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- (71) Applicants: **INNOVATIVE CELLULAR THERAPEUTICS INC.** [US/US]; 1405 Research Boulevard, Suite 210, Rockville, Maryland 20850 (US). **INNOVATIVE CELLULAR THERAPEUTICS CO., LTD.** [CN/CN]; Building 1, 6055 Jinhai Road, Fengxian District, Shanghai 201203 (CN).
- (72) Inventors: **XIAO, Lei**; Building 1, 6055 Jinhai Road, Fengxian District, Shanghai 201203 (CN). **PU, Chengfei**; Building 1, 6055 Jinhai Road, Fengxian District, Shanghai 201203 (CN). **CAO, Zhiyuan**; Building 1, 6055 Jinhai Road, Fengxian District, Shanghai 201203 (CN). **WU, Zhao**; Building 1, 6055 Jinhai Road, Fengxian District, Shanghai 201203 (CN). **MAO, Li**; Building 1, 6055 Jinhai Road, Fengxian District, Shanghai 201203 (CN). **BI, Mao**; Building 1, 6055 Jinhai Road, Fengxian District, Shanghai 201203 (CN).
- (74) Agent: **TENG, Sally P.** et al.; 601 West Riverside Avenue, Suite 1400, Spokane, Washington 99201 (US).

(54) Title: MODIFIED CELL EXPANSION AND USES THEREOF

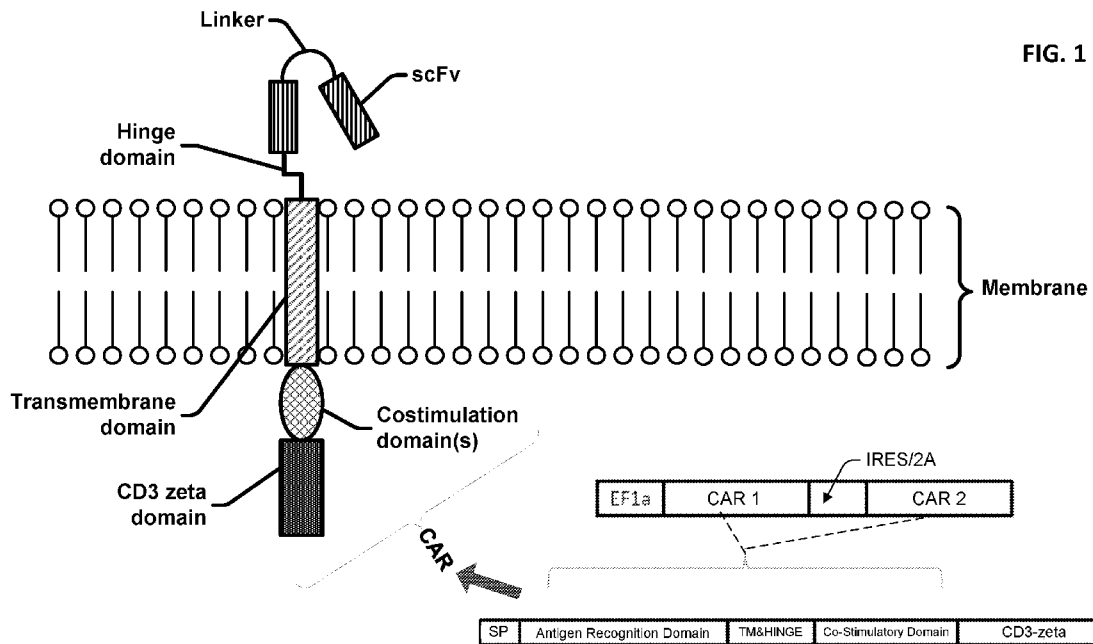


FIG. 1

*Antigen recognition domain: scFv or ligand based.

(57) Abstract: The present disclosure relates to compositions and methods for enhancing T cell response and/or CAR cell expansion in vivo and/or in vitro. For example, a cell may comprise a first chimeric antigen receptor (CAR) and a second CAR, wherein a binding domain of the first CAR binds a first antigen, and a binding domain of the second CAR binds a second antigen. The first antigen is different from the second antigen. In embodiments, the first CAR may recognize a surface molecule of a blood cell.



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Modified Cell Expansion and Uses Thereof

CROSS REFERENCE TO RELATED PATENT APPLICATIONS

[0001] This application claims the benefit of U.S. Application 16/146,218, filed on September 28, 2018; U.S. Provisional Application 62/721,791, filed on August 23, 2018; U.S. Provisional Application 62/690,892, filed on June 27, 2018; U.S. Provisional Application 62/659,233, filed on April 18, 2018; U.S. Provisional Application 62/687,059, filed on June 19, 2018; U.S. Provisional Application 62/678,836, filed on May 31, 2018; U.S. Provisional Application No. 62/659,114, filed on April 17, 2018; U.S. Provisional Application 62/626,781, filed on February 6, 2018; U.S. Provisional 62/622,601, filed on January 26, 2018; and U.S. Provisional Application No. 62/616,609, filed on January 12, 2018; U.S. Provisional Application 62/616,079, filed on January 11, 2018, which are hereby incorporated by reference in their entirety.

SEQUENCE LISTING INFORMATION

[0002] A computer readable textfile, entitled "Sequence Listing.txt," created on or about December 18, 2018 with a file size of about 949 KB, contains the sequence listing for this application and is hereby incorporated by reference in its entirety.

TECHNICAL FIELD

[0003] The present disclosure relates to compositions and methods for expanding modified cells including modified T cells, and uses thereof in the treatment of diseases, including cancer.

BACKGROUND

[0004] Chimeric Antigen Receptor (CAR) T cell therapy has achieved good clinical efficacy in cancer such as B-ALL/CLL/ lymphoma. However, progress is relatively slow for treatment of solid tumors. For CAR T cell therapy to be effective, long-term maintenance of CAR T cells in a patient is important for the prognosis of the patient in the treatment of tumors. For example, if the long-term presence of CAR T cells can be maintained, this technology may effectively reduce tumor recurrence.

[0005] Cancer is known as malignant tumors involving abnormal cell growth with the potential to invade or spread to other parts of the body. In humans, there are more than one hundred types of cancer. One example is breast cancer occurring in the epithelial tissue of the breast. Since breast cancer cells lose the characteristics of normal cells, the connection between breast cancer cells is lost. Once cancer cells are exfoliated, they spread over the entire body via the blood and/or lymph systems and therefore become life-threatening. Currently, breast cancer has become one of the common threats to women's physical and

mental health. Although immunotherapy (e.g., CAR T) has been proven to be effective for treating cancer, there is still a need to improve immunotherapy so that it is more effective for certain cancer such as solid tumors.

SUMMARY

[0006] Since a patient can survive the depletion of B cells, B cells of the patient may be used to expand the CAR T cells in the patient using the first antigen binding domain. Accordingly, more CAR T cells may be timely expanded in the patient, increasing the potency of CAR T cells. The timely expanded CAR T cells in the patient may increase the chances for the CAR T cells to come in contact with tumor cells, especially solid tumor cells having the antigen that the second CAR binds.

[0007] The present disclosure describes genetically modified cells, such as T cells, that include two different antigen binding domains: a first antigen binding domain for expanding the modified cell, and a second antigen binding domain for killing a target cell, such as a tumor cell. For example, the first antigen binding domain binds a surface marker, such as a surface antigen, of B cells, and the second antigen binding domain binds the target antigen of tumor cells. The two antigen binding domains can be on the same CAR molecule, on different CAR molecules, or on a CAR and a T cell receptor (TCR). In embodiments, the first binding domain binds a cell surface molecule of a white cell, while the second binding domain binds an antigen that is different from the cell surface molecule of a white cell and is a tumor antigen.

[0008] The two antigen binding domains can be encoded by a single nucleic acid or more than one nucleic acids. In embodiments, the cell includes a modified T cell, for example a CAR T cell. In embodiments, the target cell includes a cell of a solid tumor.

[0009] The present disclosure also describes one or more nucleic acids encoding a first CAR and a second CAR or TCR. The first CAR includes the first antigen binding domain and the second CAR or TCR includes the second antigen binding domain. In embodiments, the first CAR and the second CAR or TCR are expressed as separate polypeptides and encoded by at least two separate nucleic acids. In embodiments, a single CAR contains at least two antigen binding domains and is encoded by a single nucleic acid. Embodiments described herein relate to vectors comprising a nucleic acid described herein and to cells comprising a nucleic acid described herein.

[0010] Moreover, the present disclosure describes the release of cytokines in response to the introduction of the first CAR and second CAR or TCR. In embodiments, the cytokines are IL-6 and IFN- γ .

[0011] This Summary is not intended to identify key features or essential features of the claimed subject matter, nor is it intended to be used to limit the scope of the claimed subject matter.

BRIEF DESCRIPTION OF THE DRAWINGS

[0012] The Detailed Description is described with reference to the accompanying figures. The use of the same reference numbers in different figures indicates similar or identical items.

[0013] FIG. 1 is a schematic diagram of an exemplary CAR molecule and a portion of the cell membrane.

[0014] FIG. 2 is a schematic diagram of a nucleic acid construct including two CAR molecules and structures of a T cell having two different CAR molecules.

[0015] FIG. 3 is a schematic diagram showing an exemplary portion of a cell membrane comprising two CAR molecules.

[0016] FIG. 4 is a schematic diagram showing an exemplary portion of a cell membrane comprising a bispecific CAR molecule.

[0017] FIG. 5 is a schematic diagram showing an exemplary portion of a cell membrane comprising a bispecific CAR molecule and a T cell receptor (TCR).

[0018] FIG. 6 displays flow cytometry results showing T cells expressing anti-CD19 CAR and anti-MUC1 CAR.

[0019] FIG. 7 shows functional analysis of T cells expressing anti-CD19 CAR and anti-MUC1 CAR.

[0020] FIG. 8 displays a histogram showing T cell response to co-culturing with various substrate cells.

[0021] FIG. 9 displays a histogram showing T cell response to co-culturing with various substrate cells.

[0022] FIG. 10 displays flow cytometry analysis showing expression of anti-TSHR CAR molecules on T cells (Gated by a single live cell). Anti-TSHR CAR T cells were constructed, and the expression of CAR molecules was detected by flow cytometry. Compared to non-transduced T cells, expression of CAR molecules was observed.

[0023] FIG. 11 displays flow cytometry analysis showing overexpression of TSHR on T cells (Gated by a single live cell). Lentiviral vectors were used to construct antigen over-expressed T cells (TSHR). The expression of TSHR molecules on the surface of T cells was observed (IgG on the left and anti-TSHR FITC on the right).

[0024] FIG. 12 shows cytokine release (IL-2) in mouse peripheral blood.

[0025] FIG. 13 shows cytokine release (IFN- γ) in mouse peripheral blood.

[0026] FIG. 14 shows cytokine release (IL-4) in mouse peripheral blood.

[0027] FIG. 15 shows CAR/CD3 cell ratios were increased as compared to control in mouse peripheral blood.

[0028] FIG. 16 shows changes in the number of copies of CAR molecules with time (days) after infusion of CAR T cells to patient A.

[0029] FIG. 17 shows changes in the number of copies of CAR molecules with time (days) after infusion of CAR T cells to patient B.

[0030] FIG. 18 shows changes in the number of copies of CAR molecules with time (days) after infusion of CAR T cells to patient C.

[0031] FIG. 19 shows changes in the number of copies of CAR molecules with time (days) after infusion of CAR T cells to patient D.

[0032] FIG. 20 shows changes in the number of copies of CAR molecules with time (days) after infusion of CAR T cells to patient E.

[0033] FIG. 21 illustrates an example of a pair of ZFNs targeting an exemplary exon of a gene.

[0034] FIGS. 22, 23, 24, and 25 show sequencing results for ZFNs that target various gene fragments and are amplified by PCR. Double sequencing signals were observed for the ZFNs, and bottom portions of double sequencing signals were circled with black boxes, suggesting that the targeting gene was introduced with a mutation. The higher the density of the double sequencing signals, the higher the editing efficiency.

[0035] FIGS. 26, 27, 28, 29, and 30 show sequencing results for ZFNs that target various gene fragments and are amplified by PCR. Multiple sequencing signals were observed for the ZFNs, and bottom portions of multiple sequencing signals were circled with black boxes, suggesting that the targeting gene was introduced with a mutation. The higher the density of the multiple sequencing signals, the higher the editing efficiency is. Labels above the sequencing results represent corresponding ZFN combinations, and target sequences identified by ZFNs were circled with black boxes.

[0036] FIG. 31 shows flow cytometry of B2m expression of 293T cell with or without gRNA treatment.

[0037] FIGS. 32, 33, 34, and 35 show flow cytometry results of human leukocytes/murine leukocytes in different groups. The cells were derived from all living cells after the mouse peripheral blood lysis. The horizontal axis represents the fluorescence intensity of hCD45 corresponding staining, and the vertical axis represents the fluorescence intensity of mCD45 corresponding staining.

[0038] FIGS. 36, 37, 38, and 39 show flow cytometry results of T cells/human leukocytes. The cells were derived from human leukocyte hCD45 in FIGS. 32-35, the horizontal axis represents the fluorescence intensity of CD3 corresponding staining, and the vertical axis represents the fluorescence intensity of CD19 corresponding staining.

[0039] FIG. 40 shows release of cytokines IL-2 and IFN- γ of each of the mice. Peripheral blood samples were obtained from the mice, and the supernatant were provided in Table 13.

[0040] FIGS. 41, 42, 43, and 44 shows proportion of CD8/CD4 in mouse peripheral blood T cells. The cells are derived from CD3 in FIGS. 36-39, the horizontal axis represents the fluorescence intensity of CD4 corresponding staining, and the vertical axis represents the fluorescence intensity of CD8 corresponding staining. Detailed results are provided in Table 14.

[0041] FIG. 45 shows results of T cell / mouse white blood cell. It can be seen from the statistics and the data in Table 19 that the ratios of white blood cells in the T cells/mouse of the NT group, the 2407 group, and the Nalm6+2407+1204 group are similar, and the ratios of the white blood cells of the 2407+1204 group to the other four groups of T cells/mouse is higher.

[0042] FIG. 46 shows results of CD8/CD4. It can be seen from the statistics data in Table 20 that there is no significant difference in the ratio of the four groups of CD8/CD4.

[0043] FIG. 47 shows cytokine data from peripheral blood samples from mice and the supernatant.

[0044] FIG. 48 shows tumor volumes change in mice in response to infusion with different cell groups.

[0045] FIG. 49 shows changes in the numbers of copies of CAR molecules with time (days) after infusion of CAR T cells to patient F. The numbers of copies of CAR molecules include numbers of total copies of CAR and copies of individual CARs (i.e., Anti-CD19 CAR and Anti-tMUC1 CAR).

[0046] FIG. 50 shows cytokine release results of patient F.

[0047] FIG. 51 shows comparison of IL-6 release between patient C and patient F.

[0048] FIG. 52 shows comparison of IFN- γ release between patient C and patient F.

DETAILED DESCRIPTION

[0049] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by those of ordinary skill in the art to which the disclosure belongs. Although any method and material similar or equivalent to those described herein can be used in the practice or testing of the present disclosure, preferred methods and materials are described. For the purposes of the present disclosure, the following terms are defined below.

[0050] The articles "a" and "an" are used herein to refer to one or to more than one (i.e., to at least one) of the grammatical object of the article. By way of example, "an element" means one element or more than one element.

[0051] By "about" is meant a quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length that varies by as much as 20, 15, 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1% to a reference quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length.

[0052] The term "activation," as used herein, refers to the state of a cell that has been sufficiently stimulated to induce detectable cellular proliferation. Activation can also be associated with induced cytokine production and detectable effector functions. The term "activated T cells" refers to, among other things, T cells that are undergoing cell division.

[0053] The term "antibody" is used in the broadest sense and refers to monoclonal antibodies (including full length monoclonal antibodies), polyclonal antibodies, multi-specific

antibodies (e.g., bispecific antibodies), and antibody fragments so long as they exhibit the desired biological activity or function. The antibodies in the present disclosure may exist in a variety of forms including, for example, polyclonal antibodies, monoclonal antibodies, Fv, Fab and F(ab)₂, as well as single chain antibodies and humanized antibodies (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).

[0054] The term “antibody fragments” refers to a portion of a full-length antibody, for example, the antigen binding or variable region of the antibody. Other examples of antibody fragments include Fab, Fab', F(ab')₂, and Fv fragments; diabodies; linear antibodies; single-chain antibody molecules; and multi-specific antibodies formed from antibody fragments.

[0055] The term “Fv” refers to the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This fragment consists of a dimer of one heavy- and one light-chain variable region domain in tight, non-covalent association. From the folding of these two domains emanates six hypervariable loops (3 loops each from the H and L chain) that contribute amino acid residues for antigen binding and confer antigen binding specificity to the antibody. However, even a single variable domain (or half of an Fv including only three complementarity determining regions (CDRs) specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site (the dimer).

[0056] An “antibody heavy chain,” as used herein, refers to the larger of the two types of polypeptide chains present in all antibody molecules in their naturally occurring conformations. An “antibody light chain,” as used herein, refers to the smaller of the two types of polypeptide chains present in all antibody molecules in their naturally occurring conformations. κ and λ light chains refer to the two major antibody light chain isotypes.

[0057] The term “synthetic antibody” refers to an antibody which is generated using recombinant DNA technology, such as, for example, an antibody expressed by a bacteriophage. The term also includes an antibody which has been generated by the synthesis of a DNA molecule encoding the antibody and the expression of the DNA molecule to obtain the antibody or to obtain an amino acid encoding the antibody. The synthetic DNA is obtained using technology that is available and well known in the art.

[0058] The term “antigen” refers to a molecule that provokes an immune response, which may involve either antibody production, or the activation of specific immunologically-competent cells, or both. Antigens include any macromolecule, including all proteins or peptides, or molecules derived from recombinant or genomic DNA. For example, DNA including a nucleotide sequence or a partial nucleotide sequence encoding a protein or peptide that elicits an immune response, and therefore, encodes an “antigen” as the term is used herein. An antigen need not be encoded solely by a full-length nucleotide sequence of a gene. An antigen can be generated,

synthesized or derived from a biological sample including a tissue sample, a tumor sample, a cell, or a biological fluid.

[0059] The term “anti-tumor effect” as used herein, refers to a biological effect associated with a decrease in tumor volume, a decrease in the number of tumor cells, a decrease in the number of metastases, decrease in tumor cell proliferation, decrease in tumor cell survival, an increase in life expectancy of a subject having tumor cells, or amelioration of various physiological symptoms associated with the cancerous condition. An “anti-tumor effect” can also be manifested by the ability of the peptides, polynucleotides, cells, and antibodies in the prevention of the occurrence of tumor in the first place.

[0060] The term “auto-antigen” refers to an antigen mistakenly recognized by the immune system as being foreign. Auto-antigens include cellular proteins, phosphoproteins, cellular surface proteins, cellular lipids, nucleic acids, glycoproteins, including cell surface receptors.

[0061] The term “autologous” is used to describe a material derived from a subject which is subsequently re-introduced into the same subject.

[0062] The term “allogeneic” is used to describe a graft derived from a different subject of the same species. As an example, a donor subject may be a related or unrelated or recipient subject, but the donor subject has immune system markers which are similar to the recipient subject.

[0063] The term “xenogeneic” is used to describe a graft derived from a subject of a different species. As an example, the donor subject is from a different species than a recipient subject, and the donor subject and the recipient subject can be genetically and immunologically incompatible.

[0064] The term “cancer” is used to refer to a disease characterized by the rapid and 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 include 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.

[0065] Throughout this specification, unless the context requires otherwise, the words “comprise,” “includes” and “including” will be understood to imply the inclusion of a stated step or element or group of steps or elements but not the exclusion of any other step or element or group of steps or elements.

[0066] The phrase “consisting of” is meant to include, and is limited to, whatever follows the phrase “consisting of.” Thus, the phrase “consisting of” indicates that the listed elements are required or mandatory and that no other elements may be present.

[0067] The phrase “consisting essentially of” is meant to include any element listed after the phrase and can include other elements that do not interfere with or contribute to the activity or action specified in the disclosure for the listed elements. Thus, the phrase “consisting

essentially of' indicates that the listed elements are required or mandatory, but that other elements are optional and may or may not be present depending upon whether or not they affect the activity or action of the listed elements.

[0068] The terms "complementary" and "complementarity" refer to polynucleotides (i.e., a sequence of nucleotides) related by the base-pairing rules. For example, the sequence "A-G-T," is complementary to the sequence "T-C-A." Complementarity may be "partial," in which only some of the nucleic acids' bases are matched according to the base pairing rules, or there may be "complete" or "total" complementarity between the nucleic acids. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of hybridization between nucleic acid strands.

[0069] The term "corresponds to" or "corresponding to" refers to (a) a polynucleotide having a nucleotide sequence that is substantially identical or complementary to all or a portion of a reference polynucleotide sequence or encoding an amino acid sequence identical to an amino acid sequence in a peptide or protein; or (b) a peptide or polypeptide having an amino acid sequence that is substantially identical to a sequence of amino acids in a reference peptide or protein.

[0070] The term "co-stimulatory ligand," refers to a molecule on an antigen presenting cell (e.g., an APC, dendritic cell, B cell, and the like) that specifically binds a cognate co-stimulatory molecule on a T cell, thereby providing a signal which, in addition to the primary signal provided by, for instance, binding of a TCR/CD3 complex with an MHC molecule loaded with peptide, mediates a T cell response, including at least one of proliferation, activation, differentiation, and other cellular responses. A co-stimulatory ligand can include B7-1 (CD80), B7-2 (CD86), PD-L1, PD-L2, 4-1BBL, OX40L, inducible co-stimulatory ligand (ICOS-L), intercellular adhesion molecule (ICAM), CD30L, CD40, CD70, CD83, HLA-G, MICA, MICB, HVEM, lymphotoxin beta receptor, 3/TR6, ILT3, ILT4, HVEM, a ligand for CD7, an agonist or antibody that binds the Toll ligand receptor and a ligand that specifically binds with B7-H3. A co-stimulatory ligand also includes, inter alia, an agonist or an antibody that specifically binds with a co-stimulatory molecule present on a T cell, such as CD27, CD28, 4-1BB, OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, B7-H3, and a ligand that specifically binds CD83.

[0071] The term "co-stimulatory molecule" refers to the cognate binding partner on a T cell that specifically binds with a co-stimulatory ligand, thereby mediating a co-stimulatory response by the T cell, such as proliferation. Co-stimulatory molecules include an MHC class I molecule, BTLA, and a Toll-like receptor.

[0072] The term "co-stimulatory signal" refers to a signal, which in combination with a primary signal, such as TCR/CD3 ligation, leads to T cell proliferation and/or upregulation or downregulation of key molecules. The terms "disease" and "condition" may be used interchangeably or may be different in that the particular malady or condition may not have a

known causative agent (so that etiology has not yet been worked out), and it is therefore not yet recognized as a disease but only as an undesirable condition or syndrome, wherein a more or less specific set of symptoms have been identified by clinicians. The term “disease” is a state of health of a subject wherein the subject cannot maintain homeostasis, and wherein if the disease is not ameliorated then the subject’s health continues to deteriorate. In contrast, a “disorder” in a subject is a state of health in which the animal is able to maintain homeostasis, but in which the animal's state of health is less favorable than it would be in the absence of the disorder. Left untreated, a disorder does not necessarily cause a further decrease in the animal's state of health.

[0073] The term “effective” refers to adequate to accomplish a desired, expected, or intended result. For example, an “effective amount” in the context of treatment may be an amount of a compound sufficient to produce a therapeutic or prophylactic benefit.

[0074] 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 a template 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 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 (except that a “T” is replaced by a “U”) 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.

[0075] The term “exogenous” refers to a molecule that does not naturally occur in a wild-type cell or organism but is typically introduced into the cell by molecular biological techniques. Examples of exogenous polynucleotides include vectors, plasmids, and/or man-made nucleic acid constructs encoding the desired protein. With regard to polynucleotides and proteins, the term “endogenous” or “native” refers to naturally-occurring polynucleotide or amino acid sequences that may be found in a given wild-type cell or organism. Also, a particular polynucleotide sequence that is isolated from a first organism and transferred to a second organism by molecular biological techniques is typically considered an “exogenous” polynucleotide or amino acid sequence with respect to the second organism. In specific embodiments, polynucleotide sequences can be “introduced” by molecular biological techniques into a microorganism that already contains such a polynucleotide sequence, for instance, to create one or more additional copies of an otherwise naturally-occurring polynucleotide sequence, and thereby facilitate overexpression of the encoded polypeptide.

[0076] The term “expression” refers to the transcription and/or translation of a particular nucleotide sequence driven by its promoter.

[0077] The term “expression vector” refers to a vector including a recombinant polynucleotide including expression control sequences operably linked to a nucleotide sequence to be expressed. An expression vector includes 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, such as 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.

[0078] The term “homologous” refers to sequence similarity or sequence identity between two polypeptides or between two polynucleotides when a position in both of the two compared sequences is occupied by the same base or amino acid monomer subunit, e.g., if a position in each of two DNA molecules is occupied by adenine, then the molecules are homologous at that position. The percent of homology between two sequences is a function of the number of matching or homologous positions shared by the two sequences divided by the number of positions compared $\times 100$. For example, if 6 of 10 of the positions in two sequences are matched or homologous, then the two sequences are 60% homologous. By way of example, the DNA sequences ATTGCC and TATGGC share 50% homology. A comparison is made when two sequences are aligned to give maximum homology.

[0079] The term “immunoglobulin” or “Ig,” refers to a class of proteins, which function as antibodies. The five members included in this class of proteins are IgA, IgG, IgM, IgD, and IgE. IgA is the primary antibody that is present in body secretions, such as saliva, tears, breast milk, gastrointestinal secretions and mucus secretions of the respiratory and genitourinary tracts. IgG is the most common circulating antibody. IgM is the main immunoglobulin produced in the primary immune response in most subjects. It is the most efficient immunoglobulin in agglutination, complement fixation, and other antibody responses, and is important in defense against bacteria and viruses. IgD is the immunoglobulin that has no known antibody function but may serve as an antigen receptor. IgE is the immunoglobulin that mediates immediate hypersensitivity by causing the release of mediators from mast cells and basophils upon exposure to the allergen.

[0080] The term “isolated” refers to a material that is substantially or essentially free from components that normally accompany it in its native state. The material can be a cell or a macromolecule such as a protein or nucleic acid. For example, an “isolated polynucleotide,” as used herein, refers to a polynucleotide, which has been purified from the sequences which flank it in a naturally-occurring state, e.g., a DNA fragment which has been removed from the sequences that are normally adjacent to the fragment. Alternatively, an “isolated peptide” or an “isolated polypeptide” and the like, as used herein, refer to *in vitro* isolation and/or purification of a peptide or polypeptide molecule from its natural cellular environment, and from association with other components of the cell.

[0081] The term “substantially purified” refers to a material that is substantially free from components that are normally associated with it in its native state. For example, a substantially purified cell refers to a cell that has been separated from other cell types with which it is normally associated in its naturally occurring or native 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 a cell that has been separated from the cells with which they are naturally associated in their natural state. In embodiments, the cells are cultured *in vitro*. In embodiments, the cells are not cultured *in vitro*.

[0082] In the context of the present disclosure, the following abbreviations for the commonly occurring nucleic acid bases are used. “A” refers to adenosine, “C” refers to cytosine, “G” refers to guanosine, “T” refers to thymidine, and “U” refers to uridine.

[0083] 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 an RNA may also include introns to the extent that the nucleotide sequence encoding the protein may in some version contain an intron(s).

[0084] 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. Vectors derived from lentiviruses offer the means to achieve significant levels of gene transfer *in vivo*.

[0085] The term “modulating,” refers to mediating a detectable increase or decrease in the level of a response in a subject compared with the level of a response in the subject in the absence of a treatment or compound, and/or compared with the level of a response in an otherwise identical but untreated subject. The term encompasses perturbing and/or affecting a native signal or response thereby mediating a beneficial therapeutic response in a subject, preferably, a human.

[0086] Nucleic acid is “operably linked” when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation.

[0087] The term “under transcriptional control” refers to a promoter being operably linked to and in the correct location and orientation in relation to a polynucleotide to control the initiation of transcription by RNA polymerase and expression of the polynucleotide.

[0088] The term “overexpressed” tumor antigen or “overexpression” of the tumor antigen is intended to indicate an abnormal level of expression of the tumor antigen in a cell from a disease area such as a solid tumor within a specific tissue or organ of the patient relative to the level of expression in a normal cell from that tissue or organ. Patients having solid tumors or a hematological malignancy characterized by overexpression of the tumor antigen can be determined by standard assays known in the art.

[0089] Solid tumors are abnormal masses of tissue that usually do not contain cysts or liquid areas. Solid tumors can be benign or malignant. Different types of solid tumors are named for the type of cells that form them (such as sarcomas, carcinomas, and lymphomas). Examples of solid tumors, such as sarcomas and carcinomas, include fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma, osteosarcoma, and other sarcomas, synovioma, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, colon carcinoma, lymphoid malignancy, pancreatic cancer, breast cancer, lung cancers, ovarian cancer, prostate cancer, hepatocellular carcinoma, squamous cell carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma, medullary thyroid carcinoma, papillary thyroid carcinoma, pheochromocytomas sebaceous gland carcinoma, papillary carcinoma, papillary adenocarcinomas, medullary carcinoma, bronchogenic carcinoma, renal cell carcinoma, hepatoma, bile duct carcinoma, choriocarcinoma, Wilms' tumor, cervical cancer, testicular tumor, seminoma, bladder carcinoma, melanoma, and CNS tumors (such as a glioma (such as brainstem glioma and mixed gliomas), glioblastoma (also known as glioblastoma multiforme), astrocytoma, CNS lymphoma, germinoma, medulloblastoma, Schwannoma craniopharyngioma, ependymoma, pinealoma, hemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma, retinoblastoma, and brain metastases).

[0090] A solid tumor antigen is an antigen expressed on a solid tumor. In embodiments, solid tumor antigen is also expressed at low levels on healthy tissue. Examples of solid tumor antigens and their related disease tumors are provided in Table 1.

Table 1

Solid Tumor antigen	Disease tumor
PRLR	Breast Cancer
CLCA1	colorectal Cancer
MUC12	colorectal Cancer
GUCY2C	colorectal Cancer
GPR35	colorectal Cancer
CR1L	Gastric Cancer
MUC 17	Gastric Cancer
TMPRSS11B	esophageal Cancer
MUC21	esophageal Cancer
TMPRSS11E	esophageal Cancer
CD207	bladder Cancer
SLC30A8	pancreatic Cancer

CFC1	pancreatic Cancer
SLC12A3	Cervical Cancer
SSTR1	Cervical tumor
GPR27	Ovary tumor
FZD10	Ovary tumor
TSHR	Thyroid Tumor
SIGLEC15	Urothelial cancer
SLC6A3	Renal cancer
KISS1R	Renal cancer
QRFPR	Renal cancer:
GPR119	Pancreatic cancer
CLDN6	Endometrial cancer/ Urothelial cancer
UPK2	Urothelial cancer (including bladder cancer)
ADAM12	Breast cancer, pancreatic cancer and the like
SLC45A3	Prostate cancer
ACPP	Prostate cancer
MUC21	Esophageal cancer
MUC16	Ovarian cancer
MS4A12	Colorectal cancer
ALPP	Endometrial cancer
CEA	Colorectal carcinoma
EphA2	Glioma
FAP	Mesotelioma
GPC3	Lung squamous cell carcinoma
IL13-R α 2	Glioma
Mesothelin	Metastatic cancer
PSMA	Prostate cancer
ROR1	Breast lung carcinoma
VEGFR-II	Metastatic cancer
GD2	Neuroblastoma
FR- α	Ovarian carcinoma
ErbB2	Carcinomasb
EpCAM	Carcinomasa
EGFRvIII	Glioma—Glioblastoma
EGFR	Glioma—NSCL cancer
tMUC 1	Cholangiocarcinoma, Pancreatic cancer, Breast Cancer
PSCA	pancreas, stomach, or prostate cancer

[0091] The term “parenteral administration” of a composition includes, e.g., subcutaneous (s.c.), intravenous (i.v.), intramuscular (i.m.), intrasternal injection, or infusion techniques.

[0092] The terms “patient,” “subject,” and “individual,” and the like are used interchangeably herein and refer to any human, animal, or living organism, amenable to the methods described herein. In certain non-limiting embodiments, the patient, subject, or individual is a human or animal. In embodiments, 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, and animals such as dogs, cats, mice, rats, and transgenic species thereof.

[0093] A subject in need of treatment or in need thereof includes a subject having a disease, condition, or disorder that needs to be treated. A subject in need thereof also includes a subject that needs treatment for prevention of a disease, condition, or disorder.

[0094] The term “polynucleotide” or “nucleic acid” refers to mRNA, RNA, cRNA, rRNA, cDNA or DNA. The term typically refers to a polymeric form of nucleotides of at least 10 bases in length, either ribonucleotides or deoxynucleotides or a modified form of either type of nucleotide. The term includes all forms of nucleic acids including single and double-stranded forms of nucleic acids.

[0095] The terms “polynucleotide variant” and “variant” and the like refer to polynucleotides displaying substantial sequence identity with a reference polynucleotide sequence or polynucleotides that hybridize with a reference sequence under stringent conditions that are defined hereinafter. These terms also encompass polynucleotides that are distinguished from a reference polynucleotide by the addition, deletion or substitution of at least one nucleotide. Accordingly, the terms “polynucleotide variant” and “variant” include polynucleotides in which one or more nucleotides have been added or deleted or replaced with different nucleotides. In this regard, it is well understood in the art that certain alterations inclusive of mutations, additions, deletions, and substitutions can be made to a reference polynucleotide whereby the altered polynucleotide retains the biological function or activity of the reference polynucleotide or has increased activity in relation to the reference polynucleotide (i.e., optimized).

Polynucleotide variants include, for example, polynucleotides having at least 50% (and at least 51% to at least 99% and all integer percentages in between, e.g., 90%, 95%, or 98%) sequence identity with a reference polynucleotide sequence described herein. The terms “polynucleotide variant” and “variant” also include naturally-occurring allelic variants and orthologs.

[0096] The terms “polypeptide,” “polypeptide fragment,” “peptide,” and “protein” are used interchangeably herein to refer to a polymer of amino acid residues and to variants and synthetic analogues of the same. Thus, these terms apply to amino acid polymers in which one or more amino acid residues are synthetic non-naturally occurring amino acids, such as a chemical analogue of a corresponding naturally occurring amino acid, as well as to naturally-occurring amino acid polymers. In certain aspects, polypeptides may include enzymatic polypeptides, or “enzymes,” which typically catalyze (i.e., increase the rate of) various chemical reactions.

[0097] The term “polypeptide variant” refers to polypeptides that are distinguished from a reference polypeptide sequence by the addition, deletion, or substitution of at least one amino acid residue. In certain embodiments, a polypeptide variant is distinguished from a reference polypeptide by one or more substitutions, which may be conservative or non-conservative. In certain embodiments, the polypeptide variant comprises conservative substitutions and, in this regard, it is well understood in the art that some amino acids may be changed to others with broadly similar properties without changing the nature of the activity of the polypeptide.

Polypeptide variants also encompass polypeptides in which one or more amino acids have been added or deleted or replaced with different amino acid residues.

[0098] 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. The term “expression control sequences” refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

[0099] The term “bind,” “binds,” or “interacts with” refers to a molecule recognizing and adhering to a second molecule in a sample or organism but does not substantially recognize or adhere to other structurally unrelated molecules in the sample. The term “specifically binds,” as used herein with respect to an antibody, refers to an antibody which recognizes a specific antigen, but does not substantially recognize or bind other molecules in a sample. For example, an antibody that specifically binds an antigen from one species may also bind that antigen from one or more species. But, such cross-species reactivity does not itself alter the classification of an antibody as specific. In another example, an antibody that specifically binds an antigen may also bind different allelic forms of the antigen. However, such cross reactivity does not itself alter the classification of an antibody as specific. In some instances, the terms “specific binding” or “specifically binding,” can be used in reference to the interaction of an antibody, a protein, or a peptide with a second chemical species, to mean that the interaction is dependent upon the presence of a particular structure (e.g., an antigenic determinant or epitope) on the chemical species; for example, an antibody recognizes and binds a specific protein structure rather than to any protein. If an antibody is specific for epitope “A,” the presence of a molecule containing epitope A (or free, unlabeled A), in a reaction containing labeled “A” and the antibody, will reduce the amount of labeled A bound to the antibody.

[00100] By “statistically significant,” it is meant that the result was unlikely to have occurred by chance. Statistical significance can be determined by any method known in the art. Commonly used measures of significance include the p-value, which is the frequency or probability with which the observed event would occur if the null hypothesis were true. If the obtained p-value is smaller than the significance level, then the null hypothesis is rejected. In simple cases, the significance level is defined at a p-value of 0.05 or less. A “decreased” or “reduced” or “lesser” amount is typically a “statistically significant” or a physiologically significant amount, and may include a decrease that is about 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.5, 3, 3.5, 4, 4.5, 5, 6, 7, 8, 9, 10, 15, 20, 30, 40, or 50 or more times (e.g., 100, 500, 1000 times) (including all integers and decimal points in between and above 1, e.g., 1.5, 1.6, 1.7, 1.8, etc.) an amount or level described herein.

[00101] The term “stimulation,” refers to a primary response induced by binding of a stimulatory molecule (e.g., a TCR/CD3 complex) with its cognate ligand thereby mediating a signal transduction event, such as signal transduction via the TCR/CD3 complex. Stimulation can mediate altered expression of certain molecules, such as downregulation of TGF- β , and/or reorganization of cytoskeletal structures.

[00102] The term “stimulatory molecule” refers to a molecule on a T cell that specifically binds a cognate stimulatory ligand present on an antigen presenting cell. For example, a functional signaling domain derived from a stimulatory molecule is the zeta chain associated with the T cell receptor complex.

[00103] The term “stimulatory ligand” refers to a ligand that when present on an antigen presenting cell (e.g., an APC, a dendritic cell, a B-cell, and the like.) can specifically bind with a cognate binding partner (referred to herein as a “stimulatory molecule”) on a cell, for example a T cell, thereby mediating a primary response by the T cell, including activation, initiation of an immune response, proliferation, and similar processes. Stimulatory ligands are well-known in the art and encompass, inter alia, an MHC Class I molecule loaded with a peptide, an anti-CD3 antibody, a superagonist anti-CD28 antibody, and a superagonist anti-CD2 antibody.

[00104] The term “therapeutic” refers to a treatment and/or prophylaxis. A therapeutic effect is obtained by suppression, remission, or eradication of a disease state or alleviating the symptoms of a disease state.

[00105] The term “therapeutically effective amount” refers to the amount of the subject compound that will elicit the biological or medical response of a tissue, system, or subject that is being sought by the researcher, veterinarian, medical doctor or another clinician. The term “therapeutically effective amount” includes that amount of a compound that, when administered, is sufficient to prevent the development of, or alleviate to some extent, one or more of the signs or symptoms of the disorder or disease being treated. The therapeutically effective amount will vary depending on the compound, the disease and its severity and the age, weight, etc., of the subject to be treated.

[00106] The term “treat a disease” refers to the reduction of the frequency or severity of at least one sign or symptom of a disease or disorder experienced by a subject.

[00107] The term “transfected” or “transformed” or “transduced” refers to a process by which an 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.

[00108] The term “vector” refers to a polynucleotide that 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 linear polynucleotides, polynucleotides associated with ionic or amphiphilic compounds, plasmids, and viruses. Thus, the term “vector” includes an

autonomously replicating plasmid or a virus. The term also includes non-plasmid and non-viral compounds which facilitate the transfer of nucleic acid into cells, such as, for example, polylysine compounds, liposomes, and the like. Examples of viral vectors include adenoviral vectors, adeno-associated virus vectors, retroviral vectors, and others. For example, lentiviruses are complex retroviruses, which, in addition to the common retroviral genes gag, pol, and env, contain other genes with regulatory or structural function. Lentiviral vectors are well known in the art. Some examples of lentivirus include the Human Immunodeficiency Viruses: HIV-1, HIV-2, and the Simian Immunodeficiency Virus: SIV. Lentiviral vectors have been generated by multiply attenuating the HIV virulence genes, for example, the genes env, vif, vpr, vpu, and nef are deleted making the vector biologically safe.

[00109] Ranges: throughout this disclosure, various aspects of the disclosure 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 disclosure. 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. This applies regardless of the breadth of the range.

[00110] A "chimeric antigen receptor" (CAR) molecule is a recombinant polypeptide including at least an extracellular domain, a transmembrane domain and a cytoplasmic domain or intracellular domain. In embodiments, the domains of the CAR are on the same polypeptide chain, for example a chimeric fusion protein. In embodiments, the domains are on different polypeptide chains, for example the domains are not contiguous.

[00111] The extracellular domain of a CAR molecule includes an antigen binding domain. In embodiments, the antigen binding domain binds an antigen, for example, a cell surface molecule or marker, on the surface of a B cell. In embodiments, the cell surface molecule of a B cell includes CD19, CD22, CD20, BCMA, CD5, CD7, CD2, CD16, CD56, CD30, CD14, CD68, CD11b, CD18, CD169, CD1c, CD33, CD38, CD138, or CD13. In embodiments, the cell surface molecule of the B cell is CD19, CD20, CD22, or BCMA. In particular embodiments, the cell surface molecule of the B cell is CD19.

[00112] In embodiments, the antigen binding domain binds an antigen, on the surface of a tumor for example a tumor antigen or tumor marker. Tumor antigens are proteins that are produced by tumor cells that elicit an immune response, particularly T cell mediated immune responses. Tumor antigens are well known in the art and include, for example, tumor associated MUC1, a glioma-associated antigen, carcinoembryonic antigen (CEA), β -human chorionic gonadotropin, alphafetoprotein (AFP), lectin-reactive AFP, thyroglobulin, RAGE-1, MN-CA IX, human telomerase reverse transcriptase, RU1, RU2 (AS), intestinal carboxyl

esterase, mut hsp70-2, M-CSF, prostase, prostate-specific antigen (PSA), PAP, NY-ESO-1, LAGE-1a, p53, prostein, PSMA, Her2/neu, surviving, telomerase, prostate-carcinoma tumor antigen-1 (PCTA-1), MAGE, ELF2M, neutrophil elastase, ephrinB2, CD22, insulin growth factor (IGF)-I, IGF-II, IGF-I receptor and mesothelin. For example, when the tumor antigen is CD19, the CAR thereof can be referred to as CD19CAR.

[00113] In embodiments, the extracellular antigen binding domain of a CAR includes at least one scFv or at least a single domain antibody. As an example, there can be two scFvs on a CAR. The scFv includes a light chain variable (VL) region and a heavy chain variable (VH) region of a target antigen-specific monoclonal antibody joined by a flexible linker. Single chain variable region fragments can be made by linking light and/or heavy chain variable regions by using a short linking peptide (Bird et al., Science 242:423-426, 1988). An example of a linking peptide is the GS linker having the amino acid sequence (GGGGS)₃ (SEQ ID NO: 278), which bridges approximately 3.5 nm between the carboxy terminus of one variable region and the amino terminus of the other variable region. Linkers of other sequences have been designed and used (Bird et al., 1988, supra). In general, linkers can be short, flexible polypeptides and preferably comprised of about 20 or fewer amino acid residues. The single chain variants can be produced either recombinantly or synthetically. For synthetic production of scFv, an automated synthesizer can be used. For recombinant production of scFv, a suitable plasmid containing polynucleotide that encodes the scFv can be introduced into a suitable host cell, either eukaryotic, such as yeast, plant, insect or mammalian cells, or prokaryotic, such as E. coli. Polynucleotides encoding the scFv of interest can be made by routine manipulations such as ligation of polynucleotides. The resultant scFv can be isolated using standard protein purification techniques known in the art.

[00114] The cytoplasmic domain of the CAR molecules described herein includes one or more co-stimulatory domains and one or more signaling domains. The co-stimulatory and signaling domains function to transmit the signal and activate molecules, such as T cells, in response to antigen binding. The one or more co-stimulatory domains are derived from stimulatory molecules and/or co-stimulatory molecules, and the signaling domain is derived from a primary signaling domain, such as the CD3 zeta domain. In embodiments, the signaling domain further includes one or more functional signaling domains derived from a co-stimulatory molecule. In embodiments, the co-stimulatory molecules are cell surface molecules (other than antigens receptors or their ligands) that are required for activating a cellular response to an antigen.

[00115] In embodiments, the co-stimulatory domain includes the intracellular domain of CD27, CD28, 4-1BB, OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, B7-H3, a ligand that specifically binds with CD83, or any combination thereof. In embodiments, the signaling domain includes a CD3 zeta domain derived from a T cell receptor.

[00116] In embodiments, the cytoplasmic domain of the CAR only includes one or more stimulatory domains and no signaling domain.

[00117] The CAR molecules also include a transmembrane domain. The incorporation of a transmembrane domain in the CAR molecules stabilizes the molecule. In embodiments, the transmembrane domain of the CAR molecules is the transmembrane domain of a CD28 or 4-1BB molecule.

[00118] Between the extracellular domain and the transmembrane domain of the CAR, there may be incorporated a spacer domain. As used herein, the term "spacer domain" generally means any oligo- or polypeptide that functions to link the transmembrane domain to, either the extracellular domain or, the cytoplasmic domain on the polypeptide chain. A spacer domain may include up to 300 amino acids, preferably 10 to 100 amino acids, and most preferably 25 to 50 amino acids.

[00119] The present disclosure describes isolated nucleic acids encoding at least two different antigen binding domains. In embodiments, there is a first antigen binding domain that binds an antigen on the surface of a WBC, and there is a second antigen binding domain that binds an antigen on a tumor that is different from the antigen on the surface of a WBC. The first antigen binding domain functions to expand the cells that it is introduced into, while the second antigen binding domain functions to inhibit the growth of or kill tumor cells containing the target tumor antigen upon binding to the target antigen. In embodiments, an isolated nucleic acid described herein encodes both the first and second antigen binding domains on the same nucleic acid molecule. In embodiments, the two antigen binding domains are encoded by two separate nucleic acid molecules. For example, a first nucleic acid encodes a first antigen binding domain and a second nucleic acid encodes a second antigen binding domain.

[00120] In embodiments, the present disclosure describes nucleic acids encoding a first antigen binding domain of a binding molecule and a second antigen binding domain of a binding molecule, wherein first antigen binding domain binds a cell surface molecule of a WBC, and the second antigen binding domain binds an antigen different from the cell surface molecule of the WBC. In embodiments, the second binding domain does not bind a B cell marker. In embodiments, the second binding domain includes a scFv comprising an amino acid sequence of SEQ ID No: 264 or 265. For example, the second antigen binding domain is on a CAR having one of the amino acid sequences of SEQ ID Nos: 271-277.

[00121] In embodiments, the first and second antigen binding domains can be on two different binding molecules (first and second binding molecules) such as a first CAR and a second CAR. As an example, a first CAR includes an extracellular binding domain that binds a marker on the surface of a B cell, and a second CAR includes an extracellular binding domain that binds a target antigen of a tumor cell. In embodiments, the first CAR and second CAR are encoded by different nucleic acids. In embodiments, the first CAR and second CAR are two different binding molecules but are encoded by a single nucleic acid.

[00122] In embodiments, the two different antigen binding domains can be on the same binding molecule, for example on a bispecific CAR, and encoded by a single nucleic acid. In embodiments, the bispecific CAR can have two different scFv molecules joined together by linkers.

[00123] In embodiments, the two different antigen binding domains can be on a CAR and a T cell receptor (TCR) and are encoded by separate nucleic acids. The binding domain of a TCR can target a specific tumor antigen or tumor marker on the cell of a tumor. In embodiments the TCR binding domain is a TCR alpha binding domain or TCR beta binding domain that targets a specific tumor antigen. In embodiments, the TCR comprises the TCR γ and TCR δ chains or the TCR α and TCR β chains.

[00124] The present disclosure also describes vectors including the isolated nucleic acids described above. In embodiments, a single vector contains the isolated nucleic acid encoding the first CAR and second CAR or TCR. In embodiments, a first vector contains the first nucleic acid encoding a first CAR, a second vector contains the nucleic acid encoding the second CAR or TCR. In embodiments, the vector comprises a bispecific CAR including at least two antigen binding domains.

[00125] Moreover, the present disclosure describes cells comprising the isolated nucleic acids or vectors described above. The cells have been introduced with the isolated nucleic acids or vectors described herein and express at least two more different binding domains. In embodiments, the cells include a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain binds a cell surface molecule of a WBC, and the second antigen binding domain binds an antigen different from the cell surface molecule of a WBC. Further, the present disclosure describes compositions including a population of the cells described herein. In embodiments, the cells are lymphocytes. In particular embodiments, the lymphocytes are T cells, NK cell, or dendritic cells.

[00126] The present disclosure also describes methods of culturing cells described above. The methods described herein includes obtaining a cell comprising a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain binds a cell surface molecule of a WBC, and the second antigen binding domain binds an antigen different from the cell surface molecule of the WBC; and culturing the cell in the presence of an agent derived from a cell surface molecule of the WBC or from an antigen to which the second antigen binding domain binds. In embodiments, the agent is an extracellular domain of a cell surface molecule of a WBC.

[00127] The present disclose describes methods for *in vitro* cell preparation, wherein the method includes providing cells; introducing one or more nucleic acids encoding a first antigen binding domain and a second antigen binding domain into the cells, wherein the first antigen binding domain binds a cell surface molecule of a WBC, and the second antigen binding domain binds an antigen different from the cell surface molecule of the WBC; and culturing the cells in

the presence of an agent derived from the cell surface molecule of the WBC or from an antigen to which the second antigen binding domain binds.

[00128] The present disclosure describes using the prepared cells preparation to enhance T cell expansion in a subject having cancer. In embodiments, the method comprises introducing a plurality of nucleic acids into T cells, the plurality of nucleic acids encoding a chimeric antigen receptor (CAR) binding a solid tumor antigen and encoding a CAR binding a B cell antigen, at least a portion of the T cells comprising the CAR binding the solid tumor antigen and the CAR binding the B cell antigen; and administering an effective amount of the T cells to the subject.

[00129] Additionally, the present disclosure describes methods for introducing and/or enhancing lymphocyte (T cell) response in a subject. Embodiments described herein involve a mechanism that expands lymphocytes and a mechanism that relates to binding of an antigen on a CAR to a tumor cell. In embodiments, the first mechanism involves a molecule associated with a signal that is involved in expanding the lymphocytes in a subject, and an additional mechanism involves a molecule associated with a signal directed to binding, inhibiting the growth of, or killing a tumor cell in the subject. For example, the first mechanism includes a CAR binding to an antigen associated with blood, such as blood cells and blood plasma, or non-essential tissues, and the additional mechanism includes a CAR or TCR targeting an antigen associated with the tumor cell. Examples of non-essential tissues include the mammary gland, colon, gastric gland, ovary, blood components, such WBC, and thyroid. In embodiments, the first mechanism involves a first binding domain of a molecule, and the additional mechanism involves a second domain of a molecule. In embodiments, the first mechanism and the additional mechanism are performed by the same molecule or by separate molecules. In particular embodiments, the mechanism involves a cell expressing an antigen associated with a tumor cell, and the additional mechanism involves a lymphocyte having an antigen binding domain.

