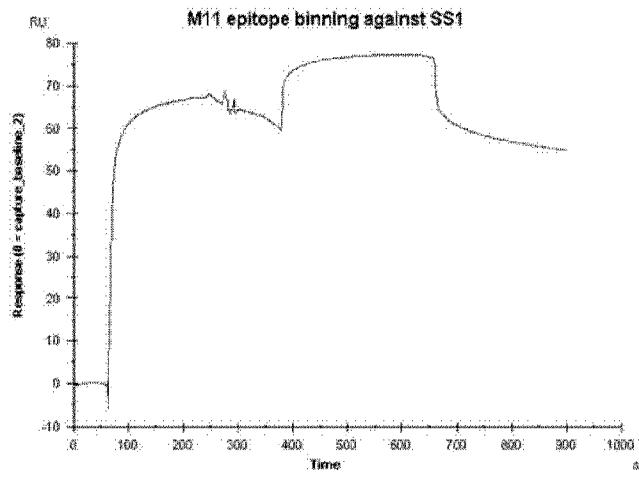
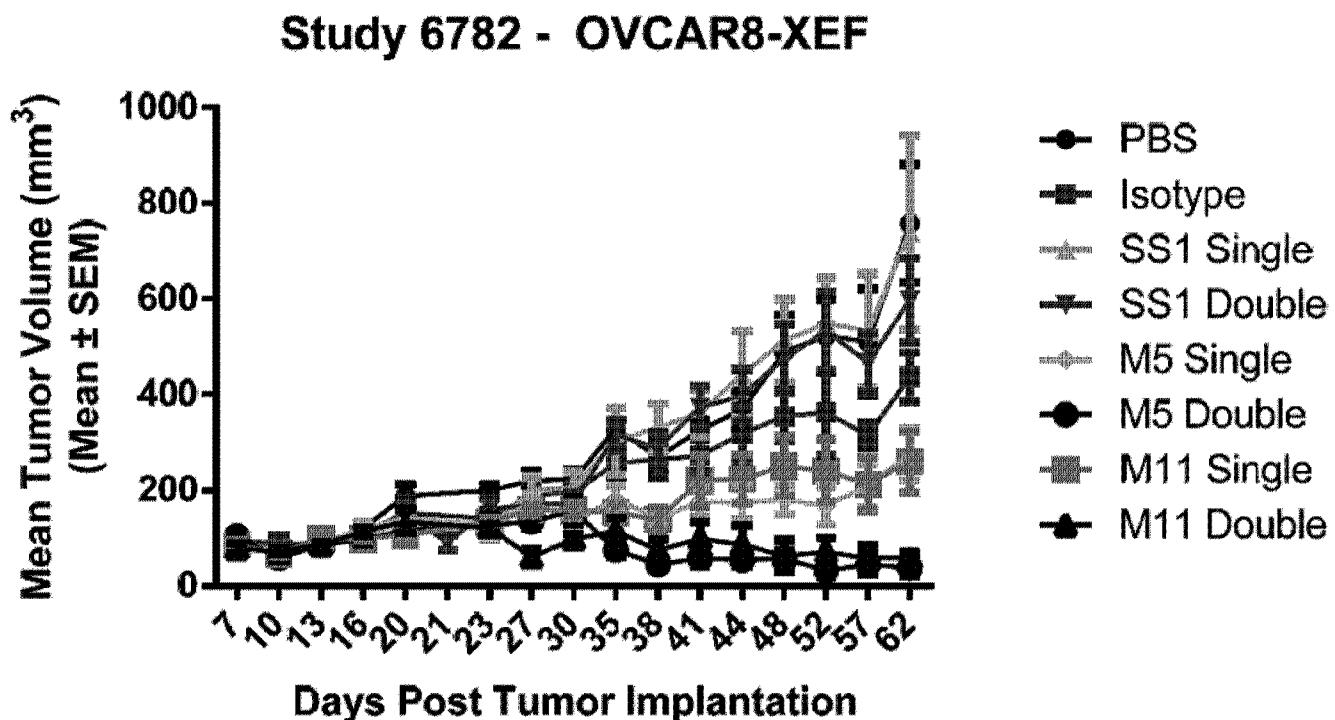


FIG. 43



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FIG. 44

E V E K T A C P S G K K A R E I D E S L I F Y K K W E L E A C V D A A
 300 305 310 315 320 325 330

L L A T Q M D R V N A I P F T Y E Q L D V L K H K L D E L Y P Q G Y P E S V I Q H L G Y L F L K M S P E D I R
 335 340 345 350 355 360 365 370 375 380 385