[00130] The methods described herein involves lymphocytes including an expansion molecule and a function molecule. In embodiments, the expansion molecule expands the lymphocytes in a subject, and/or the function molecule inhibits the growth of or kills a tumor cell in the subject. In embodiments, the expansion molecule and the function molecule are on a single CAR molecule, for example a bispecific CAR molecule. In embodiments, the expansion molecule and the function molecule are on separate molecules, for example, CAR and TCR or two different CARs. The expansion molecule can include a CAR binding to an antigen associated with blood (e.g., blood cells and blood plasma) or non-essential tissues, and the function molecule can include a CAR or TCR targeting an antigen associated with the tumor cell.

[00131] Lymphocyte or T cell response in a subject refers to cell-mediated immunity associated with a helper, killer, regulatory, and other types of T cells. For example, T cell response may include activities such as assisting other WBCs in immunologic processes and

identifying and destroying virus-infected cells and tumor cells. T cell response in the subject can be measured via various indicators such as a number of virus-infected cells and /or tumor cells that T cells kill, the amount of cytokines (e.g., IL-6 and IFN- γ) that T cells release *in vivo* and/or in co-culturing with virus-infected cells and/or tumor cells, indicates a level of proliferation of T cells in the subject, a phenotype change of T cells, for example, changes to memory T cells, and a level longevity or lifetime of T cells in the subject.

[00132] In embodiments, the method of enhancing T cell response treats a subject in need thereof, for example, a subject diagnosed with a tumor. The term tumor refers to a mass, which can be a collection of fluid, such as blood, or a solid mass. A tumor can be malignant (cancerous) or benign. Examples of blood cancers include chronic lymphocytic leukemia, acute myeloid leukemia, acute lymphoblastic leukemia, and multiple myeloma.

[00133] Solid tumors usually do not contain cysts or liquid areas. The major types of malignant solid tumors include sarcomas and carcinomas. Sarcomas are tumors that develop in soft tissue cells called mesenchymal cells, which can be found in blood vessels, bone, fat tissues, ligament lymph vessels, nerves, cartilage, muscle, ligaments, or tendon, while carcinomas are tumors that form in epithelial cells, which are found in the skin and mucous membranes. The most common types of sarcomas include undifferentiated pleomorphic sarcoma which involves soft tissue and bone cells; leiomyosarcoma which involves smooth muscle cells that line blood vessels, gastrointestinal tract, and uterus; osteosarcoma which involves bone cells, and liposarcoma which involves fat cells. Some examples of sarcomas include Ewing sarcoma, Rhabdomyosarcoma, chondrosarcoma, mesothelioma, fibrosarcoma, fibrosarcoma, and glioma.

[00134] The five most common carcinomas include adenocarcinoma which involves organs that produce fluids or mucous, such as the breasts and prostate; basal cell carcinoma which involves cells of the outer-most layer of the skin, for example, skin cancer; squamous cell carcinoma which involves the basal cells of the skin; and transitional cell carcinoma which affects transitional cells in the urinary tract which includes the bladder, kidneys, and ureter. Examples of carcinomas include cancers of the thyroid, breast, prostate, lung, intestine, skin, pancreas, liver, kidneys, and bladder, and cholangiocarcinoma.

[00135] The methods described herein can be used to treat a subject diagnosed with cancer. The cancer can be a blood cancer or can be a solid tumor, such as a sarcoma or carcinoma. The method of treating includes administering an effective amount of T cells comprising a first antigen binding domain and a second antigen binding domain to the subject to provide a T-cell response, wherein the first antigen binding domain binds a cell surface molecule of a WBC, and the second antigen binding domain binds an antigen different from the cell surface molecule of the WBC. In embodiments, enhancing the T cell response in the subject includes selectively enhancing proliferation of T cell expressing the first antigen binding domain and the second antigen binding domain *in vivo*.

[00136] In embodiments, the T cells for enhancing T cell response in a subject includes administering to the subject, T cells comprising a bispecific CAR including two different binding domains or administering T cells comprising a first CAR and a second CAR, wherein the first CAR and the second CAR, each includes a different antigen binding domain.

[00137] In embodiments, methods for enhancing T cell response in a subject includes administering a T cell including a CAR molecule and a TCR molecule. The CAR molecule targets or binds a surface marker of a white blood cell, and the TCR molecule binds a marker or an antigen of the tumor that is expressed on the surface or inside the tumor cell.

[00138] The present disclosure describes methods of expanding cells expressing an antigen binding domain *in vivo*. The method includes administering an effective amount of T cells comprising a first antigen binding domain and a second antigen binding domain to a subject in need thereof, wherein the first antigen binding domain binds a cell surface molecule of a WBC, and the second antigen binding domain binds an antigen different from the cell surface molecule of the WBC. The methods are useful for expanding T cells, NK cells, or dendritic cells.

[00139] In embodiments, the first antigen binding domain is on a first chimeric antigen receptor (CAR) and the second antigen binding domain is on a second CAR or a TCR. For example, the first CAR and the second CAR or TCR include an extracellular antigen binding domain, a transmembrane domain, and a cytoplasmic domain. The cytoplasmic domain of the first CAR include a co-stimulatory domain and a CD3 zeta domain for transmitting signals for activation of cellular responses. In embodiments, the cytoplasmic domain of the first CAR includes one or more co-stimulatory domains in the absence of a CD3 zeta domain such that activation or stimulation of the first CAR expands WBCs, such as lymphocytes, without introducing and/or activating the killing function of the WBCs. In embodiments, the lymphocytes are T cells.

[00140] In embodiments, the first and second antigen binding domains are on the same CAR (the first CAR), for example, a bispecific CAR with an extracellular antigen binding domain, a transmembrane domain, and a cytoplasmic domain. The extracellular antigen binding domain includes at least two scFvs and at least one of the scFvs function as a first antigen binding domain for binding a cell surface molecule of a WBC.

[00141] In embodiments, the antigen different from the cell surface molecule of the WBC is CD19, CD22, CD20, BCMA, CD5, CD7, CD2, CD16, CD56, CD30, CD14, CD68, CD11b, CD18, CD169, CD1c, CD33, CD38, CD138, CD13, B7, CAIX, CD123, CD133, CD171, CD171/L1-CAM, CEA, Claudin 18.2, cMet, CS1, CSPG4, Dectin1, EGFR, EGFR vIII, EphA2, ERBB receptors, ErbB T4, ERBB2, FAP, Folate receptor 1, FITC, Folate receptor 1, FSH, GD2, GPC3, HA-1 H/HLA- A2, HER2, IL-11Ra, IL13 receptor a2, IL13R, IL13R α 2 (zetakine), Kappa, Leukemia, LewisY, Mesothelin, MUC1, NKG2D, NY-ESO-1, PSMA, ROR-1, TRAIL-receptor1, or VEGFR2.

[00142] In embodiments, the MUC1 is a tumor-exclusive epitope of a human MUC1, and the first CAR and the second CAR or the TCR are expressed as separate polypeptides. In embodiments, the MUC1 is a tumor form of human MUC1 (tMUC1).

[00143] In embodiments, the first CAR includes a co-stimulatory domain without a signaling domain, such as the CD3 zeta domain, and the MUC1 CAR (second CAR) comprises the MUC1 binding domain, a transmembrane domain, a co-stimulatory, and a CD3 zeta domain.

[00144] As used herein, the term "MUC1" refers to a molecule defined as follows. MUC1 is one of the epithelial mucin family of molecules. MUC1 is a transmembrane mucin glycoprotein that is normally expressed on all glandular epithelial cells of the major organs. In normal cells, MUC1 is only expressed on the apical surface and is heavily glycosylated with its core proteins sequestered by the carbohydrates. As cells transform to a malignant phenotype, expression of MUC1 increases several folds, and the expression is no longer restricted to the apical surface, but it is found all around the cell surface and in the cytoplasm. In addition, the glycosylation of tumor associated MUC1 is aberrant, with greater exposure of the peptide core than is found on MUC1 expressed in normal tissues. Little is known regarding the specifics of the aberrant glycosylation.

[00145] MUC1 is widely expressed on a large number of epithelial cancers and is aberrantly glycosylated making it structurally and antigenically distinct from that expressed by non-malignant cells (see, e.g., Barratt-Boyes, 1996; Price et al., 1998; Peterson et al., 1991). The dominant form of MUC1 is a high molecular weight molecule comprising a large highly immunogenic extracellular mucin-like domain with a large number of twenty amino acid tandem repeats, a transmembrane region, and a cytoplasmic tail (Quin et al., 2000; McGucken et al., 1995; Dong et al., 1997).

[00146] In most epithelial adenocarcinomas including breast and pancreas, MUC1 is overexpressed and aberrantly glycosylated. Adenocarcinoma of the breast and pancreas not only overexpress MUC1 but also shed MUC1 into the circulation. High MUC1 serum levels are associated with progressive disease. MUC1 has been exploited as a prospective biomarker because of the complex and heterogeneous nature of the epitopes expressed within the antigen. MUC1 synthesized by cancerous tissues (e.g., tumor associated MUC1) usually displays an aberrant oligosaccharide profile, which gives rise to the expression of neomarkers such as sialyl-Lea (assayed in the CA19-9 test), sialyl-Lex, and sialyl-Tn (TAG-72), as well as the cryptic epitopes such as Tn.

[00147] Several antibodies are being developed against MUC1 for therapeutic use. Pentumomab (also known as HMFG1) is in Phase III clinical trials as a carrier to deliver the radioisotope Yttrium-90 into tumors in ovarian cancer (reviewed in Scott et al., 2012). CA15-3 (also the HMFG1 antibody), CA27-29, and CA19-9 are all antibodies to MUC1 that are used to assess levels of circulating MUC1 in patients with cancer. However, these antibodies have shown limited utility as therapeutic agents or as biomarkers because they cannot distinguish

effectively between MUC1 expressed on normal versus transformed tumor epithelia. In other words, none of these antibodies appear to be targeted to a tumor-specific MUC1 epitope.

[00148] A new antibody that is highly specific for a tumor-specific form of MUC1 (tMUC) is designated TAB-004 and is described in U.S. Pat. No. 8,518,405 (see also Curry et al., 2013). While Pemtumomab (HMFG1) was developed using human milk fat globules as the antigen (Parham et al., 1988), TAB-004 was developed using tumors expressing an altered form of MUC1 (Tinder et al., 2008). TAB-004 recognizes the altered glycosylated epitope within the MUC1 tandem repeat sequence. This area is accessible for antigenic detection in tMUC but is blocked from antigenic detection in normal MUC1 by large branches of glycosylation (Gendler, 2001; Mukherjee et al., 2003b; Hollingsworth & Swanson, 2004; Kufe, 2009). Importantly, TAB-004 is different from the epitopes recognized by other MUC1 antibody and has unique complementary determinant regions (CDRs) of the heavy and light chains. The antibody binds the target antigen with a high binding affinity at 3 ng/ml (20 pM) and does not bind unrelated antigens (Curry et al., 2013). Thus, TAB-004 distinguishes between normal and tumor form of MUC1 while HMFG1 (Pemtumomab) does not (see U.S. Pat. No. 8,518,405).

[00149] In embodiments, the WBC is a granulocyte, monocyte and or lymphocyte. In embodiments, the WBC is a B cell.

[00150] In embodiments, the first CAR comprises the first antigen binding domain, a transmembrane domain, a co-stimulatory domain, and a CD3 zeta domain and/or the second CAR comprises the second antigen binding domain, a transmembrane domain, a co-stimulatory domain, and a CD3 zeta domain.

[00151] In embodiments, the antigen binding domain is a Fab or a scFv. In embodiments, the first CAR comprises the amino acid sequence of one of SEQ ID NO: 5, 6, and 53-58; and the second CAR comprises the amino acid sequence of one of SEQ ID NOs: 5-17, 29, 33, 37, 71, and 72, or the amino acid sequence encoded by the nucleic acid sequence of one of SEQ ID Nos: 41, 45, 63, 67, and 68. In embodiments, a nucleic acid sequence encoding the first CAR comprises the nucleic acid sequence of SEQ ID NO: 59 or 60, and a nucleic acid sequence encoding the second CAR comprises the nucleic acid sequence of SEQ ID NO: 61. In embodiments, the isolated nucleic acid comprises one of the nucleic acid sequence of SEQ ID NO: 62-69. In embodiments, the first CAR and the second CAR are expressed as separate polypeptides.

[00152] In embodiments, the first antigen binding domain is on a CAR and the second antigen binding domain is on a T Cell Receptor (TCR). In embodiments, the TCR is a modified TCR. In embodiments, the TCR is derived from spontaneously occurring tumor-specific T cells in patients. In embodiments, the TCR binds a tumor antigen. In embodiments, the tumor antigen comprises CEA, gp100, MART-1, p53, MAGE-A3, or NY-ESO-1.

[00153] In embodiments, a T cell clone that expresses a TCR with high affinity for the target antigen may be isolated. Tumor-infiltrating lymphocytes (TILs) or peripheral blood mononuclear

cells (PBMCs) can be cultured in the presence of antigen-presenting cells (APCs) pulsed with a peptide representing an epitope known to elicit a dominant T cell response when presented in the context of a defined HLA allele. High-affinity clones may be then be selected on the basis of MHC–peptide tetramer staining and/or the ability to recognize and lyse target cells pulsed with low titrated concentrations of cognate peptide antigen. After the clone has been selected, the TCR α and TCR β chains or TCR γ and TCR δ chains are identified and isolated by molecular cloning. For example, for TCR α and TCR β chains, the TCR α and TCR β gene sequences are then used to generate an expression construct that ideally promotes stable, high-level expression of both TCR chains in human T cells. The transduction vehicle, for example, a gammaretrovirus or lentivirus, can then be generated and tested for functionality (antigen specificity and functional avidity) and used to produce a clinical lot of the vector. An aliquot of the final product can then be used to transduce the target T cell population (generally purified from patient PBMCs), which is expanded before infusion into the patient.

[00154] Various methods may be implemented to obtain genes encoding tumor-reactive TCR. More information is provided in Kershaw et al., Clin Transl Immunology. 2014 May; 3(5): e16. In embodiments, specific TCR can be derived from spontaneously occurring tumor-specific T cells in patients. Antigens included in this category include the melanocyte differentiation antigens MART-1 and gp100, as well as the MAGE antigens and NY-ESO-1, with expression in a broader range of cancers. TCRs specific for viral-associated malignancies can also be isolated, as long as viral proteins are expressed by transformed cells. Malignancies in this category include liver and cervical cancer, associated with hepatitis and papilloma viruses, and Epstein-Barr virus-associated malignancies. In embodiments, target antigens of the TCR may include CEA (e.g., for colorectal cancer), gp100, MART-1, p53 (e.g., for Melanoma), MAGE-A3 (e.g., Melanoma, esophageal and synovial sarcoma), NY-ESO-1 (e.g., for Melanoma and sarcoma as well as Multiple myelomas).

[00155] In embodiments, a binding domain of the first CAR binds CD19, and a binding domain of the second CAR binds tumor associated MUC1. In embodiments, the binding domain of the second CAR comprises: (i) a heavy chain complementary determining region 1 comprising the amino acid sequence of SEQ ID: 76 or 85, a heavy chain complementary determining region 2 comprising the amino acid sequence of SEQ ID: 77 or 86, and a heavy chain complementary determining region 3 comprising the amino acid sequence of SEQ ID: 78 or 87; and (ii) a light chain complementary determining region 1 comprising the amino acid sequence of SEQ ID: 73 or 82, a light chain complementary determining region 2 comprising the amino acid sequence of TRP-ALA-SER (WAS) or SEQ ID: 83, and a light chain complementary determining region 3 comprising the amino acid sequence of SEQ ID: 75 or 84.

[00156] In embodiments, the binding domain of the second CAR comprises: (i) a heavy chain complementary determining region 1 comprising the amino acid sequence of SEQ ID: 76, a heavy chain complementary determining region 2 comprising the amino acid sequence of SEQ

ID: 77, and a heavy chain complementary determining region 3 comprising the amino acid sequence of SEQ ID: 78; and (ii) a light chain complementary determining region 1 comprising the amino acid sequence of SEQ ID: 73, a light chain complementary determining region 2 comprising the amino acid sequence of TRP-ALA-SER (WAS), and a light chain complementary determining region 3 comprising the amino acid sequence of SEQ ID: 75.

[00157] In embodiments, the binding domain of the second CAR comprises: (i) a heavy chain complementary determining region 1 comprising the amino acid sequence of SEQ ID: 85, a heavy chain complementary determining region 2 comprising the amino acid sequence of SEQ ID: 86, and a heavy chain complementary determining region 3 comprising the amino acid sequence of SEQ ID: 87; and (ii) a light chain complementary determining region 1 comprising the amino acid sequence of SEQ ID: 82, a light chain complementary determining region 2 comprising the amino acid sequence of SEQ ID: 83, and a light chain complementary determining region 3 comprising the amino acid sequence of SEQ ID: 84. In embodiments, the binding domain of the first CAR comprises the amino acid sequence of SEQ ID: 5 or 6. In embodiments, the binding domain of the second CAR comprises one of the amino acid sequences of SEQ ID: 70 -72 and 79-81.

[00158] In embodiments, the first CAR comprises the first antigen binding domain, a transmembrane domain, a co-stimulatory domain, and a CD3 zeta domain and/or the second CAR comprises the second antigen binding domain, a transmembrane domain, a co-stimulatory domain, and a CD3 zeta domain.

[00159] In embodiments, the first CAR and the second CAR are expressed as separate polypeptides.

[00160] In embodiments, the cytoplasmic domain or the transmembrane domain of the second CAR is modified such that the second CAR is capable of activating the modified T cell via cells expressing CD19 without damaging the cells expressing CD19.

[00161] Embodiments described herein relate to a bispecific chimeric antigen receptor, comprising: a first antigen binding domain, a second antigen binding domain, a cytoplasmic domain, and transmembrane domain, wherein the first antigen binding domain recognizes a first antigen, and the second antigen binding domain recognizes a second antigen, the first antigen is different from the second antigen.

[00162] In embodiments, the first antigen and the second antigen do not express on the same cell. In embodiments, the first antigen is an antigen of a blood component, and the second antigen is an antigen of a solid tumor.

[00163] Blood cells refer to red blood cells (RBCs), white blood cells (WBCs), platelets, or other blood cells. For example, RBCs are blood cells of delivering oxygen (O₂) to the body tissues via the blood flow through the circulatory system. Platelets are cells that are involved in hemostasis, leading to the formation of blood clots. WBCs are cells of the immune system involved in defending the body against both infectious disease and foreign materials. There are

a number of different types and sub-types of WBCs and each has a different role to play. For example, granulocytes, monocytes, and lymphocytes are 3 major types of white blood cell.

There are three different forms of granulocytes: Neutrophils, Eosinophils, Basophils.

[00164] A cell surface molecule of a WBC refers to a molecule expressed on the surface of the WBC. For example, the cell surface molecule of a lymphocyte may include CD19, CD22, CD20, BCMA, CD5, CD7, CD2, CD16, CD56, and CD30. The cell surface molecule of a B cell may include CD19, CD20, CD22, BCMA. The cell surface molecule of a monocyte may include CD14, CD68, CD11b, CD18, CD169, and CD1c. The cell surface molecule of granulocyte may include CD33, CD38, CD138, and CD13.

[00165] In embodiments, the first antigen is CD19, and the second antigen is a tumor associated MUC1. In embodiments, the first antigen binding domain comprises one of the amino acid sequences of SEQ ID: 5 and 6. In embodiments, the second antigen binding domain comprises one of the amino acid sequence of SEQ ID: 70 -72 and 79-81.

[00166] In embodiments, the present disclosure describes a method of enhancing T cell response in a subject or treating a tumor of the subject, the method comprising: administering an effective amount of modified T cell to the subject to provide a T cell response such that the CAR T cell is expanded in the blood of the subject via cells expressing CD19. In embodiments, the method may further comprise infusing B cells into the subject to continue to activate and/or expand the CAR T cells. For example, the B cells of the subject or genetically modified B cells from healthy donor may be obtained and stored before CAR T cell infusion. In embodiments, the method may further comprise administering a cell expressing CD19 or a polypeptide comprising at least an extracellular domain of CD19 or the antigen that the CAR T cells recognize. For example, the cell expressing CD19 may include cell lines such as K562 and NK92 that are transduced with nucleic acid sequences encoding CD19. In embodiments, the method may further comprise identifying CAR T cells expressing both first and second CAR, as well as administering the identifier CAR T cells to the subject. For example, MUC1 may be associated as a sorting marker such that CAR T cells expressing MUC1 may be identified timely.

[00167] In embodiments, the tumor associated MUC1 is expressed on tumor cells, but not on corresponding non-malignant cells. In embodiments, a scFv against the tumor associated MUC1 directly interacts with an o-glycosylated GSTA motif (SEQ ID NO. 88).

[00168] Embodiments described herein relate to a cell comprising the bispecific CAR and to an isolated nucleic acid encoding the bispecific CAR.

[00169] In embodiments, the present disclosure describes a method of *in vivo* cell expansion. In embodiments, the method may include administering an effective amount of T cell comprising a CAR to the subject to provide a T cell response; and administering an effective amount of presenting cells (e.g., T cells) expressing a soluble agent that an extracellular domain of the CAR recognizes. In embodiments, the method may be implemented to enhance T cell response

in a subject. The method may include administering an effective amount of T cell comprising a CAR to the subject to provide a T cell response and administering an effective amount of presenting cells expressing a soluble agent that an extracellular domain of the CAR recognizes to enhance the T cell response in the subject. In certain embodiments, the presenting cells are T cells, dendritic cells, and/or antigen presenting cells. In certain embodiments, the enhancing T cell response in the subject may include selectively enhancing proliferation of T cell comprising the CAR. In embodiments, the method may be used to enhance treatment of a condition on a subject using CAR T cells. The method may include administering a population of cells that express an agent or administering an agent that is formulated as a vaccine. In these instances, the CAR T cells include a nucleic acid that encodes a CAR, and an extracellular domain of the CAR recognize the agent. In embodiments, the method may be implemented to enhance proliferation of CAR T cells in a subject having a disease. The method may include preparing CAR T cells comprising a CAR; administering an effective amount of the CAR T cells to the subject; introducing, into cells, a nucleic acid encoding an agent that an extracellular domain of the CAR recognizes; and administering an effective amount of the cells (introduced with the nucleic acid encoding the agent) to the subject. In embodiments, the T cell expansion may be measured based on an increase in copy number of CAR molecules in genomic DNA of the T cells. In embodiments, the T cell expansion may be measured based on flow cytometry analysis on molecules expressed on the T cells.

[00170] Embodiments described herein relate to an isolated T cell comprising a first CAR and a second CAR, wherein an antigen binding domain of the first CAR binds an antigen such as CD19, CD33, CD14, and BCMA, and an antigen binding domain of the second CAR binds a tumor associated MUC. In embodiments, the tumor associated MUC is MUC1 or MUC2. Embodiments described herein relate to a composition comprising a population of the isolated T cells and to a method of enhancing T cell response in a subject or treating a tumor of the subject, the method comprising: administering an effective amount of the isolated T cell.

[00171] In embodiments, the first CAR comprises the amino acid sequence of SEQ ID NO: 207, and the second CAR comprises the amino acid sequence of SEQ ID: 202. In embodiments, the first CAR comprises the amino acid sequence of SEQ ID NO: 203, 207, 216, or 219, and the second CAR comprises the amino acid sequence of SEQ ID: 202 or 205. In embodiments, the antigen binding domain of the second CAR comprises the amino acid sequence of SEQ ID NO: 70. In embodiments, the antigen binding domain of the second CAR comprises the amino acid sequence of SEQ ID NO: 5 or 6. In embodiments, the isolated T cell comprises a nucleic acid sequence of SEQ ID NO: 201, 204, 206, 208, 215, 217, 218, or 220. In embodiments, each of the first CAR and the second CAR comprises an antigen binding domain, a transmembrane domain, and a cytoplasmic domain.

[00172] In embodiments, the cytoplasmic domain comprises a co-stimulatory domain and a CD3 zeta domain.

[00173] In embodiments, the isolated T cell comprises a dominant negative variant of a receptor of programmed death 1 (PD-1), cytotoxic T lymphocyte antigen-4 (CTLA- 4), B- and T-lymphocyte attenuator (BTLA), T cell immunoglobulin mucin-3 (TIM-3), lymphocyte-activation protein 3 (LAG-3), T cell immunoreceptor with Ig and ITIM domains (TIGIT), leukocyte-associated immunoglobulin-like receptor 1 (LAIR1), natural killer cell receptor 2B4 (2B4), or CD 160. In embodiments, the isolated T cell comprises a reduced amount of TCR, as compared to the corresponding wide-type T cell. Dominant negative mutations have an altered gene product that acts antagonistically to the wild-type allele. These mutations usually result in an altered molecular function (often inactive) and are characterized by a dominant or semi-dominant phenotype.

[00174] The present disclosure describes pharmaceutical compositions. The pharmaceutical compositions include one or more of the following CAR molecules, TCR molecules, modified CAR T cells, modified cells comprising CAR or TCR, modified cells, nucleic acids, and vectors described above. Pharmaceutical compositions are 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.

[00175] When “an immunologically effective amount”, “an anti-tumor effective amount”, “a tumor-inhibiting effective amount”, or “therapeutic amount” is indicated, the precise amount of the compositions of the present disclosure 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 be stated that a pharmaceutical composition comprising the T cells described herein may be administered at a dosage of 10^4 to 10^9 cells/kg body weight, preferably 10^5 to 10^6 cells/kg body weight, including all integer values within those ranges. T 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). The optimal dosage and treatment regime for a particular patient can readily be determined by one skilled in the art of medicine by monitoring the patient for signs of disease and adjusting the treatment accordingly. In certain embodiments, it may be desired to administer activated T cells to a subject and then subsequently redraw the blood (or have apheresis performed), collect the activated and expanded T cells, and reinfuse the patient with these activated and expanded T cells. This process can be carried out multiple times every few weeks. In certain embodiments, T cells can be activated from blood draws of from 10 cc to 400 cc. In certain embodiments, T cells are activated from blood draws of 20 cc, 30 cc, 40 cc, 50 cc, 60 cc, 70 cc, 80 cc, 90 cc, or 100 cc. Not to be bound by theory, using this multiple blood draw/multiple reinfusion protocols, may select out certain populations of T cells.

[00176] The administration of the pharmaceutical compositions described herein 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 subcutaneously, intradermally, intratumorally, intranodally, intramedullary, intramuscularly, by intravenous (i. v.) injection, or intraperitoneally. In embodiments, the T cell compositions described herein are administered to subjects by intradermal or subcutaneous injection. In embodiments, the T cell compositions of the present disclosure are administered by i.v. injection. The compositions of T cells may be injected directly into a tumor, lymph node, or site of infection. In embodiments, cells activated and expanded using the methods described herein, or other methods known in the art where T cells are expanded to therapeutic levels, are administered to patients in conjunction with (e.g., before, simultaneously or following) any number of relevant treatment modalities, including but not limited to treatment with agents for antiviral therapy, cidofovir and interleukin-2, Cytarabine (also known as ARA-C); or natalizumab treatment for MS patients; or efalizumab treatment for psoriasis patients or other treatments for PML patients. In further embodiments, the T cells described herein can be used in combination with chemotherapy, radiation, immunosuppressive agents, such as cyclosporin, azathioprine, methotrexate, mycophenolate, and FK506, antibodies, or other immunoablative agents such as CAM PATH, anti-CD3 antibodies or other antibody therapies, cytoxin, fludarabine, cyclosporin, FK506, rapamycin, mycophenolic acid, steroids, FR901228, cytokines, 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; Isoniemi (supra)). In embodiments, the cell compositions described herein are administered to a subject in conjunction with (e.g., before, simultaneously or following) bone marrow 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 embodiments, the cell compositions described herein are administered following B-cell ablative therapy. For example, agents that react with CD20, e.g., Rituxan may be administered to patients. In embodiments, 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 disclosure. In embodiments, expanded cells are administered before or following surgery.

[00177] The dosage of the above treatments to be administered to a subject in need thereof 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 by a physician depending on various factors.

[00178] Additional information on the methods of cancer treatment using engineered or modified T cells is provided in U.S. Pat. No. US8,906,682, incorporated by reference in its entirety.

[00179] Embodiments described herein relate to an *in vitro* method for preparing modified cells. The method may include obtaining a sample of cells from a subject. For example, the sample may include T cells or T cell progenitors. The method may further include transfecting the sample of cells with a DNA encoding at least a CAR and culturing the population of CAR cells *ex vivo* in a medium that selectively enhances proliferation of CAR-expressing T cells.

[00180] In embodiments, the sample is a cryopreserved sample. In embodiments, the sample of cells is from umbilical cord blood or a peripheral blood sample from the subject. In embodiments, the sample of cells is obtained by apheresis or venipuncture. In embodiments, the sample of cells is a subpopulation of T cells.

[00181] Embodiments of the present disclosure relate to a Zinc Finger Nuclease (ZFN) comprising a DNA-binding domain comprising zinc finger DNA binding proteins and a DNA-cleaving domain comprising a cleavage domain and/or a cleavage half-domain.

[00182] The zinc finger DNA binding proteins may include 1, 2, 3, 4, 5, 6 or more zinc fingers, each zinc finger having a recognition helix that binds a target subsite in the target gene. In certain embodiments, the zinc finger proteins comprise 3, or 4 or 5 or 6 fingers (where the fingers are designated F1, F2, F3, F4, F5 and F6 and ordered F1 to F3, F4 or F5 or F6 from N-terminus to C-terminus) and the fingers comprise the amino acid sequence of the recognition regions shown in Table 6.

[00183] Examples of the cleavage domain and/or a cleavage half-domain include a wild-type or an engineered FokI cleavage half-domain. In embodiments, the DNA cleaving domain may comprise a wild-type cleavage domain or cleavage half-domain (e.g., a FokI cleavage half-domain). In embodiments, the cleavage domain and/or a cleavage half-domain comprises engineered (non-naturally occurring) cleavage domains or cleavage half-domains, for example, engineered FokI cleavage half-domains that form obligate heterodimers.

[00184] In embodiments, the gene is a human gene. In embodiments, the cleavage domain comprises a wild-type or engineered FokI cleavage domain.

[00185] Embodiments relate to a polynucleotide encoding the isolated ZFN as described above. Embodiments relate to a vector comprising the polynucleotide. In embodiments, the vector is an adenoviral or lentiviral vector. Embodiments relate to an isolated cell or a cell line comprising the isolated ZFN described above.

[00186] In embodiments, the isolated cell is a stem cell, a T cell or a Natural Killer (NK) cell. In embodiments, the cell is a T cell derived from a primary human T cell isolated from a human donor. In embodiments, the cell has a reduced expression of an endogenous gene of CTLA4, LAG3, BTLA, TIM3, FOXP3, SIVA1, and LGALS9.

[00187] CTLA4 is an inhibitory receptor acting as a major negative regulator of T-cell responses. T lymphocyte receptor CTLA-4 binds costimulatory molecules CD80 (B7-1) and CD86 (B7-2) with higher avidity than stimulatory co-receptor CD28 and negatively regulates T cell activation. LAG3 is a member of the immunoglobulin superfamily and is expressed on the surface of activated T and NK cells. LAG3 has also been detected on the surface of B cells, dendritic cells, TILs and Tregs. Blockage of LAG3 significantly increases T cell proliferation and function. TIM3 is an immune checkpoint receptor constitutively expressed by CD4+ T helper 1 (Th1), CD8+ T cytotoxic 1 cells (Tc1) and Th17 cells. The interaction between TIM3 and its ligand galectin-9 LGALS9 is believed to result in suppression of T-cell responses. FOXP3 is a member of the forkhead/winged-helix family of transcriptional regulators, which is crucial for the development and inhibitory function of regulatory T-cells (Treg). SIVA1 induces CD27-mediated apoptosis, inhibits BCL2L1 isoform Bcl-x(L) anti-apoptotic activity, inhibits activation of NF-kappa-B, and promotes T-cell receptor-mediated apoptosis.

[00188] Embodiments relate to an isolated cell comprising isolated nucleic acid sequence encoding a chimeric antigen receptor (CAR), wherein an endogenous gene is inactivated using the ZFN described above.

[00189] In embodiments, the CAR comprises an antigen binding domain, a transmembrane domain, a co-stimulatory domain, and a CD3 zeta signaling domain.

[00190] In embodiments, the cell has a reduced graft-versus-host disease (GVHD) response in a bioincompatible human recipient as compared to the GVHD response of the primary human T cell.

[00191] In embodiments, the antigen binding domain of the CAR binds FZD10, TSHR, PRLR, Muc17, GUCY2C, CD207, CD19, or CD20.

[00192] In embodiments, the antigen binding domain of the CAR binds at one of B7, BCMA, CAIX, CD123, CD133, CD138, CD171, CD171/L1-CAM, CD19, CD2, CD22, CD30, CD33, CEA, cMet, CS1, CSPG4, Dectin1, EGFR, EGFR vIII, EphA2, ERBB receptors, ErbB T4, ERBB2, FAP, Folate receptor 1, FITC, Folate receptor 1, GD2, GPC3, HA-1 H/HLA- A2, HER2, IL-11Ra, IL13 receptor a2, IL13R, IL13R α 2 (zetakine), Kappa, LewisY, Mesothelin, MUC1, NKG2D, NY-ESO-1, PSMA, ROR-1, TRAIL-receptor1, or VEGFR2.

[00193] In embodiments, the co-stimulatory domain of the CAR comprises the intracellular domain of a costimulatory molecule selected from the group consisting of CD27, CD28, 4-1BB, OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, B7-H3, and any combination thereof.

[00194] In embodiments, the isolated cell or the cell line is a T cell comprising a nucleic acid sequence encoding hTERT or a nucleic acid encoding SV40LT, or a combination thereof. In embodiments, the T cell comprises a nucleic acid sequence encoding hTERT and a nucleic acid encoding SV40LT. In embodiments, the expression of hTERT is regulated by an inducible expression system. In embodiments, the expression of SV40LT gene is regulated by an

inducible expression system. In embodiments, the inducible expression system is rTTA-TRE, which increases or activates the expression of SV40LT gene or hTERT gene, or a combination thereof. In embodiments, the T cell comprises a nucleic acid sequence encoding a suicide gene. In embodiments, the suicide gene includes a HSV-TK suicide gene system.

[00195] Embodiments relate to a method of treating cancer in a subject, the method comprising administering a genetically modified cell to the subject, wherein the cancer is selected from the group consisting of a lung carcinoma, pancreatic cancer, liver cancer, bone cancer, breast cancer, colorectal cancer, leukemia, ovarian cancer, lymphoma, and brain cancer.

[00196] Embodiments relate to a T/NK cell comprising a reduced amount of one or more peptides including PD1, PDL1, PDL2, CTLA4, LRBA, LAG3, Tim3, BTLA, CD160, 2B4, SOCS1, SOCS3, Foxp3, CCR4, PVRIG, CD16B, SIVA1, CD33, LAGLS9, CD122, IDO1, CD45, Cvp1b1, TNFAIP8L2, IDO2, TD02, DNMT3A, and/or Ceacam-1 (list 1), as compared to a corresponding wild-type cell. In embodiments, the T/NK cell has an enhanced T/NK cell response when the T cell is administrated into a subject.

[00197] Embodiments relate to T/NK cell comprising an increased amount of one or more peptides including Runx3, Ixmx, PILRA, Ptnns1L3, Fcgr3a, Nat8, Ccl9, Hck, Trem2, Ccl6, Cd36, Igf1, Ctss, Gzmc, Batf, Cxcl2, TNFAIP8L3, Il1b, TRPV1, TRPV2, TRPV3, TRPV4, Rgs1, PLSCR1, ITGB2, C3AR1, ITGA3, ITGA5, ITGAL, batf, batf3, Cxcl2, CARD11, and/or CD83 (list 2), as compared to a corresponding wild-type cell. In embodiments, the T/NK cell has an enhanced T cell response when the T/NK cell is administrated to a subject.

[00198] In embodiments, various gene editing techniques or overexpression techniques (e.g., Cas9, TALEN, and ZFN) may be used to regulate T/NK cell functions by knocking out/knocking down/overexpressing/inserting one or more genes. For example, the modified cell has reduced or increase expression of one or more genes of a biosynthesis or transportation pathway of a peptide in list 1 and list 2 (see above), as compared to the corresponding wild-type cell.

[00199] In embodiments, the target gene is Runx3. For example, the modified T/NK cell has increased expression of Runx3 as compared to the corresponding wild-type cell. In these instances, the increased expression of Runx3 may help, for example, T cells' infiltration or long-term residence within tumor cells, therefore increasing T cell killing effects.

[00200] For example, T cell response in a subject refers to cell-mediated immunity associated with helper, killer, regulatory, and other types T cells. For example, T-cell response may include activities such as assistance to other white blood cells in immunologic processes and identifying and destroying virus-infected cells and tumor cells. T-cell response in the subject may be measured via various indicators such as a number of virus-infected cells and /or tumor cells that T cells kill, an amount of cytokines that T cells release in co-culturing with virus-infected cells and/or tumor cells, a level of proliferation of T cells in the subject, a phenotype

change of T cells (e.g., changes to memory T cells), and a level longevity or lifetime of T cells in the subject.

[00201] T cell response also includes the release of cytokines. Although cytokine release is often associated with systemic inflammation and complication of disease, the release of cytokines appear to be also associated with the efficacy of a CAR T cell therapy. The release of cytokines may correlate with expansion and progressive immune activation of adoptively transferred cells, such as in CAR T cell therapy. The present disclosure describes the release of effector cytokines, such as IFN- γ , and pro- and anti-inflammatory cytokines, such as IL-6, in response to CAR T cell therapy, especially in response to the presence of a first CAR and second CAR. In embodiments, the present disclosure describes the release of IL-6 and IFN- γ in a subject introduced with the first CAR and second CAR described herein. In embodiments, the subject is in need of cancer treatment, and the cancer treatment is pancreatic cancer treatment. In embodiments, the present disclosure describes determining the efficacy or monitoring the efficacy of a CAR T cell therapy by measuring the level of cytokine release. In embodiments, the release of cytokines (e.g., IL-6 and/or IFN- γ) in the subject in response to CAR T cell therapy using T cells comprising the first and the second CARs is more than that using T cells comprising the second CAR without the first CARs.

[00202] The present disclosure is further described by reference to the following exemplary embodiments and examples. These exemplary embodiments and examples are provided for purposes of illustration only and are not intended to be limiting unless otherwise specified. Thus, the present disclosure should in no way be construed as being limited to the following exemplary embodiments and examples, but rather, should be construed to encompass any and all variations which become evident as a result of the teaching provided herein.

EXEMPLARY EMBODIMENTS

[00203] The following are exemplary embodiments:

1. A nucleic acid encoding a first chimeric antigen receptor (CAR) and a second CAR, wherein a binding domain of the first CAR binds a cell surface molecule of a white blood cell (WBC), and a binding domain of the second CAR binds an antigen different from the cell surface molecule of a WBC.
2. A vector comprising the nucleic acid of embodiment 1.
3. A cell comprising the nucleic acid of embodiment 1.
4. A cell comprising a first CAR and a second CAR, wherein a binding domain of the first CAR binds a cell surface molecule of a cell surface molecule of a WBC, and a binding domain of the second CAR binds an antigen different from the cell surface molecule of a WBC.
5. The cell of any one of embodiments 1-4, wherein the cell is a T cell, NK cell, or dendritic cells.
6. A composition comprising a population of the cells of any one of embodiments 3-5.
7. A method of culturing the cells of any one of embodiments 3-5, the method comprising:

obtaining the cell of any one of embodiments 3-5, wherein a binding domain of the first CAR binds a cell surface molecule of a cell surface molecule of a WBC, and a binding domain of the second CAR binds an antigen different from the cell surface molecule of a WBC; and culturing the cell in the presence of an agent derived from the cell surface molecule of the WBC cell or from an antigen to which a second CAR binds.

8. The method of embodiment 7, wherein the agent is an extracellular domain of the cell surface molecule of the WBC.

9. A method for *in vitro* CAR cell preparation, the method comprising:
providing cells;

introducing a nucleic acid encoding a first CAR and a second CAR into the cells, wherein a binding domain of the first CAR binds a cell surface molecule of a WBC, and a binding domain of the second CAR binds an antigen different from the cell surface molecule of the WBC; and culturing the cells in the presence of an agent derived from the cell surface molecule of the WBC or from an antigen to which the second CAR binds.

10. A method of enhancing T cell response in a subject or treating a tumor of the subject, the method comprising: administering an effective amount of T cell comprising a first CAR and a second CAR to the subject to provide a T cell response, wherein a binding domain of the first CAR binds a cell surface molecule of a WBC, and a binding domain of the second CAR binds an antigen different from the cell surface molecule of the WBC, and wherein the T cell response is measured by the number of copies of CAR(s) and/or the amount of cytokine released (e.g., IL-6 and IFN- γ). In embodiments, the T cell response is enhanced as compared to T cells that include the second CAR but don't comprise the first CAR.

11. The method of embodiment 10, wherein enhancing the T cell response in the subject comprises selectively enhancing proliferation of T cell comprising the first and second CARs *in vivo*.

12. A method of expanding cells expressing CAR *in vivo*, the method comprising:
administering an effective amount of T cell comprising a first CAR and a second CAR to the subject, wherein a binding domain of the first CAR binds a cell surface molecule of a WBC, and a binding domain of the second CAR binds an antigen different from the cell surface molecule of the WBC, the cells being T cells, NK cells, or dendritic cells.

13. The nucleic acid, the vector, the cell, the composition, or the method of any one of embodiments 1-12, wherein the antigen different from the cell surface molecule of the WBC is CD19, CD22, CD20, BCMA, CD5, CD7, CD2, CD16, CD56, CD30, CD14, CD68, CD11b, CD18, CD169, CD1c, CD33, CD38, CD138, CD13, B7, CAIX, CD123, CD133, CD171, CD171/L1-CAM, CEA, Claudin 18.2, cMet, CS1, CSPG4, Dectin1, EGFR, EGFR vIII, EphA2, ERBB receptors, ErbB T4, ERBB2, FAP, Folate receptor 1, FITC, Folate receptor 1, FSH, GD2, GPC3, HA-1 H/HLA-A2, HER2, IL-11Ra, IL13 receptor α 2, IL13R, IL13R α 2 (zetakine), Kappa,

Leukemia, LewisY, Mesothelin, MUC1, NKG2D, NY-ESO-1, PSMA, ROR-1, TRAIL-receptor1, or VEGFR2.

14. The nucleic acid, the vector, the cell, the composition, or the method of embodiment 13, wherein the MUC1 is a tumor-exclusive epitope of a human MUC1, and the first CAR and the second CAR are expressed as separate polypeptides.

15. The nucleic acid, the vector, the cell, the composition, or the method of embodiment 13, wherein the MUC1 is a tumor form of human MUC1 (tMUC1).

16. The nucleic acid, the vector, the cell, the composition, or the method of any one of embodiments 1-12, wherein the WBC is a granulocyte, a monocyte, or lymphocyte.

17. The nucleic acid, the vector, the cell, the composition, or the method of any one of embodiments 1-12, wherein the WBC is a B cell.

18. The nucleic acid, the vector, the cell, the composition, or the method of any one of embodiments 1-12, wherein the cell surface molecule of the WBC is CD19, CD22, CD20, BCMA, CD5, CD7, CD2, CD16, CD56, CD30, CD14, CD68, CD11b, CD18, CD169, CD1c, CD33, CD38, CD138, or CD13.

19. The nucleic acid, the vector, the cell, the composition, or the method of any one of embodiments 1-12, wherein the cell surface molecule of the WBC is CD19, CD20, CD22, or BCMA.

20. The nucleic acid, the vector, the cell, the composition, or the method of any one of embodiments 1-12, wherein the cell surface molecule of the WBC is CD19.

21. The nucleic acid, the vector, the cell, the composition, or the method of any one of embodiments 1-12, wherein the first CAR comprises the first antigen binding domain, a transmembrane domain, a co-stimulatory domain, and a CD3 zeta domain; and/or the second CAR comprises the second antigen binding domain, a transmembrane domain, a co-stimulatory domain, and a CD3 zeta domain.

22. The nucleic acid, the vector, the cell, the composition, or the method of any one of embodiments 1-12, wherein the co-stimulatory domain comprises the intracellular domain of CD27, CD28, 4-1BB, OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, B7-H3, a ligand that specifically binds with CD83, or a combination thereof.

23. The nucleic acid, the vector, the cell, the composition, or the method of any one of embodiments 1-12, wherein the antigen binding domain is a Fab or a scFv.

24. The nucleic acid, the vector, the cell, the composition, or the method of any one of embodiments 1-12, wherein the first CAR comprises the amino acid sequence of SEQ ID NO: 5, 6, 53 and 54, 55 and 56, or 57 and 58, and the second CAR comprises the amino acid sequence of SEQ ID NO: 5-17, 29, 33, 37, 71, or 72, or the amino acid sequence encoded by nucleic acid sequence SEQ ID NO: 41, 45, 63, 67, or 68.

25. The nucleic acid, the vector, the cell, the composition, or the method of any one of embodiments 1-12, wherein a nucleic acid encoding the first CAR comprises the nucleic acid sequence of SEQ ID NO: 59, or 60, and a nucleic acid sequence encoding the second CAR comprises the nucleic acid sequence of SEQ ID NO: 61.

26. The nucleic acid, the vector, the cell, the composition, or the method of any one of embodiments 1-12, wherein the nucleic acid comprises one of the nucleic acid sequences of SEQ ID NO: 62-69.

27. The nucleic acid, the vector, the cell, the composition, or the method of any one of embodiments 1-12, wherein the first CAR and the second CAR are expressed as separate polypeptides.

28. A modified T cell comprising a first CAR and a second CAR, wherein a binding domain of the first CAR binds CD19, and a binding domain of the second CAR binds tumor associated MUC1.

29. The modified T cell of embodiment 28, wherein the binding domain of the second CAR comprises:

(i) a heavy chain complementary determining region 1 comprising the amino acid sequence of SEQ ID: 76 or 85, a heavy chain complementary determining region 2 comprising the amino acid sequence of SEQ ID: 77 or 86, and a heavy chain complementary determining region 3 comprising the amino acid sequence of SEQ ID: 78 or 87; and (ii) a light chain complementary determining region 1 comprising the amino acid sequence of SEQ ID: 73 or 82, a light chain complementary determining region 2 comprising the amino acid sequence of TRP-ALA-SER (WAS) or SEQ ID: 83, and a light chain complementary determining region 3 comprising the amino acid sequence of SEQ ID: 75 or 84.

30. The modified T cell of embodiment 28, wherein the binding domain of the second CAR comprises:

(i) a heavy chain complementary determining region 1 comprising the amino acid sequence of SEQ ID: 76, a heavy chain complementary determining region 2 comprising the amino acid sequence of SEQ ID: 77, and a heavy chain complementary determining region 3 comprising the amino acid sequence of SEQ ID: 78; and (ii) a light chain complementary determining region 1 comprising the amino acid sequence of SEQ ID: 73, a light chain complementary determining region 2 comprising the amino acid sequence of TRP-ALA-SER (WAS), and a light chain complementary determining region 3 comprising the amino acid sequence of SEQ ID: 75.

31. The modified T cell of embodiment 28, wherein the binding domain of the second CAR comprises: (i) a heavy chain complementary determining region 1 comprising the amino acid sequence of SEQ ID: 85, a heavy chain complementary determining region 2 comprising the amino acid sequence of SEQ ID: 86, and a heavy chain complementary determining region 3 comprising the amino acid sequence of SEQ ID: 87; and (ii) a light chain complementary determining region 1 comprising the amino acid sequence of SEQ ID: 82, a light chain

complementary determining region 2 comprising the amino acid sequence of SEQ ID: 83, and a light chain complementary determining region 3 comprising the amino acid sequence of SEQ ID: 84.

32. The modified T cell of embodiment 28, wherein the binding domain of the first CAR comprises the amino acid sequence of SEQ ID: 5 or 6.

33. The modified T cell of embodiment 28, wherein the binding domain of the second CAR comprises one of the amino acid sequences of SEQ ID: 70 -72 and 79-81.

34. The modified T cell of any one of embodiments 28-33, wherein the first CAR comprises the first antigen binding domain, a transmembrane domain, a co-stimulatory domain, and a CD3 zeta domain and/or the second CAR comprises the second antigen binding domain, a transmembrane domain, a co-stimulatory domain, and a CD3 zeta domain.

35. The modified T cell of embodiment 34, wherein the co-stimulatory domain comprises the intracellular domain of CD27, CD28, 4-1BB, OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, B7-H3, a ligand that specifically binds with CD83, or a combination thereof.

36. The modified T cell of any one of embodiments 28-35, wherein the first CAR and the second CAR are expressed as gene products that are separate polypeptides.

37. The modified T cell of any one of embodiments 28-35, wherein a cytoplasmic domain or a transmembrane domain of the second CAR is modified such that the second CAR is capable of activating the modified T cell via cells expressing CD19 without damaging the cells expressing CD19.

38. A bispecific CAR, comprising:

a first antigen binding domain, a second antigen binding domain, a cytoplasmic domain, and a transmembrane domain, wherein the first antigen binding domain recognizes a first antigen, the second antigen binding domain recognize a second antigen, and the first antigen is different from the second antigen.

39. The bispecific CAR of embodiment 38, wherein the first antigen and the second antigen are not expressed on the same cell.

40. The bispecific CAR of embodiment 38, wherein the first antigen is an antigen of a blood component, and the second antigen is an antigen of a solid tumor.

41. The bispecific CAR of embodiment 38, wherein the first antigen is CD19, and the second antigen is a tumor associated MUC1.

42. The bispecific CAR of embodiment 38, wherein the first antigen binding domain comprises amino acid sequence of SEQ ID: 5 or 6.

43. The modified T cell of embodiment 28, wherein the second antigen binding domain comprises one of the amino acid sequences of SEQ ID: 70 -72 and 79-81.

44. A method of enhancing T cell response in a subject or treating a tumor of the subject, the method comprising: administering an effective amount of the modified T cell of any one of

embodiments 28-37 to the subject to provide a T-cell response such that the modified T cell is expanded in the blood of the subject via cells expressing CD19.

45. The modified T cell of any one of embodiments 28-37, wherein the tumor associated MUC1 is expressed on tumor cells and not on corresponding non-malignant cells.

46. The modified T cells of any one of embodiments 28-37, wherein the binding domain of the second CAR comprises a scFv against the tumor associated MUC1 that directly interacts with an o-glycosylated GSTA motif (SEQ ID NO. 88).

47. A cell comprising the bispecific CAR of any one of embodiments 38-43.

48. A nucleic acid encoding the bispecific CAR of any one of embodiments 38-43.

49. A nucleic acid encoding a first CAR and a second CAR, wherein a binding domain of the first CAR binds an antigen selected from the group consisting of CD19, CD33, CD14, and BCMA, and a binding domain of the second CAR binds a tumor associated MUC1.

50. A T cell comprising a first CAR and a second CAR, wherein a binding domain of the first CAR binds an antigen selected from the group consisting of CD19, CD33, CD14, and BCMA, a binding domain of the second CAR binds a tumor associated MUC1.

51. A T cell comprising a first nucleic acid encoding a first CAR and a second nucleic acid encoding a second CAR, wherein a binding domain of the first CAR binds an antigen selected from the group consisting of CD19, CD33, CD14, and BCMA, a binding domain of the second CAR binds a tumor associated MUC1.

52. A composition comprising a population of the T cells of embodiment 50 or 51.

53. The T cell of embodiment 50 or 51, wherein the first CAR and the second CAR are expressed as separate polypeptides.

54. The nucleic acid of embodiment 1 or the T cell of embodiment 50 or 51, wherein the nucleic acid comprises one of the nucleic acid sequences of SEQ ID NO: 201, 204, 206, 208, 209, 211, 213-215, 217, 218, 220-225, 227, 228, 230-235, 237, 238, 240-244, 247, 249-254, 256, 257, 259, and 260-263.

55. The nucleic acid of embodiment 49 or the T cell of embodiment 50 or 51, wherein the nucleic acid comprises one of the nucleic acid sequences of SEQ ID NO: 201, 204, 206, 208, 215, 217, 218, and 220.

56. The nucleic acid of embodiment 49 or the cell of embodiment 50 or 51, wherein the first CAR comprises the amino acid sequence of SEQ ID NO: 203, 207, 216, 219, 226, 229, 236, 239, 245, 248, 255, or 258, and the second CAR comprises the amino acid sequence of SEQ ID: 202, 205, 210, or 212.

57. The nucleic acid of embodiment 49 or the cell of embodiment 50 or 51, wherein the first CAR comprises the amino acid sequence of SEQ ID NO: 207, and the second CAR comprises the amino acid sequence of SEQ ID NO: 202.

58. The nucleic acid of embodiment 49 or the cell of embodiment 50 or 51, wherein the first CAR comprises the amino acid sequence of SEQ ID NO: 203, 207, 216, or 219, and the second CAR comprises the amino acid sequence of SEQ ID NO: 202 or 205.
59. A vector comprising the nucleic acid of embodiment 49.
60. A cell comprising the nucleic acid of embodiment 49.
61. A composition comprising a population of the cells of embodiment 60.
62. The cell of embodiments 60 or 61, wherein the cell is a T cell, NK cell, or dendritic cells.
63. A genetically modified T cell comprising one or more nucleic acids encoding a CAR and one or more TCR chains or a TCR of an innate T cell.
64. The genetically modified T cell of embodiment 63, wherein the nucleic acid encoding the one or more TCR chains or a TCR of an innate T cell is a nucleic acid insert within a target genomic locus.
65. The genetically modified T cell of embodiment 63, wherein integration of the nucleic acid insert causes replacement of at least of a portion of a gene at the target genomic locus.
66. The genetically modified T cell of embodiment 63, wherein the nucleic acid is introduced into the T cell using a nuclease agent.
67. A method of modifying a target genomic locus in a T cell, the method comprising: introducing into the T cell a nuclease agent that makes a single or double-strand break within the target genomic locus; and introducing into the T cell a nucleic acid insert comprising a nucleic acid encoding one or more TCR chains or a TCR of an innate T cell; and selecting the T cell comprising the nucleic acid insert integrated into the target genomic locus.
68. The method of embodiment 67, wherein the nucleic acid insert is flanked by a 5' homology arm and a 3' homology arm, and the 3' homology arm of the nucleic acid insert and the 5' homology arm of the nucleic acid insert are homologous to corresponding genomic segments within the target genomic locus.
69. The method of embodiment 67, wherein the target genomic locus is modified by integration of the nucleic acid insert between the corresponding genomic segments.
70. The method of embodiment 67, wherein the nuclease agent is a zinc finger nuclease (ZFN), a Transcription Activator-Like Effector Nuclease (TALEN), or a meganuclease.
71. The method of embodiment 67, wherein the nuclease agent comprises a Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)-associated (Cas) protein and a guide RNA (gRNA).
72. The method of embodiment 71, wherein the Cas protein is Cas9.
73. The genetically modified T cell or the method of any one of embodiments 63-72, wherein the innate T cell comprises a $\gamma\delta$ T cell, an iNKT cell, or a MAIT cell.
74. The genetically modified T cell or the method of any one of embodiments 63-72, wherein the innate T cell comprises a $\gamma\delta$ T cell.

75. The genetically modified T cell or the method of any one of embodiments 63-72, wherein the innate T cell comprises a V γ 9V δ 2 T cell.
76. The genetically modified T cell or the method of embodiment 75, wherein the one or more nucleic acids encoding one or more TCR chains encodes a TCR γ chain and a TCR δ chain.
77. The genetically modified T cell or the method of embodiment 75, wherein the one or more nucleic acids encoding one or more TCR chains encodes an endogenous TCR γ chain and an endogenous TCR δ chain.
78. The genetically modified T cell or the method of embodiment 75, wherein the nucleic acid insert comprises a nucleic acid that corresponds to one or more the amino acid sequences of SEQ ID No.: 99 and 185, or a combination thereof.
79. The genetically modified T cell or the method of any one of embodiments 63-72, wherein the innate T cell comprises an iNKT cell.
80. The genetically modified T cell or the method of embodiment 79, wherein the nucleic acid encoding the TCR of an innate T cell encodes an iNKT α chain and/or an iNKT β chain.
81. The genetically modified T cell or the method of embodiment 79, wherein the nucleic acid encoding the TCR of an innate T cell encodes an endogenous iNKT α chain or an endogenous iNKT β chain.
82. The genetically modified T cell or the method of any one of embodiments 63-72, wherein the innate T cell comprises a MAIT cell.
83. The genetically modified T cell or the method of embodiment 82, wherein the nucleic acid encoding the TCR of an innate T cell encodes a MAIT α chain and/or a MAIT β chain.
84. The genetically modified T cell or the method of embodiment 82, wherein the nucleic acid encoding the TCR of an innate T cell encodes an endogenous MAIT α chain or an endogenous MAIT β chain.
85. The genetically modified T cell or the method of any one of embodiments 63-84, wherein the target genomic locus is α or β TCR gene locus of an $\alpha\beta$ T cell.
86. The genetically modified T cell or the method of any one of embodiments 63-84, wherein the integration of the nucleic acid insert causes replacement a sequence at α or β TCR gene locus of an $\alpha\beta$ T cell such that expression of overall endogenous TCR is not reduced.
87. The genetically modified T cell or the method of any one of embodiments 63-84, wherein corresponding genomic segments of the target genomic locus comprise the amino acid sequence of α chain of TCR.
88. The genetically modified T cell or the method of any one of embodiments 63-84, wherein the genetically modified cell elicits a reduced graft versus host disease response against allogeneic cells as compared to a corresponding cell that does not include nucleic acid sequence.
89. The genetically modified T cell or the method of any one of embodiments 63-84, wherein the T cell is a T cell derived from a primary human T cell isolated from a human donor.

90. The genetically modified T cell or the method of any one of embodiments 63-84, wherein the T cell comprises a CAR.
91. The genetically modified cell or the method of any one of embodiments 63-90, wherein the genetically modified cell has functional TCRs comprising the one or more TCR chains.
92. The genetically modified cell or the method of any one of embodiments 63-90, wherein the TCR of the innate T cells and $\alpha\beta$ TCR originate from the donor.
93. The genetically modified cell or the method of any one of embodiments 63-92, wherein the innate T cell exhibits a non-MHC class I or II restriction requirement for antigen recognition.
94. A method of causing a T- cell response in a subject or treating a tumor of the subject, the method comprising: administering an effective amount of the T cell of any one of embodiments 63-92.
95. A nucleic acid encoding a binding molecule comprising a first domain and a second binding domain, wherein the first binding domain and the second binding domain bind to an antigen.
96. The nucleic acid of embodiment 95, wherein one or more targeting antigen binding sites of the first binding domain and the second binding domain are different, and the binding molecule is a CAR comprising the first binding domain, a linker, the second binding domain, a transmembrane domain, and a co-stimulatory domain and/or a CD3 zeta domain.
97. The nucleic acid of embodiment 95, wherein the antigen is Epidermal growth factor receptor (EGFR), Variant III of the epidermal growth factor receptor (EGFRvIII), Human epidermal growth factor receptor 2 (HER2), Mesothelin (MSLN), Prostate-specific membrane antigen (PSMA), Carcinoembryonic antigen (CEA), Disialoganglioside 2 (GD2), Interleukin-13Ra2 (IL13R α 2), Glypican-3 (GPC3), Carbonic anhydrase IX (CAIX), L1 cell adhesion molecule (L1-CAM), Cancer antigen 125 (CA125), Cluster of differentiation 133 (CD133), Fibroblast activation protein (FAP), Cancer/testis antigen 1B (CTAG1B), Mucin 1 (MUC1), Folate receptor- α (FR- α), CD19, FZD10, TSHR, PRLR, Mucin 17 (MUC17), GUCY2C, CD207, CD3, CD5, B-Cell Maturation Antigen (BCMA), or CD4.
98. The nucleic acid of embodiment 95, wherein the first binding domain binds tumor associated Muc1, TSHR, FZD10, PRLR, Mucin 16 (MUC16), MUC17, GUCY2C, CD207, CLDN18.2, CLDN6, or SIGL1C.
99. The nucleic acid of embodiment 95, wherein the nucleic acid encodes a polypeptide comprising one of the amino acid sequences of SEQ ID NO: 264 and 265.
100. A vector comprising a nucleic acid of any one of embodiments 95-99.
101. A host cell transformed or transfected with the nucleic acid of any one of embodiments 95-99 or with the vector of embodiment 100.
102. A method for the production of a binding molecule encoded by the nucleic acid of any one of embodiments 95-99, the method comprising culturing a host cell of embodiment 101 under conditions allowing expression of the binding molecule of any one of embodiments 95-99 and recovering the binding molecule from the culture.

103. A pharmaceutical composition comprising a binding molecule encoded by the nucleic acid of any one of embodiments 95-99 or produced according to the method of embodiment 102.
104. A kit comprising a binding molecule encoded by the nucleic acid of any one of embodiments 95-99, a nucleic acid of any one of embodiments 95-99, a vector of embodiment 100, and/or a host cell of embodiment 101.
105. A method for the treatment or amelioration of a disease, comprising administering to a subject in need thereof the binding molecule encoded by the nucleic acid of any one of embodiments 95-99.
106. A nucleic acid encoding a first antigen binding molecule and a second antigen binding molecule, wherein a binding domain of the first antigen binding molecule binds a cell surface molecule of a WBC, and a binding domain of the second antigen binding molecule binds a solid tumor antigen that is different from the cell surface molecule of the WBC.
107. A vector comprising the nucleic acid of embodiment 106.
108. A cell comprising the nucleic acid of embodiment 106.
109. A cell comprising a first antigen binding molecule and a second antigen binding molecule, wherein a binding domain of the first antigen binding molecule binds a cell surface molecule of a WBC, and a binding domain of the second antigen binding molecule binds a solid tumor antigen that is different from the cell surface molecule of a WBC.
110. A composition comprising a population of the cell of any one of embodiments 108-109.
111. The cell of any one of embodiments 108-109, wherein the cell is a T cell, NK cell, or dendritic cells.
112. A method of culturing cells, the method comprising: obtaining a cell comprising a first antigen binding molecule and a second antigen binding molecule, wherein a binding domain of the first antigen binding molecule binds a cell surface molecule of a WBC, and a binding domain of the second antigen binding molecule binds a solid tumor antigen that is different from the cell surface molecule of the WBC; and culturing the cell in the presence of an agent derived from the cell surface molecule of the WBC or from an antigen to which the second antigen binding molecule binds.
113. The method of embodiment 112, wherein the agent is an extracellular domain of the cell surface molecule of the WBC.
114. A method for *in vitro* cell preparation, the method comprising: preparing cells; introducing a nucleic acid encoding a first antigen binding molecule and a second antigen binding molecule into the cells, a binding domain of the first antigen binding molecule binding to a cell surface molecule of a WBC, and a binding domain of the second antigen binding molecule binding to an antigen different from the cell surface molecule of the WBC; and culturing the cells in the presence of an agent derived from the cell surface molecule of the WBC or from an antigen to which the second antigen binding molecule binds.

115. A method of enhancing T cell response in a subject or treating a tumor of the subject, the method comprising: administering an effective amount of T cell comprising a first antigen binding molecule and a second antigen binding molecule to the subject to provide a T cell response, wherein a binding domain of the first antigen binding molecule binds a cell surface molecule of a WBC, and a binding domain of the second antigen binding molecule binds an antigen different from the cell surface molecule of the WBC.

116. The method of embodiment 115, wherein enhancing T cell response in the subject comprises selectively enhancing proliferation of T cell comprising the first antigen binding molecule and the second antigen binding molecule *in vivo*.

117. A method of expanding cells expressing an antigen binding molecule *in vivo*, the method comprising: administering an effective amount of T cell comprising a first antigen binding molecule and a second antigen binding molecule to the subject, wherein a binding domain of the first antigen binding molecule binds a cell surface molecule of a WBC, and a binding domain of the second antigen binding molecule binds a solid tumor antigen that is different from the cell surface molecule of the WBC, the cells being T cells, NK cells, or dendritic cells.

118. The nucleic acid, the vector, the cell, or the method of any one of embodiments 106-117, wherein the first antigen binding molecule is a first chimeric antigen receptor (CAR) and the second antigen binding molecule is a second CAR.

119. The nucleic acid, the vector, the cell, or the method of embodiment 118, wherein the antigen different from the cell surface molecule of the WBC is CD19, CD22, CD20, BCMA, CD5, CD7, CD2, CD16, CD56, CD30, CD14, CD68, CD11b, CD18, CD169, CD1c, CD33, CD38, CD138, CD13, B7, CAIX, CD123, CD133, CD171, CD171/L1-CAM, CEA, Claudin 18.2, cMet, CS1, CSPG4, Dectin1, EGFR, EGFR vIII, EphA2, ERBB receptors, ErbB T4, ERBB2, FAP, Folate receptor 1, FITC, Folate receptor 1, FSH, GD2, GPC3, HA-1 H/HLA- A2, HER2, IL-11Ra, IL13 receptor a2, IL13R, IL13R α 2 (zetakine), Kappa, Leukemia, LewisY, Mesothelin, MUC1, NKG2D, NY-ESO-1, PSMA, ROR-1, TRAIL-receptor1, or VEGFR2.

120. The nucleic acid, the vector, the cell, or the method of embodiment 118, wherein the MUC1 is a tumor-exclusive epitope of a human MUC1, and the first CAR and the second CAR are expressed as polypeptides.

121. The nucleic acid, the vector, the cell, or the method of embodiment 118, wherein the MUC1 is a tumor form of human MUC1 (tMUC1).

122. The nucleic acid, the vector, the cell, or the method of embodiment 118, wherein the WBC is a granulocyte, a monocyte and or lymphocyte.

123. The nucleic acid, the vector, the cell, or the method of embodiment 118, wherein the WBC is a B cell.

124. The nucleic acid, the vector, the cell, or the method of embodiment 118, wherein the cell surface molecule of the WBC is CD19, CD22, CD20, BCMA, CD5, CD7, CD2, CD16, CD56,

CD30, CD14, CD68, CD11b, CD18, CD169, CD1c, CD33, CD38, CD138, or CD13, or the cell surface molecule of the WBC is CD19, CD20, CD22, or BCMA.

125. The nucleic acid, the vector, the cell, or the method of embodiment 118, wherein the cell surface molecule of the WBC is CD19.

126. The nucleic acid, the vector, the cell, or the method of embodiment 118, wherein the first CAR comprises the first antigen binding domain, a transmembrane domain, a co-stimulatory domain, and a CD3 zeta domain and/or the second CAR comprises the second antigen binding domain, a transmembrane domain, a co-stimulatory domain, and a CD3 zeta domain.

127. The nucleic acid, the cell, or the method of embodiment 110, wherein the co-stimulatory domain comprises the intracellular domain of a co-stimulatory molecule selected from the group consisting of CD27, CD28, 4-1BB, OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, B7-H3, a ligand that specifically binds with CD83, or a combination thereof.

128. The nucleic acid, the vector, the cell, or the method of embodiment 118, wherein the antigen binding domain is a Fab or a scFv.

129. The nucleic acid, the vector, the cell, or the method of embodiment 118, wherein the first CAR comprises the amino acid sequence of SEQ ID NO: 5, 6, 53 and 54, 55 and 56, or 57 and 58, and the second CAR comprises the amino acid sequence of one of SEQ ID NOs: 5-17, 29, 33, 37, 71, and 72, or the amino acid sequence encoded by the nucleic acid of SEQ ID NO: 41, 45, 63, 67, or 68.

130. The nucleic acid, the vector, the cell, or the method of embodiment 118, wherein a nucleic acid encoding the first CAR comprises the nucleic acid sequence of SEQ ID NO: 59, or 60, and a nucleic acid encoding the second CAR comprises the nucleic acid sequence of SEQ ID NO: 61.

131. The nucleic acid, the vector, the cell, or the method of embodiment 118, wherein the nucleic acid comprises one of the nucleic acid sequence of SEQ ID NO: 62-69.

132. The nucleic acid, the vector, the cell, or the method of embodiment 118, wherein the first CAR and the second CAR are expressed as gene products that are separate polypeptides.

133. The nucleic acid, the vector, the cell, or the method of any one of embodiments 106-132, wherein the first antigen binding molecule is a chimeric antigen receptor (CAR) and the second antigen binding molecule is a T Cell Receptor (TCR).

134. The nucleic acid, the vector, the cell, or the method of embodiment 133, wherein the TCR is modified TCR.

135. The nucleic acid, the vector, the cell, or the method of embodiment 133, wherein the TCR is derived from spontaneously occurring tumor-specific T cells in patients.

136. The nucleic acid, the cell, or the method of embodiment 133, wherein the TCR binds a tumor antigen.

137. The nucleic acid, the vector, the cell, or the method of embodiment 133, wherein the tumor antigen comprises CEA, gp100, MART-1, p53, MAGE-A3, or NY-ESO-1, or the TCR comprises TCR γ and TCR δ Chains or TCR α and TCR β chains, or a combination thereof.

138. A modified T cell comprising a first CAR and a second CAR, wherein a binding domain of the first CAR binds CD19, and a binding domain of the second CAR binds tumor associated MUC1.

139. The modified T cell of embodiment 138, wherein the binding domain of the second CAR comprises: (i) a heavy chain complementary determining region 1 comprising the amino acid sequence of SEQ ID: 76 or 85, a heavy chain complementary determining region 2 comprising the amino acid sequence of SEQ ID: 77 or 86, and a heavy chain complementary determining region 3 comprising the amino acid sequence of SEQ ID: 78 or 87; and (ii) a light chain complementary determining region 1 comprising the amino acid sequence of SEQ ID: 73 or 82, a light chain complementary determining region 2 comprising the amino acid sequence of TRP-ALA-SER (WAS) or SEQ ID: 83, and a light chain complementary determining region 3 comprising the amino acid sequence of SEQ ID: 75 or 84.

140. The modified T cell of embodiment 138, wherein the binding domain of the second CAR comprises: (i) a heavy chain complementary determining region 1 comprising the amino acid sequence of SEQ ID: 76, a heavy chain complementary determining region 2 comprising the amino acid sequence of SEQ ID: 77, and a heavy chain complementary determining region 3 comprising the amino acid sequence of SEQ ID: 78; and (ii) a light chain complementary determining region 1 comprising the amino acid sequence of SEQ ID: 73, a light chain complementary determining region 2 comprising the amino acid sequence of TRP-ALA-SER (WAS), and a light chain complementary determining region 3 comprising the amino acid sequence of SEQ ID: 75.

141. The modified T cell of embodiment 138, wherein the binding domain of the second CAR comprises: (i) a heavy chain complementary determining region 1 comprising the amino acid sequence of SEQ ID: 85, a heavy chain complementary determining region 2 comprising the amino acid sequence of SEQ ID: 86, and a heavy chain complementary determining region 3 comprising the amino acid sequence of SEQ ID: 87; and (ii) a light chain complementary determining region 1 comprising the amino acid sequence of SEQ ID: 82, a light chain complementary determining region 2 comprising the amino acid sequence of SEQ ID: 83, and a light chain complementary determining region 3 comprising the amino acid sequence of SEQ ID: 84.

142. The modified T cell of embodiment 138, wherein the binding domain of the first CAR comprises the amino acid sequence of SEQ ID: 5 or 6.

143. The modified T cell of embodiment 138, wherein the binding domain of the second CAR comprises one of the amino acid sequences of SEQ ID: 70 -72 and 79-81.

144. The modified T cell of any one of embodiments 138-143, wherein the first CAR comprises the first antigen binding domain, a transmembrane domain, a co-stimulatory domain, and a CD3 zeta domain and/or the second CAR comprises the second antigen binding domain, a transmembrane domain, a co-stimulatory domain, and a CD3 zeta domain.
145. The modified T cell of embodiment 144, wherein the co-stimulatory domain comprises the intracellular domain of a co-stimulatory molecule selected from the group consisting of CD27, CD28, 4-1BB, OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, B7-H3, a ligand that specifically binds with CD83, or a combination thereof.
146. The modified T cell of any one of embodiments 138-145, wherein the first CAR and the second CAR are expressed as gene products that are separate polypeptides.
147. The modified T cell of any one of embodiments 138-146, wherein a cytoplasmic domain or a transmembrane domain of the second CAR is modified such that the second CAR is capable of activating the modified T cell via cells expressing CD19 without damaging the cells expressing CD19.
148. A bispecific chimeric antigen receptor, comprising: a first antigen binding domain, a second antigen binding domain, a cytoplasmic domain, and transmembrane domain, wherein the first antigen binding domain recognizes a first antigen, and the second antigen binding domain recognize a second antigen, the first antigen is different from the second antigen.
149. The bispecific chimeric antigen receptor of embodiment 148, wherein the first antigen and the second antigen are not expressed on the same cell.
150. The bispecific chimeric antigen receptor of embodiment 148 or 149, wherein the first antigen is an antigen of a blood component, and the second antigen is an antigen of a solid tumor.
151. The bispecific chimeric antigen receptor of any one of embodiments 148-150, wherein the first antigen is CD19, and the second antigen is a tumor associated MUC1.
152. The bispecific chimeric antigen receptor of any one of embodiments 148-151, wherein the first antigen binding domain comprises one of the amino acid sequences of SEQ ID: 5 and 6.
153. The modified T cell of any one of embodiments 138-147, wherein the second antigen binding domain comprises one of the amino acid sequence of SEQ ID: 70 -72 and 79-81.
154. A method of enhancing T cell response in a subject or treating a tumor of the subject, the method comprising: administering an effective amount of modified T cell of any one of embodiments 138-147 to the subject to provide a T-cell response such that the CAR T cell is expanded in the blood of the subject via cells expressing CD19.
155. The modified T cells of any one of embodiments 138-147, wherein the tumor associated MUC1 are expressed on tumor cells and not on corresponding non-malignant cells.
156. The modified T cells of any one of embodiments 138-147, wherein a scFv against the tumor associated MUC1 directly interacts with an o-glycosylated GSTA motif (SEQ ID NO. 88).

157. A cell comprising the bispecific CAR of any one of embodiments 148-152.
158. A nucleic acid encoding the bispecific CAR of any one of embodiments 148-152.
159. A T cell comprising a first CAR and a second CAR, wherein an antigen binding domain of the first CAR binds an antigen selected from the group consisting of CD19, CD33, CD14, and BCMA, and an antigen binding domain of the second CAR binds a tumor associated MUC1.
160. The T cell of embodiment 159, wherein the first CAR comprises the amino acid sequence of SEQ ID NO: 207, and the second CAR comprises the amino acid sequence of SEQ ID: 202.
161. The T cell of embodiment 159, wherein the first CAR comprises the amino acid sequence of SEQ ID NO: 203, 207, 216, or 219, and the second CAR comprises the amino acid sequence of SEQ ID: 202 or 205.
162. The T cell of embodiment 159, wherein the antigen binding domain of the second CAR comprises the amino acid sequence of SEQ ID NO: 70.
163. The T cell of embodiment 159, wherein the antigen binding domain of the second CAR comprises the amino acid sequence of SEQ ID NO: 5 or 6.
164. The T cell of embodiment 159, wherein the Isolated T cell comprises one of the nucleic acid sequences of SEQ ID NO: 201, 204, 206, 208, 215, 217, 218, and 220.
165. The T cell of any one of embodiments 159-164, wherein each of the first CAR and the second CAR comprises an antigen binding domain, a transmembrane domain, and a cytoplasmic domain.
166. The T cell of embodiment 165, wherein the cytoplasmic domain comprises a co-stimulatory domain and a CD3 zeta domain.
167. The T cell of embodiment 166, wherein the co-stimulatory domain comprises the intracellular domain of CD27, CD28, 4-1BB, OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, B7-H3, a ligand that specifically binds with CD83, or a combination thereof.
168. The T cell of embodiment 159, wherein the T cell comprises a dominant negative variant of a receptor of programmed death 1 (PD-1), cytotoxic T lymphocyte antigen-4 (CTLA- 4), B- and T-lymphocyte attenuator (BTLA), T cell immunoglobulin mucin-3 (TIM-3), lymphocyte-activation protein 3 (LAG-3), T cell immunoreceptor with Ig and ITIM domains (TIGIT), leukocyte-associated immunoglobulin-like receptor 1 (LAIR1), natural killer cell receptor 2B4 (2B4), or CD 160.
169. The T cell of embodiment 159, wherein the T cell comprises a reduced amount of TCR, as compared to the corresponding wide-type T cell.
170. A composition comprising a population of the T cell of any one of embodiments 159-169.
171. A method of enhancing T cell response in a subject or treating a tumor of the subject, the method comprising: administering an effective amount of the T cell of any one of embodiments 159-169.

172. The nucleic acid, the vector, the cell (including T cell and modified T cell), the bispecific CAR, the composition, or the method of any one of embodiments 1-171, wherein the tumor antigen, is a solid tumor antigen.

173. The nucleic acid, the vector, the cell (including T cell and modified T cell), the bispecific CAR, the composition, or the method of any one of embodiments 1-172, wherein the solid tumor antigen is tMUC 1, PRLR, CLCA1, MUC12, GUCY2C, GPR35, CR1L, MUC 17, TMPRSS11B, MUC21, TMPRSS11E, CD207, SLC30A8, CFC1, SLC12A3, SSTR1, GPR27, FZD10, TSHR, SIGLEC15, SLC6A3, KISS1R, QRFPR, GPR119, CLDN6, UPK2, ADAM12, SLC45A3, ACPP, MUC21, MUC16, MS4A12, ALPP, CEA, EphA2, FAP, GPC3, IL13-R α 2, Mesothelin, PSMA, ROR1, VEGFR-II, GD2, FR- α , ErbB2, EpCAM, EGFRvIII, or EGFR, and wherein the B cell antigen is CD19, CD20, CD22, or BCMA.

174. A method for enhancing T cell expansion and/or cytokine release (e.g., IL-6 and INF- γ) in a subject having cancer, the method comprising: providing a plurality of nucleic acids into T cells, the plurality of nucleic acids encoding a chimeric antigen receptor (CAR) binding a solid tumor antigen and encoding a CAR binding a B cell antigen; and administering an effective amount of the T cells to the subject.

175. A method for enhancing T cell response and/or cytokine release (e.g., IL-6 and INF- γ) in a subject having cancer, the method comprising: providing a plurality of nucleic acids into T cells, the plurality of nucleic acids encoding a chimeric antigen receptor (CAR) binding a solid tumor antigen, a CAR binding a B cell antigen, and a modified PD-1 lacking a functional PD-1 intracellular domain; and administering an effective amount of the T cells to the subject.

176. A modified cell comprising a plurality of nucleic acids encoding a chimeric antigen receptor (CAR) binding a solid tumor antigen associated with tumor of a subject, a CAR binding a B cell antigen, and a modified PD-1 lacking a functional PD-1 intracellular domain.

177. The modified cell or the method of embodiments of 175 or 176, wherein the subject has a higher level of T cell expansion and a higher amount of memory T cells as compared with a subject that is administered an effective amount of the CAR T cells that do not have the CAR binding the B cell antigen nor the modified PD-1.

178. The modified cell or the method of embodiments of 175 or 176, wherein the modified PD-1 comprises one of the amino acid sequences of SEQ ID NO: 89-95.

179. The modified cell or the method of embodiments of any one of embodiments 174-178, wherein the solid tumor antigen is tMUC 1, PRLR, CLCA1, MUC12, GUCY2C, GPR35, CR1L, MUC 17, TMPRSS11B, MUC21, TMPRSS11E, CD207, SLC30A8, CFC1, SLC12A3, SSTR1, GPR27, FZD10, TSHR, SIGLEC15, SLC6A3, KISS1R, QRFPR, GPR119, CLDN6, UPK2, ADAM12, SLC45A3, ACPP, MUC21, MUC16, MS4A12, ALPP, CEA, EphA2, FAP, GPC3, IL13-R α 2, Mesothelin, PSMA, ROR1, VEGFR-II, GD2, FR- α , ErbB2, EpCAM, EGFRvIII, or EGFR, and the B cell antigen is CD19, CD20, CD22, or BCMA.

180. The modified cell or the method of embodiments of any one of embodiments 174-178, wherein the B cell antigen comprises CD19.

181. The modified cell or the method of embodiment 180, wherein the solid tumor antigen comprises tumor associated MUC1.

182. The modified cell or the method of embodiment 181, wherein a binding domain of the CAR binding the B cell antigen comprises an amino acid sequence of SEQ ID NO: 5 or 6, and a binding domain of the CAR binding the solid tumor antigen comprises an amino acid sequence of SEQ ID NO: 70.

183. The modified cell or the method of embodiment 181, wherein the CAR binding the B cell antigen comprises an amino acid sequence of SEQ ID NO: 207, and the CAR binding the solid tumor antigen comprises an amino acid sequence of SEQ ID NO: 202.

184. The modified cell or the method of embodiment 181, wherein the CAR binding the B cell antigen comprises an antigen binding domain, a transmembrane domain, a cytoplasmic domain, and the CAR binding the solid tumor antigen comprises an antigen binding domain, a transmembrane domain, and a cytoplasmic domain.

185. The modified cell or the method of embodiment 184, wherein the cytoplasmic domain of the CAR comprises a co-stimulatory domain or a CD3 zeta domain, or a combination thereof.

186. The modified cell or the method of embodiment 180, wherein the T cell expansion is greater than a T cell expansion obtained by administering T cells having the CAR binding the solid tumor antigen in the absence of the CAR binding the B cell antigen.

187. The modified cell or the method of embodiment 186, wherein the T cell expansion is measured based on an increase in copy number of CAR molecules in genomic DNA of the T cells.

188. The modified cell or the method of embodiment 180, wherein at least one of the nucleic acids comprises a nucleic acid sequence of SEQ ID NO: 201.

189. The modified cell or the method of embodiment 178, wherein the B cell antigen comprises CD19, CD20, CD22, or BCMA.

190. The modified cell or the method of embodiment 188, wherein the solid tumor antigen comprises B7, CAIX, CD123, CD133, CD171, CD171/L1-CAM, CEA, Claudin 18.2, cMet, CS1, CSPG4, Dectin1, EGFR, EGFR vIII, EphA2, ERBB receptors, ErbB T4, ERBB2, FAP, Folate receptor 1, FITC, Folate receptor 1, FSH, GD2, GPC3, HA-1 H/HLA- A2, HER2, IL-11Ra, IL13 receptor a2, IL13R, IL13R α 2 (zetakine), Kappa, Leukemia, LewisY, Mesothelin, MUC1, NKG2D, NY-ESO-1, PSMA, ROR-1, TRAIL-receptor1, or VEGFR2.

191. The modified cell or the method of embodiment 178, wherein the CAR binding the B cell antigen comprises an amino acid sequence of SEQ ID NO: 203, 207, 216, or 219.

192. The modified cell or the method of embodiment 178, wherein the CAR binding the solid tumor antigen comprises an amino acid sequence of SEQ ID NO: 202 or 205.

193. The modified cell or the method of embodiment 178, wherein at least one of nucleic acids comprises a nucleic acid sequence of SEQ ID NO: 201, 204, 206, 208, 215, 217, 218, or 220.

194. A method for increasing a number or ratio of an immune cell subpopulation and/or increasing or extending persistence of the immune cell subpopulation in a subject having cancer, the method comprising: administering an effective amount of a composition comprising T-cells to the subject, the T-cells including a chimeric antigen receptor (CAR) and a modified PD-1, the modified PD-1 lacking a functional PD-1 intracellular domain; and monitoring T-cell response in the subject, the immune cell subpopulation comprising naive T-cells, stem cell memory T-cells, and/or central memory T-cells, wherein the number or ratio of the immune cell subpopulation in the subject is increased as compared to corresponding T-cells that do not include the modified PD-1; or monitoring the persistence of the immune cell subpopulation in the subject, whether it is increased or extended as compared to the corresponding T-cells that do not include the modified PD-1.

195. The method of claim 194, wherein monitoring the T-cell response in the subject comprises at least one of: detecting mRNA of the modified PD-1; detecting a number of one or more white blood cells; detecting a number of at least one of naive T-cells, stem cell memory T-cells, and central memory T-cells; detecting a CAR copy number; detecting CD3 positive cell number; detecting a number of T-cells expressing CAR; and detecting a level of one or more cytokines.

196. The method of claim 194, wherein the T-cells has more memory T-cells in the subject than those of T-cells that are introduced with the CAR and do not include the modified PD-1.

197. The method of claim 194, wherein the modified PD-1 comprises one sequences of SEQ ID: 89-93 or the modified PD-1 do not include SEQ ID: 94 or 95.

198. The method of claim 194, wherein the T-cells comprise a dominant negative variant of PD-1, and endogenous gene of PD-1 of the T cells is not disrupted.

199. The method of claim 194, wherein the CAR comprises an extracellular domain, a transmembrane domain, and an intracellular domain, the extracellular domain binds an antigen.

200. The method of claim 199, wherein the intracellular domain comprises a co-stimulatory domain that comprises an intracellular domain of a costimulatory molecule selected from the group consisting of CD27, CD28, 4-1BB, OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, B7-H3, and any combination thereof.

201. The method of claim 199, wherein the antigen is Epidermal growth factor receptor (EGFR), Variant III of the epidermal growth factor receptor (EGFRvIII), Human epidermal growth factor receptor 2 (HER2), Mesothelin (MSLN), Prostate-specific membrane antigen (PSMA), Carcinoembryonic antigen (CEA), Disialoganglioside 2 (GD2), Interleukin-13Ra2 (IL13R α 2), Glypican-3 (GPC3), Carbonic anhydrase IX (CAIX), L1 cell adhesion molecule (L1-CAM), Cancer antigen 125 (CA125), Cluster of differentiation 133 (CD133), Fibroblast activation protein (FAP), Cancer/testis antigen 1B (CTAG1B), Mucin 1 (MUC1), Folate receptor- α (FR- α),

CD19, FZD10, TSHR, PRLR, Muc 17, GUCY2C, CD207, CD3, CD5, B-Cell Maturation Antigen (BCMA), or CD4.

202. The method of claim 194, wherein the T-cells comprise a CAR binding a solid tumor antigen and a CAR binding a white cell antigen.

203. The method of claim 202, wherein the the solid tumor antigen is tMUC 1, PRLR, CLCA1, MUC12, GUCY2C, GPR35, CR1L, MUC 17, TMPRSS11B, MUC21, TMPRSS11E, CD207, SLC30A8, CFC1, SLC12A3, SSTR1, GPR27, FZD10, TSHR, SIGLEC15, SLC6A3, KISS1R, QRFPR, GPR119, CLDN6, UPK2, ADAM12, SLC45A3, ACPP, MUC21, MUC16, MS4A12, ALPP, CEA, EphA2, FAP, GPC3, IL13-R α 2, Mesothelin, PSMA, ROR1, VEGFR-II, GD2, FR- α , ErbB2, EpCAM, EGFRvIII, or EGFR, and the B cell antigen is CD19, CD20, CD22, or BCMA.

204. The method of claim 202, wherein the white cell antigen is a B cell antigen.

205. The method of claim 202, wherein the B cell antigen is CD19, CD20, CD22, or BCMA.

206. A method for increasing a number or ratio of an immune cell subpopulation and/or increasing or extending persistence of the immune cell subpopulation, the method comprising: providing T-cells with a nucleic acid sequence encoding a chimeric antigen receptor (CAR); and providing T-cells with a nucleic acid sequence encoding a modified PD-1, the modified PD-1 lacking a functional PD-1 intracellular domain, the immune cell subpopulation comprising naive T-cells, stem cell memory T-cells, and/or central memory T-cells, wherein the number or ratio of the immune cell subpopulation is increased as compared to corresponding T-cells that do not include the modified PD-1; or monitoring the persistence of the immune cell subpopulation, whether it is increased or extended as compared to the corresponding T-cells that do not include the modified PD-1.

207. An isolated zinc finger nuclease (ZFN) comprising: a first zinc finger protein (ZFP) binding to a first target site in a CTLA4 gene, the first ZFP comprising three or more zinc finger domains; a second ZFP binding to a second target site in the CTLA4 gene, the second ZFP comprising three or more zinc finger domains; and a cleavage domain, wherein the first ZFP comprises amino acid sequences SEQ ID NOS.: 301, 302, and 303 ordered from a N-terminal of the first ZFP to a C-terminal of the first ZFP, and the second ZFP comprises amino acid sequences SEQ ID NOS.: 305, 306, and 307 ordered from a N-terminal of the second ZFP to a C-terminal of the second ZFP.

208. An isolated ZFN that binds a target site in a CTLA4 gene, the target site comprising a nucleotide sequence SEQ ID NO.: 304.

209. An isolated zinc finger nuclease (ZFN) comprising: a first zinc finger protein (ZFP) binding to a first target site in a LAG3 gene, the first ZFP comprising three or more zinc finger domains; a second ZFP binding to a second target site in the LAG3 gene, the second ZFP comprising three or more zinc finger domains; and a cleavage domain, wherein: the first ZFP comprises amino acid sequences SEQ ID NOS.: 308, 309, and 310 ordered from a N-terminal of the first ZFP to a C-terminal of the first ZFP, and the second ZFP comprises amino acid sequences

SEQ ID NOS.: 309, 308, and 312 ordered from a N-terminal of the second ZFP to a C-terminal of the second ZFP, or the first ZFP comprises amino acid sequences SEQ ID NOS.: 313, 314, and 315 ordered from a N-terminal of the first ZFP to a C-terminal of the first ZFP, and the second ZFP comprises amino acid sequences SEQ ID NOS.: 316, 317, and 318 ordered from a N-terminal of the second ZFP to a C-terminal of the second ZFP.

210. An isolated ZFN that binds a target site in a LAG3 gene, the target site comprising a nucleotide sequence SEQ ID NO.: 311 or 319.

211. An isolated zinc finger nuclease (ZFN) comprising: a first zinc finger protein (ZFP) binding to a first target site in a BTLA gene, the first ZFP comprising three or more zinc finger domains; a second ZFP binding to a second target site in the BTLA gene, the second ZFP comprising three or more zinc finger domains; and a cleavage domain, wherein the first ZFP comprises amino acid sequences SEQ ID NOS.: 320, 321, and 322 ordered from a N-terminal of the first ZFP to a C-terminal of the first ZFP, and the second ZFP comprises amino acid sequences SEQ ID NOS.: 323, 324, and 325 ordered from a N-terminal of the second ZFP to a C-terminal of the second ZFP.

212. An isolated ZFN that binds a target site in a BTLA gene, the target site comprising a nucleotide sequence SEQ ID NO.: 326.

213. An isolated zinc finger nuclease (ZFN) comprising: a first zinc finger protein (ZFP) binding to a first target site in a TIM3 gene, the first ZFP comprising three or more zinc finger domains; a second ZFP binding to a second target site in the TIM3 gene, the second ZFP comprising three or more zinc finger domains; and a cleavage domain, wherein: the first ZFP comprises amino acid sequences SEQ ID NOS.: 327, 328, and 329 ordered from a N-terminal of the first ZFP to a C-terminal of the first ZFP, and the second ZFP comprises amino acid sequences SEQ ID NOS.: 330, 331, and 332 ordered from a N-terminal of the second ZFP to a C-terminal of the second ZFP; or the first ZFP comprises amino acid sequences SEQ ID NOS.: 334, 335, and 336 ordered from a N-terminal of the first ZFP to a C-terminal of the first ZFP, and the second ZFP comprises amino acid sequences SEQ ID NOS.: 337, 338, and 339 ordered from a N-terminal of the second ZFP to a C-terminal of the second ZFP.

214. An isolated ZFN that binds a target site in a TIM3 gene, the target site comprising a nucleotide sequence SEQ ID NO.: 333 or 340.

215. An isolated zinc finger nuclease (ZFN) comprising: a first zinc finger protein (ZFP) binding to a first target site in a FOXP3 gene, the first ZFP comprising three or more zinc finger domains; a second ZFP binding to a second target site in the FOXP3 gene, the second ZFP comprising three or more zinc finger domains; and a cleavage domain, wherein: the first ZFP comprises amino acid sequences SEQ ID NOS.: 341, 328, and 342 ordered from a N-terminal of the first ZFP to a C-terminal of the first ZFP, and the second ZFP comprises amino acid sequences SEQ ID NOS.: 343, 344, and 345 ordered from a N-terminal of the second ZFP to a C-terminal of the second ZFP, the first ZFP comprises amino acid sequences SEQ ID NOS.:

347, 348, and 349 ordered from a N-terminal of the first ZFP to a C-terminal of the first ZFP, and the second ZFP comprises amino acid sequences SEQ ID NOS.: 350, 344, and 351 ordered from a N-terminal of the second ZFP to a C-terminal of the second ZFP; or the first ZFP comprises amino acid sequences SEQ ID NOS.: 288, 310, and 314 ordered from a N-terminal of the first ZFP to a C-terminal of the first ZFP, and the second ZFP comprises amino acid sequences SEQ ID NOS.: 308, 308, and 284 ordered from a N-terminal of the second ZFP to a C-terminal of the second ZFP.

216. An isolated ZFN that binds a target site in a FOXP3 gene, the target site comprising a nucleotide sequence SEQ ID NO.: 346, 352, or 283.

217. An isolated zinc finger nuclease (ZFN) comprising: a first zinc finger protein (ZFP) binding to a first target site in a SIVA1 gene, the first ZFP comprising three or more zinc finger domains; a second ZFP binding to a second target site in the SIVA1 gene, the second ZFP comprising three or more zinc finger domains; and a cleavage domain, wherein: the first ZFP comprises amino acid sequences SEQ ID NOS.: 353, 331, and 354 ordered from a N-terminal of the first ZFP to a C-terminal of the first ZFP, and the second ZFP comprises amino acid sequences SEQ ID NOS.: 355, 300, and 299 ordered from a N-terminal of the second ZFP to a C-terminal of the second ZFP; or the first ZFP comprises amino acid sequences SEQ ID NOS.: 308, 314, and 312 ordered from a N-terminal of the first ZFP to a C-terminal of the first ZFP, and the second ZFP comprises amino acid sequences SEQ ID NOS.: 288, 287, and 286 ordered from a N-terminal of the second ZFP to a C-terminal of the second ZFP.

218. An isolated ZFN that binds a target site in a SIVA1 gene, the target site comprising a nucleotide sequence SEQ ID NO.: 296 or 285.

219. An isolated zinc finger nuclease (ZFN) comprising: a first zinc finger protein (ZFP) binding a first target site in a LGALS9 gene, the first ZFP comprising three or more zinc finger domains; a second ZFP binding to a second target site in the LGALS9 gene, the second ZFP comprising three or more zinc finger domains; and a cleavage domain, wherein the first ZFP comprises amino acid sequences SEQ ID NOS.: 298, 324, and 297 ordered from a N-terminal of the first ZFP to a C-terminal of the first ZFP, and the second ZFP comprises amino acid sequences SEQ ID NOS.: 295, 300, and 294 ordered from a N-terminal of the second ZFP to a C-terminal of the second ZFP.

220. An isolated ZFN that binds a target site in a CD33 gene, the target site comprising a nucleotide sequence SEQ ID NO.: 293.

221. An isolated zinc finger nuclease (ZFN) comprising: a first zinc finger protein (ZFP) binding to a first target site in a CD33 gene, the first ZFP comprising three or more zinc finger domains; a second ZFP binding to a second target site in the CD33 gene, the second ZFP comprising three or more zinc finger domains; and a cleavage domain, wherein the first ZFP comprises amino acid sequences SEQ ID NOS.: 301, 292, and 312 ordered from a N-terminal of the first ZFP to a C-terminal of the first ZFP, and the second ZFP comprises amino acid sequences

SEQ ID NOS.: 291, 290, and 310 ordered from a N-terminal of the second ZFP to a C-terminal of the second ZFP.

222. An isolated ZFN that binds a target site in a LGALS9 gene, the target site comprising a nucleotide sequence SEQ ID NO.: 289.

223. The isolated ZFN of any one of embodiments 207-222, wherein the gene is a human gene.

224. The isolated ZFN of any one of embodiments 207-222, wherein the cleavage domain comprises a wild-type or engineered FokI cleavage domain.

225. A polynucleotide encoding the isolated ZFN of any one of embodiments 207-222.

226. A vector comprising the polynucleotide of embodiment 225.

227. The vector of embodiment 226, wherein the vector is an adenoviral or lentiviral vector.

228. An isolated cell or a cell line comprising the isolated ZFN of any one of embodiments 207-222.

229. The isolated cell or the cell line of embodiment 228, wherein the isolated cell is a stem cell, a T cell or a Natural Killer (NK) cell.

230. The isolated cell or the cell line of embodiment 228, wherein the cell is a T cell derived from a primary human T cell isolated from a human donor.

231. The isolated cell or the cell line of embodiment 228, wherein the cell has a reduced expression of an endogenous gene of CTLA4, LAG3, BTLA, TIM3, FOXP3, SIVA1, and LGALS9.

232. An isolated cell comprising isolated nucleic acid sequence encoding a chimeric antigen receptor (CAR), wherein an endogenous gene is inactivated using the ZFN of any one of embodiments 207-222.

233. The isolated cell or the cell line of embodiment 232, wherein the CAR comprises an antigen binding domain, a transmembrane domain, a co-stimulatory domain, and a CD3 zeta signaling domain.

234. The isolated cell or the cell line of embodiment 233, wherein the cell has a reduced graft-versus-host disease (GVHD) response in a bioincompatible human recipient as compared to the GVHD response of the primary human T cell.

235. The isolated cell or the cell line of embodiment 232, wherein an antigen binding domain of the CAR binds FZD10, TSHR, PRLR, Muc17, GUCY2C, CD207, CD19, or CD20.

236. The isolated cell or the cell line of embodiment 232, wherein a co-stimulatory domain of the CAR comprises the intracellular domain of a costimulatory molecule selected from the group consisting of CD27, CD28, 4-1BB, OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, B7-H3, and any combination thereof.

237. The isolated cell or the cell line of embodiment 228, wherein the isolated cell or the cell line is a T cell comprising a nucleic acid sequence encoding hTERT or a nucleic acid encoding SV40LT, or a combination thereof.

238. The isolated cell or the cell line of embodiment 237, wherein the T cell comprises a nucleic acid sequence encoding hTERT and a nucleic acid encoding SV40LT.
239. The isolated cell or the cell line of embodiment 237, wherein expression of hTERT is regulated by an inducible expression system.
240. The isolated cell or the cell line of embodiment 237, wherein expression of SV40LT gene is regulated by an inducible expression system.
241. The isolated cell or the cell line of embodiment 240, wherein the inducible expression system is rTTA-TRE, which increases or activates the expression of SV40LT gene or hTERT gene, or a combination thereof.
242. The isolated cell or the cell line of embodiment 237, wherein the T cell comprises a nucleic acid sequence encoding a suicide gene, and/or the suicide gene comprises a HSV-TK suicide gene system.
243. A method of treating cancer in a subject, the method comprising administering a genetically modified cell of embodiment 232 to the subject, wherein the cancer is selected from the group consisting of a lung carcinoma, pancreatic cancer, liver cancer, bone cancer, breast cancer, colorectal cancer, leukemia, ovarian cancer, lymphoma, and brain cancer.
244. An isolated zinc finger nuclease (ZFN) comprising: a first zinc finger protein (ZFP) binding to a first target site in a B2M gene, the first ZFP comprising three or more zinc finger domains; a second ZFP binding to a second target site in the B2M gene, the second ZFP comprising three or more zinc finger domains; and a cleavage domain, wherein the first ZFP comprises amino acid sequences listed in Table 8, and the second ZFP comprises amino acid sequences listed in Table 8.
245. An isolated ZFN that binds a target site in a B2M gene, the target site comprising a nucleotide sequence listed in Table 8.
246. An isolated zinc finger nuclease (ZFN) comprising: a first zinc finger protein (ZFP) binding to a first target site in a ClITA gene, the first ZFP comprising three or more zinc finger domains; a second ZFP binding to a second target site in the ClITA gene, the second ZFP comprising three or more zinc finger domains; and a cleavage domain, wherein: the first and second ZFP comprises amino acid sequences listed in Table 8.
247. The isolated ZFN of any one of embodiments 244-246, wherein the gene is a human gene.
248. The isolated ZFN of any one of embodiments 244-246, wherein the cleavage domain comprises a wild-type or engineered *FokI* cleavage domain.
249. A polynucleotide encoding the isolated ZFN of any one of embodiments 244-248.
250. A vector comprising the polynucleotide of embodiments 249.
251. The vector of embodiments 250, wherein the vector is an adenoviral or lentiviral vector.
252. An isolated cell or a cell line comprising the isolated ZFN of any one of embodiments 244-248.

253. The isolated cell or the cell line of embodiments 252, wherein the isolated cell is a stem cell, a T cell or a Natural Killer (NK) cell.
254. The isolated cell or the cell line of embodiments 253, wherein the cell is a T cell derived from a primary human T cell isolated from a human donor.
255. The isolated cell or the cell line of embodiments 254, wherein the cell has a reduced expression of an endogenous gene of B2M or CIITA.
256. An isolated cell comprising isolated nucleic acid sequence encoding a chimeric antigen receptor (CAR), wherein an endogenous gene of the CAR is inactivated using the ZFN of any one of embodiments 244-256.
257. The isolated cell or the cell line of embodiments 256, wherein the CAR comprises an antigen binding domain, a transmembrane domain, a co-stimulatory domain, and a CD3 zeta signaling domain.
258. The isolated cell or the cell line of embodiments 257, wherein the cell has a reduced host-versus-graft disease (HVGD) response in a bioincompatible human recipient as compared to the HVGD response of the primary human T cell.
259. The isolated cell or the cell line of embodiments 258, wherein an antigen binding domain of the CAR binds FZD10, TSHR, PRLR, Muc17, GUCY2C, CD207, CD19, or CD20.
260. The isolated cell or the cell line of embodiments 258, wherein a co-stimulatory domain of the CAR comprises the intracellular domain of a costimulatory molecule selected from the group consisting of CD27, CD28, 4-1BB, OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, B7-H3, and any combination thereof.
261. The isolated cell or the cell line of embodiments 260, wherein the isolated cell or the cell line is a T cell comprising a nucleic acid sequence encoding hTERT or a nucleic acid encoding SV40LT, or a combination thereof.
262. The isolated cell or the cell line of embodiments 261, wherein the T cell comprises a nucleic acid sequence encoding hTERT and a nucleic acid encoding SV40LT.
263. The isolated cell or the cell line of embodiments 262, wherein expression of hTERT is regulated by an inducible expression system.
264. The isolated cell or the cell line of embodiments 262, wherein expression of SV40LT gene is regulated by an inducible expression system.
265. The isolated cell or the cell line of embodiments 264, wherein the inducible expression system is rTTA-TRE, which increases or activates the expression of SV40LT gene or hTERT gene, or a combination thereof.
266. The isolated cell or the cell line of embodiment 262, wherein the T cell comprises a nucleic acid sequence encoding a suicide gene, and/or the suicide gene comprises a HSV-TK suicide gene system.
267. A method of treating cancer in a subject, the method comprising administering a genetically modified cell of embodiment 25 to the subject, wherein the cancer is selected from

the group consisting of lung carcinoma, pancreatic cancer, liver cancer, bone cancer, breast cancer, colorectal cancer, leukemia, ovarian cancer, lymphoma, and brain cancer.