K W N V T S L E T L K A L L E V N K G H E M S P Q A P R R P Q V A T L I D R F V K G R G Q L D K D T L D T
 390 395 400 405 410 415 420 425 430 435 440

L T A F Y P G Y L C S L S P E E L S S V P P S S I W A V R P Q D L D T C D P R Q L D V L Y P K A R L A F Q N M
 445 450 455 460 465 470 475 480 485 490 495

N G S E Y F V K I Q S F L G G A P T E D L K A L S Q Q N V S M D L A T F M K L R T D A V L P L T V A E V Q K L
 500 505 510 515 520 525 530 535 540 545 550

L G P H V E G L K A E E R H R P V R D W I L R Q R Q D D L D T L G L G L Q G (SEQ ID NO: 278)
 555 560 565 570 575 580 585

FIG. 45A

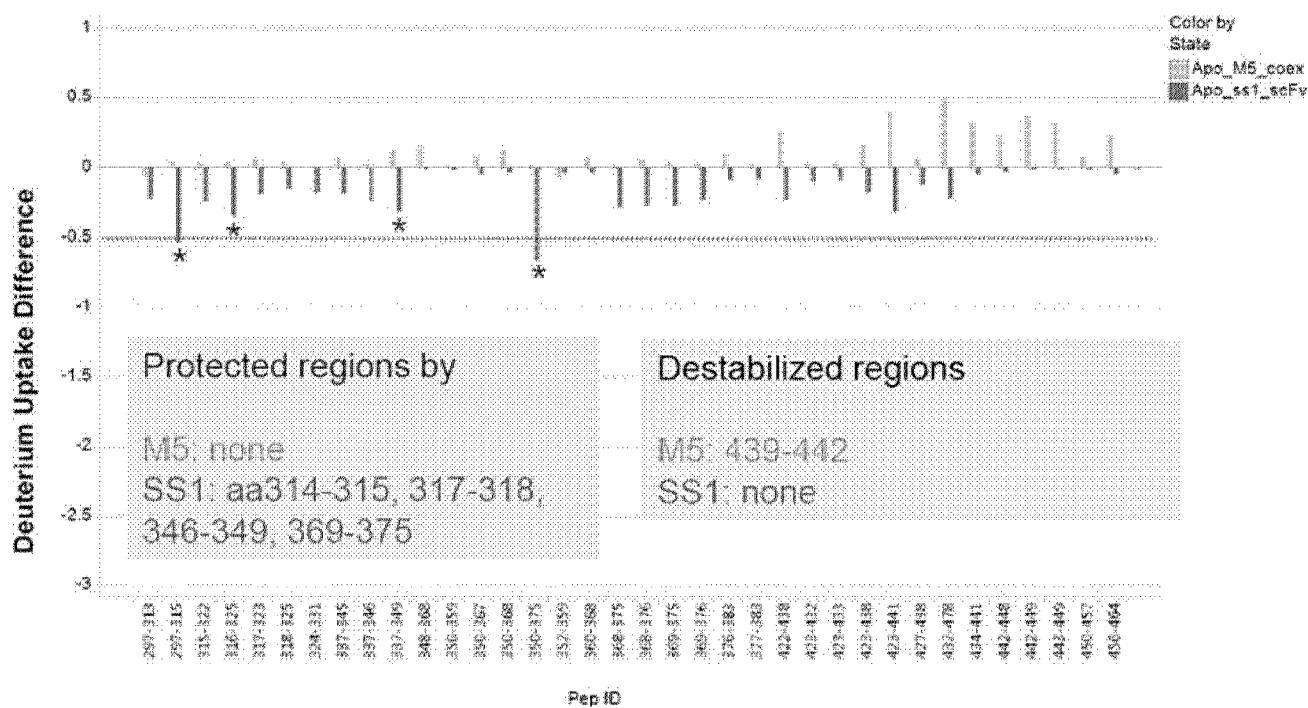


FIG. 46

E₂₉₆ VEKT₃₀₀

A₃₀₁CPSGKKAREIDESLIFYKKWELEACVDAALLATQMDRVNAIPFTYEQLD₃₅₀

V₃₅₁LKHKLDELYPQGYPESVIQHLGFLKMSPEDIRKWNVTSLETLKALLE₄₀₀

V₄₀₁NKGHEMSPQAPRRPLPVATLIDRFVKGRGQLDKDTLTLTAFYPGILC₄₅₀

S₄₅₁LSPEELSSVPPSSIWAVRPQQLDTCDPRQLDVLYPKARLAFAQNMNGSEY₅₀₀

F₅₀₁VKIQSFLGGAPTEDLKALSQQNVSMMLATFMKLRTDAVLPLTVAEVQKL₅₅₀

L₅₅₁ GPHVEGLKAEERHRPVRDWILRQRQDDLTLGLGLQG₅₈₈ (SEQ ID NO: 278)