268. A modified cell comprising a reduced amount of Major Histocompatibility Complex II (MHC II) as compared to a corresponding wild-type cell, wherein the modified cell has decreased immunogenicity as compared to the corresponding wild-type cell.

269. A method for generating modified cells for transplantation, comprising culturing in a culture media modified cells that have a reduced amount of Major Histocompatibility Complex II (MHC II) as compared to corresponding wild-type cells, wherein the modified cells have decreased immunogenicity as compared to the corresponding wild-type cells.

270. A method for treating a condition, comprising administering to a subject a therapeutically effective amount of modified cells that have a reduced amount of Major Histocompatibility Complex II (MHC II) as compared to corresponding wild-type cells, wherein the modified cells have decreased immunogenicity as compared to the corresponding wild-type cells.

271. The modified cell of any one of embodiments 268-270, wherein the modified cell has reduced expression of one or more genes of a biosynthesis or transportation pathway of MHC II as compared to the corresponding wild-type cell.

272. The modified cell of any one of embodiments 268-270, wherein the modified cell accumulates a reduced amount of MHC II on the modified cell as compared to the corresponding wild-type cell.

273. The modified cell of any one of embodiments 268-270, wherein the modified cell has a disruption in an endogenous gene associated with a biosynthesis or transportation pathway of MHC II.

274. The modified cell of any one of embodiments 268-270, wherein the disruption comprises a disruption of MHC class II transactivator (*CIIITA*).

275. The modified cell of any one of embodiments 268-270, wherein the disruption results from deletion of at least a portion of *CIIITA*.

276. The modified cell of any one of embodiments 268-270 the MHC II comprises Human Leukocyte antigen II (HLA II).

277. The modified cell of any one of embodiments 268-270, wherein the decreased immunogenicity comprises a decreased level of inflammatory responses induced by the modified cell as compared to the corresponding wild-type cell.

278. A modified cell comprising a reduced amount of Major Histocompatibility Complex I (MHC I) as compared to a corresponding wild-type cell, wherein the modified cell has decreased immunogenicity as compared to the corresponding wild-type cell.

279. The modified cell of embodiment 278, wherein the modified cell has a disruption in an endogenous gene associated with a biosynthesis or transportation pathway of MHC I.

280. The modified cell of embodiment 279, wherein the disruption comprises a disruption of one or more exons of Transporter associated with antigen presentation 1 (TAP1) gene or a disruption of one or more exons of TAP-associated glycoprotein (TAPBP) gene.
281. The modified cell of embodiment 280, wherein the disruption of the one or more exons of TAP1 gene comprises a disruption of an exon of TAP1 gene.
282. The modified cell of embodiment 280, wherein the disruption of TAPBP gene comprises a heterozygous disruption of TAP1 gene, and the modified cell expresses a wild-type TAPBP gene.
283. The modified cell of embodiment 280, wherein the disruption of the one or more exons of TAPBP gene comprises a disruption of an exon of TAPBP gene.
284. The modified cell of embodiment 280, wherein the decreased immunogenicity comprises a decreased level of inflammatory responses induced by the modified cell as compared to the corresponding wild-type cell.
285. The modified cell of embodiment 280, wherein a karyotype of the modified cell is the same as a karyotype of the corresponding wild-type cell.
286. The modified cell of embodiment 280, wherein a level of pluripotency of the modified cell is substantially the same as a level of pluripotency of the corresponding wild-type cell.
287. The modified cell of any one of embodiments 268-286, wherein the cell is a T cell or a NK cell.
288. The modified cell of any one of embodiments 268-286, wherein the modified cell comprises a CAR.
289. The modified cell of embodiment 288, wherein the CAR comprises an extracellular domain, a transmembrane domain, and an intracellular domain, and the extracellular domain binds a tumor antigen.
290. The modified cell of embodiment 289, wherein the tumor antigen includes HER2, CD19, CD20, CD22, Kappa or light chain, CD30, CD33, CD123, CD38, ROR1, ErbB3/4, EGFR, EGFRvIII, EphA2, FAP, carcinoembryonic antigen, EGP2, EGP40, mesothelin, TAG72, PSMA, NKG2D ligands, B7-H6, IL-13 receptor α 2, IL-11 receptor α , MUC1, MUC16, CA9, GD2, GD3, HMW-MAA, CD171, Lewis Y, G250/CAIX, HLA-AI MAGE A1, HLA-A2 NY-ESO-1, PSC1, folate receptor- α , CD44v7/8, 8H9, NCAM, VEGF receptors, 5T4, Fetal AchR, NKG2D ligands, CD44v6, TEM1, or TEM8.
291. The modified cell of embodiment 289, wherein the intracellular domain comprising a co-stimulatory domain that comprises an intracellular domain of a costimulatory molecule selected from the group consisting of CD27, CD28, 4-1BB, OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, B7-H3, and any combination thereof.
292. The modified cell of embodiments 289, wherein the intracellular domain comprises a CD3 zeta signaling domain.

293. A method for improving infusion of cells or cells derived from the cells, the method comprising: culturing in a culture media the modified cells of the embodiments 246; and administering a subject a composition comprising the modified cells, wherein immune responses of the subject in response to the infusion is less than infusion using wild type cells.
294. The method of embodiments 293, wherein the infusion is an allogeneic infusion.
295. A modified human T cell comprising: a nucleic acid sequence encoding a CAR; a disruption of TCR gene; a disruption of MHC class II transactivator (CIITA) gene; and a disruption of Transporter associated with antigen presentation 1 (TAP1) gene or a disruption of TAP-associated glycoprotein (TAPBP) gene, wherein the modified human T cell has: a reduced amount of TCR, a reduced amount of MHC I, or a reduced amount of MHC II, as compared to human T cells without the disruption; or a reduced host-versus-graft disease (HVGD) response in a bioincompatible human recipient as compared to the HVGD response of the primary human T cell.
296. The modified cell of embodiments 295, wherein the CAR comprises an extracellular domain, a transmembrane domain, and an intracellular domain, and the extracellular domain binds a tumor antigen.
297. The modified cell of embodiments 296, wherein the tumor antigen includes HER2, CD19, CD20, CD22, Kappa or light chain, CD30, CD33, CD123, CD38, ROR1, ErbB3/4, EGFR, EGFRvIII, EphA2, FAP, carcinoembryonic antigen, EGP2, EGP40, mesothelin, TAG72, PSMA, NKG2D ligands, B7-H6, IL-13 receptor α 2, IL-11 receptor α , MUC1, MUC16, CA9, GD2, GD3, HMW-MAA, CD171, Lewis Y, G250/CAIX, HLA-AI MAGE A1, HLA-A2 NY-ESO-1, PSC1, folate receptor- α , CD44v7/8, 8H9, NCAM, VEGF receptors, 5T4, Fetal AchR, NKG2D ligands, CD44v6, TEM1, or TEM8.
298. The modified cell of embodiments 296, wherein the intracellular domain comprises a co-stimulatory domain that comprises an intracellular domain of a costimulatory molecule selected from the group consisting of CD27, CD28, 4-1BB, OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, B7-H3, and any combination thereof.
299. The modified cell of embodiments 296, wherein the intracellular domain comprises a CD3 zeta signaling domain.
300. A method of modifying a target genomic locus in a lymphocyte, the method comprising: introducing into the lymphocyte a nuclease agent that make a single or double-strand break within the target genomic locus; and selecting the lymphocyte of which endogenous B2M, CIITA, TAP1, and/or TAPBP genes are disrupted.
301. A genetically modified lymphocyte comprising a nuclease agent targeting endogenous B2M, CIITA, TAP1, and/or TAPBP genes.

302. The method or the genetically modified lymphocyte of any one of embodiments 300-301, wherein the nuclease agent is a zinc finger nuclease (ZFN), a Transcription Activator-Like Effector Nuclease (TALEN), or a meganuclease.
303. The method or the genetically modified lymphocyte of any one of embodiments 300-301, wherein the nuclease agent comprises a Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)-associated (Cas) protein and a guide RNA (gRNA).
304. The method of embodiments 303, wherein the Cas protein is Cas9.
305. The method or the genetically modified lymphocyte of any one of embodiments 300-301, wherein the nuclease agent comprising at least one of the amino acid sequence listed in Tables 9-10.
306. The method or the genetically modified lymphocyte of one of embodiments 300-301, wherein the nuclease agent comprises: one or more ZFNs targeting one or more exons of Transporter associated with antigen presentation 1 (TAP1) gene or a disruption of one or more exons of TAP-associated glycoprotein (TAPBP) gene, or an exon of TAP1 gene, or the isolated ZFN of any one of embodiments 1-4.
307. The genetically modified lymphocyte or the method of any one of embodiments 300-306, wherein the lymphocyte is NK cell or T cell.
308. The genetically modified lymphocyte or the method of any one of embodiments 300-306, wherein the genetically modified cell elicits a reduced graft versus host disease response against allogeneic cells as compared to a corresponding cell that does not include nucleic acid sequence.
309. The genetically modified lymphocyte or the method of any one of embodiments 300-306, wherein the lymphocyte is a T cell derived from a primary human T cell isolated from a human donor.
310. The genetically modified lymphocyte or the method of any one of embodiments 300-306, wherein the T cell comprises a CAR.
311. The genetically modified lymphocyte or the method of embodiment 310, wherein the CAR comprises an extracellular domain, a transmembrane domain, and an intracellular domain, and the extracellular domain binds a tumor antigen.
312. The genetically modified lymphocyte or the method of embodiment 311, wherein the tumor antigen includes HER2, CD19, CD20, CD22, Kappa or light chain, CD30, CD33, CD123, CD38, ROR1, ErbB3/4, EGFR, EGFRvIII, EphA2, FAP, carcinoembryonic antigen, EGP2, EGP40, mesothelin, TAG72, PSMA, NKG2D ligands, B7-H6, IL-13 receptor α 2, IL-11 receptor α , MUC1, MUC16, CA9, GD2, GD3, HMW-MAA, CD171, Lewis Y, G250/CAIX, HLA-AI MAGE A1, HLA-A2 NY-ESO-1, PSC1, folate receptor- α , CD44v7/8, 8H9, NCAM, VEGF receptors, 5T4, Fetal AchR, NKG2D ligands, CD44v6, TEM1, or TEM8.
313. The genetically modified lymphocyte or the method of embodiment 311, wherein the intracellular domain comprising a co-stimulatory domain that comprises an intracellular domain

of a costimulatory molecule selected from the group consisting of CD27, CD28, 4-1BB, OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, B7-H3, and any combination thereof.

314. The genetically modified lymphocyte or the method of embodiments 311, wherein the intracellular domain comprises a CD3 zeta signaling domain.

315. The genetically modified lymphocyte or the method of any one of embodiments 300-306, wherein the T cell comprises a modified T Cell Receptor (TCR).

316. The genetically modified lymphocyte or the method of 315, wherein the TCR is derived from spontaneously occurring tumor-specific T cells in patients.

317. The genetically modified lymphocyte or the method of 315, wherein the TCR binds a tumor antigen.

318. The genetically modified lymphocyte or the method of 317, wherein the tumor antigen comprises CEA, gp100, MART-1, p53, MAGE-A3, or NY-ESO-1.

319. The genetically modified lymphocyte or the method of 317, wherein the TCR comprises TCR γ and TCR δ Chains or TCR α and TCR β chains, or a combination thereof.

320. A method of causing a T- cell response in a subject or treating a tumor of the subject, the method comprising: administering an effective amount of the T cell of any one of embodiments 301-319.

321. A method of determining the efficacy of a CAR T cell therapy, wherein the method comprises administering the nucleic acid, the cells, the composition, the modified T cell, or the bispecific CAR of any one of embodiments 1-6, 14-43, 45, and 46 to a subject in need thereof and measuring the levels of cytokine release over a period of time after introducing the CAR T cell to a subject.

322. A method of monitoring the efficacy of a CAR T cell therapy, wherein the method comprises administering the nucleic acid, the cells, or the composition of any one of embodiments 1-6 and 14-27 to a subject in need thereof and measuring the levels of cytokine release over a period of time after introducing the CAR T cell to a subject.

323. The method of embodiment 321 or 322, wherein the method further comprises comparing the level of cytokine release with control subject and wherein the control subject comprises a subject that is not introduced with CAR T cell therapy or a subject that is administered with T cells comprising a single CAR molecule (e.g., anti-solid tumor CAR).

324. The method of any one of embodiments 321-323, wherein the cytokine is IL-6, IFN- γ , or a combination thereof.

325. The method of any one of embodiments 321-324, wherein the method comprises measuring cytokine release from day 0 (one day before introducing CAR T cell therapy) to day 10, to day 9, to day 8, to day 7, to day 6, to day 5, to day 4, to day 3, to day 2, or to day 1 of CAR T cell therapy.

326. The method of any one of embodiments 321-325, wherein the subject has thyroid cancer, cholangiocarcinoma, breast cancer, or pancreatic cancer.

327. The method of any one of embodiments 321-326, wherein the subject is a mammal.

328. The method of any one of embodiments 321-327, wherein the mammal is a human.

EXAMPLES

Example 1. Expression of CARs on T cells

[00204] Lentiviral vectors that encode a CD19 CAR (CAR: SEQ ID NO. 207 and scFv: SEQ ID NO. 6) and tumor associated MUC1 CAR (CAR: SEQ ID NO. 202 and scFv: SEQ ID NO. 70) were generated, as shown in FIG. 1 (see "Chimeric Receptors Containing CD137 Signal Transduction Domains Mediate Enhanced Survival of T Cells and Increased Antileukemic Efficacy *In Vivo*," Molecular Therapy, Aug. 2009, vol. 17 no. 8, 1453–1464 incorporated herein by reference in its entirety).

[00205] Primary T cells were obtained from patients. The obtained primary T cells were transduced with lentiviral vectors to obtain modified T cells. Flow-cytometry was performed and analyzed to confirm the expression of CARs in primary T cells (See FIG. 6). Techniques related to cell cultures, construction of lentiviral vectors, and flow cytometry may be found in "Control of large, established tumor xenografts with genetically retargeted human T cells containing CD28 and CD137 domains," PNAS, March 3, 2009, vol. 106 no. 9, 3360–3365, which is incorporated herein by reference in its entirety.

Example 2. IFN- γ release in co-cultivation assays

[00206] T cells were transfected with the lentiviral vectors encoding dual CARs (CD19 and TA-MUC1 CARs, see dual CARs in FIGS. 8 and 9) and lentiviral vectors encoding single CAR (TA-MUC1 CAR, see 5E5 CAR in FIGS. 8 and 9), respectively. Two types of T cells and different single type or multiple types of substrate cells were co-cultured and the release of IFN- γ was observed. Substrate cells include MUC1-positive tumor cells (MCF-7), MUC1-negative tumor cells (231), and CD19-positive tumor cells (RK19). A ratio of E:T (Effector Cell: Target Cell) 1:1/3:1/10:1/30:1 (i.e., CAR T cells: target tumor cells) of CAR T cells and target tumor cells were co-cultured for 24 hours. Subsequently, the supernatant was collected, and release of IFN- γ was measured. Various levels of IFN- γ release were observed when CAR T cells and the substrate cells were co-cultured (See FIG. 7). As further shown in FIGS. 8 and 9, dual CAR T cells released IFN- γ in response to co-culturing with CD19-positive tumor cells and MUC1-positive tumor cells, while single CAR T cells released little IFN- γ in response to co-culturing with CD19-positive tumor cells. Further, in response to co-culturing with CD19-positive tumor cells and MUC1-positive tumor cells, dual CAR T cells released a greater amount of IFN- γ as compared to single CAR T cells. Techniques related to cell cultures, construction of cytotoxic T-lymphocyte assay may be found in "Control of large, established tumor xenografts with

genetically retargeted human T cells containing CD28 and CD137 domains,” PNAS, March 3, 2009, vol. 106 no. 9, 3360–3365, which is incorporated herein by reference in its entirety.

Example 3. Expression of CAR/antigen on primary T cells

[00207] Primary T cells were obtained from a patient. The obtained primary T cells were divided into two groups. Primary T cells in Group 1 were transduced with lentiviral vectors including a nucleic acid sequence encoding Anti-TSHR CAR (SEQ ID: 8). Primary T cells in Group 2 were transduced with lentiviral vectors including a nucleic acid sequence encoding TSHR (SEQ ID: 20). Flow-cytometry was performed and analyzed to determine the expression of CAR and TSHR in primary T cells, respectively (FIGS. 8 and 9). Techniques related to cell cultures, construction of lentiviral vectors, and flow cytometry may be found in “Control of large, established tumor xenografts with genetically retargeted human T cells containing CD28 and CD137 domains,” PNAS March 3, 2009, vol. 106 no. 9, 3360–3365, which is incorporated herein by reference in its entirety.

Example 4. *In vivo* cytokine release assay

[00208] Primary T cells of Group 1 and Group 2 were infused into mice (Experimental Group). As a control, Primary T cells of Group 1 alone or buffer were infused into mice (Control Group 1 and Control Group 2). Several parameters regarding cell infusion are provided in Table 1 below. NPG™ (NOD Prkdc^{scid} IL2rg^{null}) mice were irradiated, and a certain number of CAR T cells and corresponding control agents were infused into mice. For Control Group 2, three consecutive buffers were returned to the mice. For Control Group 1, T cells that did not express antigen were returned three times in succession. For Experimental Group, T cells expressing antigens were continuously transfused three times in succession. After the transfusion was completed, blood from the limb vein was collected to analyze the T cells and factor release (e.g., cytokine release) in the peripheral blood of the mice. The mice were then sacrificed, and T ratios of each organ/CAR T Cell ratio / CAR T copy and other data were collected. Cytokine release assay was then performed. Various cytokines (e.g., IFN-γ, IL4, IL2) in mice peripheral blood were measured for Experimental Group and Control Group. As shown in FIGS. 10-13, the amount of cytokine released in the Experimental Group was greater than those in the Control Group. These results demonstrate that infusion of cells expressing an antigen enhances the corresponding CAR T cells' T cell response. Table 2 summarizes the infusion of T cells into mice, and Table 3 provides the schedule for *in vivo* analysis cytokine release.

Table 2

Experimental Group	Control Group 1	Control Group 2
Anti-TSHR CAR T cells about 4 x 10 ⁶ /mouse	Anti-TSHR CAR T cells about 4 x 10 ⁶ /mouse	Anti-TSHR CAR T cells about 4 x 10 ⁶ /mouse
Antigen T (TSHR-overexpressed T cell) about 4 x 10 ⁶ /mouse per time	NT (non-transduced T cell) about 4 x 10 ⁶ /mouse per time	NT (non-transduced T cell) about 4 x 10 ⁶ /mouse per time

Table 3

Day 1	Day 3	Day 5	Day 9	Day 12	Day 14	Day 21	Day 28
irradiation at 1.5 Gy	anti-TSHR CAR T cells infusion	buffers/nt/antigen T infusion	buffers/nt/antigen T infusion	buffers/nt/antigen T infusion	bleeding and analysis	bleeding and analysis	sacrifice and analysis

[00209] The following table (Table 4) shows various polypeptide domains and nucleic acid constructs and their Sequence Identifiers (SEQ ID NO). (CD19 refers to CD19 CAR; MUC1 refers to tMUC1 CAR; A, B, C, and D refer to specific sequences of hinge and/or transmembrane domain of corresponding CARs)

Table 4

Name	SEQ ID NO	Name	SEQ ID NO	Name	SEQ ID No
SP	1	UPK2	101	Construct of MUC1-5E5-A-IRES-CD19-A	201
Hinge & transmembrane domain	2	ADAM12	102	CAR 1 of MUC1-5E5-A-IRES-CD19-A	202
Co-stimulatory domain	3	SLC45A3	103	CAR 2 of MUC1-5E5-A-IRES-CD19-A	203
CD3-zeta	4	ACPP	104	Construct of MUC1-5E5-B-IRES-CD19-A	204
scFV Humanized CD19	5	MUC21	105	CAR 1 of MUC1-5E5-B-IRES-CD19-A	205
scFV CD19	6	MUC16	106	CAR 2 of MUC1-5E5-B-IRES-CD19-A	203
scFv FZD10	7	MS4A12	107	Construct of MUC1-5E5-A-IRES-CD19-B	206

Name	SEQ ID NO	Name	SEQ ID NO	Name	SEQ ID No
scFv TSHR	8	ALPP	108	CAR 1 of MUC1-5E5-A-IRES-CD19-B	202
scFv PRLR	9	SLC2A14	109	CAR 2 of MUC1-5E5-A-IRES-CD19-B	207
scFv Muc 17	10	GS1-259H13.2	110	Construct of MUC1-5E5-B-IRES-CD19-B	208
scFv GUCY2C	11	ERVFRD-1	111	CAR 1 of MUC1-5E5-B-IRES-CD19-B	205
scFv CD207	12	ADGRG2	112	CAR 2 of MUC1-5E5-B-IRES-CD19-B	207
Prolactin (ligand)	13	ECEL1	113	Construct of MUC1-2-A-IRES-CD19-A	209
scFv CD3	14	CHRNA2	114	CAR 1 of MUC1-2-A-IRES-CD19-A	210
scFv CD4	15	GP2	115	CAR 2 of MUC1-2-A-IRES-CD19-A	203
scFv CD4-2	16	PSG9	116	Construct of MUC1-2-B-IRES-CD19-A	211
scFv CD5	17	SIGLEC15	117	CAR 1 of MUC1-2-B-IRES-CD19-A	212
CD19 antigen	18	SLC6A3	118	CAR 2 of MUC1-2-B-IRES-CD19-A	203
FZD10 antigen	19	KISS1R	119	Construct of MUC1-2-A-IRES-CD19-B	213
TSHR antigen	20	QRFPR	120	CAR 1 of MUC1-2-A-IRES-CD19-B	210
PRLR antigen	21	GPR119	121	CAR 2 of MUC1-2-A-IRES-CD19-B	207
Muc 17 antigen	22	CLDN6	122	Construct of MUC1-2-B-IRES-CD19-B	214
GUCY2C antigen	23	SP-2	123	CAR 1 of MUC1-2-B-IRES-CD19-B	212
CD207 antigen	24	Linker-2	124	CAR 2 of MUC1-2-B-IRES-CD19-B	207
CD3 antigen	25	Hinge-2	125	Construct of MUC1-5E5-A-IRES-hCD19-A	215
CD4 antigen	26	TM-2	126	CAR 1 of MUC1-5E5-A-IRES-hCD19-A	202
CD5 antigen	27	4-1BB-2	127	CAR 2 of MUC1-5E5-A-IRES-hCD19-A	216

Name	SEQ ID NO	Name	SEQ ID NO	Name	SEQ ID No
CAR CD19 nucleic acid	28	CD3 zeta-2	128	Construct of MUC1-5E5-B-IRES-hCD19-A	217
Hinge & TM domain B	29	CLDN6-CAR-1	129	CAR 1 of MUC1-5E5-B-IRES-hCD19-A	205
Hinge & TM domain A	30	ScFv CLDN6-CAR-1	130	CAR 2 of MUC1-5E5-B-IRES-hCD19-A	216
Hinge & TM domain D	31	ScFv VL CLDN6-CAR-1	131	Construct of MUC1-5E5-A-IRES-hCD19-B	218
Hinge & TM domain C	32	ScFv VH CLDN6-CAR-1	132	CAR 1 of MUC1-5E5-A-IRES-hCD19-B	202
Hinge domain D	33	CLDN6-CAR-2	133	CAR 2 of MUC1-5E5-A-IRES-hCD19-B	219
Hinge domain C	34	ScFv CLDN6-CAR-2	134	Construct of MUC1-5E5-B-IRES-hCD19-B	220
Hinge domain B	35	ScFv VL CLDN6-CAR-2	135	CAR 1 of MUC1-5E5-B-IRES-hCD19-B	205
Hinge domain A	36	ScFv VH CLDN6-CAR-2	136	CAR 2 of MUC1-5E5-B-IRES-hCD19-B	219
TM domain D	37	CLDN6-CAR-3	137	Construct of MUC1-2-A-IRES-hCD19-A	221
TM domain A	38	scFv CLDN6-CAR-3	138	CAR 1 of MUC1-2-A-IRES-hCD19-A	210
CD19 extracellular domain	39	scFv VL CLDN6-CAR-3	139	CAR 2 of MUC1-2-A-IRES-hCD19-A	216
TM domain C or B	40	scFv VH CLDN6-CAR-3	140	Construct of MUC1-2-B-IRES-hCD19-A	222
WTCD3zeta	41	CLDN6-CAR-4	141	CAR 2 CAR 1 of MUC1-2-B-IRES-hCD19-A	212
WTCD3zeta-BCMACAR full length	42	scFv CLDN6-CAR-4	142	Construct of MUC1-2-B-IRES-hCD19-A	216
BCMA	43	scFv VL CLDN6-CAR-4	143	Construct of MUC1-2-A-IRES-hCD19-B	223
BCMA CAR vector	44	scFv VH CLDN6-CAR-4	144	CAR 1 of MUC1-2-A-IRES-hCD19-B	210
BCMA CAR vector	45	SIGLEC-15-CAR-1	145	CAR 2 of MUC1-2-A-IRES-hCD19-B	219
VL anti-CD5	46	scFv SIGLEC-15-CAR-1	146	Construct of MUC1-2-B-IRES-hCD19-B	224

Name	SEQ ID NO	Name	SEQ ID NO	Name	SEQ ID NO
VH anti-CD5	47	scFv VL SIGLEC-15-CAR-1	147	CAR 1 of MUC1-2-B-IRES-hCD19-B	212
VL anti-CD4	48	scFv VH SIGLEC-15-CAR-1	148	CAR 2 of MUC1-2-B-IRES-hCD19-B	219
VH anti-CD4	49	VL1 VH1 SIGLEC-15-CAR-2	149	Construct of MUC1-5E5-A-IRES-CD22-A	225
VL anti-CD3	50	VL1 VH2 SIGLEC-15-CAR-3	150	CAR 1 of MUC1-5E5-A-IRES-CD22-A	202
VH anti-CD3	51	VL1 VH3 SIGLEC-15-CAR-4	151	CAR 2 of MUC1-5E5-A-IRES-CD22-A	226
TSHR extracellular domain	52	VL1 VH 4 SIGLEC-15-CAR-5	52	Construct of MUC1-5E5-B-IRES-CD22-A	227
VH region of BCMA scFv	53	VL2 VH 1 SIGLEC-15-CAR-6	153	CAR 1 of MUC1-5E5-A-IRES-CD22-A	205
VL region of BCMA scFv	54	VL2 VH2 SIGLEC-15-CAR-7	154	CAR 2 of MUC1-5E5-A-IRES-CD22-A	226
VH region of CD14 scFv	55	VL2 VH3 SIGLEC-15-CAR-8	155	Construct of MUC1-5E5-A-IRES-CD22-B	228
VL region of CD14 scFv	56	VL2 VH4 SIGLEC-15-CAR-9	156	MUC1-5E5-A-IRES-CD22-B CAR 1	202
VH region of CD33 scFv	57	VL1 SIGLEC-15-CAR	157	MUC1-5E5-A-IRES-CD22-B CAR 2	229
VL region of CD33 scFv	58	VL2 SIGLEC-15-CAR	158	MUC1-5E5-B-IRES-CD22-B	230
CD22CAR	59	VH1 SIGLEC-15-CAR	159	CAR 1 of MUC1-5E5-B-IRES-CD22-B	205
BCMACAR	60	VH2 SIGLEC-15-CAR	160	CAR 2 of MUC1-5E5-B-IRES-CD22-B	229
MUC1CAR	61	VH3 SIGLEC-15-CAR	161	Construct of MUC1-2-A-IRES-CD22-A	231
m19CAR-IRES-MUC1CAR	62	VH4 SIGLEC-15-CAR	162	CAR 1 of MUC1-2-A-IRES-CD22-A	210
hCD19CAR-IRES-MUC1CAR	63	MUC16-CAR-1	163	CAR 2 of MUC1-2-A-IRES-CD22-A	226
hCD22CAR-IRES-MUC1CAR	64	scFv MUC16-CAR-1	164	MUC1-2-B-IRES-CD22-A	232
BCMACAR-IRES-MUC1CAR	65	scFv VL MUC16-CAR-1	165	MUC1-2-B-IRES-CD22-A CAR 1	212
mCD19CAR-2A-MUC1CAR	66	scFv VH MUC16-CAR-1	166	MUC1-2-B-IRES-CD22-A CAR 2	226

Name	SEQ ID NO	Name	SEQ ID NO	Name	SEQ ID NO
hCD19CAR-2A-MUC1CAR	67	MUC16-CAR-2	167	MUC1-2-A-IRES-CD22-B	233
hCD22CAR-2A-MUC1CAR	68	scFv MUC16-CAR-2	168	MUC1-2-A-IRES-CD22-B CAR 1	210
BCMA-2A-MUC1CAR	69	scFv VL MUC16-CAR-2	169	MUC1-2-A-IRES-CD22-B CAR 2	229
Tumor associated MUC1 scFv 1	70	scFv VH MUC16-CAR-2	170	Construct of MUC1-2-B-IRES-CD22-B	234
Tumor associated MUC1 scFv-1 VH	71	KISS1R-CAR	171	CAR 1 of MUC1-2-B-IRES-CD22-B	212
Tumor associated MUC1 scFv-1 VL	72	Ligand peptide KISS1R-CAR	172	CAR 2 of MUC1-2-B-IRES-CD22-B	229
Tumor associated MUC1 scFv-1 VL CDR 1	73	ZFLm1 (left) RS aa	173	Construct of MUC1-5E5-A-IRES-CD14-A	235
L2D8-2 (hCAR VL)	74	ZFLm1 (left) F1	174	CAR 1 of MUC1-5E5-A-IRES-CD14-A	202
Tumor associated MUC1 scFv-1 VL CDR 3	75	ZFLm1 (left) F2	174	CAR 2 of MUC1-5E5-A-IRES-CD14-A	236
Tumor associated MUC1 scFv-1 VH CDR 1	76	ZFLm1 (left) F3	176	Construct of MUC1-5E5-B-IRES-CD14-A	237
Tumor associated MUC1 scFv-1 VH CDR 2	77	ZFLm1 (left) F4	177	CAR 1 of MUC1-5E5-B-IRES-CD14-A	205
Tumor associated MUC1 scFv-1 VH CDR 3	78	ZFLm1 (left) F5	178	CAR 2 of MUC1-5E5-B-IRES-CD14-A	236
Tumor associated MUC1 scFv 2	79	ZFLm1 (left) F6	179	Construct of MUC1-5E5-A-IRES-CD14-B	238
Tumor associated MUC1 scFv2 VH	80	ZFRm1-4 (right) RS aa	180	CAR 1 of MUC1-5E5-A-IRES-CD14-B	202
Tumor associated MUC1 scFv2 VL	81	ZFRm1-4 (right) F1	181	CAR 2 of MUC1-5E5-A-IRES-CD14-B	239
Tumor associated MUC1 scFv-2 VL CDR 1	82	ZFRm1-4 (right) F2	182	Construct of MUC1-2-A-IRES-CD14-A	240
Tumor associated MUC1 scFv-2 VL CDR 2	83	ZFRm1-4 (right) F3	184	CAR 1 of MUC1-2-A-IRES-CD14-A	210
Tumor associated MUC1 scFv-2 VL CDR 3	84	ZFRm1-4 (right) F4	184	CAR 2 of MUC1-2-A-IRES-CD14-A	236
Tumor associated MUC1 scFv-2VH CDR 1	85	δ chain-1 of Vγ9Vδ2	185	Construct of MUC1-2-B-IRES-CD14-A	241

Name	SEQ ID NO	Name	SEQ ID NO	Name	SEQ ID No
Tumor associated MUC1 scFv-2 VH CDR 2	86	γ chain-2 of V γ 9V δ 2	186	CAR 1 of MUC1-2-B-IRES-CD14-A	212
Tumor associated MUC1 scFv-2 VH CDR 3	87	δ chain-2 of V γ 9V δ 2	187	CAR 2 of MUC1-2-B-IRES-CD14-A	236
GSTA motif	88	V γ 9V δ 2 TCR-1 : DG. SF13 γ chain	188	Construct of MUC1-2-A-IRES-CD14-B	242
Modified intracellular domain -1	PD-1 89	V γ 9V δ 2 TCR-1 : DG. SF13 δ chain	189	CAR 1 of MUC1-2-A-IRES-CD14-B	210
Modified intracellular domain -2	PD-1 90	V γ 9V δ 2 TCR-2: DG. SF68: γ chain	190	CAR 2 of MUC1-2-A-IRES-CD14-B	239
Modified intracellular domain -3	PD-1 91	V γ 9V δ 2 TCR-2 : DG. SF68 : δ chain	191	Construct of MUC1-2-B-IRES-CD14-B	243
Modified intracellular domain -4	PD-1 92	V γ 9V δ 2 TCR-3: 12G12: γ chain	192	CAR 1 of MUC1-2-B-IRES-CD14-B	212
Modified intracellular domain -5	PD-1 93	V γ 9V δ 2 TCR-3: 12G12: δ chain	193	CAR 2 of MUC1-2-B-IRES-CD14-B	239
Removed intracellular domain -1	PD-1 94	V γ 9V δ 2 TCR-4: CP.1.15 γ chain	194	Construct of MUC1-5E5-A-IRES-BCMA-A	244
Removed intracellular domain -2	PD-1 95	TCR-4: CP.1.15 δ chain	195	CAR 1 of MUC1-5E5-A-IRES-BCMA-A	202
FokI WC	96	WT CD3-zeta	196	CAR 2 of MUC1-5E5-A-IRES-BCMA-A	245
M FokI	97	Invariant sequence for iNKT α chain (hV α 24-J α Q-TRAC)	197	Construct of MUC1-5E5-B-IRES-BCMA-A	246
M FokI	98	An example for iNKT β chain sequence (containing V β 11):	198	CAR 1 of MUC1-5E5-B-IRES-BCMA-A	205
γ chain-1 of V γ 9V δ 2	99	Invariant sequence for MAIT α chain (hAV7S2-AJ33 α chain) (version1)	199	CAR 2 of MUC1-5E5-B-IRES-BCMA-A	245
VL anti-CD4-2	100	VH anti- CD4-2	200	Construct of MUC1-5E5-A-IRES-BCMA-B	247

Name	SEQ ID NO	Name	SEQ ID NO	Name	SEQ ID No
CAR 1 of MUC1-2-A-IRES-CD33-A	210	CAR 1 of MUC1-5E5-B-IRES-CD33-A	205	CAR 1 of MUC1-5E5-A-IRES-BCMA-B	202
CAR 2 of MUC1-2-A-IRES-CD33-A	255	CAR 2 of MUC1-5E5-B-IRES-CD33-A	255	CAR 2 of MUC1-5E5-A-IRES-BCMA-B	248
Construct of MUC1-2-B-IRES-CD33-A	261	Construct of MUC1-5E5-A-IRES-CD33-B	257	Construct of MUC1-5E5-B-IRES-BCMA-B	249
CAR 1 of MUC1-2-B-IRES-CD33-A	212	CAR 1 of MUC1-5E5-A-IRES-CD33-B	202	CAR 1 of MUC1-5E5-B-IRES-BCMA-B	
CAR 2 of MUC1-2-B-IRES-CD33-A	255	CAR 2 of MUC1-5E5-A-IRES-CD33-B	258	CAR 2 of MUC1-5E5-B-IRES-BCMA-B	
Construct of MUC1-2-A-IRES-CD33-B	262	Construct of MUC1-5E5-B-IRES-CD33-B	259	Construct of MUC1-2-A-IRES-BCMA-A	250
CAR 1 of MUC1-2-A-IRES-CD33-B	210	CAR 1 of MUC1-5E5-B-IRES-CD33-B	205	CAR 1 of MUC1-2-A-IRES-BCMA-A	210
CAR 2 of MUC1-2-A-IRES-CD33-B	258	CAR 2 of MUC1-5E5-B-IRES-CD33-B	258	CAR 2 of MUC1-2-A-IRES-BCMA-A	245
Construct of MUC1-2-B-IRES-CD33-B	263	Construct of MUC1-2-A-IRES-CD33-A	260	Construct of MUC1-2-B-IRES-BCMA-A	251
CAR 1 of MUC1-2-B-IRES-CD33-B	212	Construct of MUC1-2-B-IRES-BCMA-B	253	CAR 1 of MUC1-2-B-IRES-BCMA-A	212
CAR 2 of MUC1-2-B-IRES-CD33-B	258	CAR 1 of MUC1-2-B-IRES-BCMA-B	212	CAR 2 of MUC1-2-B-IRES-BCMA-A	245
Construct of MUC1-5E5-A-IRES-CD33-A	254	MUC1-2-B-IRES-BCMA-B CAR 2	248	Construct of MUC1-2-A-IRES-BCMA-B	252
CAR 1 of MUC1-5E5-A-IRES-CD33-A	202	MUC1-5E5-B-IRES-CD33-A	256	CAR 1 of MUC1-2-A-IRES-BCMA-B	210
CAR 2 of MUC1-5E5-A-IRES-CD33-A	255	CAR 2 of MUC1-2-A-IRES-BCMA-B	248	Mcu1-5e5Panko-enhanced scFc	264
Mcu1-Panko5e5 – enhanced scFc	265	hinge and/or transmembrane domain A	266	hinge and/or transmembrane domain B	267
hinge and/or transmembrane domain C	268	hinge and/or transmembrane domain D	269	Mcu1-5e5Panko-enhanced scFc A 41BB CD2 zeta	270
Mcu1-5e5Panko-enhanced scFc B 41BB CD2 zeta	271	Mcu1-5e5Panko-enhanced scFc C 41BB CD2 zeta	272	Mcu1-5e5Panko-enhanced scFc D 41BB CD2 zeta	273
Mcu1-Panko5e5-enhanced	274	Mcu1-Panko5e5-enhanced	275	Mcu1-Panko5e5-enhanced	276

Name	SEQ ID NO	Name	SEQ ID NO	Name	SEQ ID NO
scFc A 41BB CD2 zeta		scFc B 41BB CD2 zeta		scFc C 41BB CD2 zeta	
Mcu1-Panko5e5-enhanced scFc D 41BB CD2 zeta	277	GS linker	278	Construct of TSHR CAR	279
M <i>FokI</i> -1	280	M <i>FokI</i> -2	281	<i>FokI</i> WC	282
PSCA-CAR ScFv	356				

Example 5. *In Vivo* Cell Expansion

[00210] These clinical studies were designed to assess the safety and efficacy of infusing autologous T cells modified to express several solid tumor markers specific CAR/4-1BB/CD3- ζ into patients. On the first arm of the studies, patients received solid tumor marker-specific CAR T cells only. The solid tumor marker included TSHR and tMuc1. On the second arm, patients received CAR T cells directed to CD19 and tMuc1. T cells of the patients were obtained, modified, and infused to the patients. T cell responses of patients from the first and second arms were measured and compared using the following protocols, which were approved by the hospitals where the trials were conducted. All patients were provided with written informed consent.

[00211] Lentiviruses were produced by transfecting 293T cells with TSHR-4-1BB vectors, tMuc1-4-1BB vector, CARtMuc1/CAR19-4-1BB vectors, and viral packaging plasmids, which were frozen in -80 °C, were thawed immediately before transduction. The lentivirus supernatant was harvested. CD3+ T cells were isolated and activated as described (see Kalos M. et al, *Sci Transl Med* 2011;3:95ra73). The CD3+ T cells were then cultured in X-VIVO 15 medium (Lonza) containing 100 U/ml interleukin-2 (IL-2) and transduced with the lentivirus supernatant at high multiplicity of infection (MOI) from 5:1 to 10:1 within 24-48 hours. The CAR transduced T cells (TSHR-CAR T cell, tMuc1-CAR T cell, or tMuc1-CAR/CD19-CAR T cell, hereafter “dual CAR T cells”) were cultured for about 11 days. Three days before administration, fresh culture media were replaced. After that, the cells were not manipulated until transportation for infusion. The transduction efficiency was evaluated by flow cytometry (FACS) on days 5-7 after lentivirus transduction. The following anti-human antibodies were used: anti-hCD45 APC (BD Bioscience), anti-hCD3 FITC (BD Bioscience), biotin-labeled goat-anti-mouse IgG specific for F(ab')₂ fragment (Jackson immuno-Research, Cat# 115-065-072) and PE streptavidin (BD Bioscience). Data acquisition was performed using a CytoFLEX flow cytometer (Beckman).

[00212] Prior to CAR T cell infusion, FACS analysis of transduction efficiency and *in vitro* cytotoxicity assays of CAR T cells were performed for each patient as described in this Example and Examples 1 and 2. Additionally, CAR T cell cultures were checked twice for possible contaminations by fungus, bacteria, mycoplasma, chlamydia, and endotoxin.

[00213] Peripheral blood mononuclear cells (PBMCs) were obtained from patients by leukapheresis for CAR T cell preparation on day 8, and the first day of CAR T infusion was set as study day 0. Patients were given a conditioning treatment for lymphodepletion. Fludarabine- and cyclophosphamide-based conditioning treatment varied according to the tumor burden in the bone marrow (BM) and peripheral blood (PB). CAR T cells were transfused to patients. Each day CAR T cells were transported to hospital, washed, counted, checked for viability and then prepared for administration to patients, who were then observed closely for at least 2 hours. CRS was graded according to a revised grading system (See Lee DW. et al, Blood 2014;124:188-95). Other toxicities during and after therapy were assessed according to the National Institutes of Health Common Terminology Criteria for Adverse Events Version 4.0 (<http://ctep.cancer.gov/>). Therapy responses were assessed by flow cytometry and morphological analysis. When possible, patients were assessed by chimeric gene expression levels. The response type was defined as minimal residual disease (MRD) negative, complete response, complete response with incomplete count recovery, stable disease, and progressive disease.

[00214] Serial BM and PB samples after CAR T cell infusion were collected in K2EDTA BD vacutainer tubes (BD). The persistence of CAR19 T cells from fresh PB and BM in patients was determined by FACS. Circulating CAR T cell numbers per μl were calculated on the basis of measured absolute CD3+ T lymphocyte counts. Simultaneously, CAR DNA copies were evaluated as another method of determining CAR T cell expansion and persistence. Genomic DNA was extracted using a QIAamp DNA Blood Mini Kit (Qiagen) from cryopreserved PB and BM. CAR DNA copies were assessed by quantitative real-time PCR as described in the supplementary materials. The levels of cytokines IFN- γ , TNF- α , IL-4, IL-6, IL-10, IL-17, etc. in serum and CSF were measured in a multiplex format according to the manufacturer's instructions.

[00215] Genomic DNA was extracted using a QIAamp DNA Blood Mini Kit (Qiagen) from cryopreserved peripheral blood and bone marrow. Quantitative PCR (qPCR) was performed in real-time in triplicates using the ABI 2 \times TaqMan Universal Master Mix with AmpErase UNG (Applied Biosystems) in a 7500 real-time PCR system (Applied Biosystems). Copy numbers per microgram of genomic DNA were calculated from a standard curve of 10-fold serial dilutions of purified CAR plasmid containing 102-108 copies/ μL . Amplification of an internal control gene was used for normalization of DNA quantities. Primers/probes specific for the CAR19 transgene and an internal control gene were as previously described (see Gökbuğet N. et al., Blood 2012;120:2032-41 and O'Brien S. et al, J Clin Oncol 2013;31:676-83).

[00216] CAR T cell expansion and cytokine release of these patients are shown in FIGS. 16-20 and 49-52. These results demonstrate that T cells expressing CD19 CAR and tumor marker specific CAR expanded more and released more cytokines (e.g., IL-6 and IFN- γ) than T cells

expressing only the tumor maker specific CAR. Information regarding the patients and their corresponding T cells are provided below in Table 5.

Table 5

Patient ID	Cancer type	solid tumor antigen	CAR binding solid tumor antigen SEQ ID	B cell antigen	CAR binding B cell Antigen SEQ ID	Vector SEQ ID	Infusion (date dosage)
A	Thyroid cancer	TSHR	8	N/A	N/A	280	1st: 1.08×10^5 /kg
B	Cholangiocarcinoma	tMuc1	70	N/A	N/A	61	1st: 1.01×10^7 /kg
C	Pancreatic cancer	tMuc1	70	N/A	N/A	61	1st: 1.27×10^6 /kg 2nd : 71Days after the 1st: (1.29×10^7 /Kg)
D	Breast Cancer	tMuc1	70	N/A	N/A	61	1st Date: 1×10^5 /kg 2nd : 24Days after the 1st: (1.24×10^6 /Kg) 3rd : 37 days after the 2nd: 9.65×10^6
E	Breast cancer	tMuc1	70	CD19	5	201	1st: 1.15×10^5 /kg
F	Pancreatic cancer	tMuc1	70	CD19	5	201	1st: 1.15×10^6 /kg

[00217] FIGS. 51-52 show an elevated release of cytokines IL-6 and IFN- γ in patient F administered with a first CAR and a second CAR and compared with patient C administered with only one CAR. The elevated release of cytokines IL-6 and IFN- γ confirms the efficacy of the CAR T cell therapy using a first and a second CAR molecule, each CAR molecule binds a different antigen.

Example 6. Design of ZFNs I

[00218] Multiple gene-specific ZFNs were constructed to enable the site specific introduction of mutations at these genes. Various ZFNs were designed and incorporated into plasmid vectors essentially as described in Mala et al. (2005) *Biochem Biophys Res Commun* 335(2):447-57, Liu et al. (2002) *J Bio Chem* 277(6):3850-6, Sander et al. (2011) *Nat Methods*. 8(1):67-9, Urnov et al. (2005) *Nature* 435(7042):646-651, and U.S. Patent Publication 2008/0131962. The ZFNs included various combinations of Zinc finger binding domains (e.g., ZFN-left and ZFN-right binding domains), which are listed in Table 6 and Table 7. The cleavage domain of the ZFNs comprised an engineered FokI cleavage domain (SEQ ID NOS.: 280, 281, or 282).

Table 6: Exemplary ZFN pairs as well as the target sequences (Target site: the target sequence for ZFN include two 9-bp recognition sites (i.e., upper case letters) are separated by a 6-bp spacer)

Gene Name	ICT ZFN Number	ZFN	Finger 1	SEQ ID NO:	Finger 2	SEQ ID NO:	Finger 3	SEQ ID NO:	Target site	SEQ ID NO:
CTLA4	ICTZF1 L	ZFN-L	QSGSL TR	301	DRSDL TR	302	QSSAL TR	303	TGCGGCA ACctacatGA	304
	ICTZF1 R	ZFN-R	QRSNL VR	305	RSDHL TR	306	TSANL SR	307	TGGGGAA	
LAG3	ICTZF2 L	ZFN-L	QSSDL TR	308	RSDNL AR	309	QSGH LQR	310	AGCCTCTC CagccaGG	311
	ICTZF2 R	ZFN-R	RSDNL AR	309	QSSDL TR	308	RSDHL SR	312	GGCTGAG	
LAG3	ICTZF3 L	ZFN-L	RSDHL AR	313	QSGD LTR	314	RSDDL TR	315	CCCTGCC GCctgcctGC	319
	ICTZF3 R	ZFN-R	RSDAL TR	316	TSGHL VR	317	QSSDL QR	318	TGGTGTG	
BTLA	ICTZF4 L	ZFN-L	GGTAL RM	320	QRSSL VR	321	QRNN LGR	322	GTTTACTT CcttggGGG	326
	ICTZF4 R	ZFN-R	RKRNL IM	323	VRHNL TR	324	RGDKL GP	325	GATTGC	
TIM3	ICTZF5 L	ZFN-L	SRFTL GR	327	RREHL VR	328	QTATL KR	329	CACCCCTG CaccgacTC	333
	ICTZF5 R	ZFN-R	KHSNL AR	330	QSTTL KR	331	RADGL QL	332	GGCAGAG	
TIM3	ICTZF6 L	ZFN-L	TRQKL ET	334	RQDN LGR	335	QQHG LRH	336	ACCCTCAC AaccttTGG	340
	ICTZF6 R	ZFN-R	TKKILT V	337	HKSSL TR	338	RSDHL SL	339	GTTGTC	
FOXP3	ICTZF7 L	ZFN-L	RKHHL GR	341	RREHL VR	28	VSNSL AR	342	CCCCCA GCaccttTC	346
	ICTZF7 R	ZFN-R	RTSSL KR	343	QRSDL TR	344	RSDGL RG	345	GGCTGTG	
FOXP3	ICTZF8 L	ZFN-L	DSPTL RR	347	QSAHL KR	348	QDVSL VR	349	GGCTCCT GCtgcacGT	352
	ICTZF8 R	ZFN-R	MKNTL TR	350	QRSDL TR	344	QSGTL TR	351	AGCTGCT	
SIVA1	ICTZF9 L	ZFN-L	TKQIL GR	353	QSTTL KR	331	RTEHL AR	354	AGCTGCC CCttcgcgGA	296
	ICTZF9 R	ZFN-R	KRRDL DR	355	RREVL EN	300	DPSNL RR	299	CGTGGCC	
LGALS9	ICTZF1 OL	ZFN-L	MKHH LDA	298	VRHNL TR	324	HHNSL TR	297	ACCATCAA CagactgGA	293
	ICTZF1 OR	ZFN-R	KKDHL HR	295	RREVL EN	300	QTVNL DR	294	AGTGGGG	
CD33	ICTZF1 1L	ZFN-L	QSGSL TR	301	RSDDL QR	292	RSDHL SR	312	TGCCGCC CCtactgtGG	289
	ICTZF1 1R	ZFN-R	QSGH LAR	291	TSGNL VR	290	QSGH LQR	310	AGATGGA	
SIVA1	ICTZF1 2L	ZFN-L	QSSDL TR	308	QSGD LTR	314	RSDHL SR	312	AGCTGCC CCttcgcgGA	285
	ICTZF1 2R	ZFN-R	ERGTL AR	288	RSDAL SR	287	DRSNL TR	286	CGTGGCC	

FOXP3	ICTZF1 3L	ZFN-L	ERGT LAR	288	QSGH LQR	310	QSGD LTR	314	GGCTCCT GctgcatcGT	283
	ICTZF1 3R	ZFN-R	QSSDL TR	308	QSSDL TR	308	QRASL TR	284	AGCTGCT	

Example 7. ZFN Activity In Vitro I

[00219] ZFN-left arm plasmid vectors and ZFN-right arm plasmid vectors were transfected into HeLa cells using fugene transfection reagent, respectively. After transfection of 24 hours, HeLa cells were treated with 1 µg / ml puromycin for 48 hours to obtain cells rich in ZFNs. The HeLa cells were then collected, and lysed DNA fragment containing ZFNs were amplified by PCR using primers specific to various gene (i.e., CTLA4, LAG3, BTLA, TIM3, FOXP3, SIVA1, or LGALS9) and the genome of HeLa cells as templates. The DNA fragments were sequenced using forward primers, and the sequencing results are shown in Fig. 21-25.

[00220] The DNA fragments were cloned into vectors. The DNA fragments of about 30 monoclonal cells were sequenced to determine whether the DNA fragments include mutations. The results of the sequencing were shown in Table 7.

Table 7: Monoclonal sequencing results for ZFNs that target genes fragments and are amplified by PCR

ZFN		Number of clones analyzed	Number of clones mutated	Mutation frequency
Left	Right			
ICTZF1L	ICTZF1R	31	6	19%
ICTZF2L	ICTZF2R	26	3	12%
ICTZF3L	ICTZF3R	30	9	30%
ICTZF4L	ICTZF4R	30	4	13%
ICTZF5L	ICTZF5R	29	1	3%
ICTZF6L	ICTZF6R	30	4	13%
ICTZF7L	ICTZF7R	29	5	17%
ICTZF8L	ICTZF8R	33	7	21%
ICTZF9L	ICTZF9R	34	10	29%
ICTZF10L	ICTZF10R	27	2	7%
ICTZF11L	ICTZF11R	34	14	41%
ICTZF12L	ICTZF12R	24	3	13%
ICTZF13L	ICTZF13R	21	5	24%

Example 8. Design of ZFNs II

[00221] Multiple gene-specific ZFNs were constructed to enable the site-specific introduction of mutations in these genes. Various ZFNs were designed and incorporated into plasmid vectors essentially as described in Mala et al. (2005) *Biochem Biophys Res Commun* 335(2):447-57, Liu et al. (2002) *J Bio Chem* 277(6):3850-6, Sander et al. (2011) *Nat Methods*. 8(1):67-9, Handel et al. (2009) *Mol Ther. Jan*;17(1):104-11, Urnov et al. (2005) *Nature* 435(7042):646-651, and U.S. Patent Publication 2008/0131962. The ZFNs included various combinations of Zinc finger binding domains (e.g., ZFN-left and ZFN-right binding domains), which are listed in Table 8. The cleavage domain of the ZFNs comprised an engineered FokI cleavage domain (SEQ ID NOS.: 96, 97, or 98).

[00222] Table 8: Exemplary ZFN pairs as well as the target sequences (Target site: the target sequence for ZFN include two 9-bp recognition sites (i.e., uppercase letters) are separated by a 6-bp spacer).

Gene Name	ICT ZFN #	ZFN	Finger 1	Finger 2	Finger 3	Target site	Linker between ZFP and Fok1
B2M	ICTZ F14L	ZFN-L	RTSSLK R (SEQ ID NO: 357)	QRSDLT R (SEQ ID NO: 358)	RSDHLS L (SEQ ID NO: 359)	CACAGCC CAagatagtT AAGTGGG	TGPGAAARA (SEQ ID NO: 417)
	ICTZ F14R	ZFN-R	KKDHLH R (SEQ ID NO:361)	RREVLN N (SEQ ID NO: 362)	QRGNL NM (SEQ ID NO: 363)	G (SEQ ID NO: 360)	TGPGAAARA (SEQ ID NO: 417)
CIITA	ICTZ F15L	ZFN-L	VPSKLR R (SEQ ID NO: 364)	EAHHLR R (SEQ ID NO: 265)	QDGNL TR (SEQ ID NO: 366)	GCCACCT TCccccGC TGAAGTC (SEQ ID NO: 400)	LRGSQ (SEQ ID NO: 418)
	ICTZ F15R	ZFN-R	TSTLLN R (SEQ ID NO: 367)	QQTNLT R (SEQ ID NO: 368)	VGNSLT R (SEQ ID NO: 369)		LRGSQ (SEQ ID NO: 418)
	ICTZ F16L	ZFN-L	QSGSLT R (SEQ ID NO: 370)	TSGNLV R (SEQ ID NO: 371)	QSGDL TR (SEQ ID NO: 372)	TGCATCT GCgacgtgG GAGCCGA	LRGSQ (SEQ ID NO: 418)
	ICTZ F16R	ZFN-R	RSDNLA R (SEQ ID NO: 373)	DRSDLT R (SEQ ID NO: 374)	QSGHL QR (SEQ ID NO: 375)	G (SEQ ID NO: 401)	LRGSQ (SEQ ID NO: 418)
	ICTZ F17L	ZFN-L	DRSHLT R (SEQ ID NO: 376)	RSDALS R (SEQ ID NO: 377)	QSSDL QR (SEQ ID NO: 378)	GCCCCA GCcactcGT GGCGGCC (SEQ ID NO: 402)	LRGSQ (SEQ ID NO: 418)
	ICTZ F17R	ZFN-R	ERGTLA R (SEQ ID NO: 379)	RSDDL QR (SEQ ID NO: 380)	RSDALT R (SEQ ID NO: 381)		LRGSQ (SEQ ID NO: 418)
	ICTZ F18L	ZFN-L	RSDHLA R	QSGDL TR	QSGHL QR		LRGSQ (SEQ ID NO: 418)

		(SEQ ID NO: 382)	(SEQ ID NO: 383)	(SEQ ID NO: 384)	CCCTGCT CCctccgGG GGCTGCT (SEQ ID NO: 403)	LRGSQ (SEQ ID NO: 418)
ICTZ F18R	ZFN-R	QSSDLT R (SEQ ID NO: 385)	QSSDLT R (SEQ ID NO: 386)	RSDHLS R (SEQ ID NO: 387)		
ICTZ F19L	ZFN-L	QSGHL AR (SEQ ID NO: 388)	DRSDLT R (SEQ ID NO: 389)	QSGNL AR (SEQ ID NO: 390)	TCCGGCT TCtccatGG AGCAGGC (SEQ ID NO:404)	LRGSQ (SEQ ID NO: 407)
ICTZ F19R	ZFN-R	DRSHLT R (SEQ ID NO: 391)	QSGDL TR (SEQ ID NO: 392)	QSGHL QR (SEQ ID NO: 393)		LRGSQ (SEQ ID NO: 418)
ICTZ F20L	ZFN-L	RSHILT N (SEQ ID NO: 394)	QSTTLK R (SEQ ID NO: 395)	DGGHL TR (SEQ ID NO: 396)	CACTGCG CCcaccgagG CCGAGGA	LRGSQ (SEQ ID NO: 418)
ICTZ F20R	ZFN-R	RQMNL DR (SEQ ID NO: 397)	RQDNL GR (SEQ ID NO: 398)	DKSVLA R (SEQ ID NO: 399)	G (SEQ ID NO: 405)	LRGSQ (SEQ ID NO: 418)

Example 9. ZFN Activity In Vitro II

[00223] ZFN-left arm plasmid vectors and ZFN-right arm plasmid vectors were transfected into HeLa cells using fugene transfection reagent, respectively. After transfection of 24 hours, HeLa cells were treated with 1 µg/ml puromycin for 48 hours to obtain cells rich in ZFNs. The HeLa cells were then collected, and lysed DNA fragment containing ZFNs were amplified by PCR using primers specific to the various gene (i.e., B2M and CIITA) and the genome of HeLa cells as templates. The DNA fragments were sequenced using forward primers, and the sequencing results are shown in FIGS. 27-30.

[00224] The DNA fragments were cloned into vectors. The DNA fragments of about 30 monoclonal cells were sequenced to determine whether the DNA fragments include mutations. The results of the sequencing were shown in Table 10.

Example 10. Design of ZFNs III

[00225] T cells were introduced with TRAC-specific ZFNs constructed to enable the site-specific introduction of mutations at TRAC gene. Various ZFNs were designed and incorporated into plasmids vectors essentially as described in Urnov et al. (2005) Nature 435(7042):646-651, Lombardo et al. (2007) Nat Biotechnol. November; 25(11):1298-306, and U.S. Patent Publication 2008/0131962. The ZFNs included various combinations of Zinc finger binding domains (e.g., ZFN-left and ZFN-right binding domains), which are listed in Table 9. The cleavage domain of the ZFNs comprised a FokI cleavage domain (SEQ ID NOS.: 96, 97, or 98). mRNA encoding a pair

of ZFNs (See Table 9) was introduced into the transduced cells to modify a target genomic locus associated with α chain of TCR.

Table 9

ZFN	Recognition Sequence	F1	F2	F3	F4	F5	F6
ZFLm1 (left)	GTTGCTCCAGG CCACAGCA (SEQ ID: 408)	QSGDLTR (SEQ ID: 409)	QWGTRYR (SEQ ID: 410)	ERGTLAR (SEQ ID: 411)	RSDNLRE (SEQ ID: 408)	QSGDLTR (SEQ ID: 412)	TSGALTR (SEQ ID: 413)
ZFRm1-4 (right)	GACTTTGCATG T(SEQ ID: 414)	WRSSLAS (SEQ ID: 415)	QSGSLTR (SEQ ID: 416)	HKWVLR Q(SEQ ID: 406)	DRSNLTR (SEQ ID: 407)		

Example 11. TALENs efficiency detection

[00226] TALENs for CIITA were designed to target exon2 (2L1: gctgacccctgtgctt (SEQ ID NO: 426); 2L2: gacccctgtgctct (SEQ ID NO: 427); 2R1: ctccagccagggtccatct (SEQ ID NO: 419); 2R2: tctccagccagggtccat (SEQ ID NO: 420)) and exon3 (3L1: tcagcaggctgttgt (SEQ ID NO: 421); 3L2: tcagcaggctgtgtgt (SEQ ID NO: 422); 3R1: ccctggtcttctcat (SEQ ID NO: 423); 3R2: aagcctccctggtctt (SEQ ID NO: 424); 3R3: aagcctccctggtct (SEQ ID NO: 425)). The TALENs were constructed with FastTALE TALEN Assembly Kit (Sidansai), and their activities were confirmed in 293T cells as previous description. The constructed TALENs were transfected into 293T cells and selected with 2 μ g/ml puromycin (Sigma). The genomic DNA of 293T cells was harvested after selection. Then, PCR and sequencing were performed to examine the efficiency of the TALENs.

Table 10: Monoclonal sequencing results for ZFNs that target various gene fragments and are amplified by PCR

ZFN		Number of clones analyzed	Number of clones mutated	Mutation frequency
Left	Right			
ICTZF14L	ICTZF14R	33	10	30%
ICTZF15L	ICTZF15R	26	3	12%
ICTZF16L	ICTZF16R	31	7	23%
ICTZF17L	ICTZF17R	35	3	9%
ICTZF18L	ICTZF18R	27	6	22%
ICTZF19L	ICTZF19R	32	9	28%
ICTZF20L	ICTZF20R	30	1	3%

Example 12. Cas9 design and analysis

[00227] The plasmids expressing Cas9 and gRNA were co-transfected into 293T cells with fugene transfection reagent. After 72 hours, 293T cells were collected and the expression of B2m and HLA proteins was detected by flow cytometry (FIG. 31).

Example 13. MCF-7 and double CAR reinfusion I

[00228] 8 NPG female mice were used, and they were 6 weeks old. On day 0, each of the mice was inoculated with 350w MCF-7 cells to establish an orthotopic tumor model. On day 35, each of the mice was infused with the corresponding cells as shown in Table 11.

Table 11: Experimental protocol

Tumor Modeling	Infusion Dose	Infused Cells	ID of Mice
MCF-7	1000w/Per Mouse	NT	827
			831
		2407 (T cells expressing anti-MUC1 CAR T cells, and the CAR binding domain comprises SEQ ID NO: 70) (CARtMuc1 4-1BB)	823
			830
		1204+2407 (T cells expressing anti-CD19 and MUC1 CAR T cells, and the CAR of anti-CD19 comprises SEQ ID NO: 5) (CARtMuc1/CAR19-4-1BB)	822
			828
		N/A	824
			829

[00229] On Day 42, about 150 ul of blood from each mice was collected from the orbital venous plexus. On day 49, mice blood of the mice was collected from the orbital venous plexus about 150 ul each. Each peripheral blood was centrifuged to separate plasma, and plasma was used to measure cytokines. Peripheral blood-precipitated cells were stained with antibodies after being subjected to red-breaking treatment, followed by flow cytometry.

[00230] Percentages of T cells/mouse white blood cells in mouse peripheral blood were measured. Results are provided in FIGS. 32-39 and Table 12.

[00231] FIGS. 32-35 show flow cytometry results of human leukocytes/murine leukocytes in different groups. The cells were derived from all living cells after the mouse peripheral blood lysis. The horizontal axis represents the fluorescence intensity of hCD45 corresponding staining, and the vertical axis represents the fluorescence intensity of mCD45 corresponding staining.

[00232] FIGS. 36-39 show flow cytometry results of T cells/human leukocytes. The cells were derived from human leukocyte hCD45 in FIGS. 32-35, the horizontal axis represents the fluorescence intensity of CD3 corresponding staining, and the vertical axis represents the fluorescence intensity of CD19 corresponding staining.

Table 12: Leukocytes/murine leukocytes %

Tumor Modeling	Infused Cells	ID of Mice	Leukocytes/murine leukocytes %
MCF-7	NT	827	0.54
		831	4.9
	2407	823	37.12
		830	12.16
	1204+2407	822	11.80
		828	9.91
	N/A	824	0
		829	0

[00233] As shown above, the proportion of T cells in the Mock group (N/A Infused Cells) was 0%, and the T cells in the NT group were less, which was in line with expectations. The proportion of T cells in group 2407 was greater than that in group 1204+2407, but further experiments were needed because the number of mice was small. Thus, double CAR cells can be activated like a single CAR cell.

[00234] FIG. 40 shows release of cytokines IL-2 and IFN-γ of each of the mice. Peripheral blood samples were obtained from the mice, and the supernatant were provided as follows (unit: pg/mL) in Table 13.

Table 13: Cytokine data

Tumor Modeling	Infused Cells	ID of Mice	IL-2	IFN-γ
MCF-7	NT	827	7	1.04
		831	5.64	0
	2407	823	9.13	385.9
		830	11.57	711.68
	1204+2407	822	11.57	736.36
		828	8.49	1235.00
	N/A	824	7.29	3.23
		829	7.29	1.04

[00235] As shown above, the IL-2 release levels of IL-2:2407 and 1204+2407 were slightly higher than those of NT and Mock (N/A Infused Cells). The IFN-γ release in the NT group and the Mock group was basically 0, and the IFN-γ release in the 1204+2407 group was much higher than that in the 2407 group. Thus, double CAR cells can release cytokines like a single CAR cell.

[00236] FIGS. 41-44 shows proportion of CD8/CD4 in mouse peripheral blood T cells. The cells were derived from CD3 positive cells in FIGS. 36-39, and the horizontal axis represents the fluorescence intensity of CD4 corresponding staining, and the vertical axis represents the fluorescence intensity of CD8 corresponding staining. Detailed results are provided in Table 14.

Table 14: CD8/CD4 in T Cells

Tumor Modeling	Infused Cells	ID of Mice	CD8/CD4 in T Cells
MCF-7	NT	827	3.33:1
		831	4:11:1
	2407	823	0.90:1
		830	0.79:1
	1204+2407	822	0.88:1
		828	0.99:1
	N/A	824	N/A
		829	N/A

[00237] As shown above, the Mock group (N/A Infused Cells) has no CD8 and CD4. The 2407 group and the 1204+2407 group were basically flat, and the NT group CD8/CD4 ratio was much higher than the two groups.

Example 14. MCF-7 and double CAR reinfusion II

[00238] 17 NPG female mice were used, and they were 8 weeks old. After the animals arrived, they were sterilized and transferred to the animal room. The experimental animals were acclimatized for 7 days. The animals were observed in the cage daily during the adaptation period. After the end of the animal adaptation period, the animals were irradiated on the day before the experimental modeling. The irradiation dose was 1 Gy.

[00239] Mice were modeled on the second day after irradiation. MCF-7 cells were injected into the mammary fat pad of mice by in situ vaccination with a mammary fat pad to establish a tumor model. The day of modeling is Day 0.

Table 15: Mice modeling protocol

Number of animals / gender	Modeling cell	Modeling method	Modeling cell mass
17/F	MCF-7	In situ inoculation of breast fat pad	500w / Mouse

[00240] The modeled 17 mice were divided into 4 groups according to a random grouping as shown in Table 16.

Table 16: Experimental protocol

Returning cells	Nalm6 stimulation	Number of animals
2407+1204 (T cells expressing anti-CD19 and MUC1 CAR T cells)	NA	4
2407 (T cells expressing anti-MUC1 CAR T cells)	NA	5
2407+1204 (Nalm6 stimulation)	Stimulation of Nalm6 cells prior to cell reinfusion	5
NT	NA	3

[00241] After modeling, volumetric measurements of mouse tumors were initiated when visible tumors were visible to the naked eye. Nalm6 cell stimulation was performed as follow. Five mice in the 2407+1204 (Nalm6 stimulation) group in Day9 were injected with Nalm6 cells for stimulation. Nalm6 cells were injected into mice by tail vein injection using the protocol in Table 17.

Table 17: Experimental protocol

Stimulating cell	Stimulating cell mass
Nalm6	50w / Mouse

[00242] On day 10, each of the mice was infused (tail vein injection) with the corresponding cells as shown in Table 18.

Table 18: Experimental protocol

Modeling cell	Return volume	Nalm6 stimulation	Animal number
2407+1204	1000w / Mouse	no	921、 922、 923、 924
2407	1000w / Mouse	no	903、 904、 905、 906、 907

2407+1204 (Nalm6 stimulation)	1000w / Mouse	Yes	934、938、939、940、958
NT	1000w / Mouse	no	908、909、910

[00243] Peripheral blood collection was performed on mice one week after cell reinfusion, and blood was collected through the orbital venous plexus. On day 17, the first blood collection was performed.

[00244] Peripheral blood was centrifuged to separate the plasma, and plasma was used to measure cytokines. Peripheral blood-precipitated cells were stained with antibodies after being subjected to red-breaking treatment, followed by flow cytometry. The data was analyzed and shown in FIGS. 45-47 (Peripheral blood flow data).

[00245] FIG. 45 shows results of T cell / mouse white blood cell. It can be seen from the statistics and the data in Table 19 that the ratios of white blood cells in the T cells/mouse of the NT group, the 2407 group, and the Nalm6+2407+1204 group are similar, and the ratios of the white blood cells of the 2407+1204 group to the other four groups of T cells/mouse are higher.

Table 19: T cell / mouse white blood cell

Modeling cell	Returning cells	Numbering	T cell / mouse white blood cell
MCF-7	NT	908	13.58%
		909	11.41%
		910	16.35%
	2407	903	20.63%
		904	8.60%
		905	6.33%
		906	8.66%
		907	19.43%
	2407+1204	921	17.01%
		922	14.75%
		923	36.67%
		924	19.54%
	Nalm6+2407+1204	934	14.20%
		938	13.18%
		939	19.02%
		940	8.79%
958		19.41%	

[00246] FIG. 46 shows results of CD8/CD4. It can be seen from the statistics data in Table 20 that there is no significant difference in the ratio of the four groups of CD8/CD4.

Table 20: Ratios of CD8/CD4

Modeling cell	Returning cells	Numbering	CD8/CD4
MCF-7	NT	908	8.25
		909	8.48
		910	7.41

	2407	903	8.12
		904	7.35
		905	7.51
		906	10.33
		907	9.01
	2407+1204	921	10.23
		922	10.48
		923	9.73
		924	9.71
	Nalm6+2407+1204	934	9.59
		938	7.89
		939	11.92
		940	11.09
		958	10.55

[00247] Peripheral blood samples from mice and the supernatant (unit: pg/mL) and cytokine data was analyzed (Table 21) and shown in FIG. 47. It can be seen from the statistical graph and tabular data that the release of IL-2 in group 2407 is higher than that in the other three groups. Further, it can be seen from the statistics and tabular data that the release of IFN in the 2407 group was significantly higher than the other three groups. The amount of IFN released in the 2407+1204 group and the Nalm6+2407+1204 group was relatively close.

Table 21: Cytokine data

Modeling cell	Returning cells	Numbering	IL-2	IFN
MCF-7	NT	908	7.29	4.62
		909	8.18	12.01
		910	11.57	185.82
	2407	903	21.18	590.23
		904	21.74	2033.41
		905	19.57	1697.69
		906	33.8	1348.12
		907	9.46	182.51
	2407+1204	921	8.18	44.02
		922	9.13	214.25
		923	8.18	41.91
		924	9.46	221.94
	Nalm6+2407+1204	934	8.49	325.22
		938	9.46	17.94
		939	9.13	54.42
		940	11.2	406.14
		958	9.13	166.75

[00248] FIG. 48 shows tumor volumes change in mice in response to infusion with different cell groups. The tumor volumes in different mice were measured (unit: mm³, volume formula according to $V = \text{long diameter} * \text{short diameter} * \text{short diameter} * 0.5$) in certain time periods after

the infusion of the various cells. results are shown in the figure. It can be seen from the above figure that the tumor volume of the 2407+1204 group remained basically unchanged after the reinfusion, and the tumor volume was reduced in the Nalm6+2407+1204 group and the 2407 group, and the tumor volume of the NT group increased. Thus, both double CAR and single CAR have similar anti-tumor functions.

[00249] All publications, patents and patent applications cited in this specification are incorporated herein by reference in their entireties as if each individual publication, patent or patent application were specifically and individually indicated to be incorporated by reference. While the foregoing has been described in terms of various embodiments, the skilled artisan will appreciate that various modifications, substitutions, omissions, and changes may be made without departing from the spirit thereof.

CLAIMS

1. A modified cell comprising a plurality of nucleic acids encoding a chimeric antigen receptor (CAR) binding a solid tumor antigen and encoding a CAR binding a B cell antigen.
2. The modified cell of claim 1, wherein the solid tumor antigen is tMUC 1, PRLR, CLCA1, MUC12, GUCY2C, GPR35, CR1L, MUC 17, TMPRSS11B, MUC21, TMPRSS11E, CD207, SLC30A8, CFC1, SLC12A3, SSTR1, GPR27, FZD10, TSHR, SIGLEC15, SLC6A3, KISS1R, QRFPR, GPR119, CLDN6, UPK2, ADAM12, SLC45A3, ACPP, MUC21, MUC16, MS4A12, ALPP, CEA, EphA2, FAP, GPC3, IL13-R α 2, Mesothelin, PSMA, ROR1, VEGFR-II, GD2, FR- α , ErbB2, EpCAM, EGFRvIII, or EGFR, and the B cell antigen is CD19, CD20, CD22, or BCMA.
3. The modified cell of claim 1, wherein the B cell antigen comprises CD19.
4. The modified cell of claim 3, wherein the solid tumor antigen comprises tumor associated MUC1.
5. The modified cell of claim 4, wherein a binding domain of the CAR binding the B cell antigen comprises an amino acid sequence of SEQ ID NO: 5 or 6, and a binding domain of the CAR binding the solid tumor antigen comprises an amino acid sequence of SEQ ID NO: 70.
6. The modified cell of claim 4, wherein the CAR binding the B cell antigen comprises an amino acid sequence of SEQ ID NO: 207, and the CAR binding the solid tumor antigen comprises an amino acid sequence of SEQ ID NO: 202.
7. The modified cell of claim 4, wherein the CAR binding the B cell antigen comprises an antigen binding domain, a transmembrane domain, a cytoplasmic domain, and the CAR binding the solid tumor antigen comprises an antigen binding domain, a transmembrane domain, and an intracellular domain.
8. The modified cell of claim 7, wherein the cytoplasmic domain comprises a co-stimulatory domain or a CD3 zeta domain, or a combination thereof.
9. The modified cell of claim 3, wherein T cell expansion by the modified cell is greater than a T cell expansion obtained by administering T cells having the CAR binding the solid tumor antigen in the absence of the CAR binding the B cell antigen.
10. The modified cell of claim 9, wherein the T cell expansion is measured based on an increase in copy number of CAR molecules in genomic DNA of the T cells.
11. The modified cell of claim 3, wherein at least one of the nucleic acids comprises a nucleic acid sequence of SEQ ID NO: 201.
12. The modified cell of claim 1, wherein the B cell antigen comprises CD19, CD20, CD22, or BCMA.
13. The modified cell of claim 1, wherein the solid tumor antigen comprises B7, CAIX, CD123, CD133, CD171, CD171/L1-CAM, CEA, Claudin 18.2, cMet, CS1, CSPG4, Dectin1, EGFR, EGFR vIII, EphA2, ERBB receptors, ErbB T4, ERBB2, FAP, Folate receptor 1, FITC,

Folate receptor 1, FSH, GD2, GPC3, HA-1 H/HLA- A2, HER2, IL-11Ra, IL13 receptor a2, IL13R, IL13R α 2 (zetakine), Kappa, Leukemia, LewisY, Mesothelin, MUC1, NKG2D, NY-ESO-1, PSMA, ROR-1, TRAIL-receptor1, or VEGFR2.

14. The modified cell of claim 1, wherein the CAR binding the B cell antigen comprises an amino acid sequence of SEQ ID NO: 203, 207, 216, or 219.

15. The modified cell of claim 1, wherein the CAR binding the solid tumor antigen comprises an amino acid sequence of SEQ ID NO: 202 or 205.

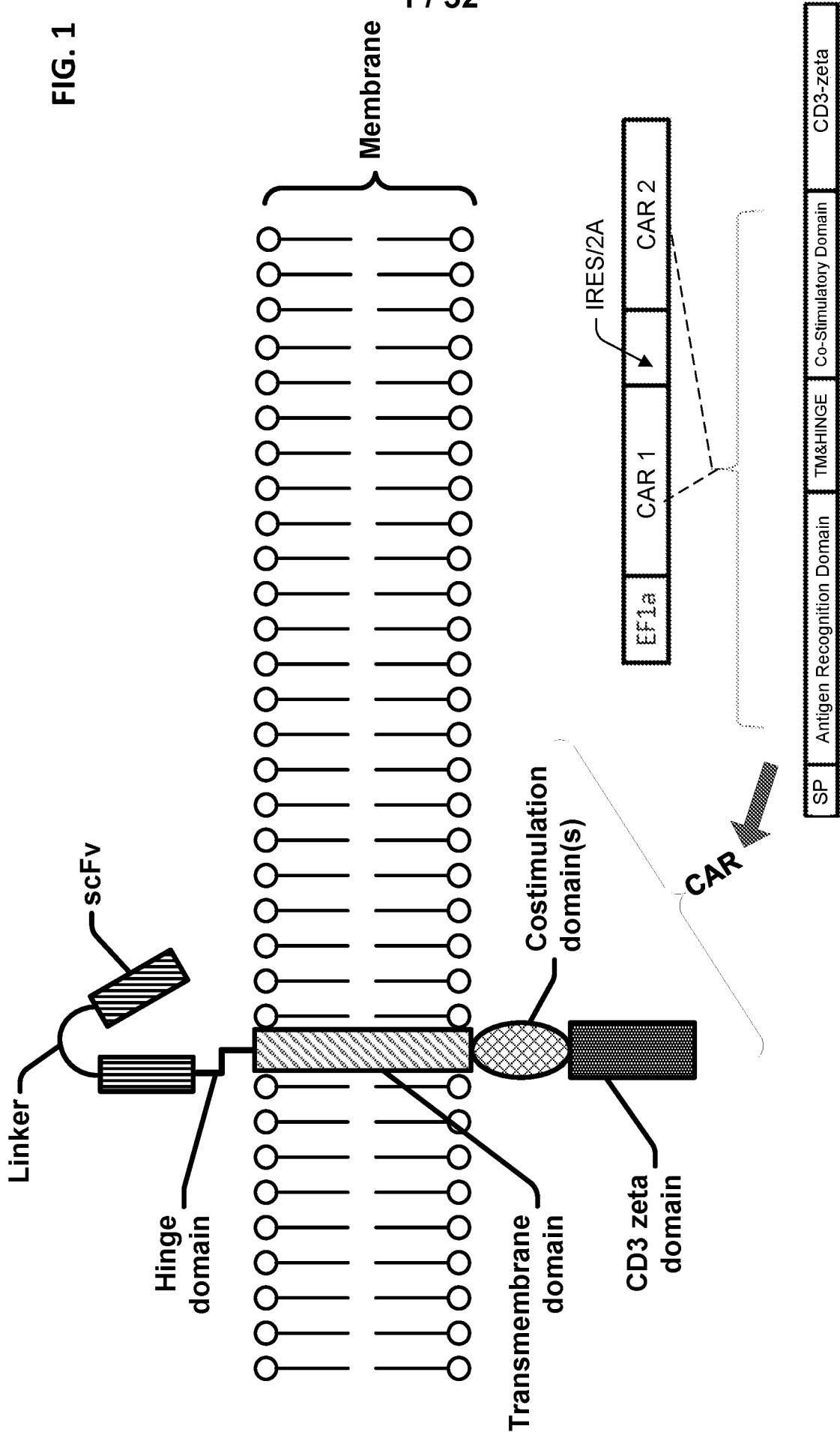
16. The modified cell of claim 1, wherein at least one of nucleic acids comprises a nucleic acid sequence of SEQ ID NO: 201, 204, 206, 208, 215, 217, 218, or 220.

17. A pharmaceutical composition comprising a population of the modified cells of any of claims 1-16.

18. A method of promoting T cell response in a subject in need thereof and/or treating a tumor of the subject, the method comprising administering an effective amount of the composition of claim 17 to the subject.

19. A method of enhancing T cell expansion in a subject in need thereof, the method comprising administering an effective amount of the composition of claim 17 to the subject, the subject having a higher level of T cell expansion as compared with a subject that is administered an effective amount of the CAR T cells that do not have the CAR binding the B cell antigen.

FIG. 1



*Antigen recognition domain: scFv or ligand based.

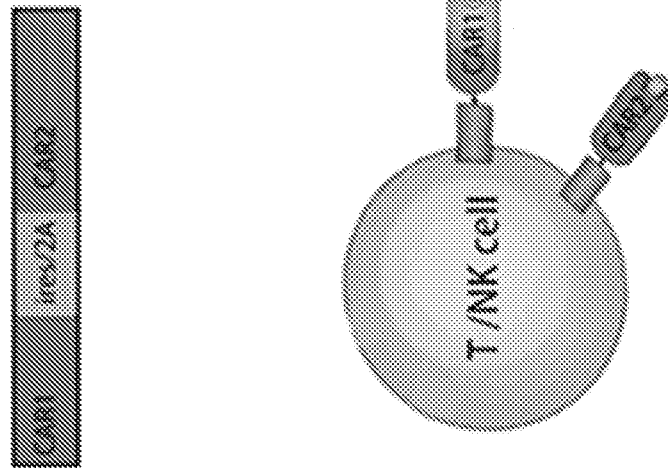


FIG. 2

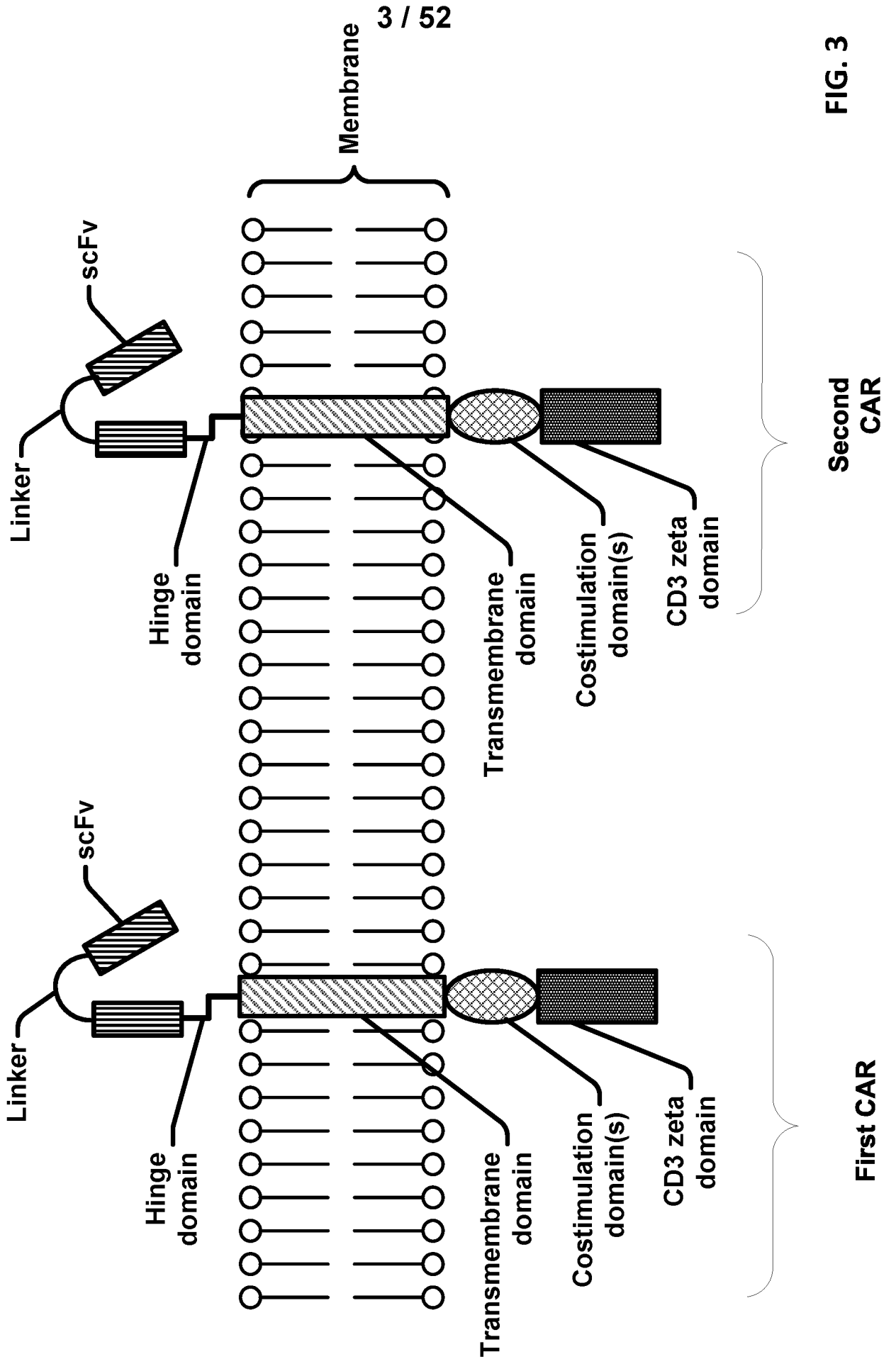


FIG. 3

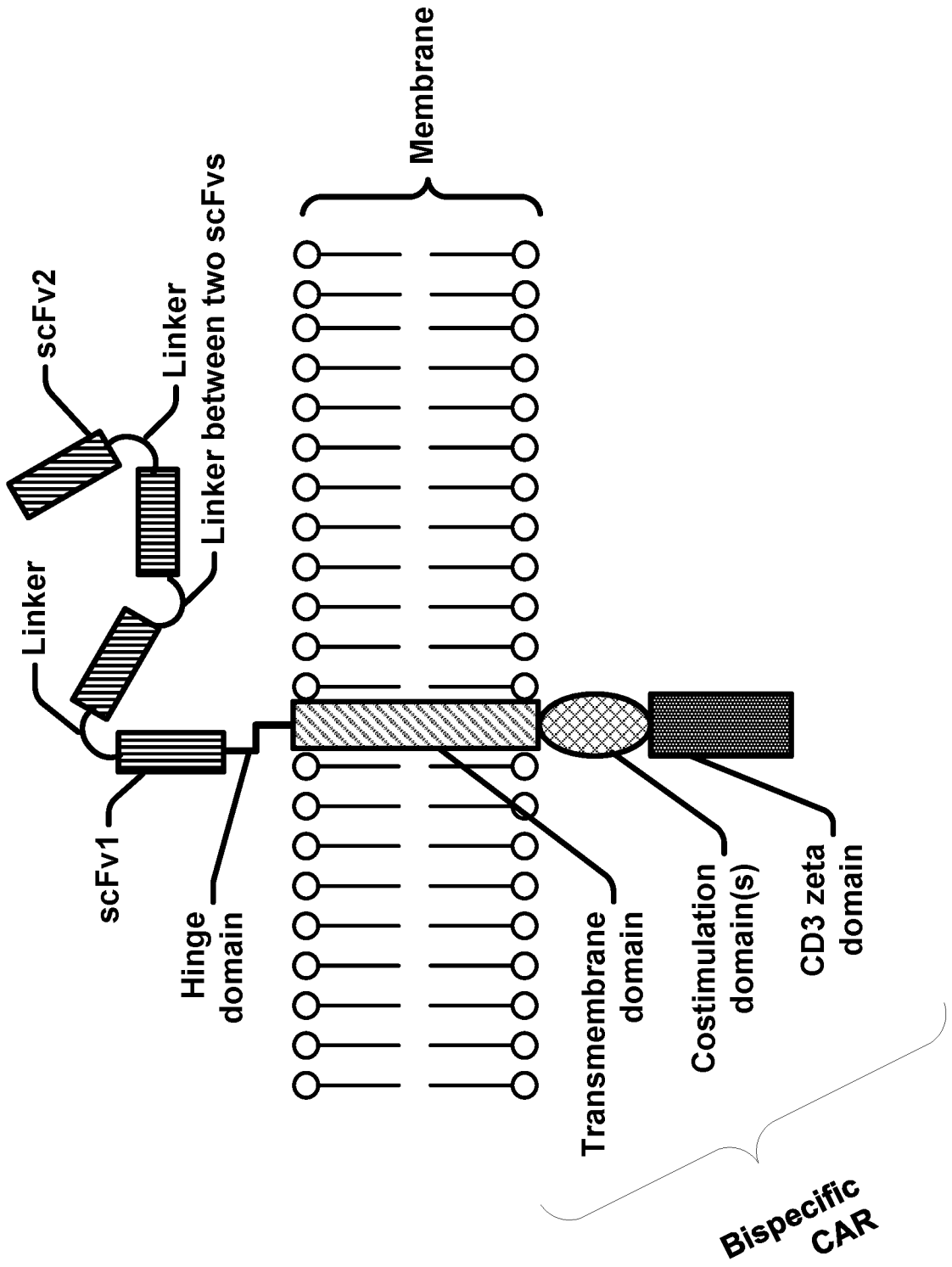


FIG. 4

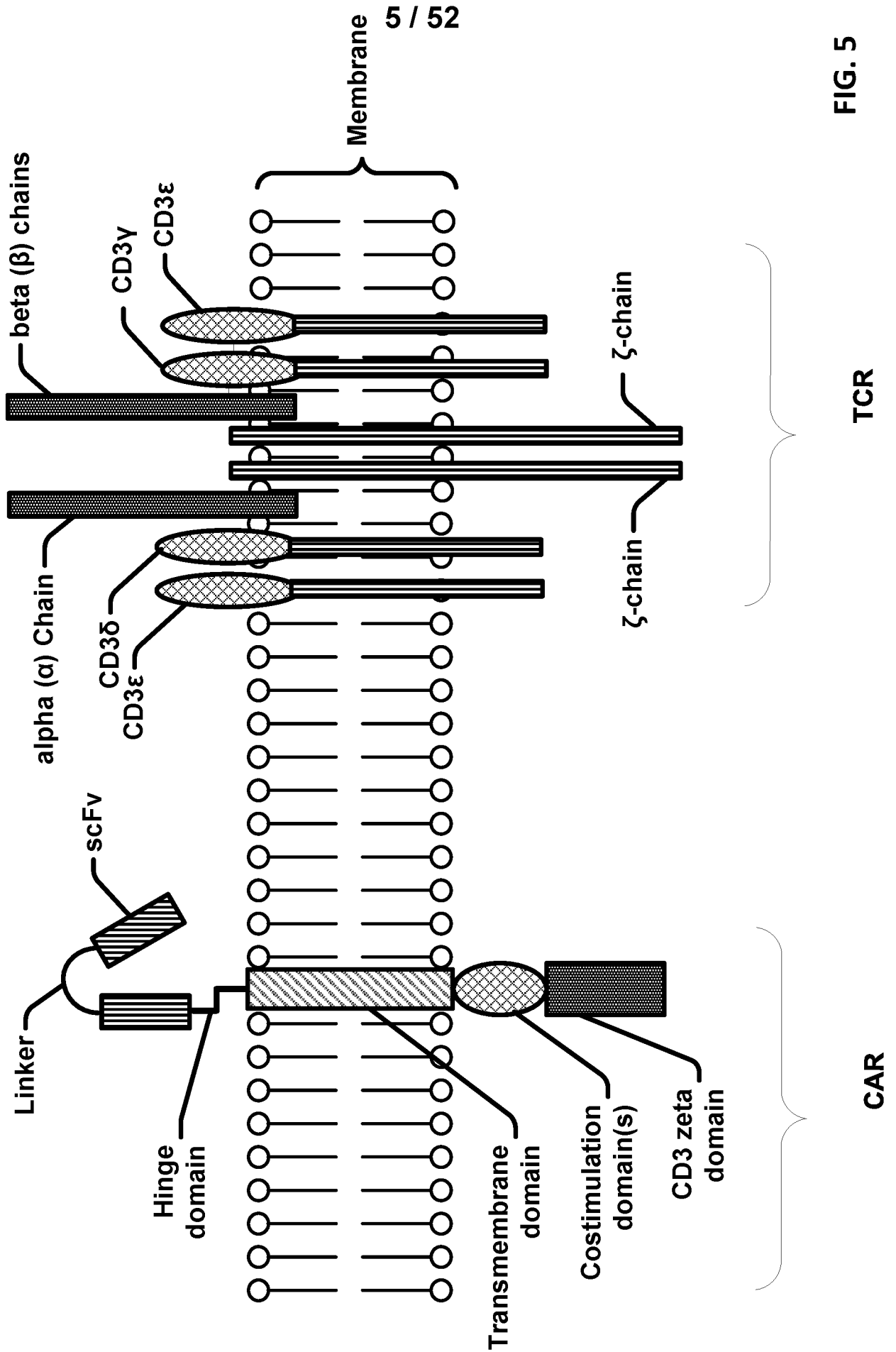
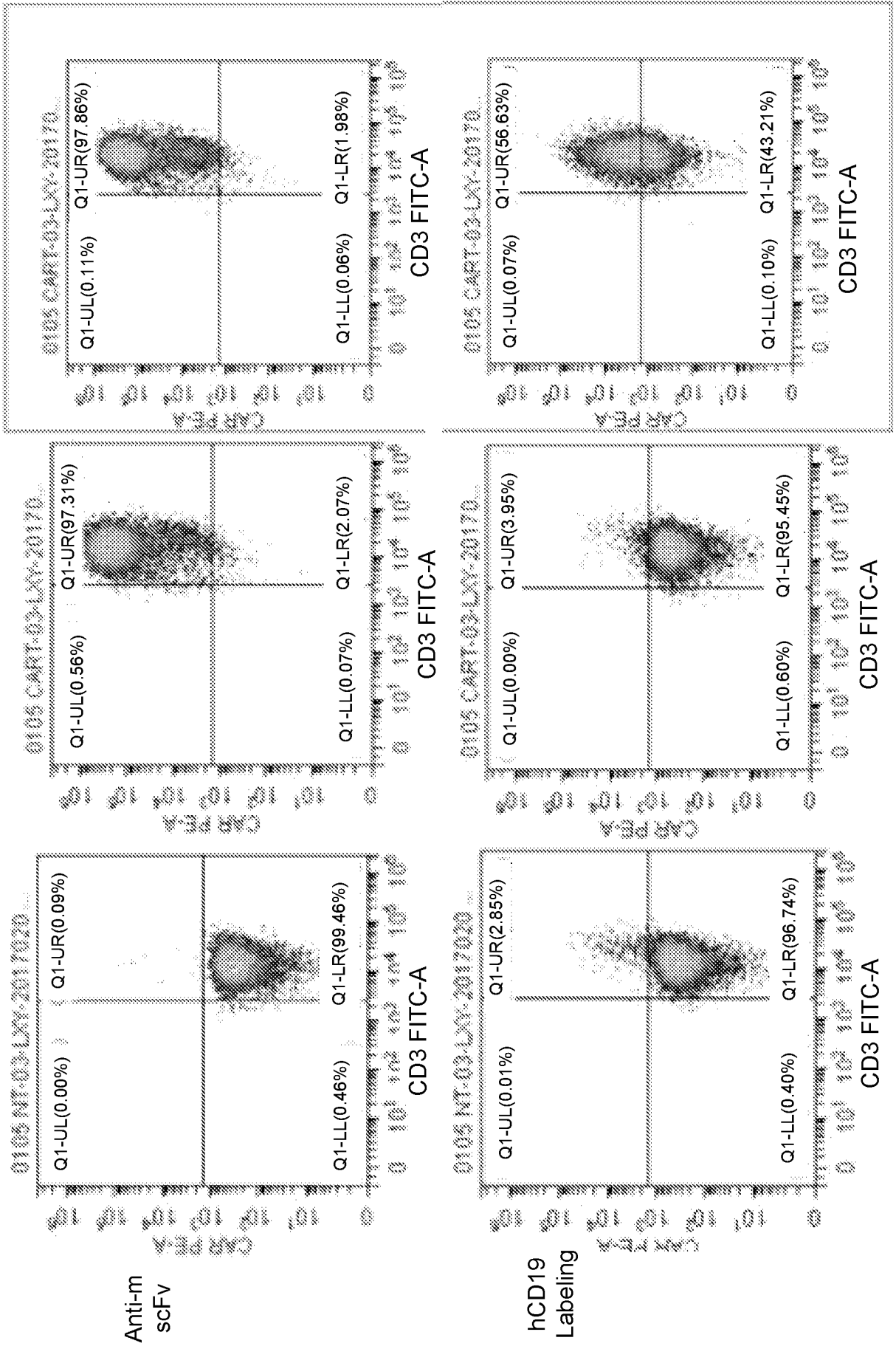


FIG. 5

Anti-Muc1 & anti-CD19 CAR T cells, derived.



dual CAR: anti-muc1 & CD19
5E5 CAR: anti-muc1

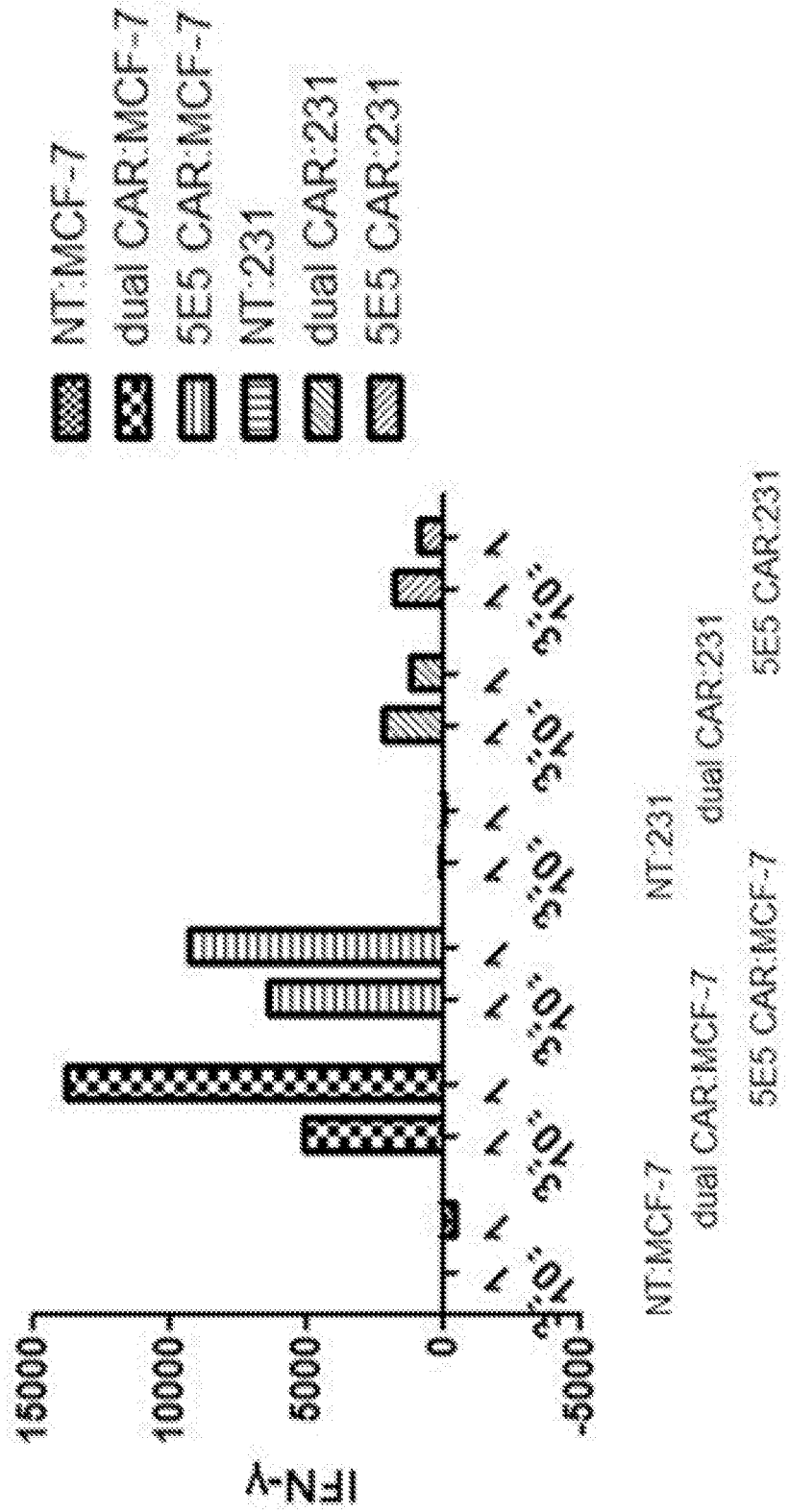


FIG. 8

dual CAR: anti-muc1 & CD19
5E5 CAR: anti-muc1

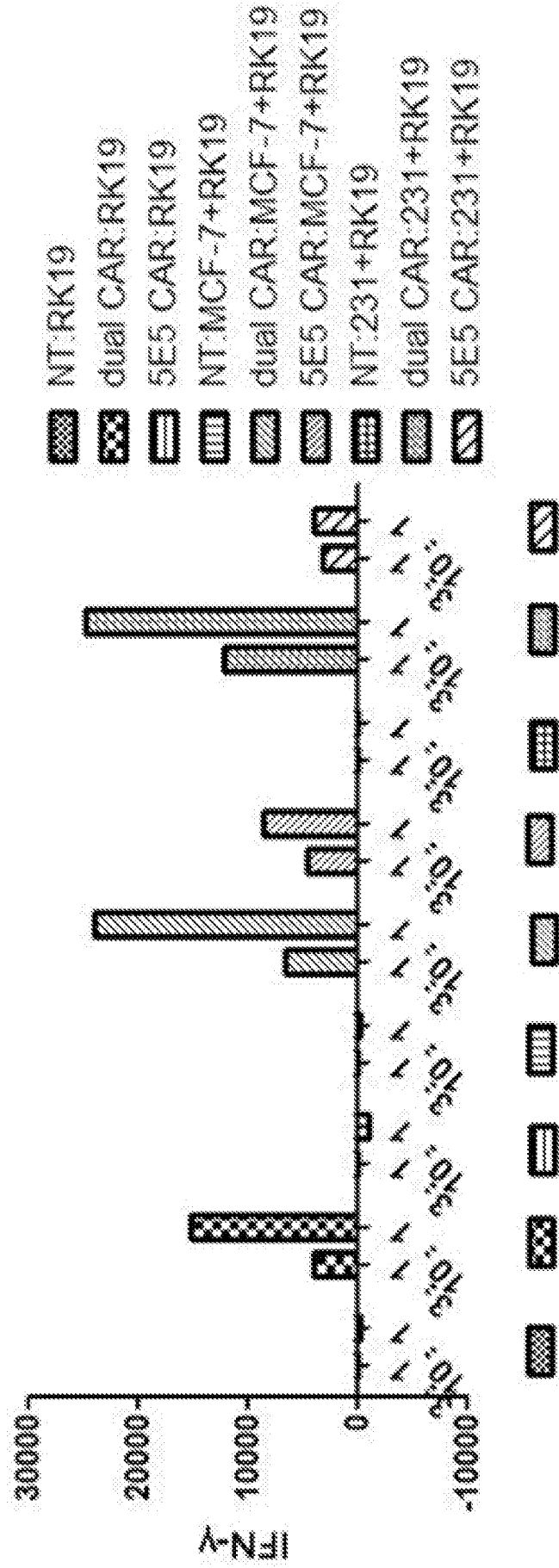


FIG. 9

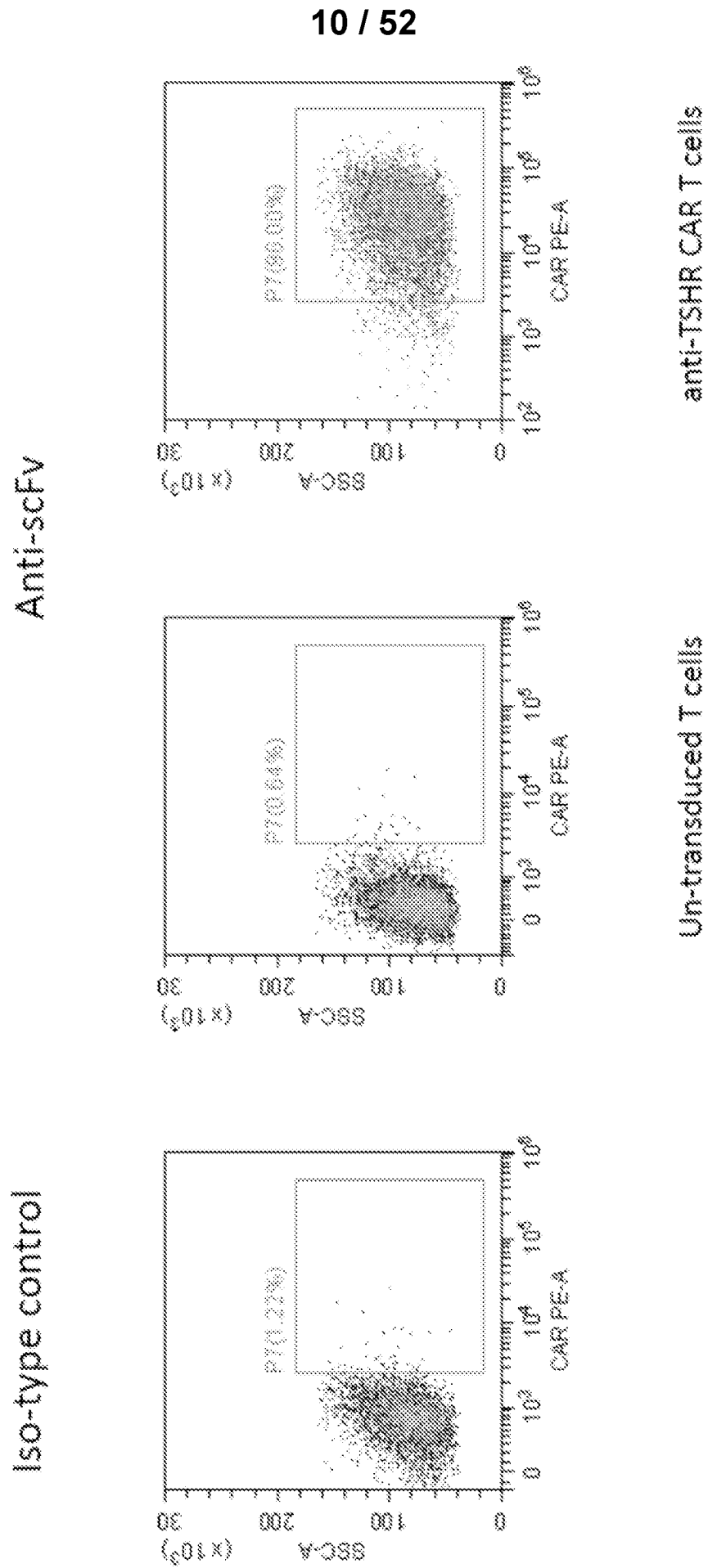
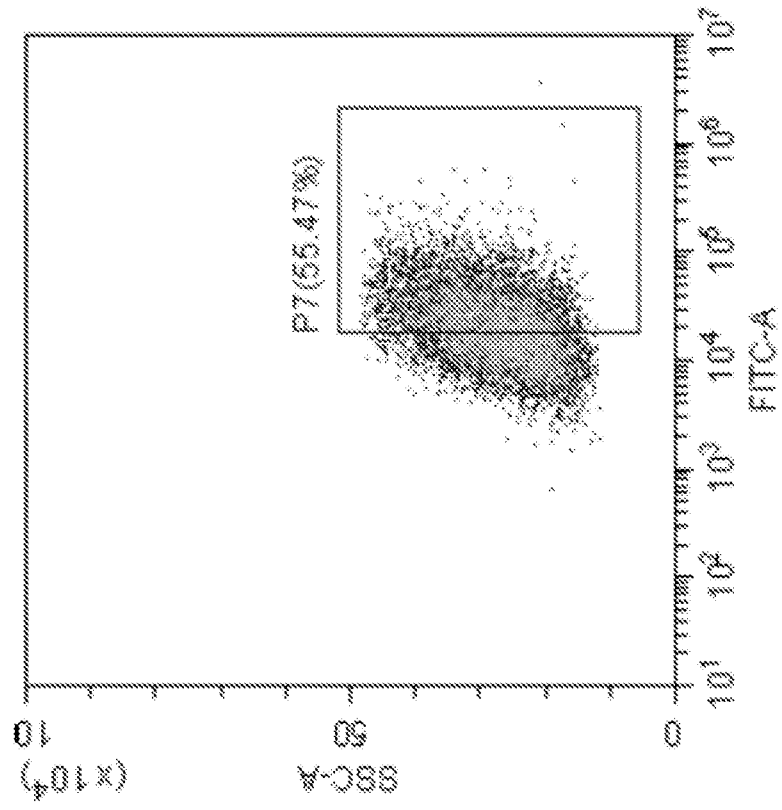