Protected by M5
Protected by SS1

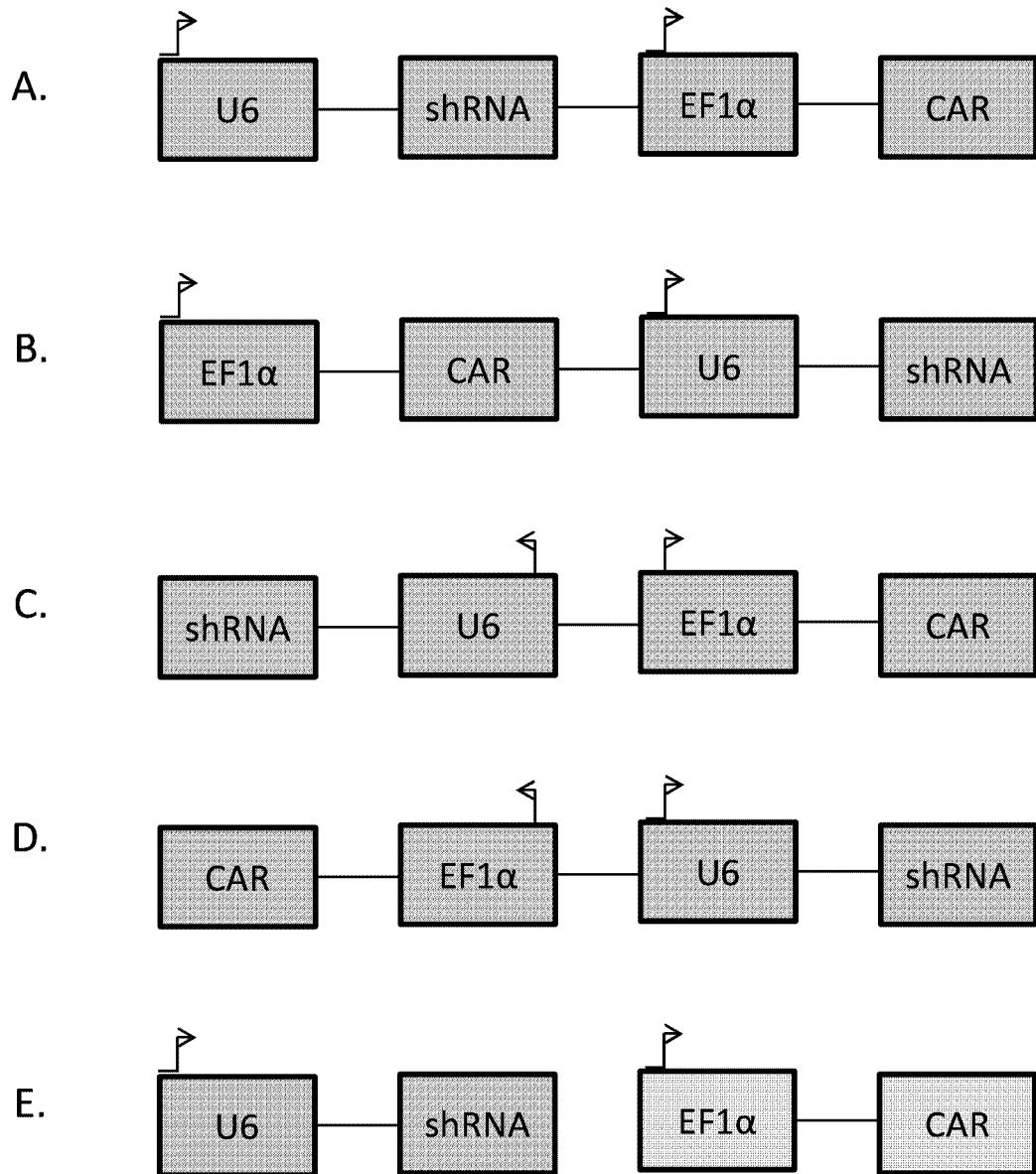
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FIG. 47*Vector constructs*

FIG. 48

Regulatable CAR (RCAR)