FIG. 10

Anti-TSHR fitc



Iso-type control

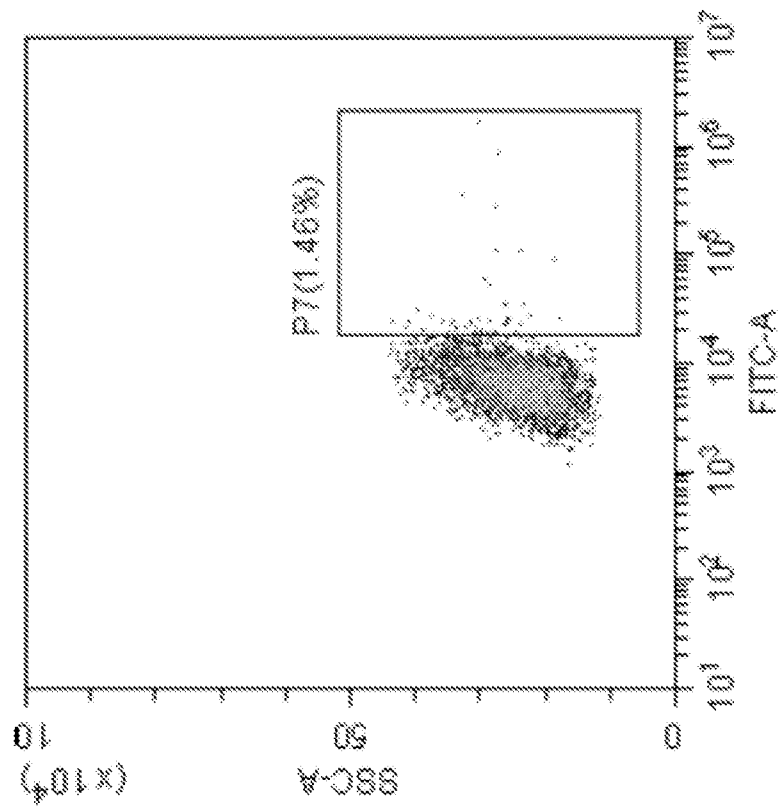


FIG. 11

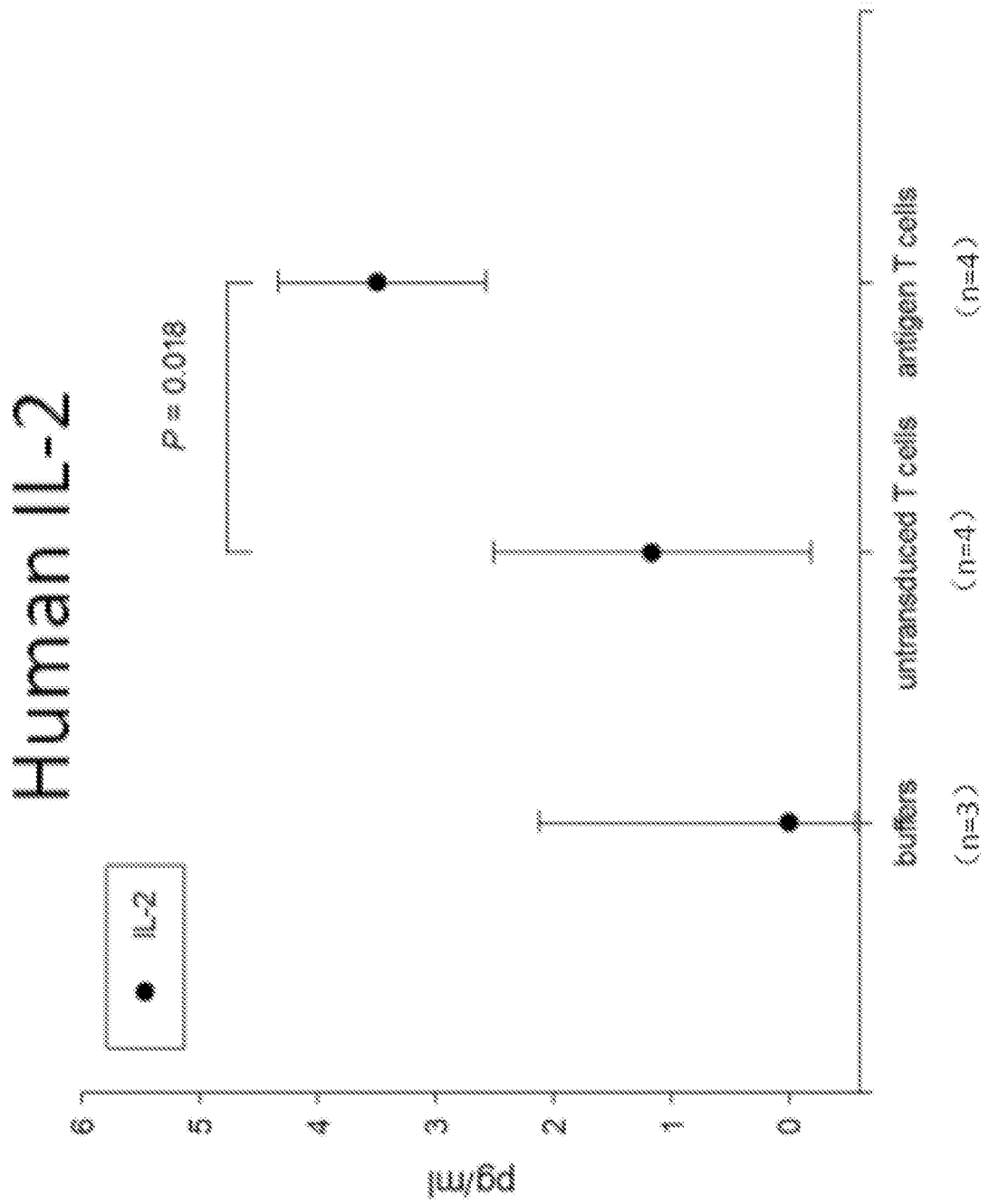


FIG. 12

Human IFN-gamma

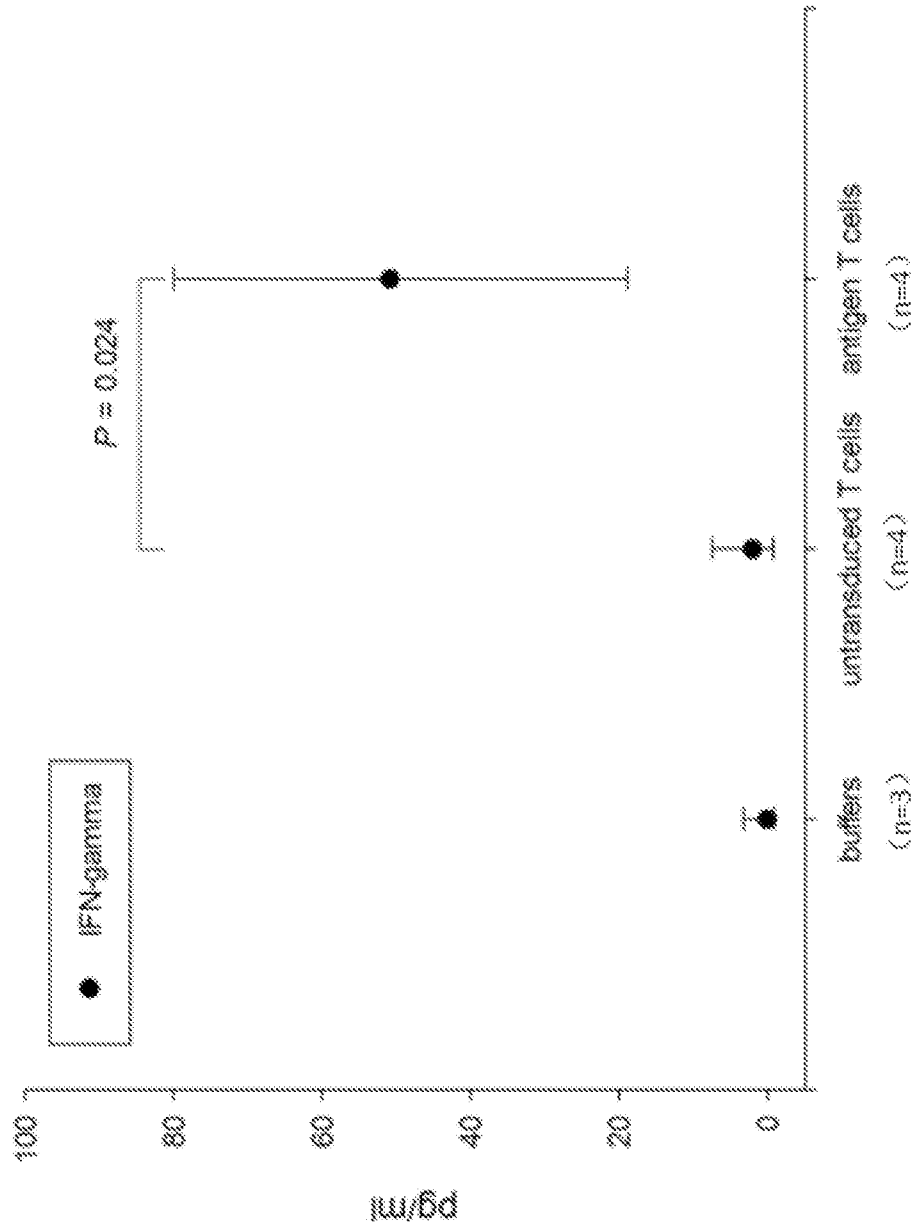


FIG. 13

Human IL-4

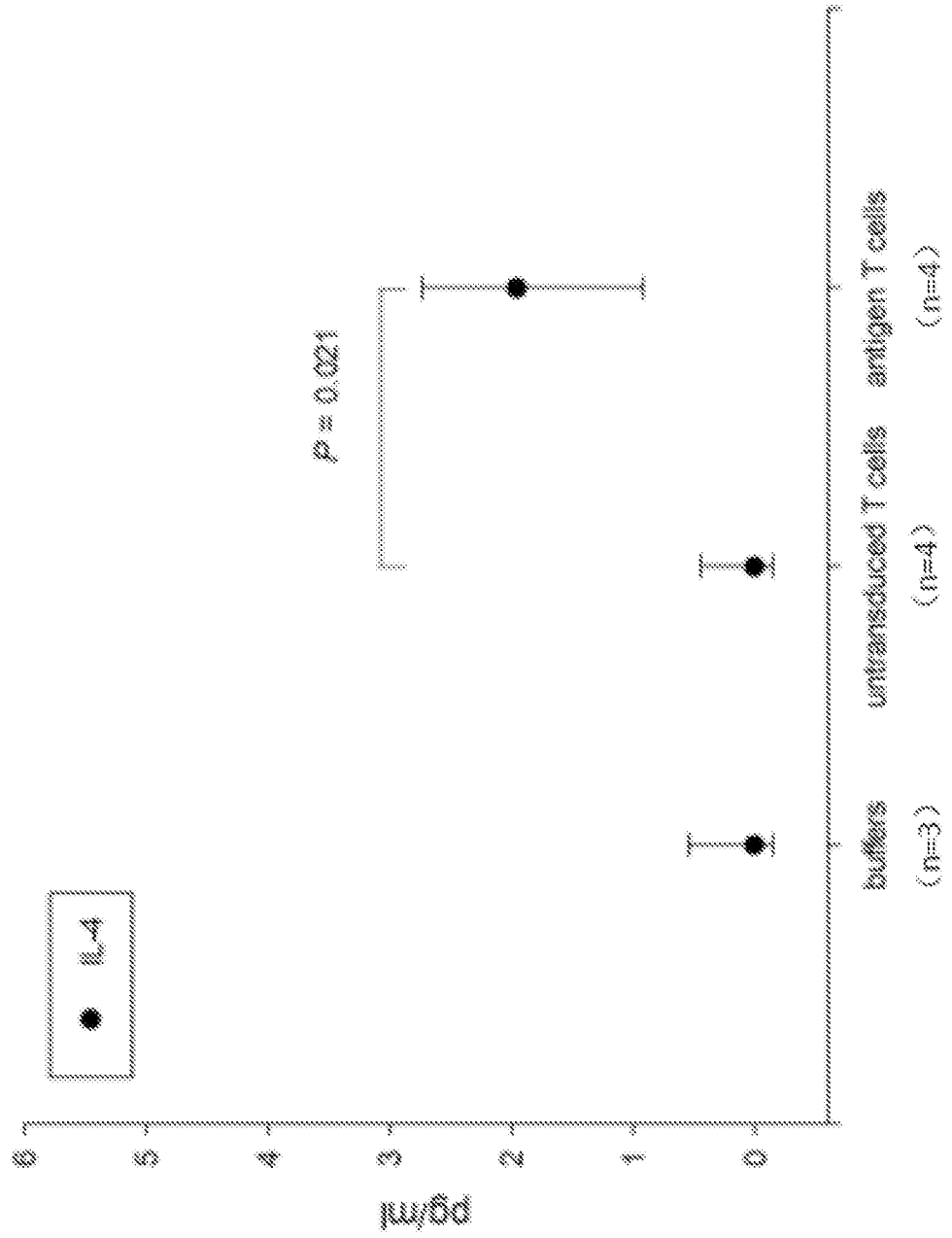


FIG. 14

Gated by single live mCD45-hCD3+ cells, mouse p8

Anti-scFv

IgG

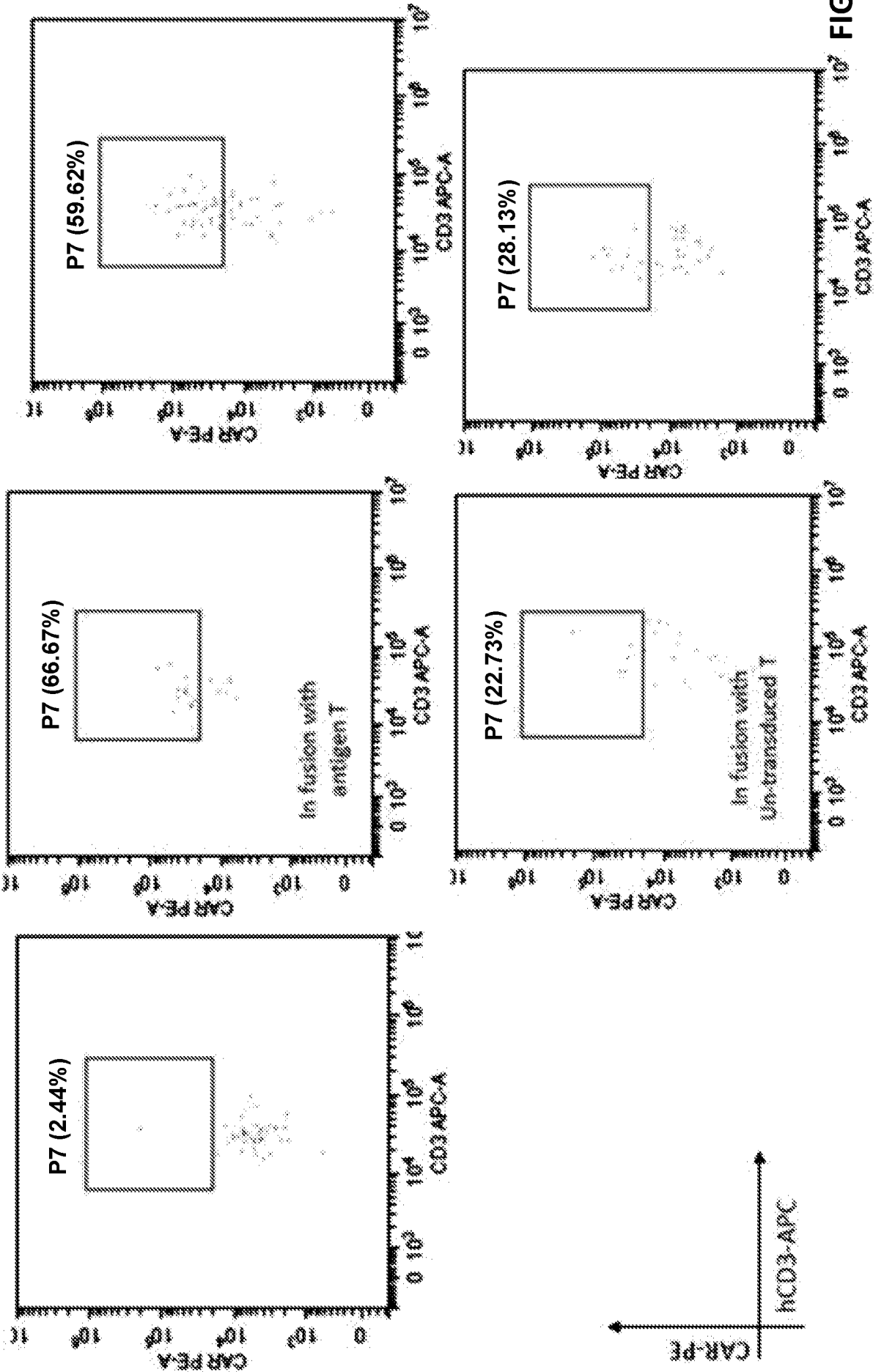
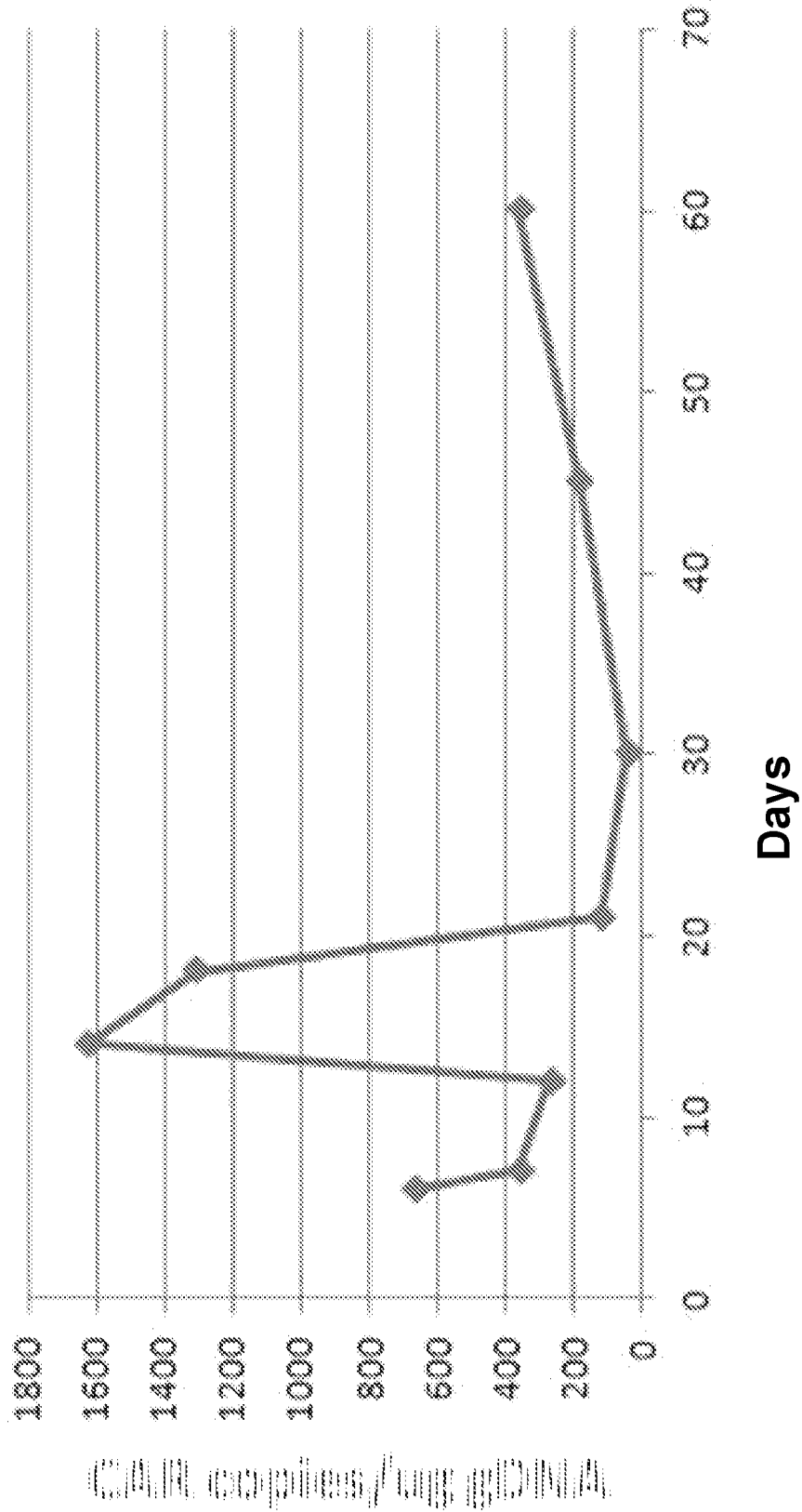


FIG. 15

Patient A



Patient B

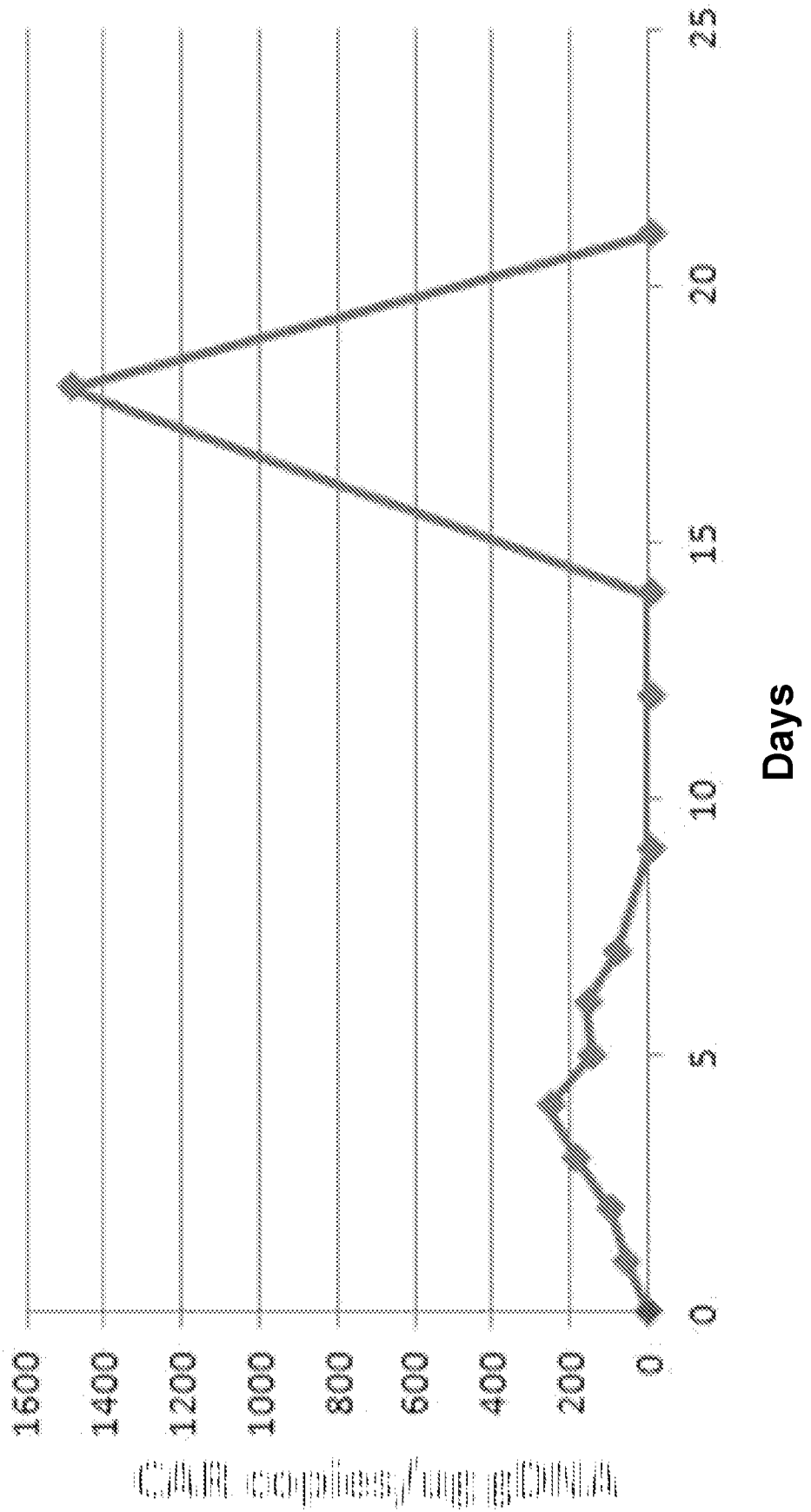


FIG. 17

Patient C

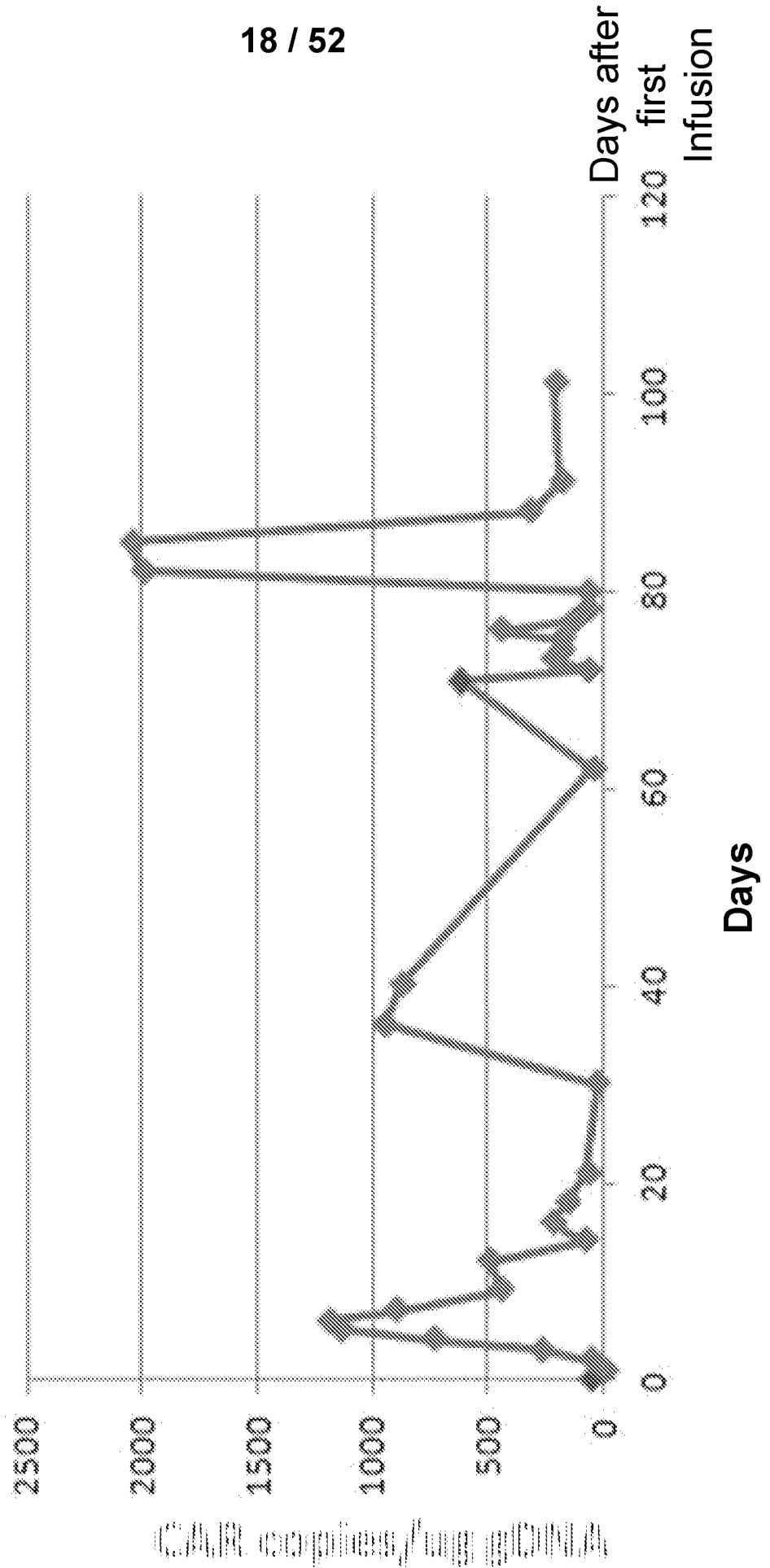


FIG. 18

Patient D

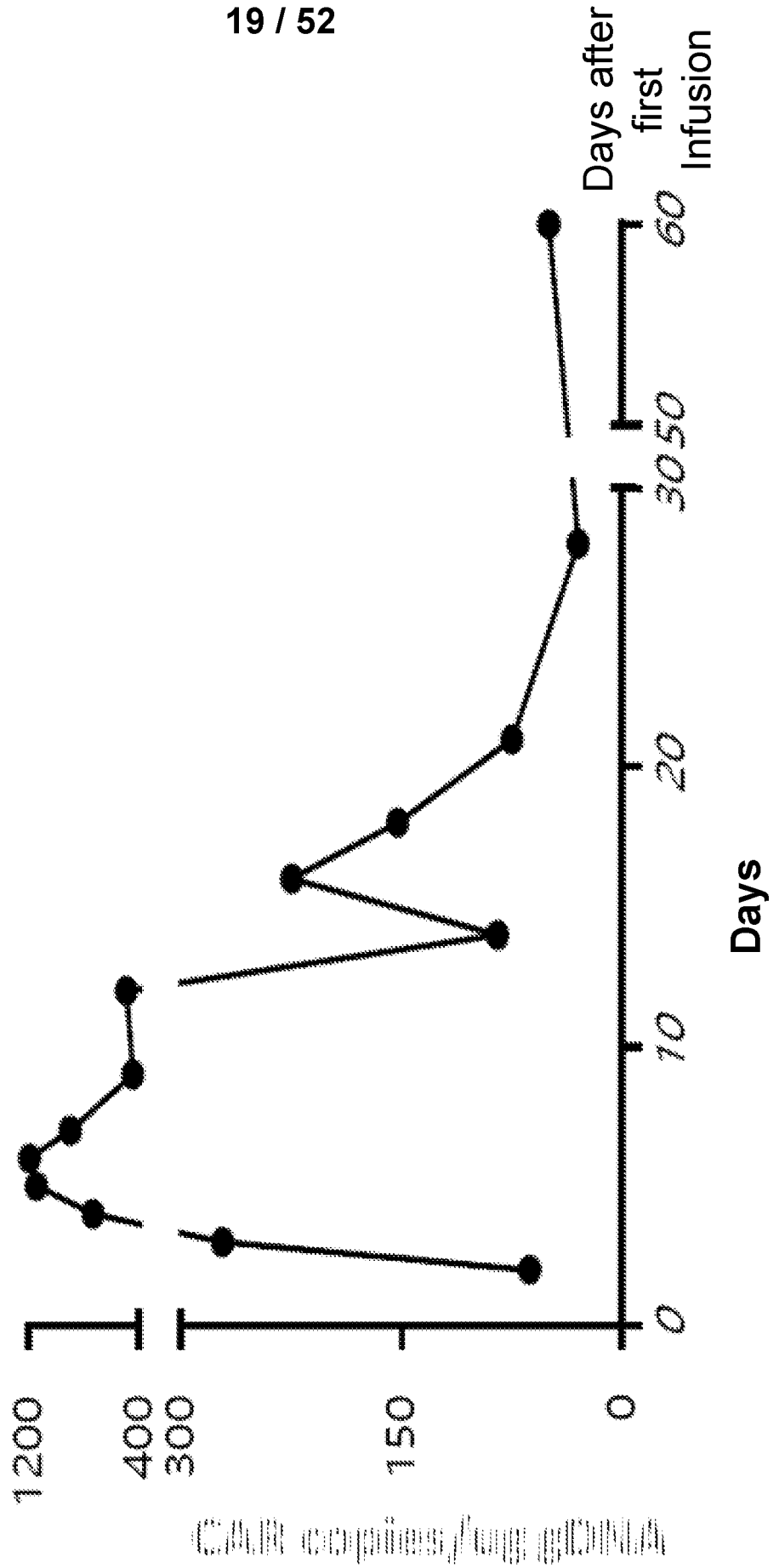
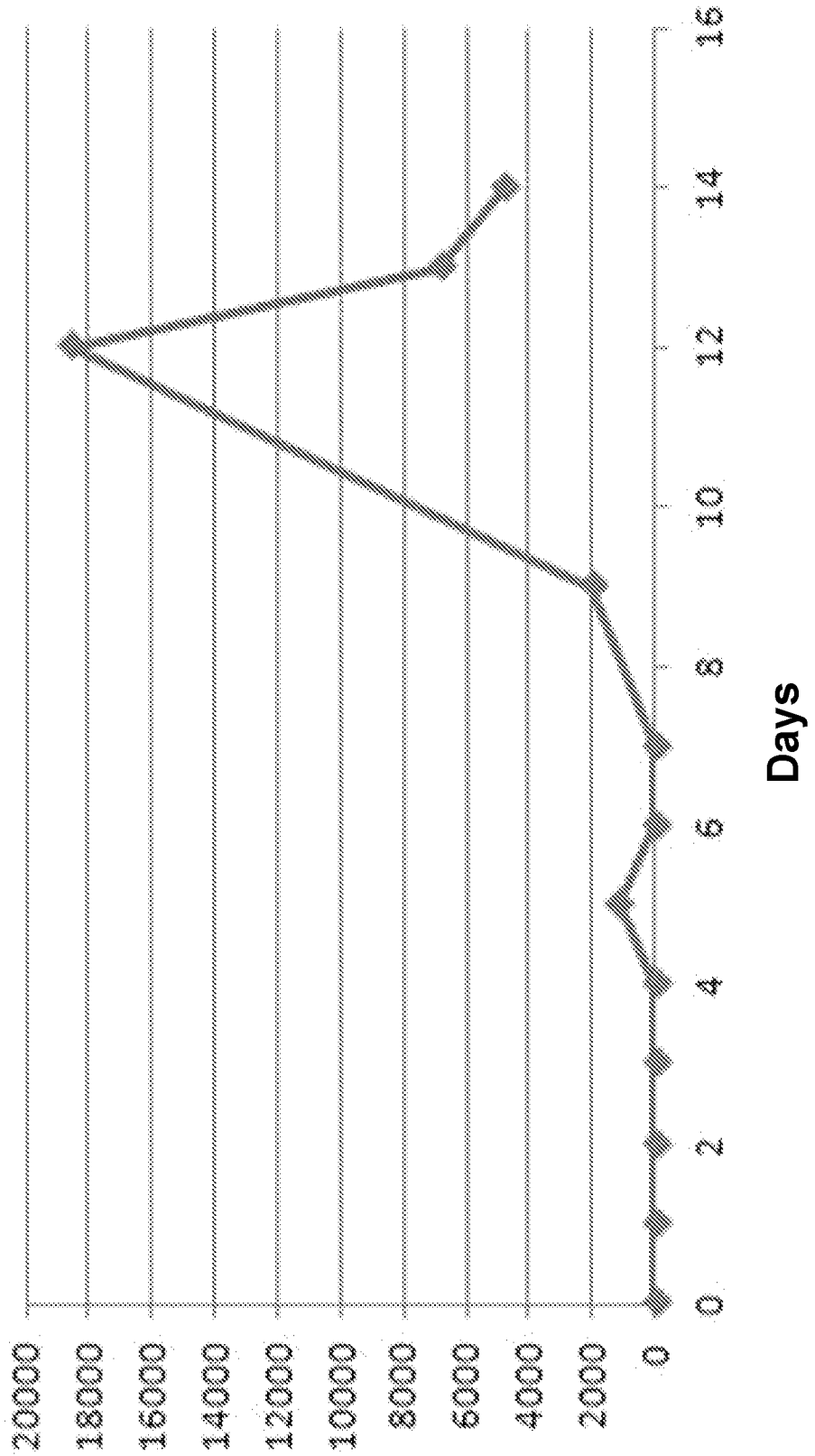


FIG. 19

Patient E



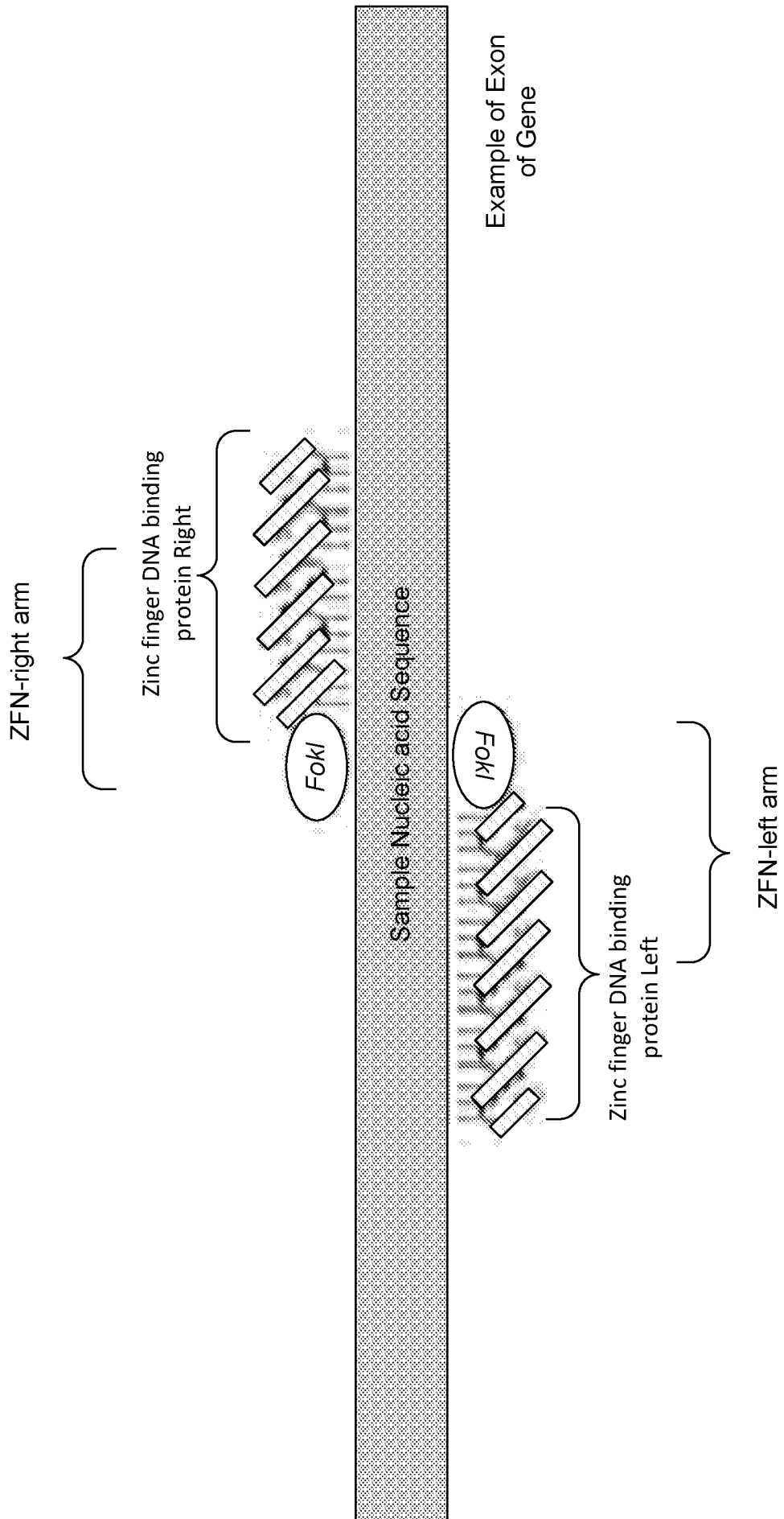
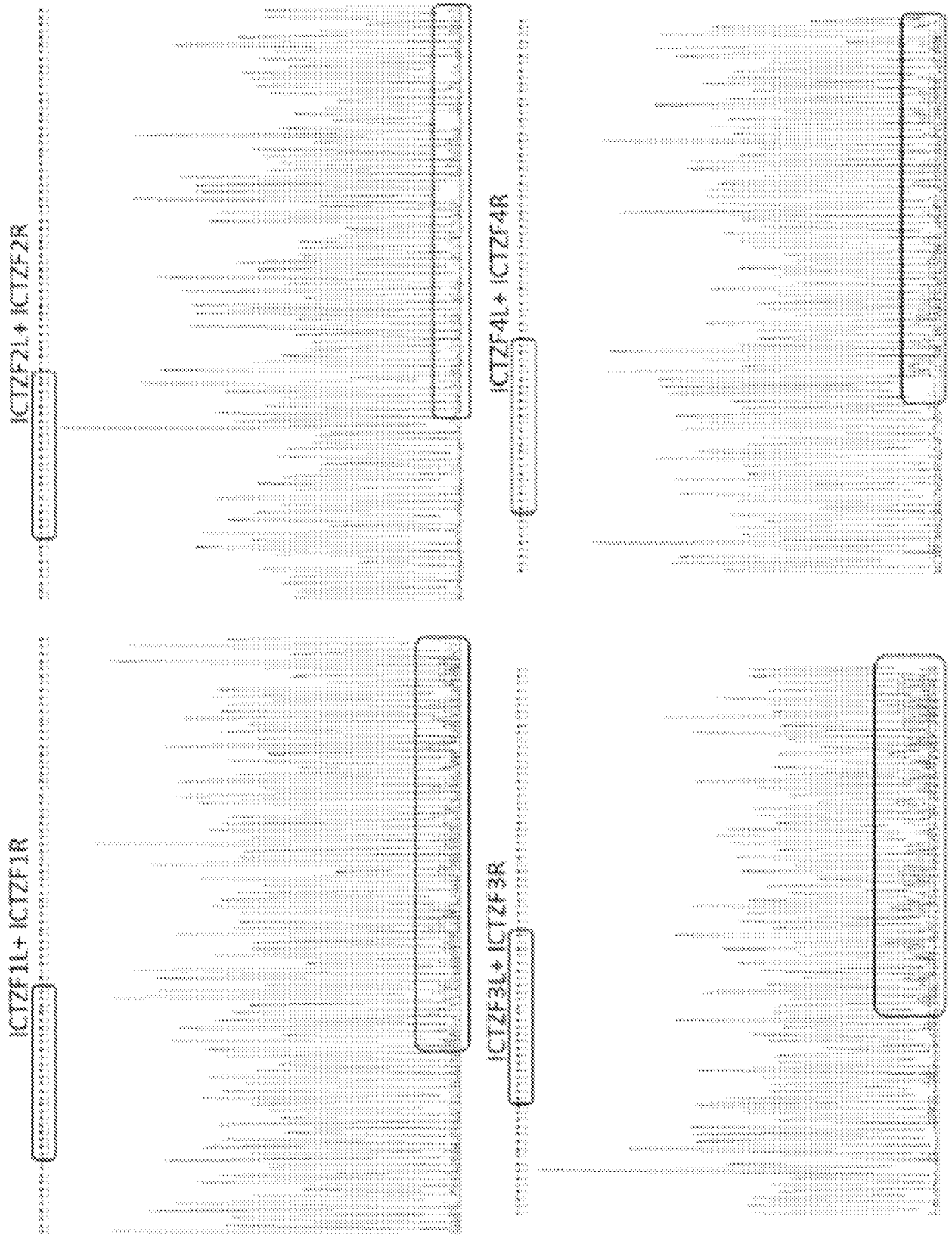
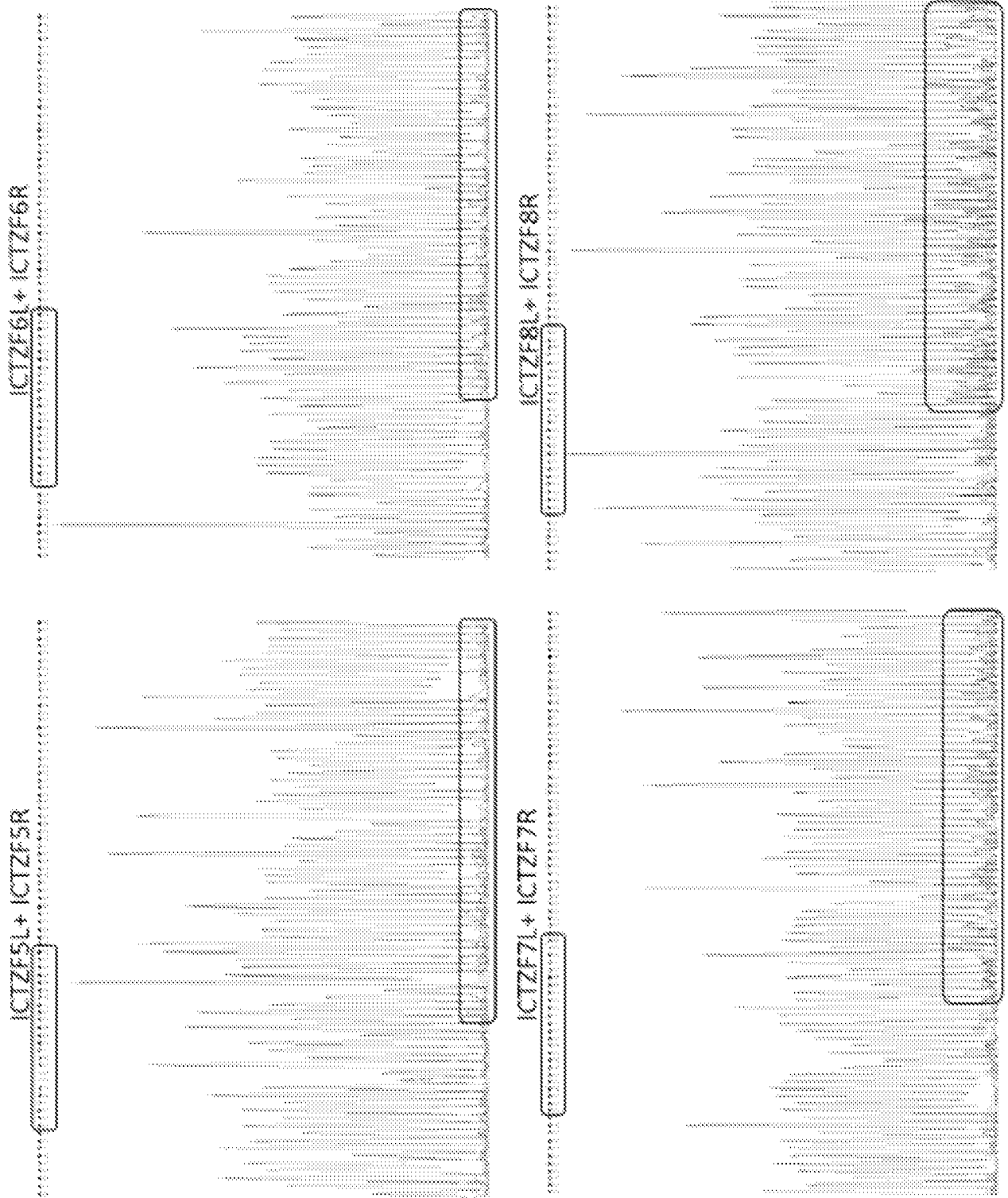
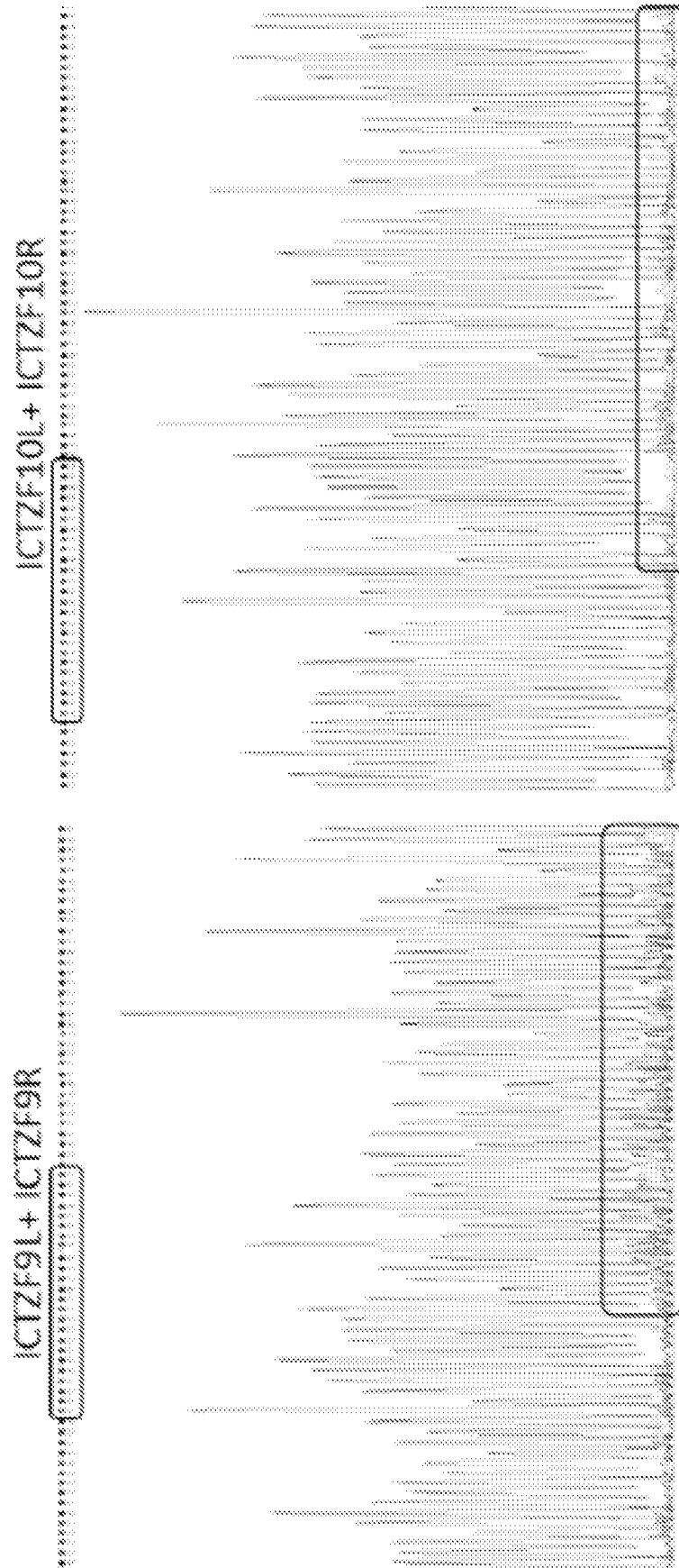


FIG. 21







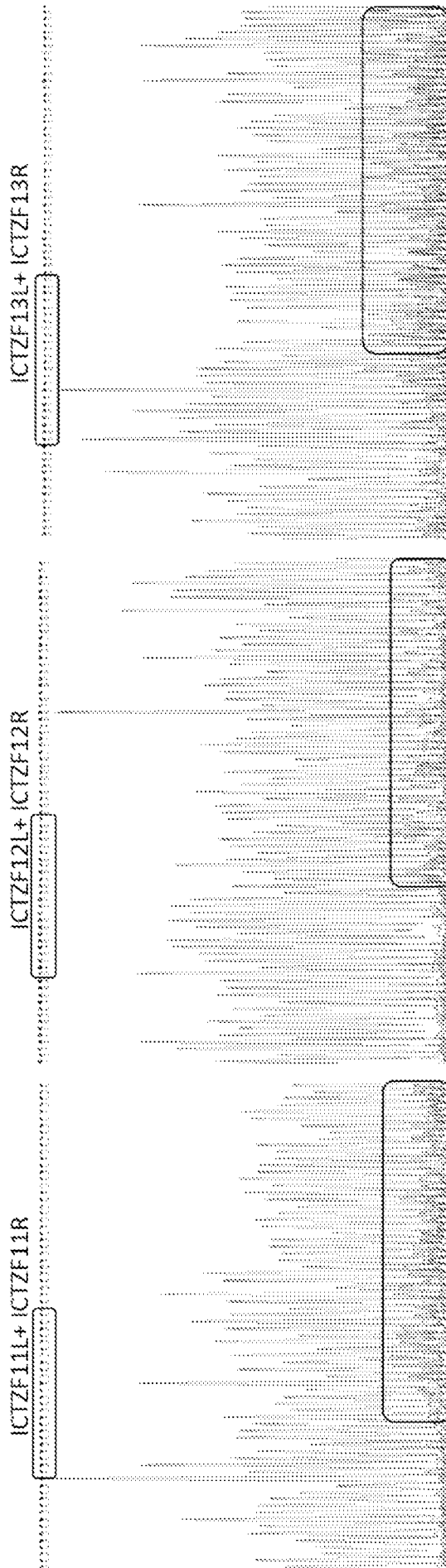


FIG. 25

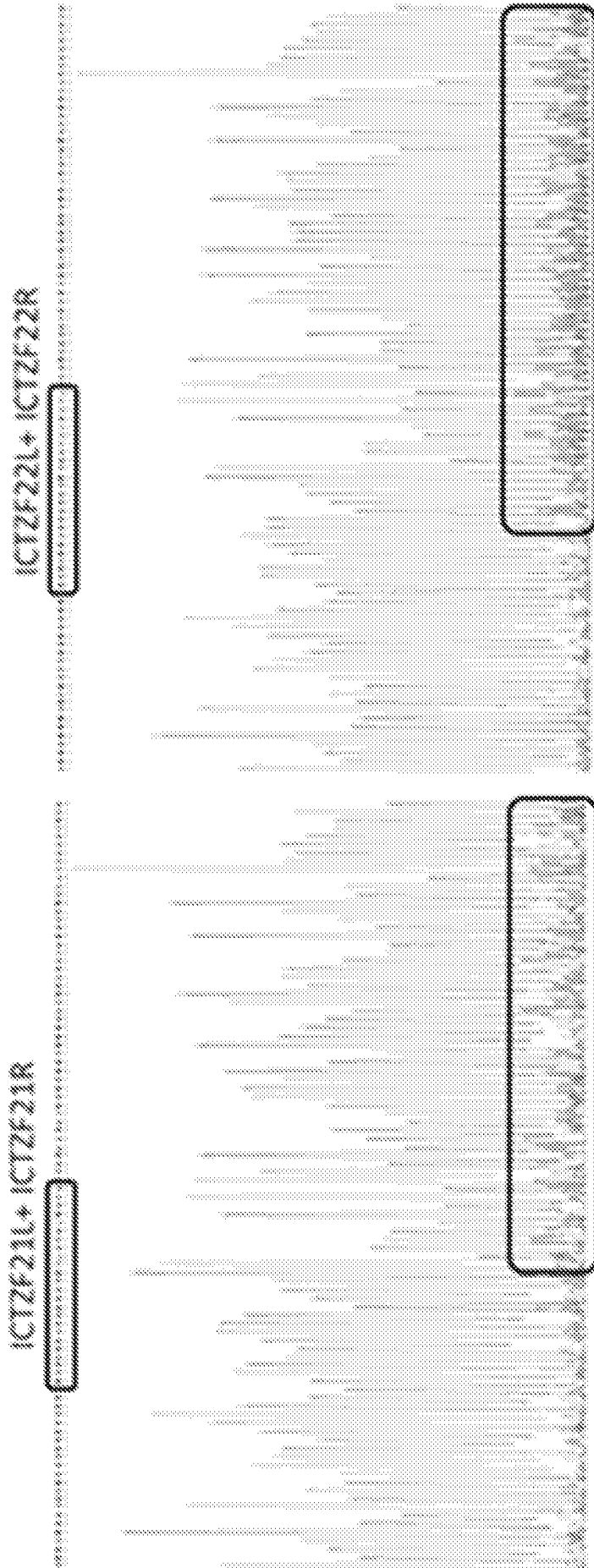


FIG. 26

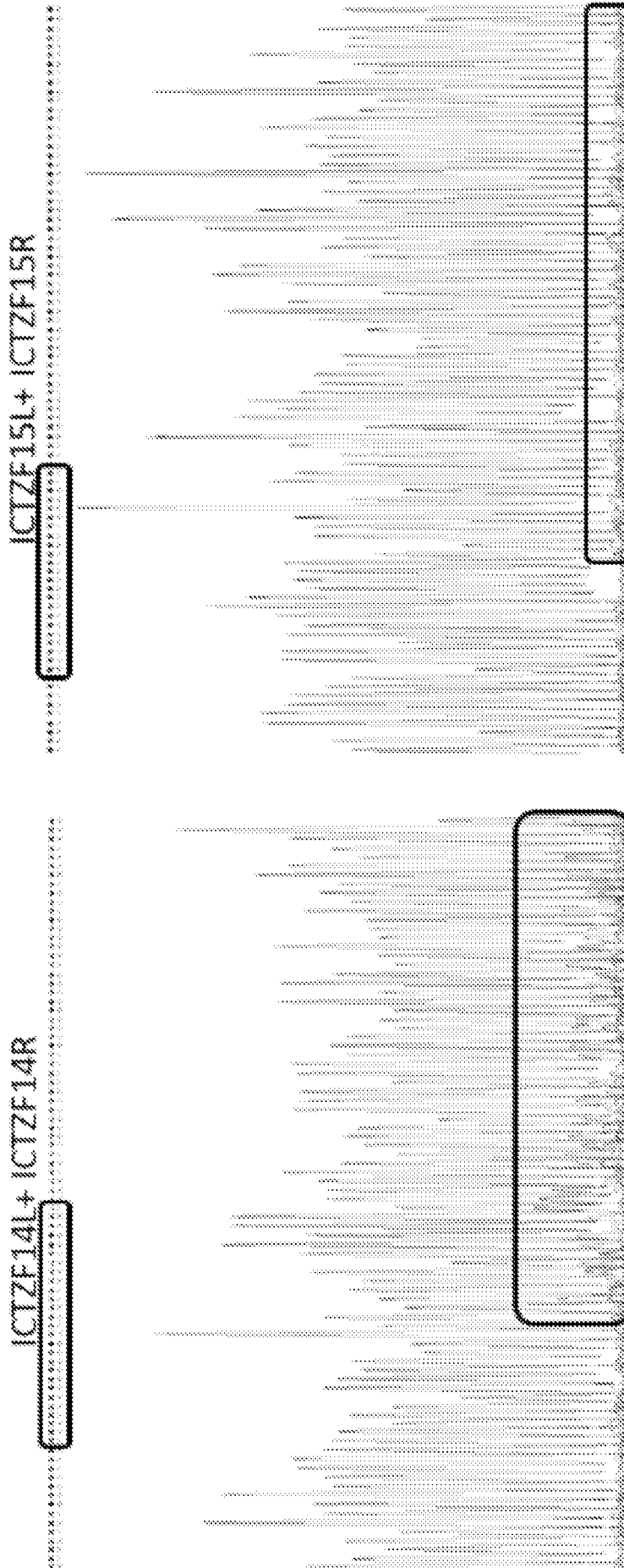


FIG. 27

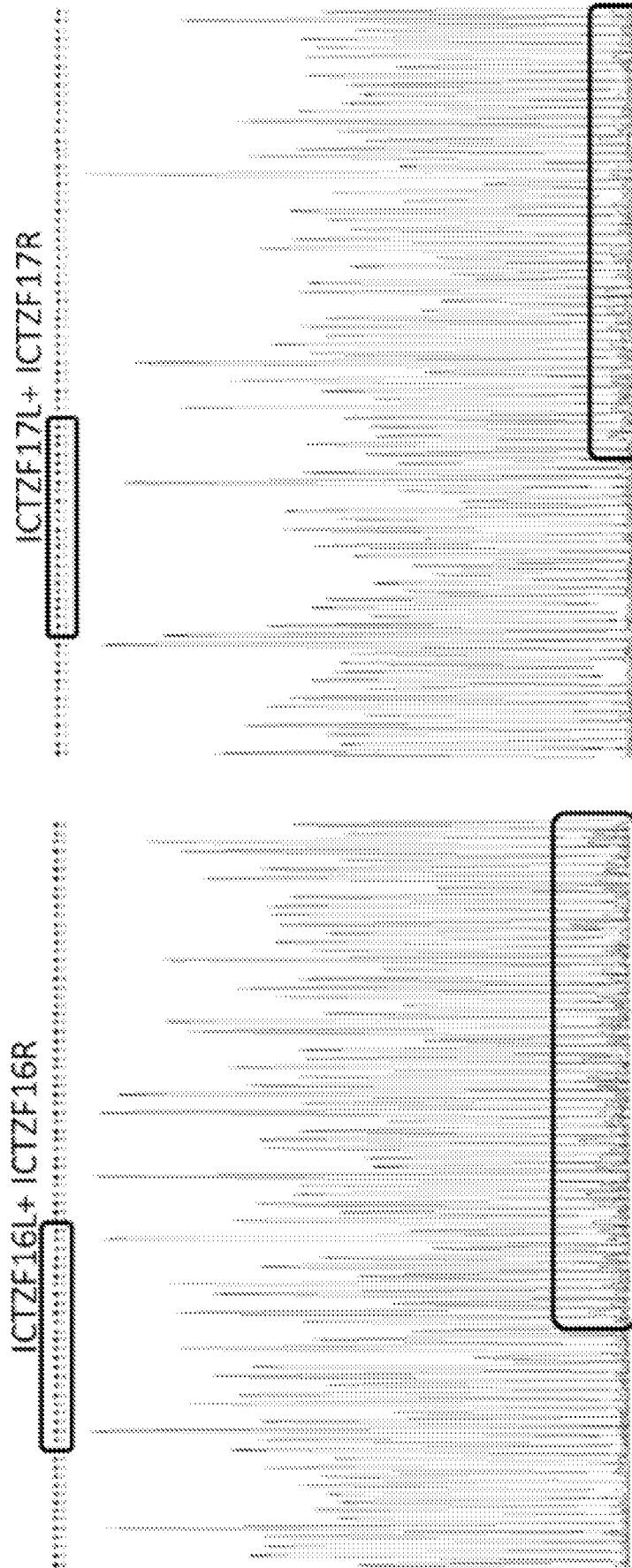


FIG. 28

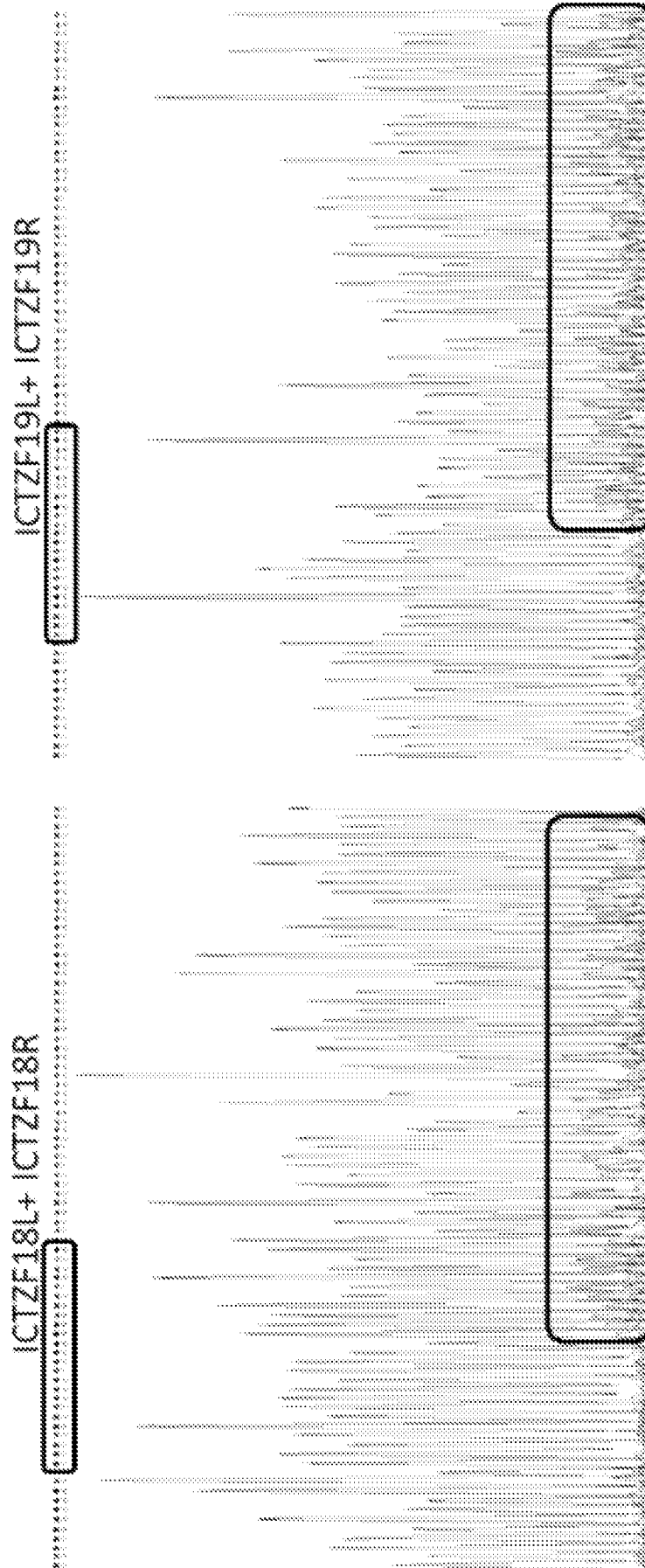
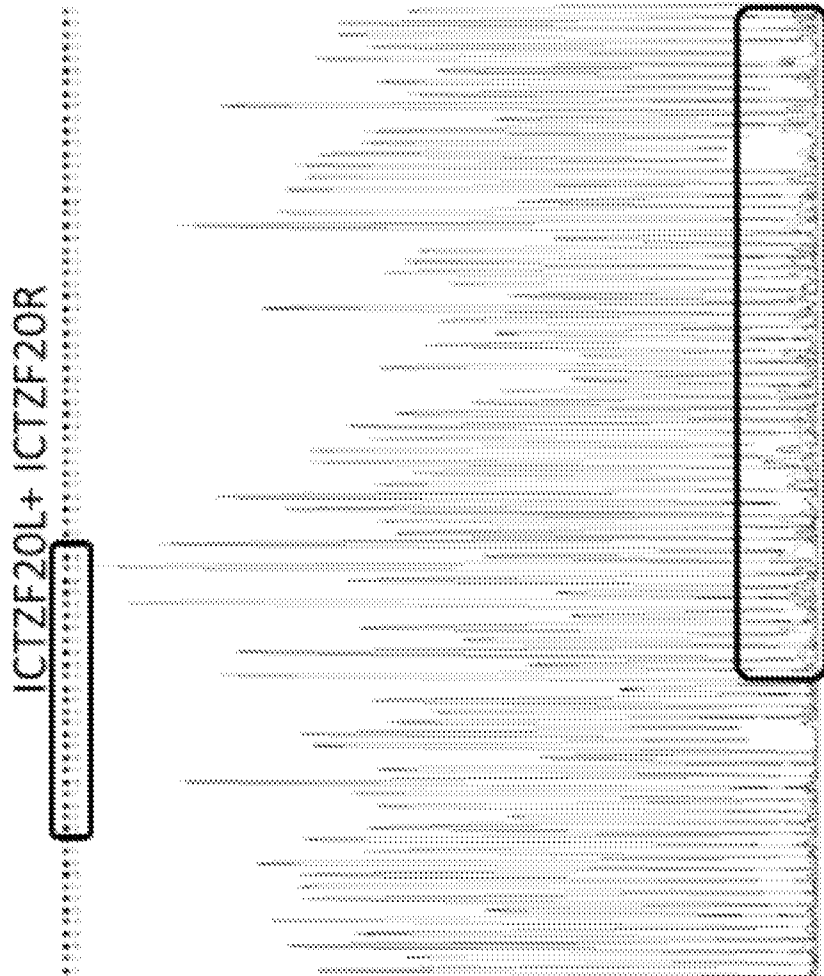


FIG. 29



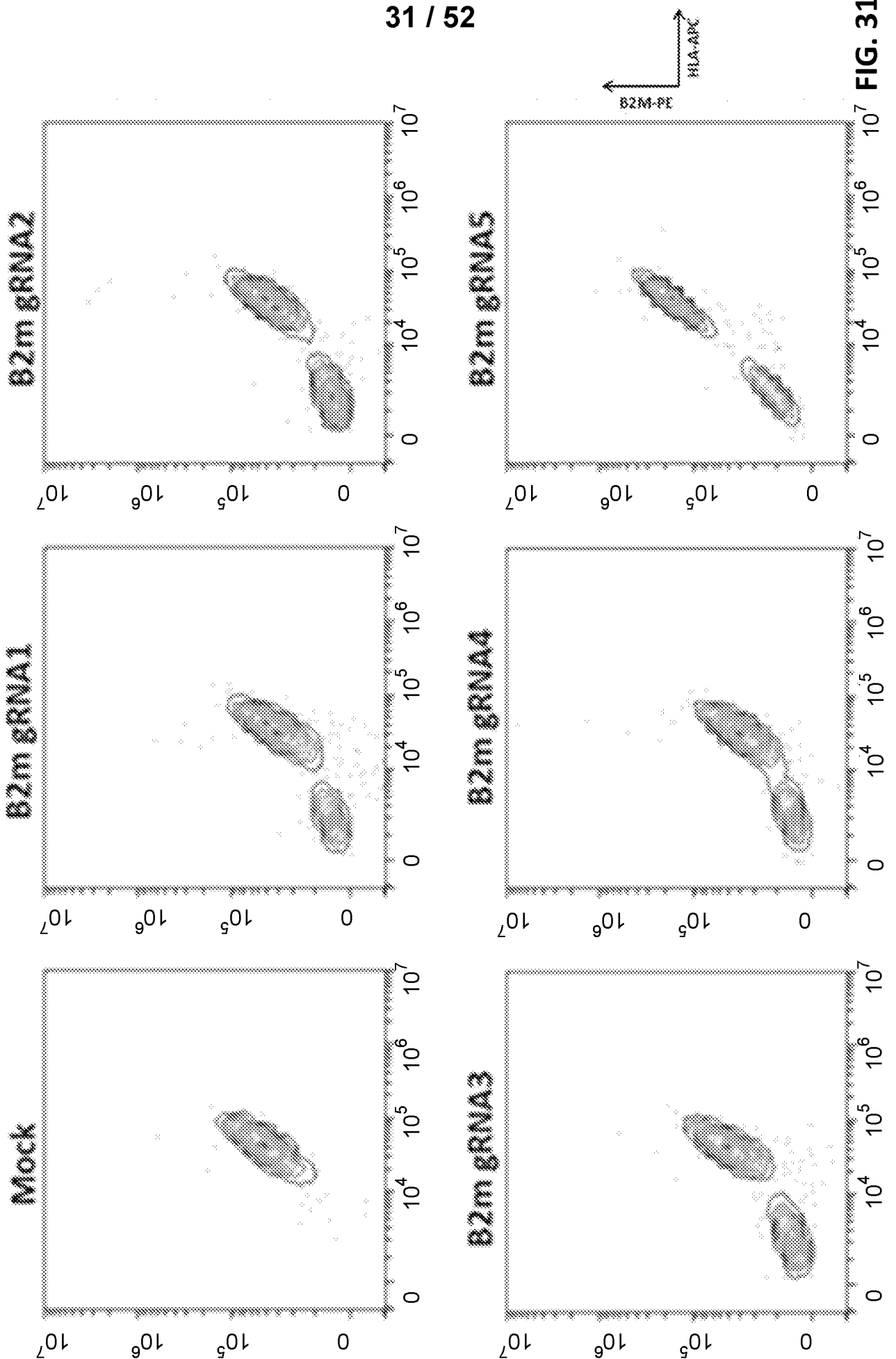
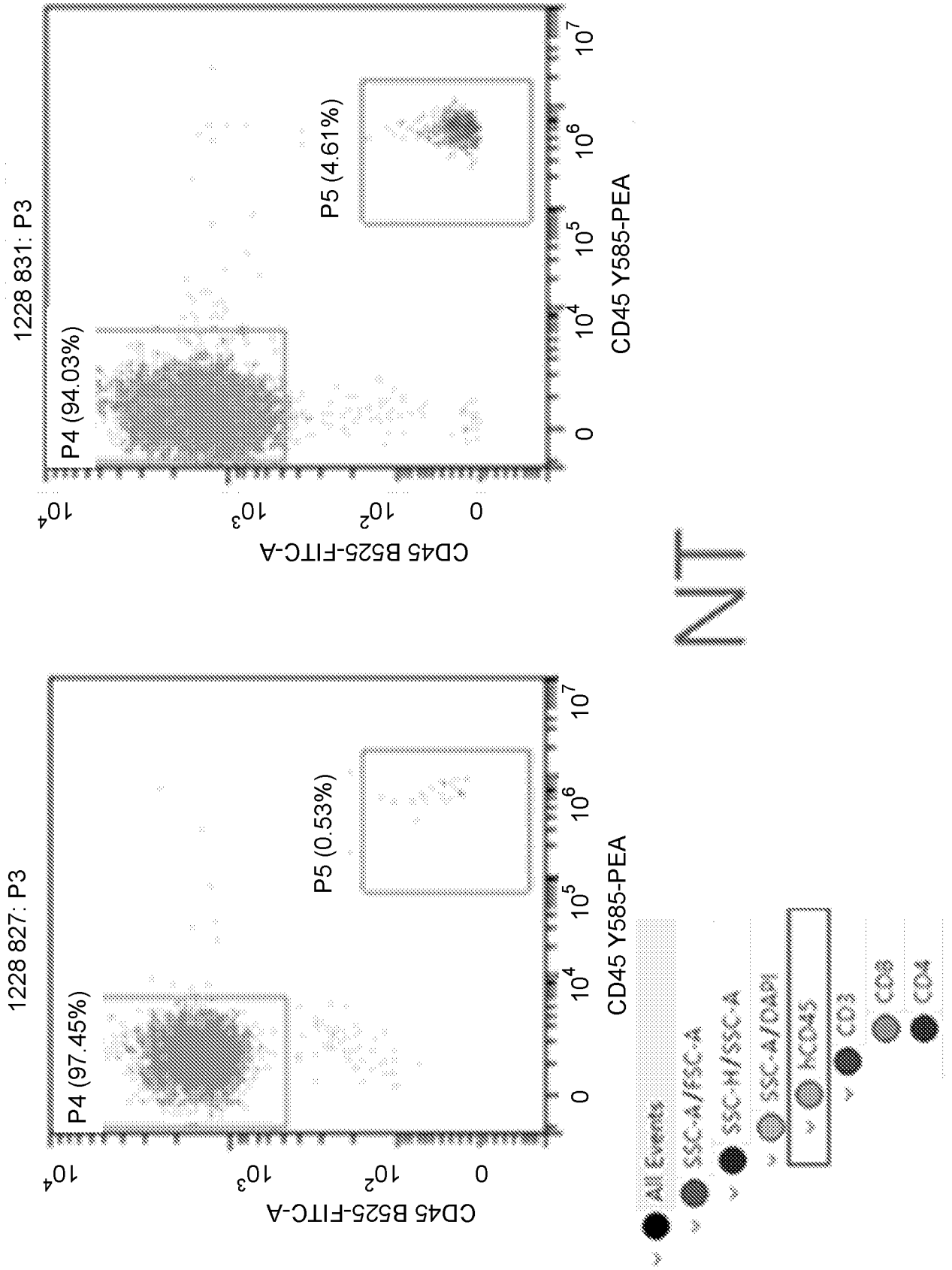
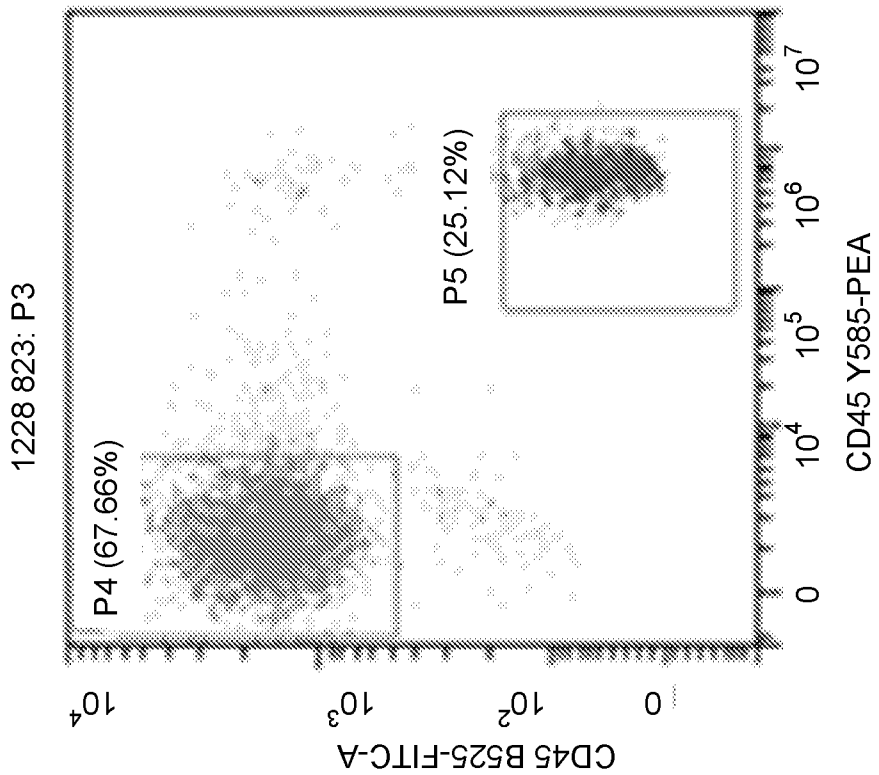
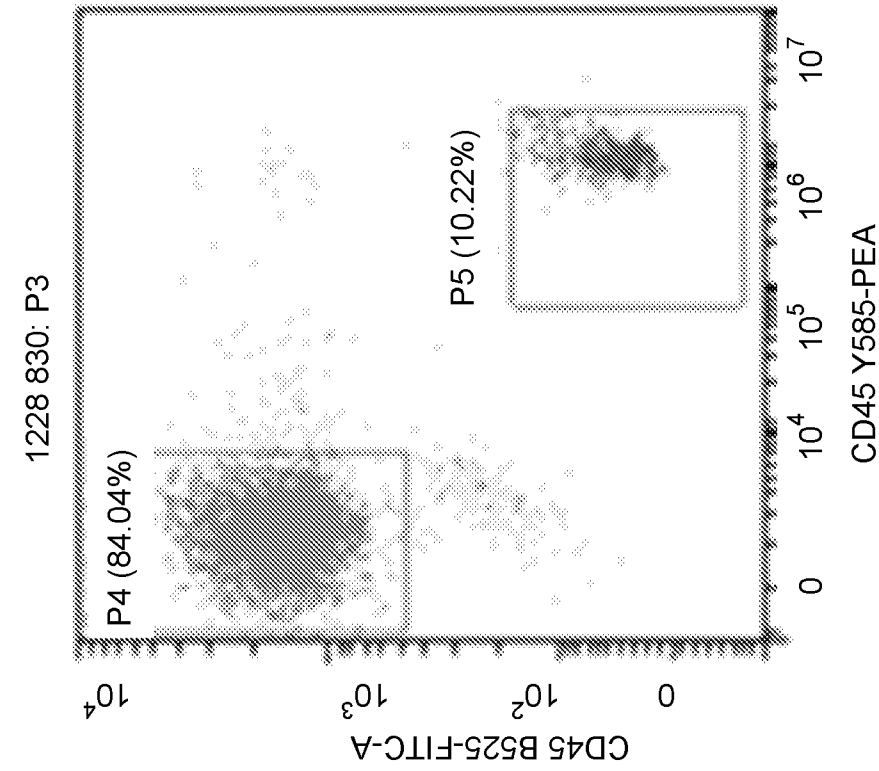
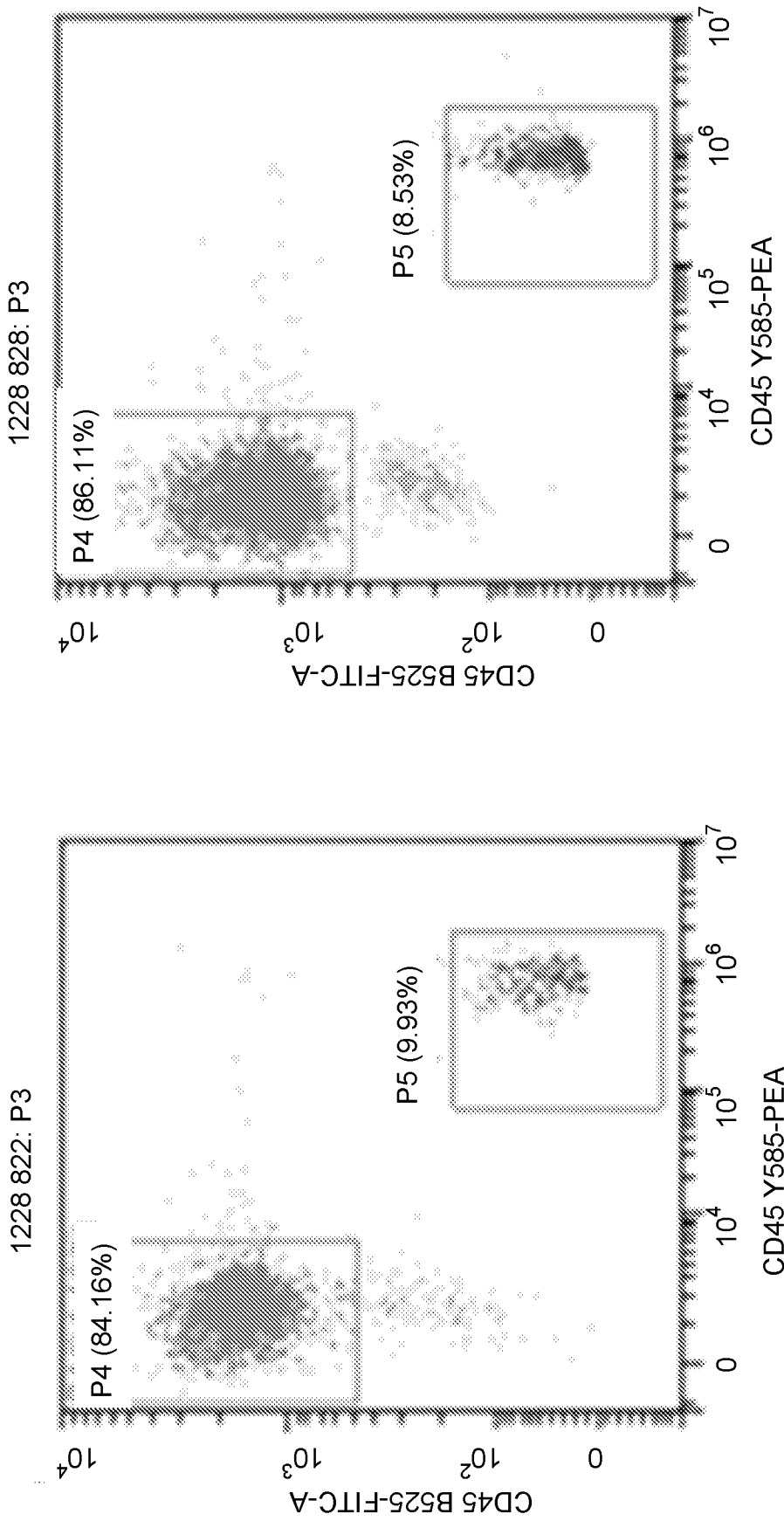


FIG. 31



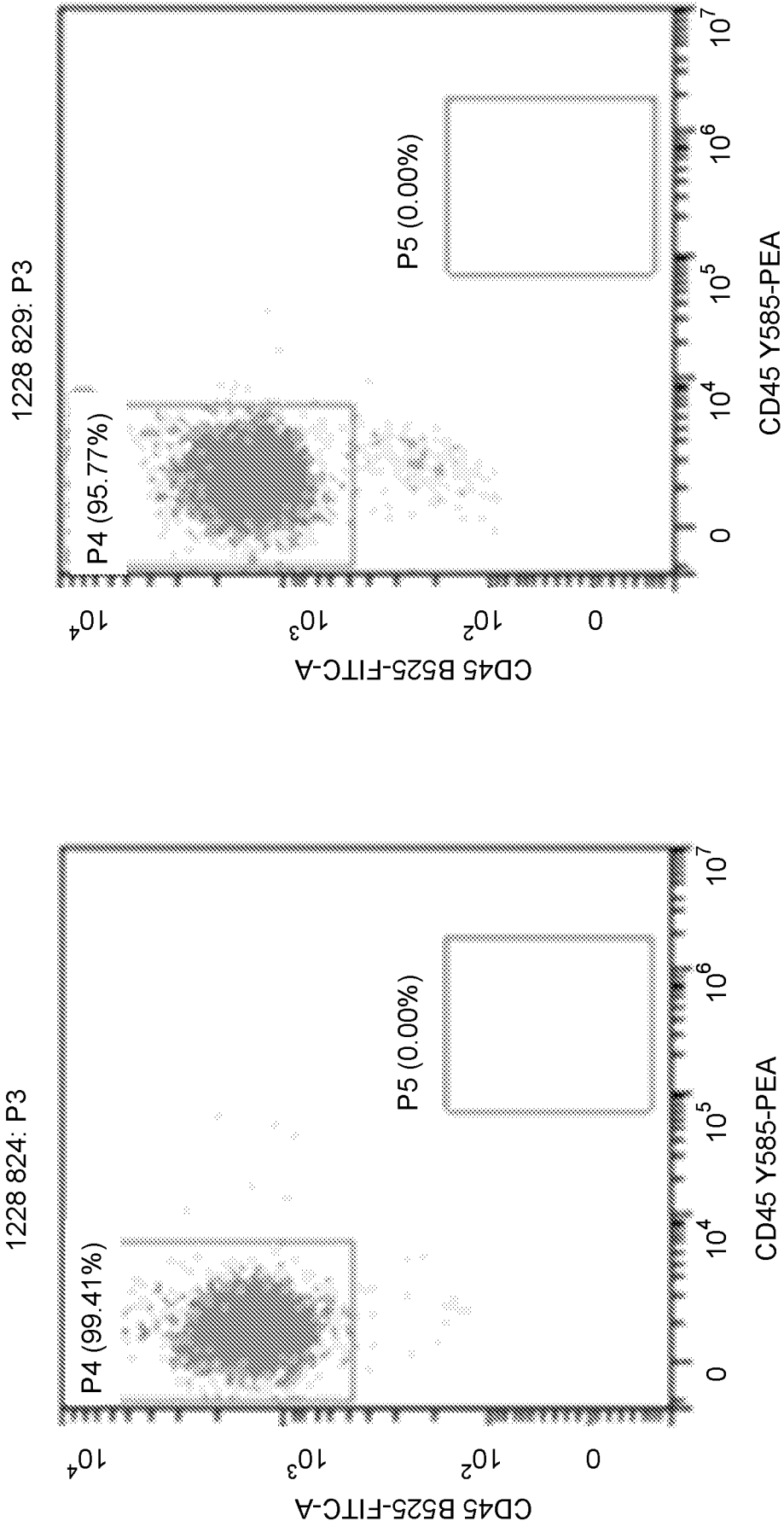


2407



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FIG. 34



MOCK

FIG. 35

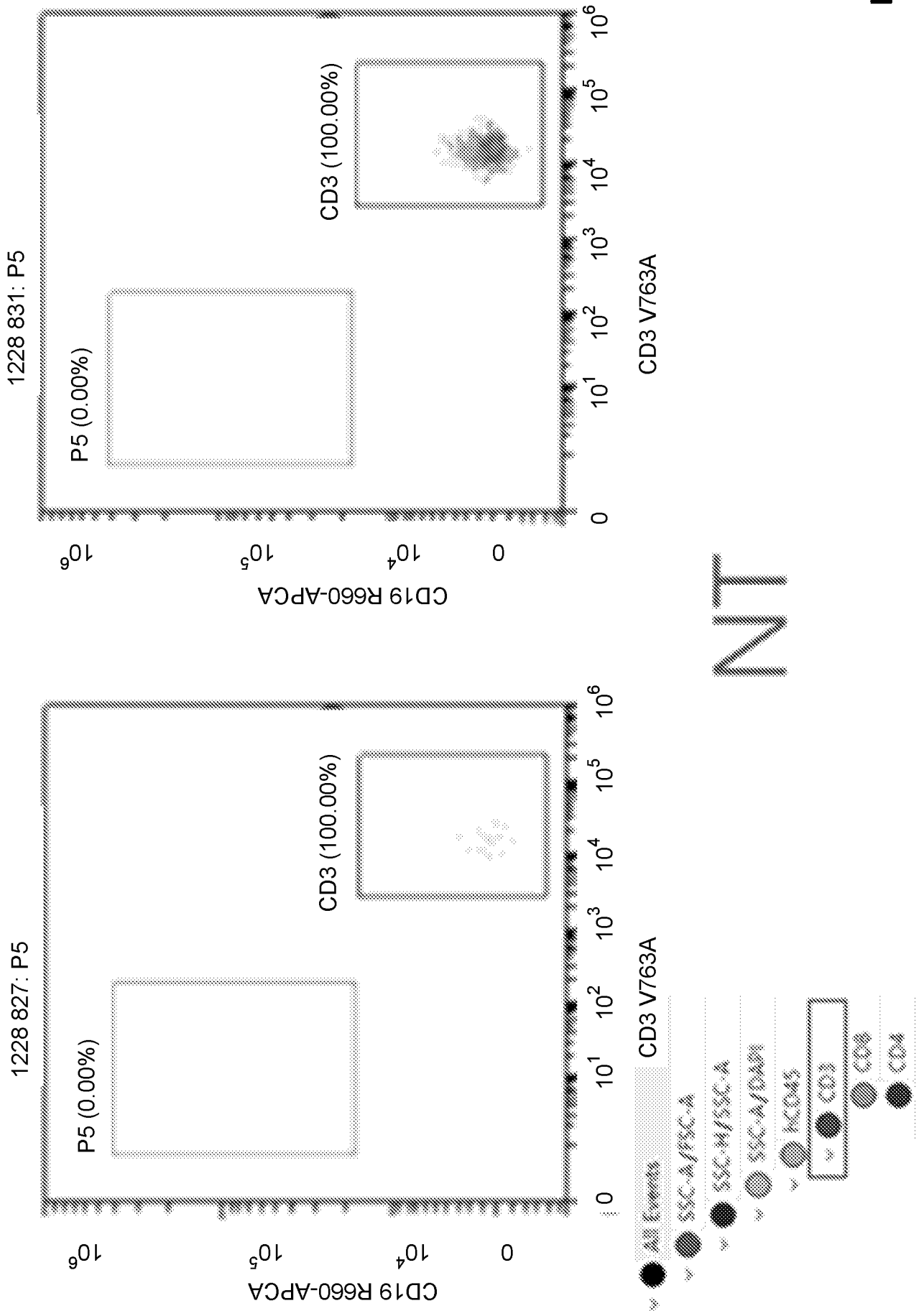
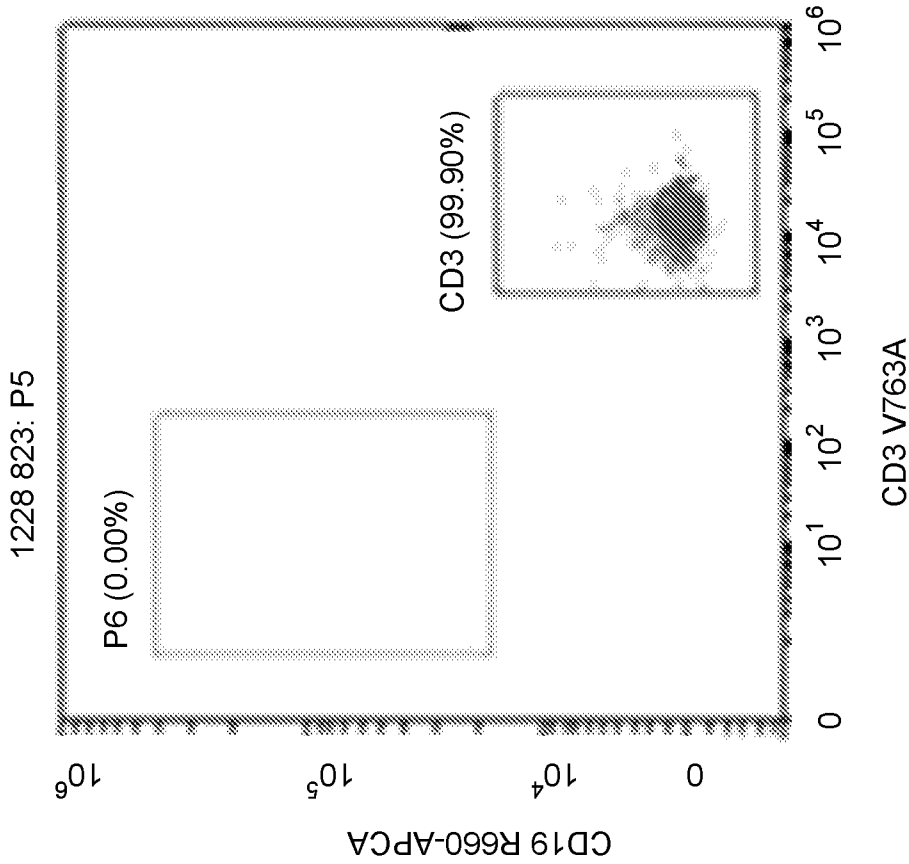
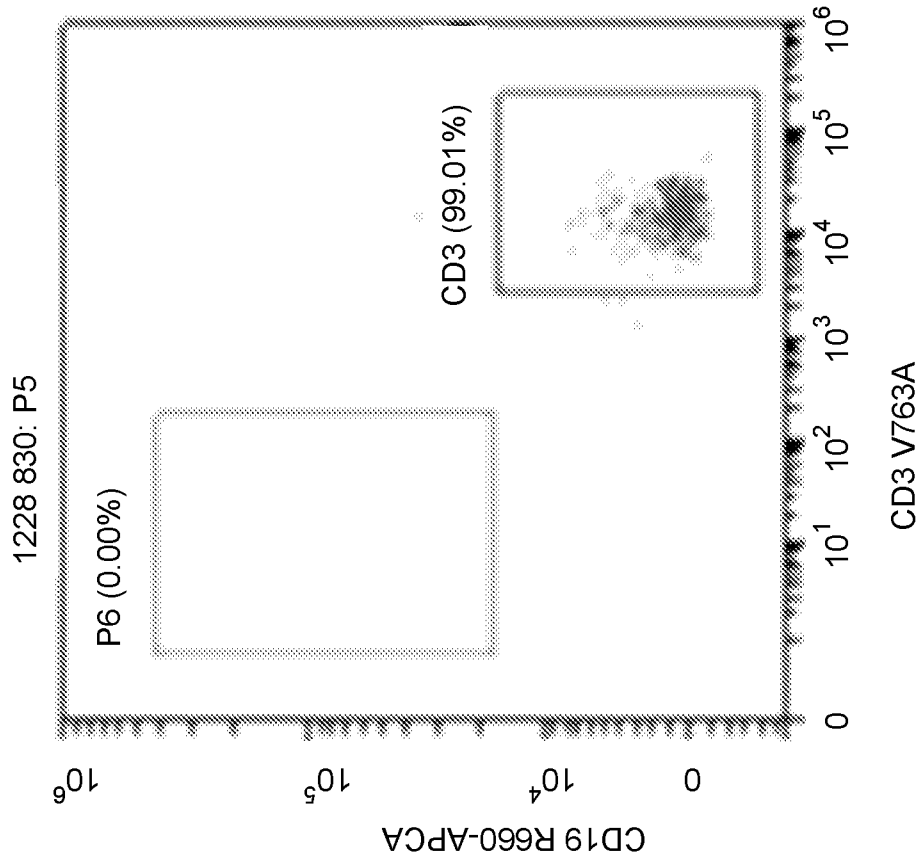
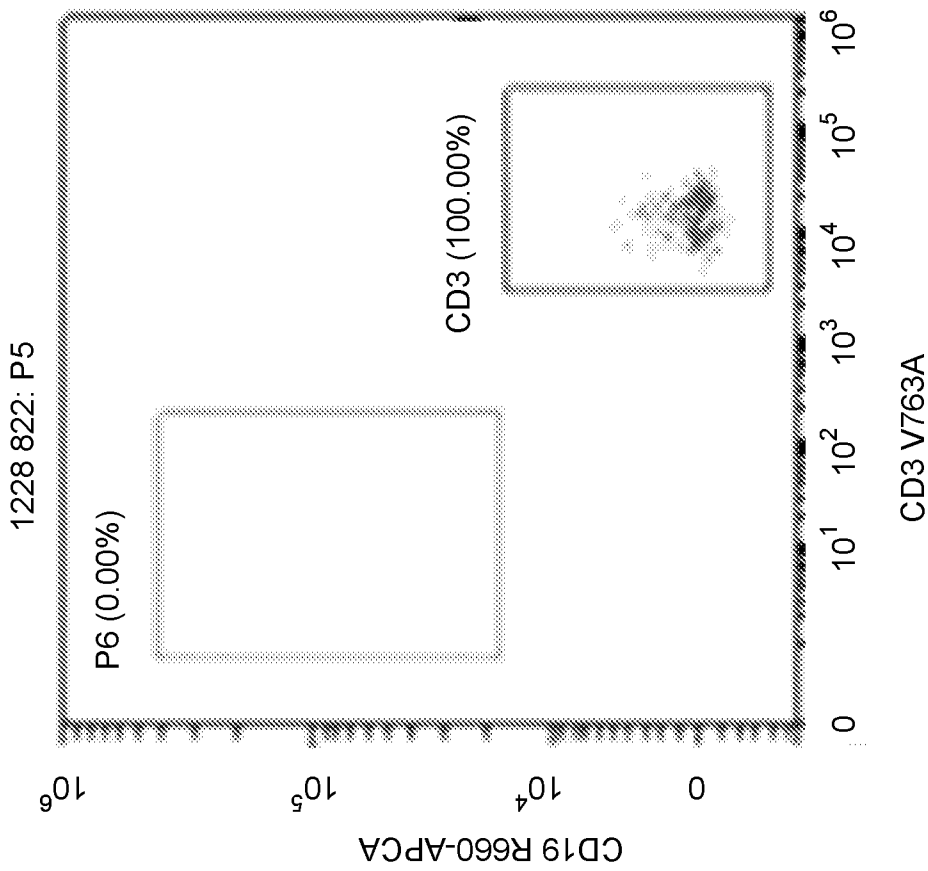
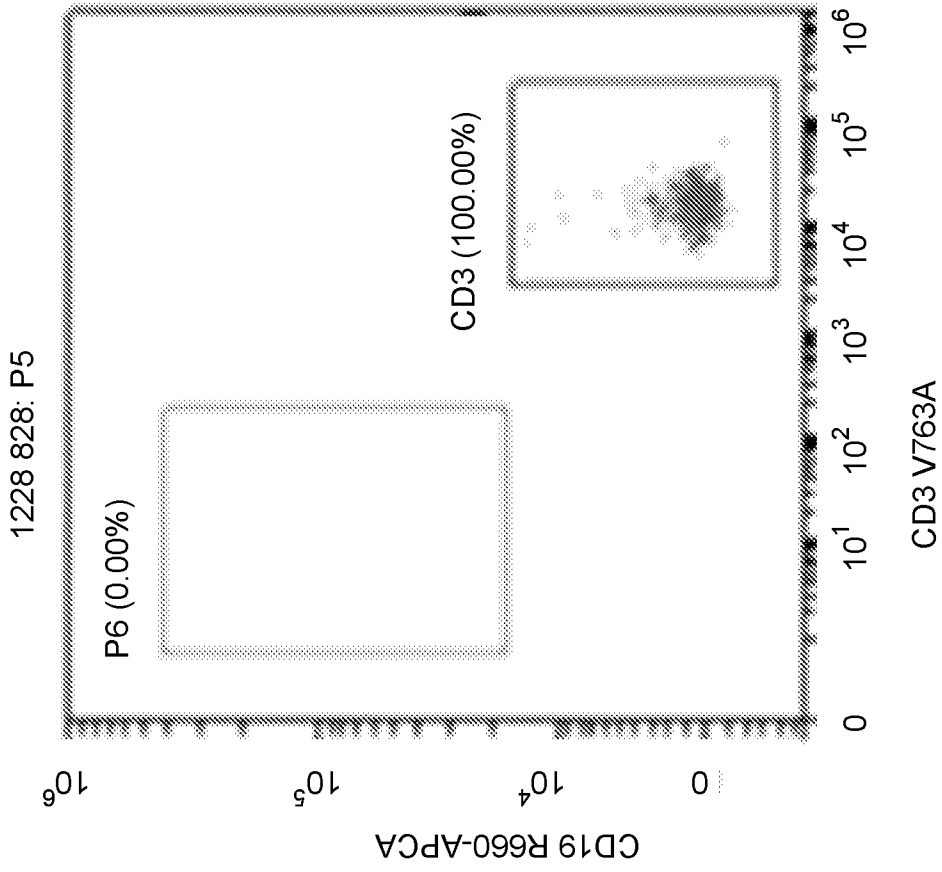


FIG. 36



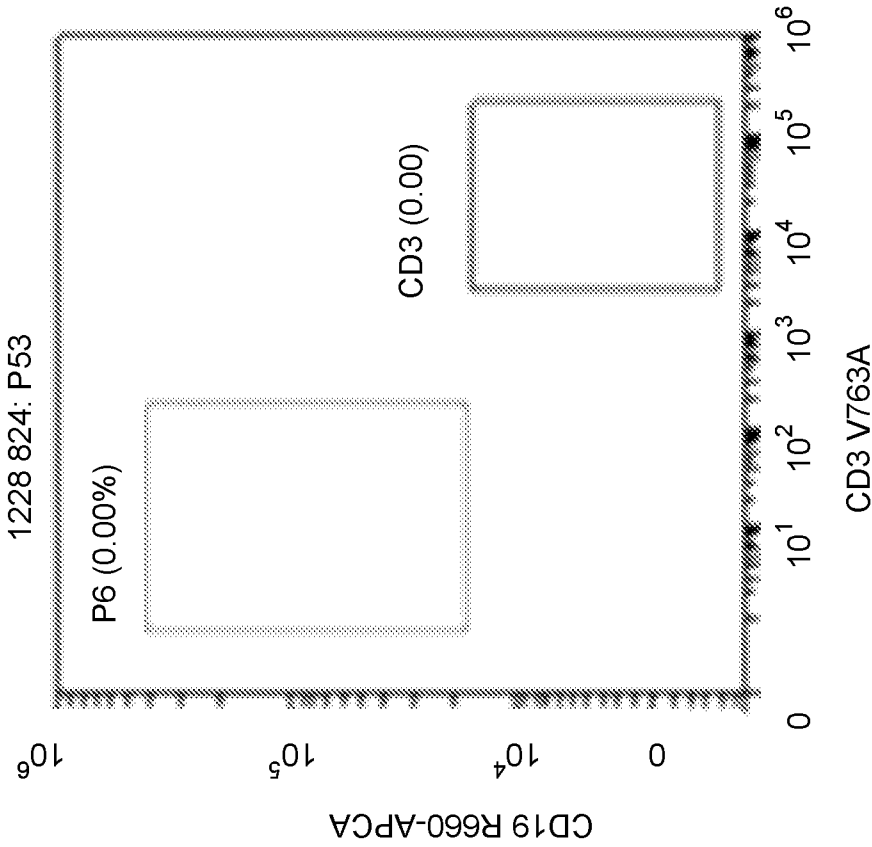
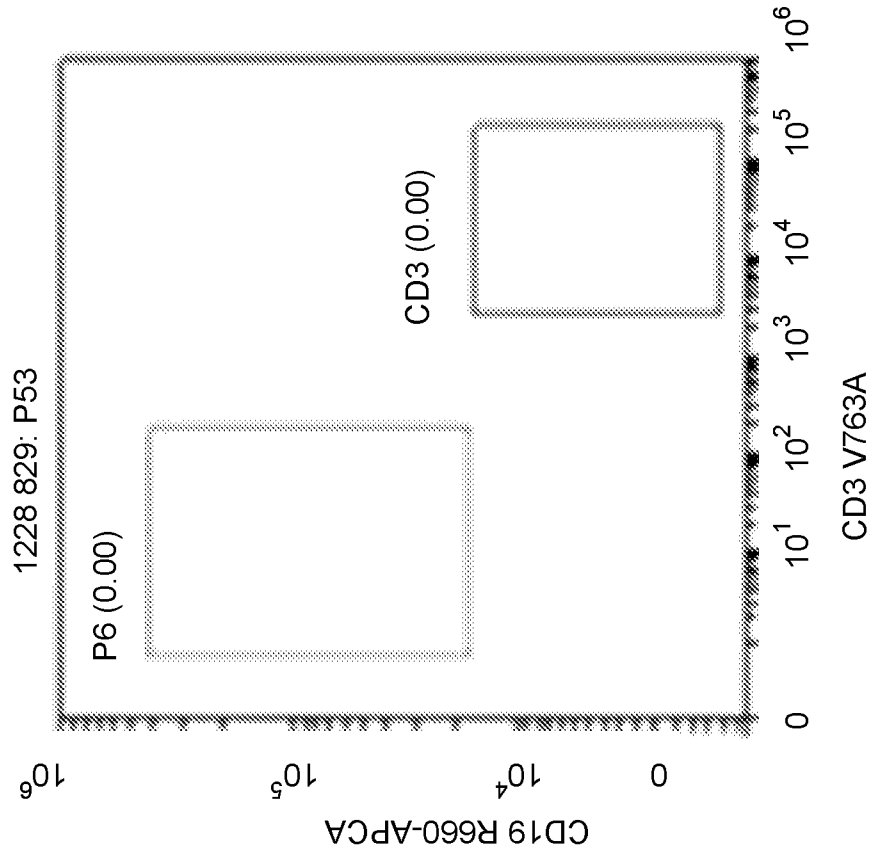
2407

FIG. 37



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FIG. 38



MOCK

FIG. 39

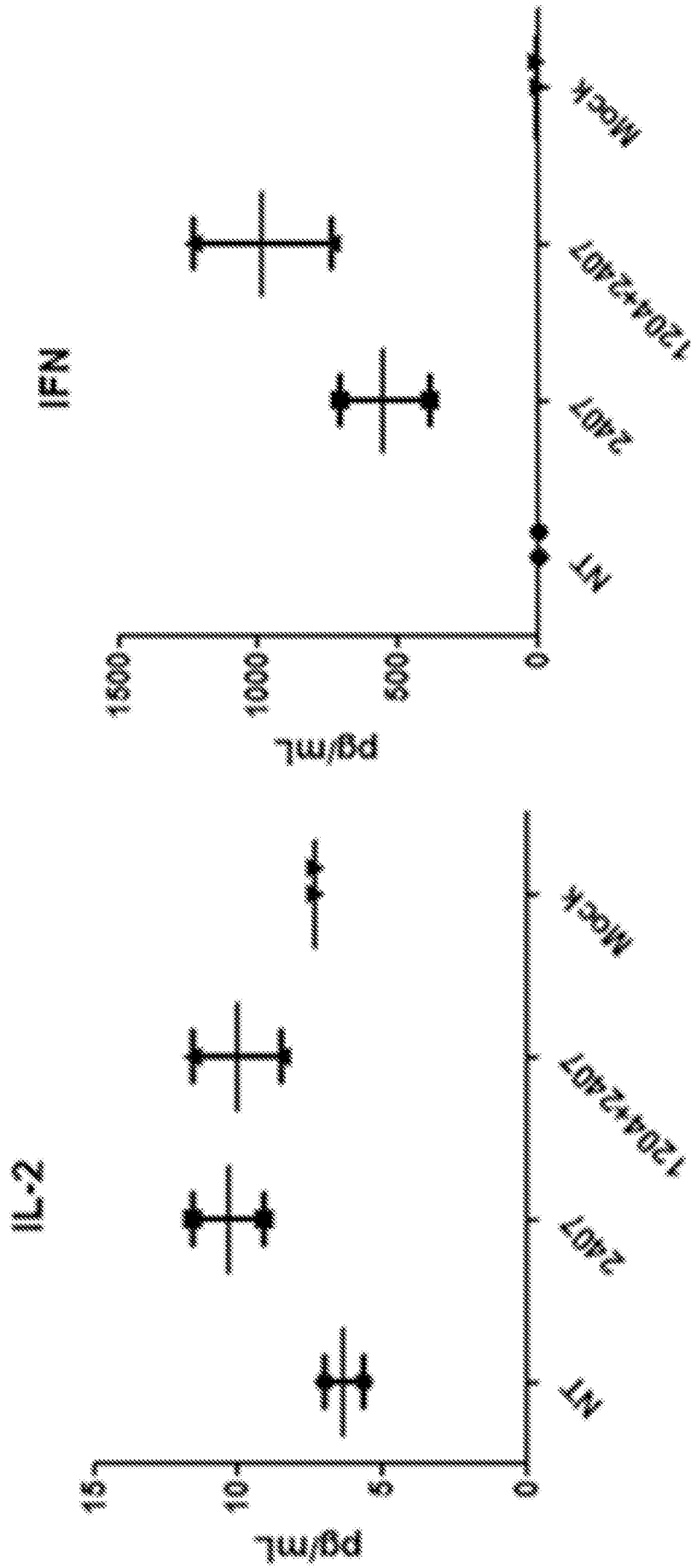


FIG. 40

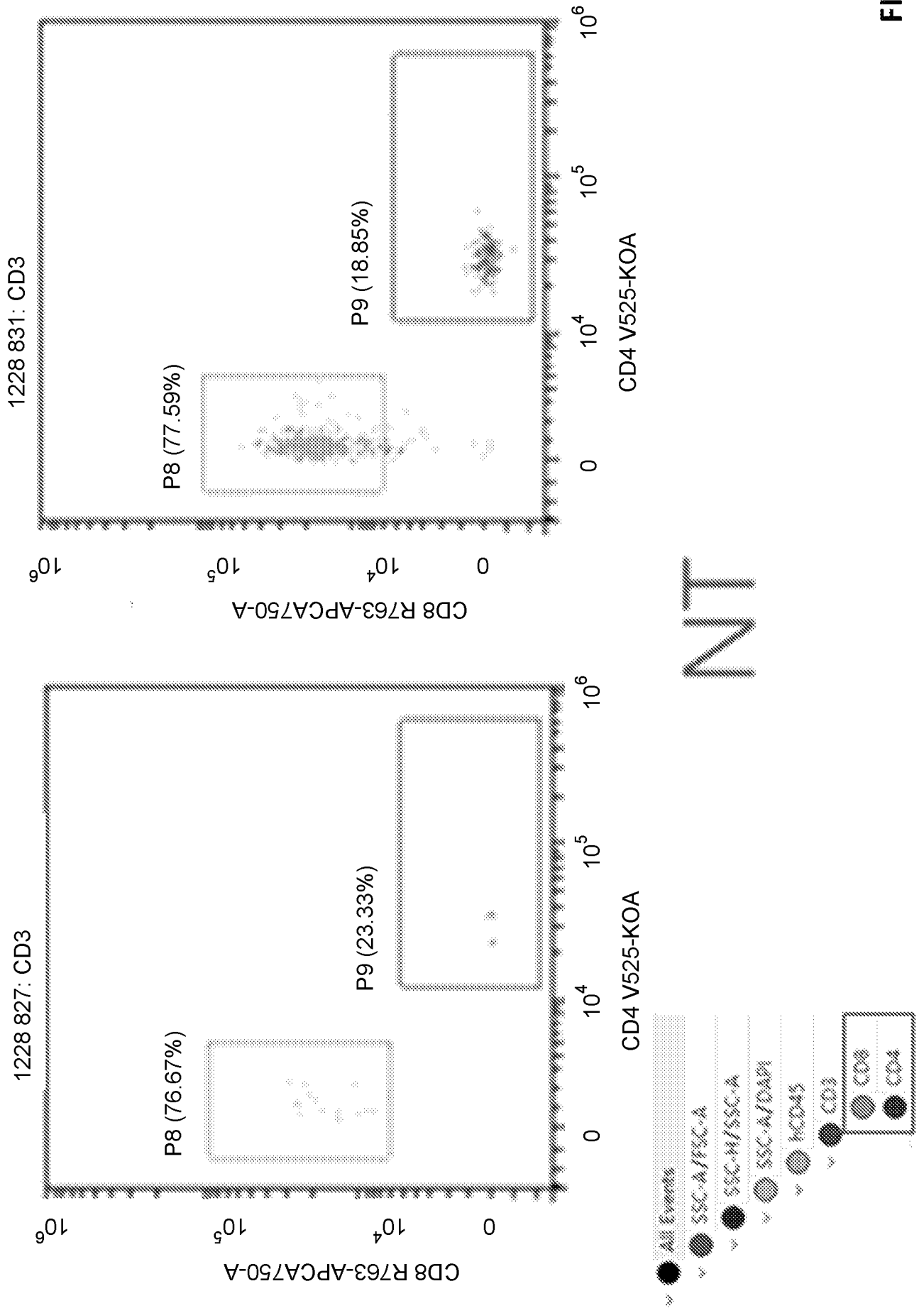
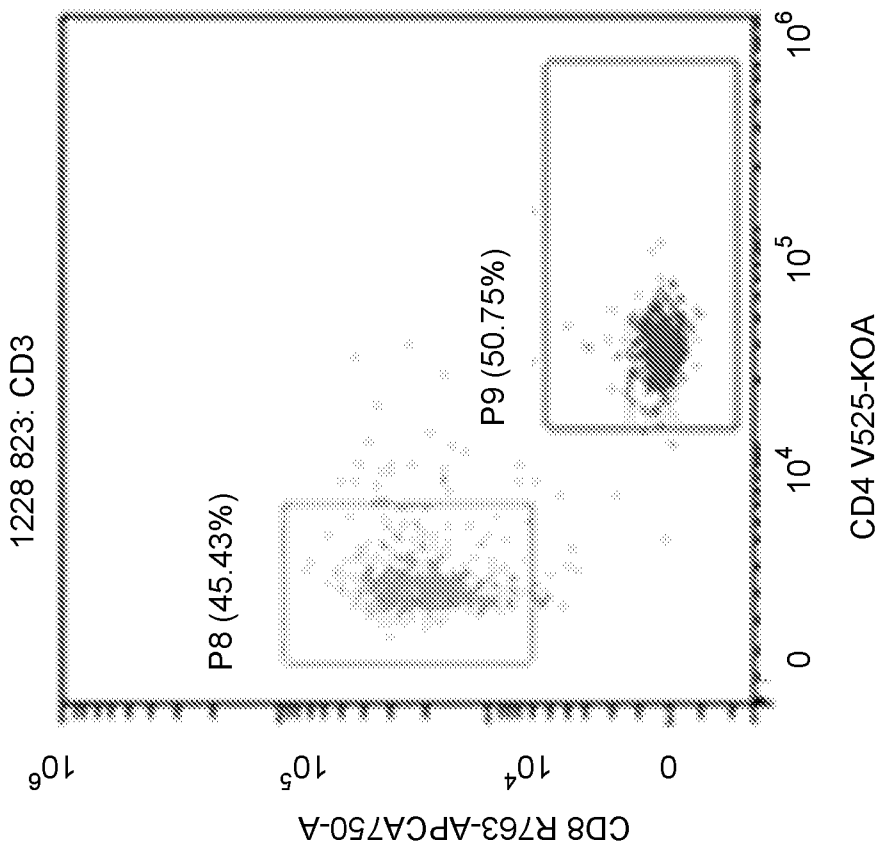
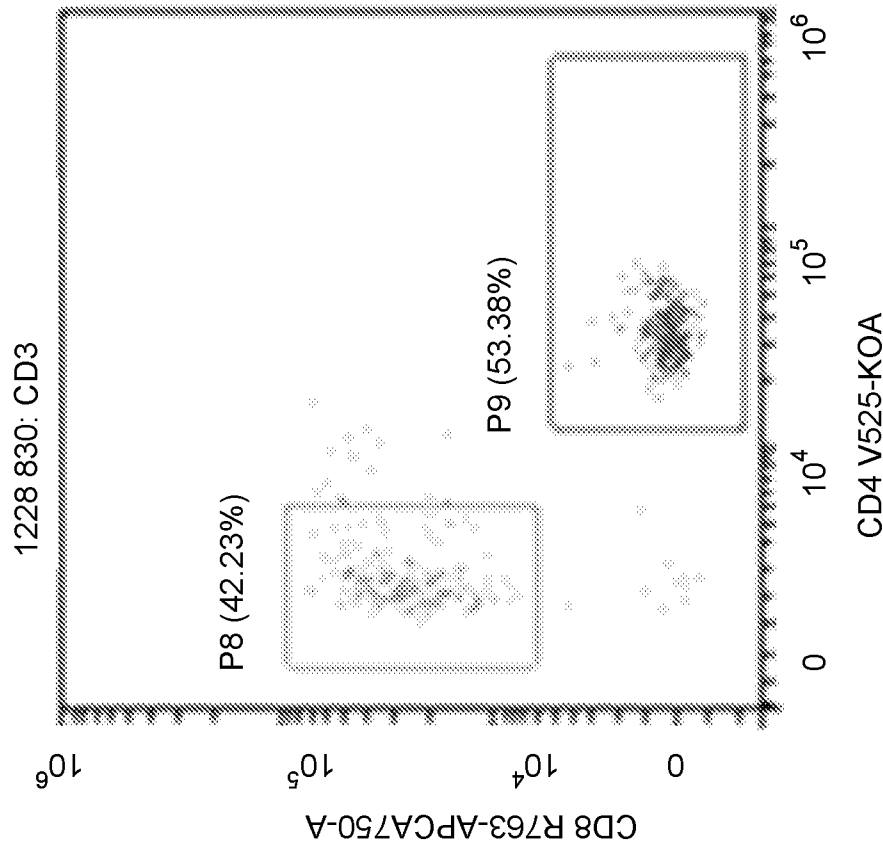
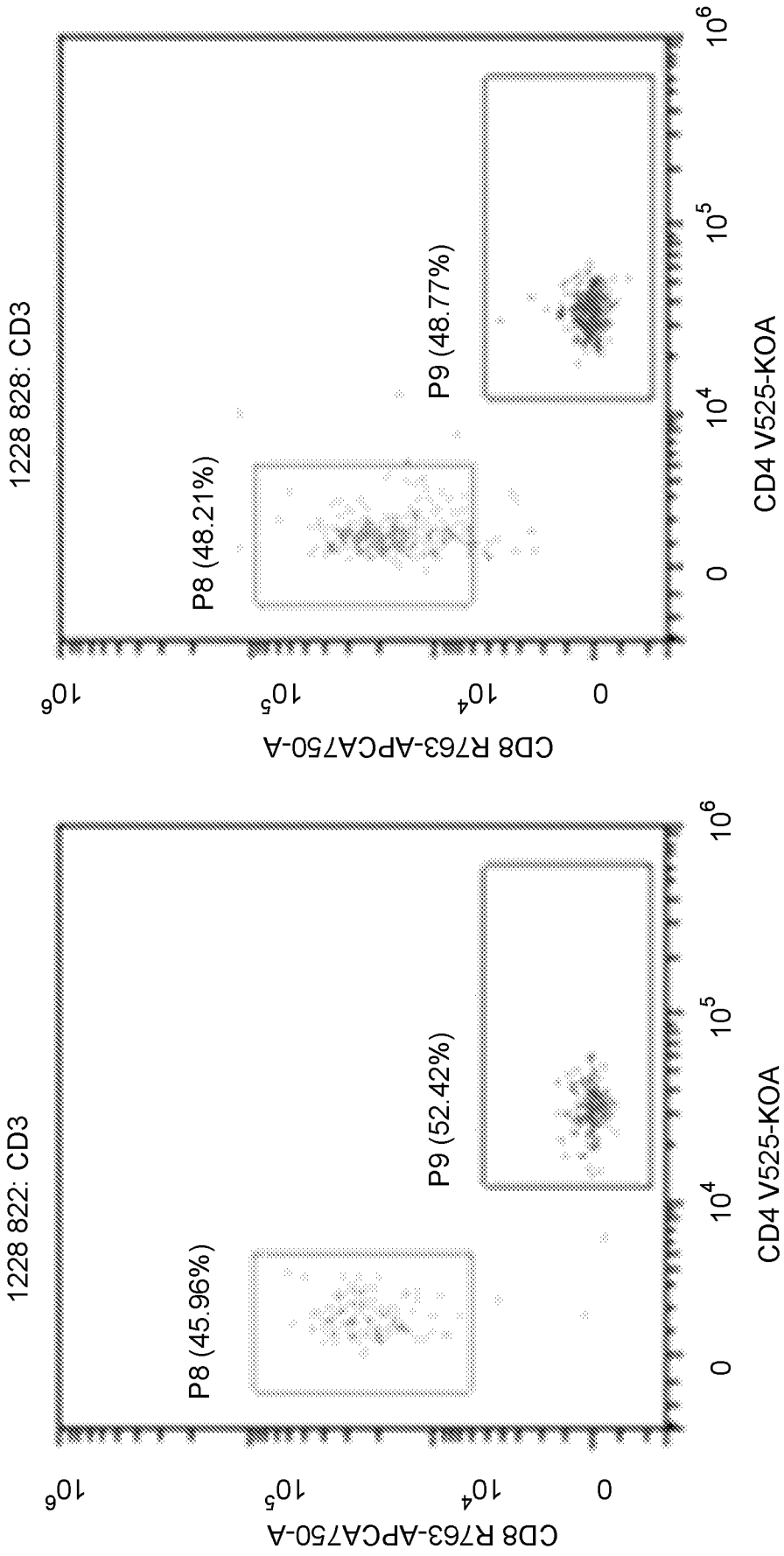


FIG. 41



2407

FIG. 42



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FIG. 43

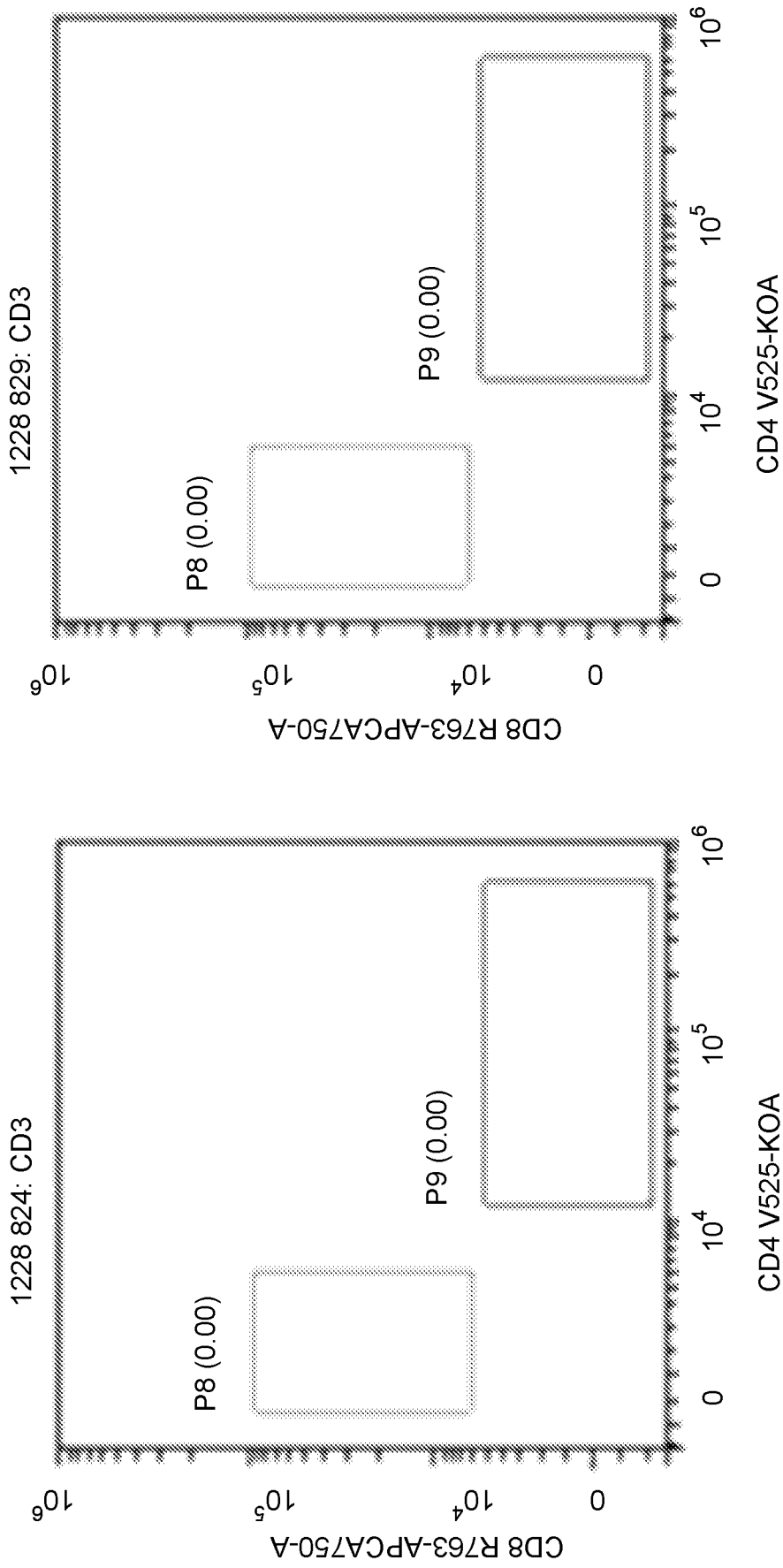


FIG. 44

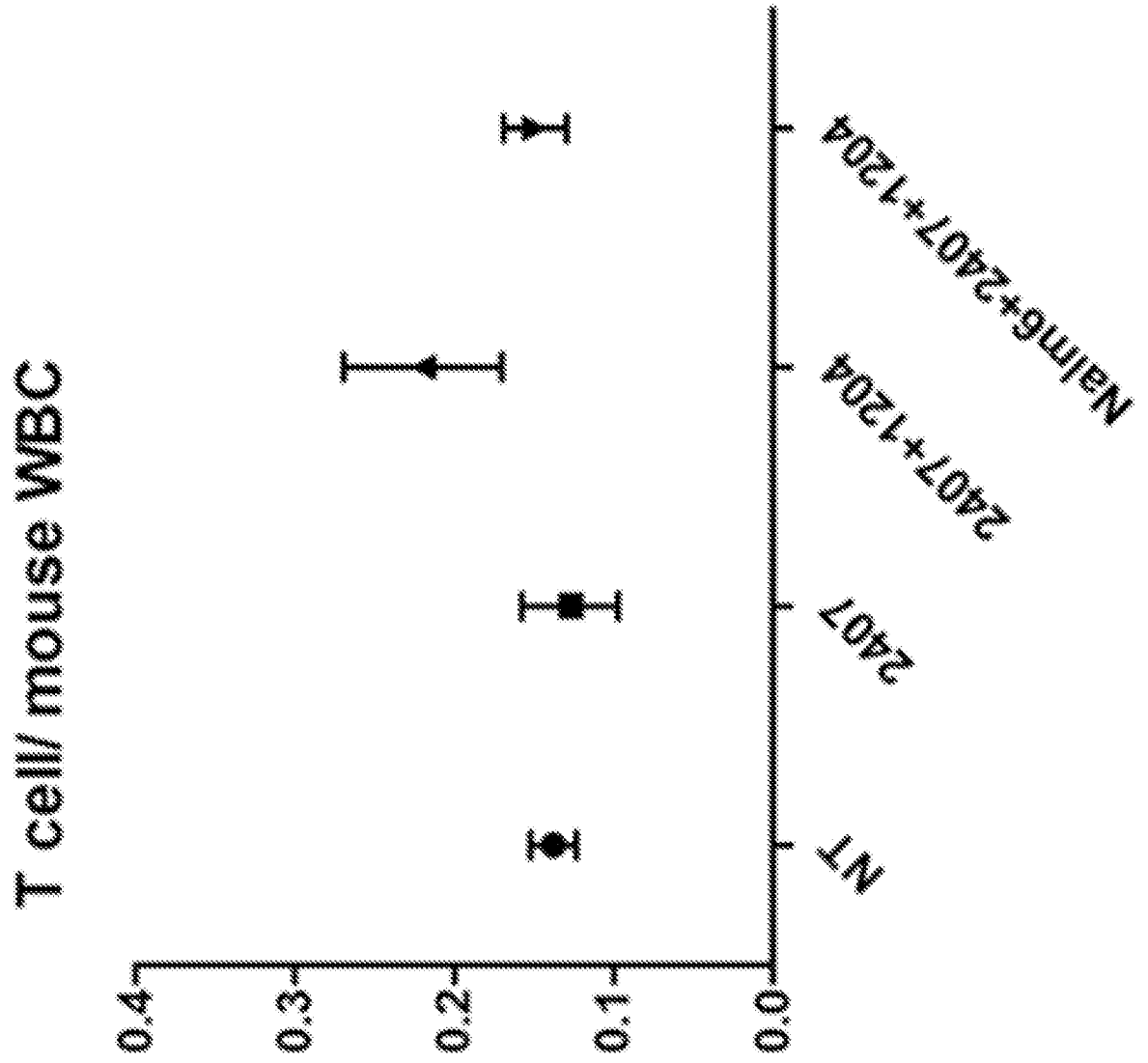


FIG. 45

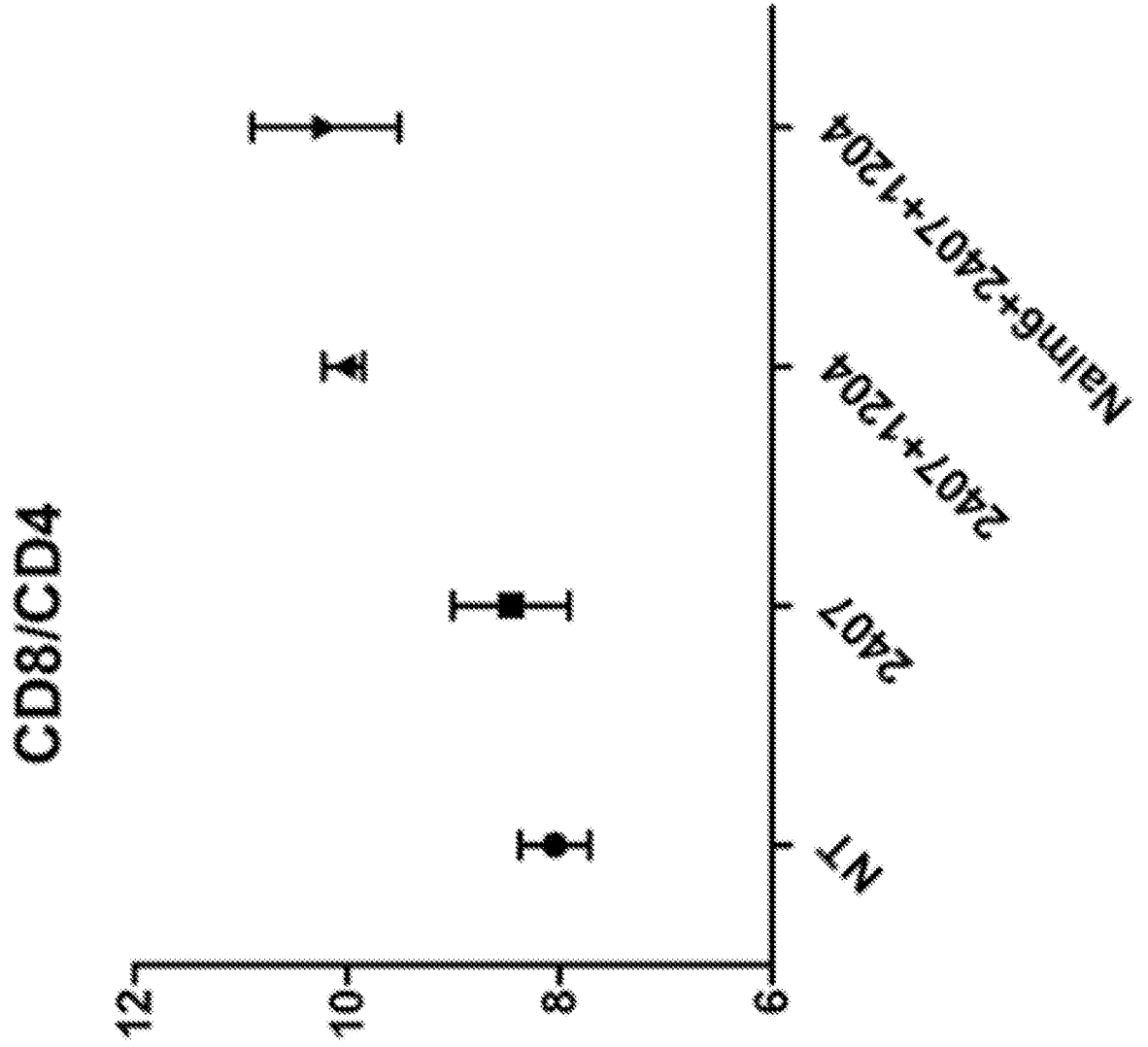


FIG. 46

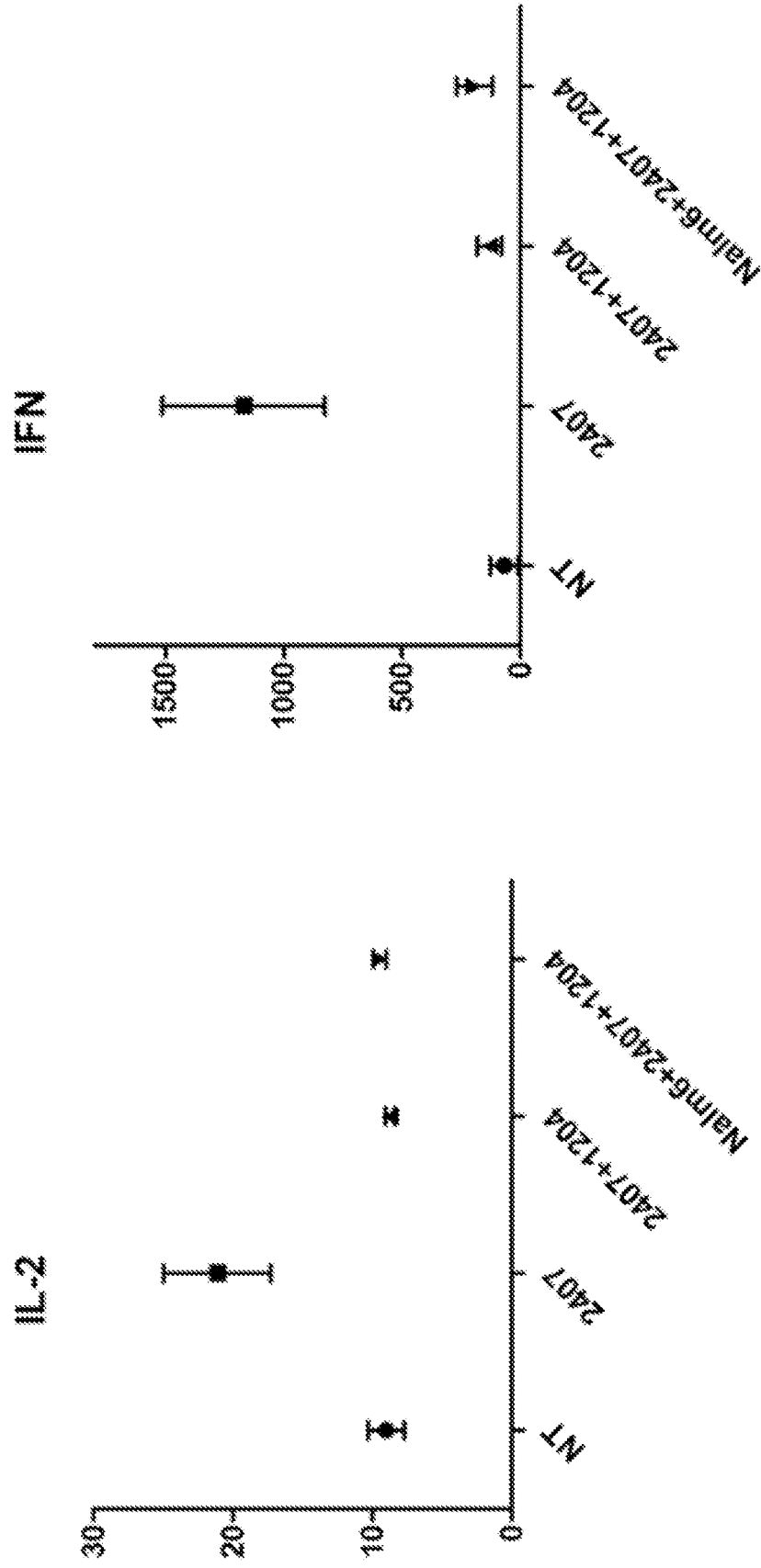


FIG. 47

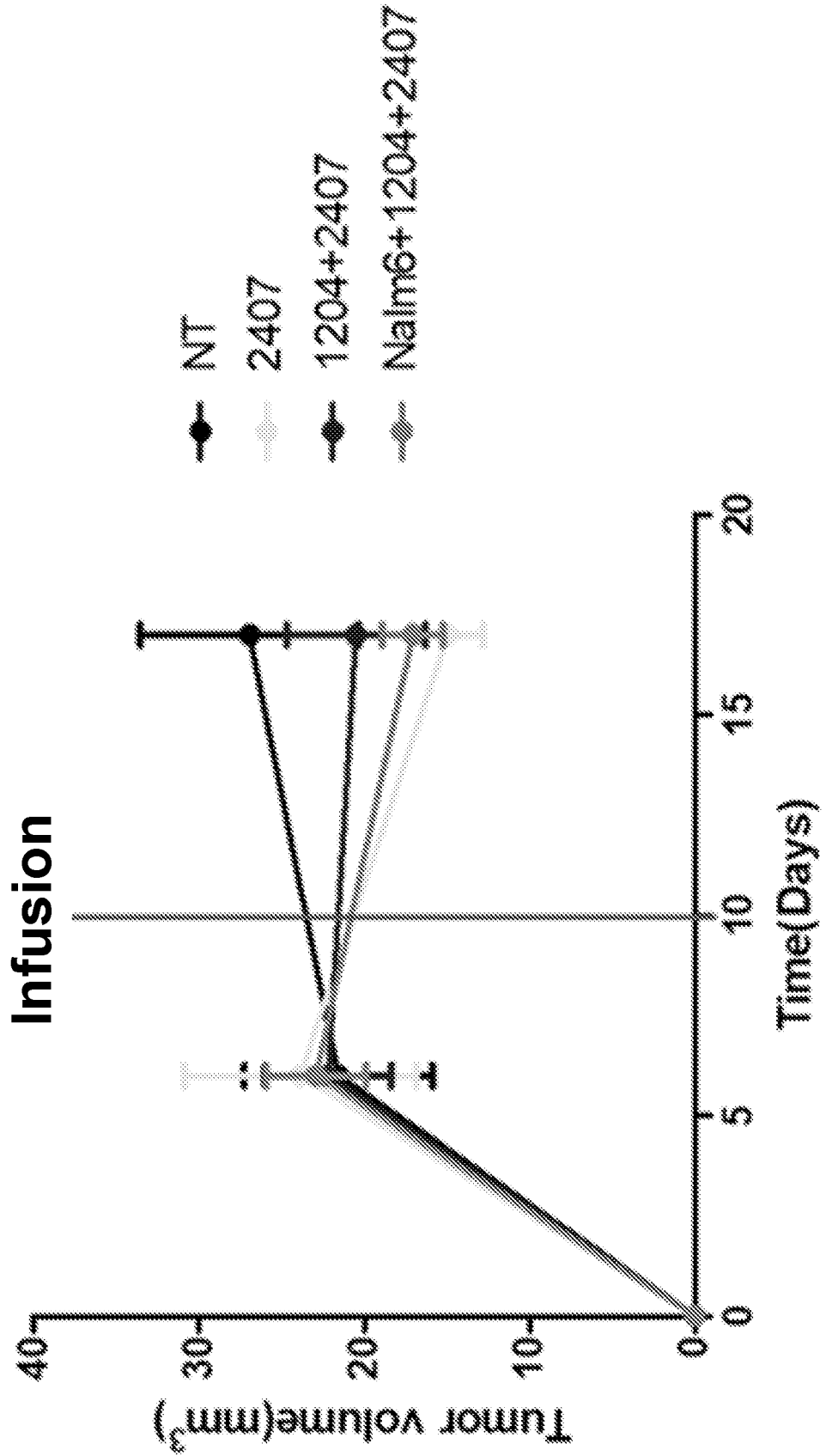


FIG. 48

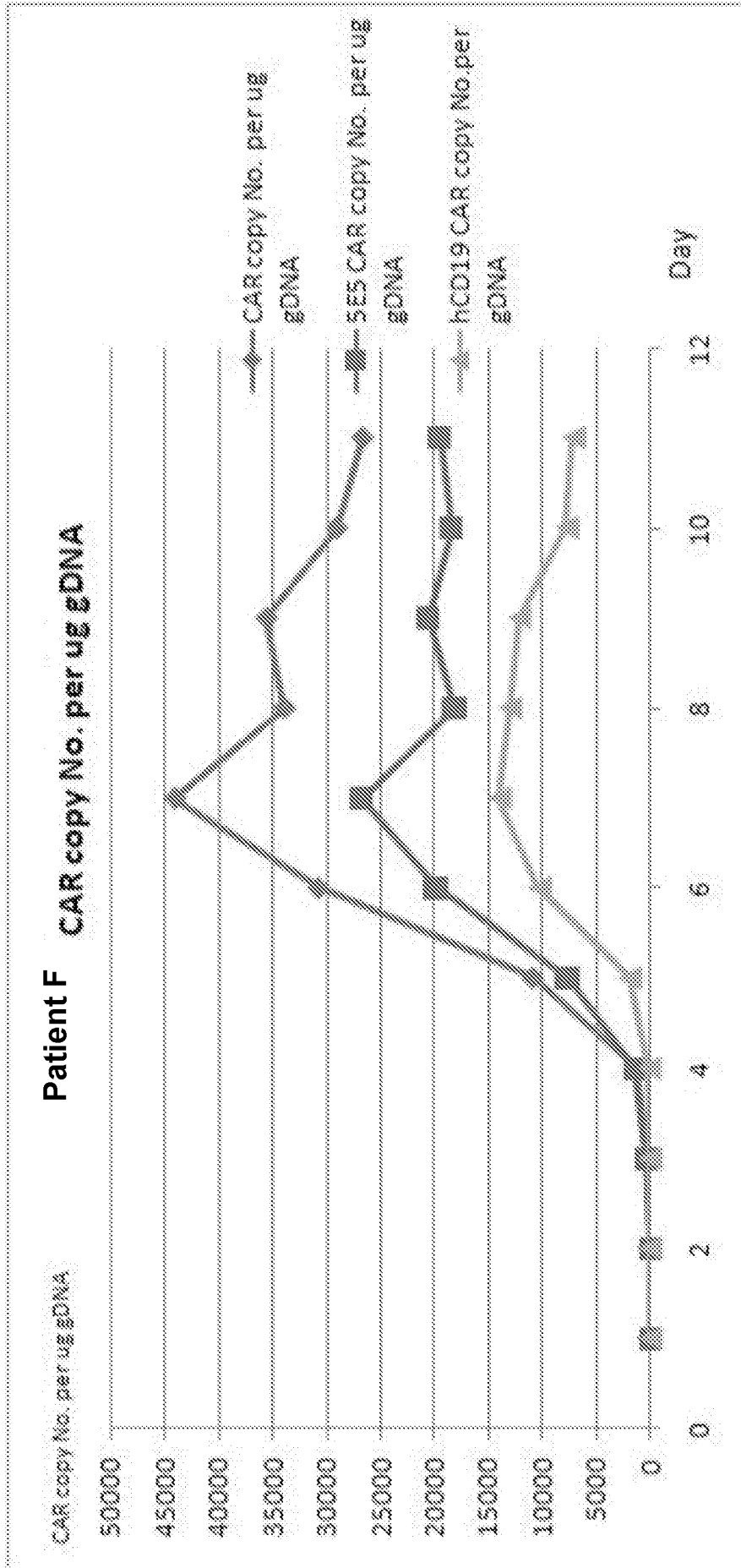
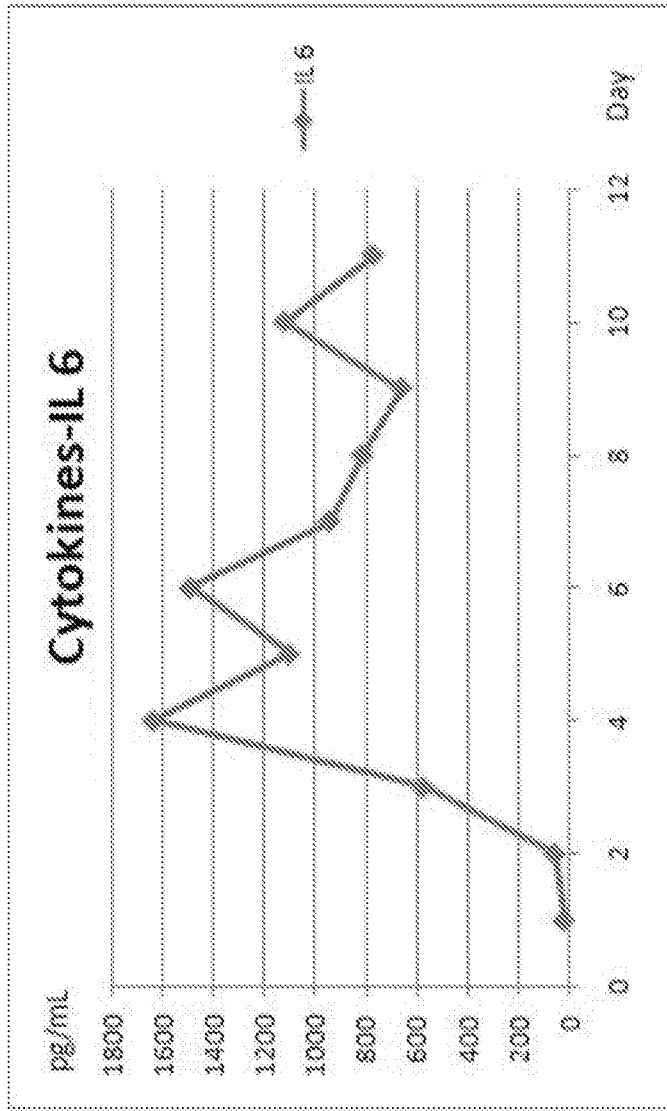


FIG. 49



Patient F

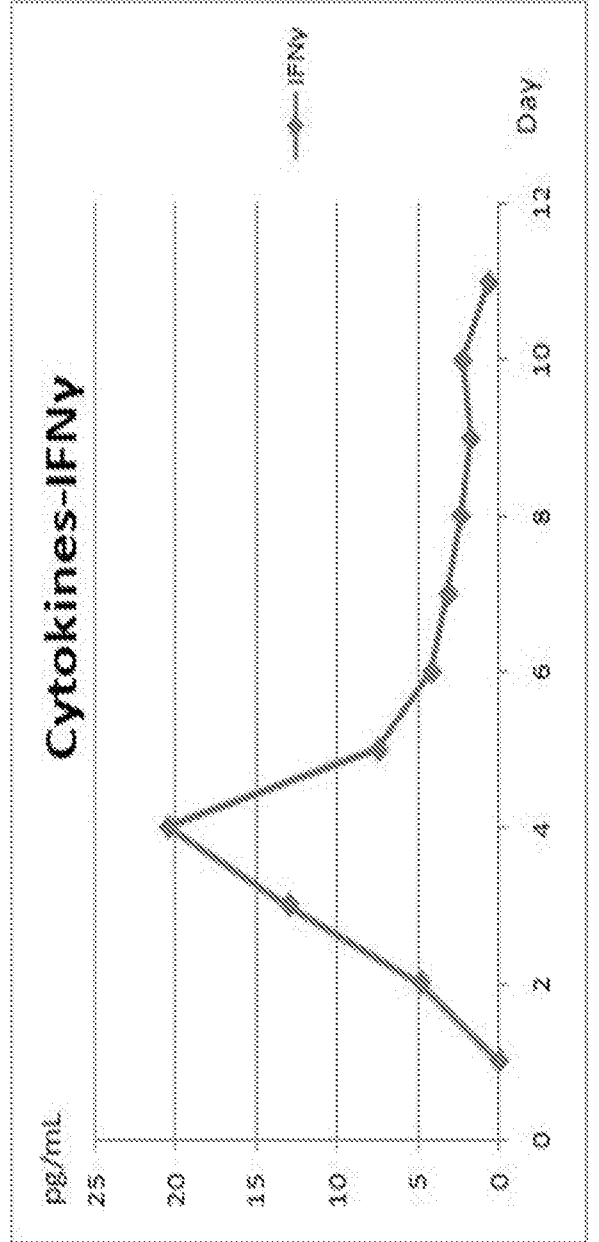


FIG. 50

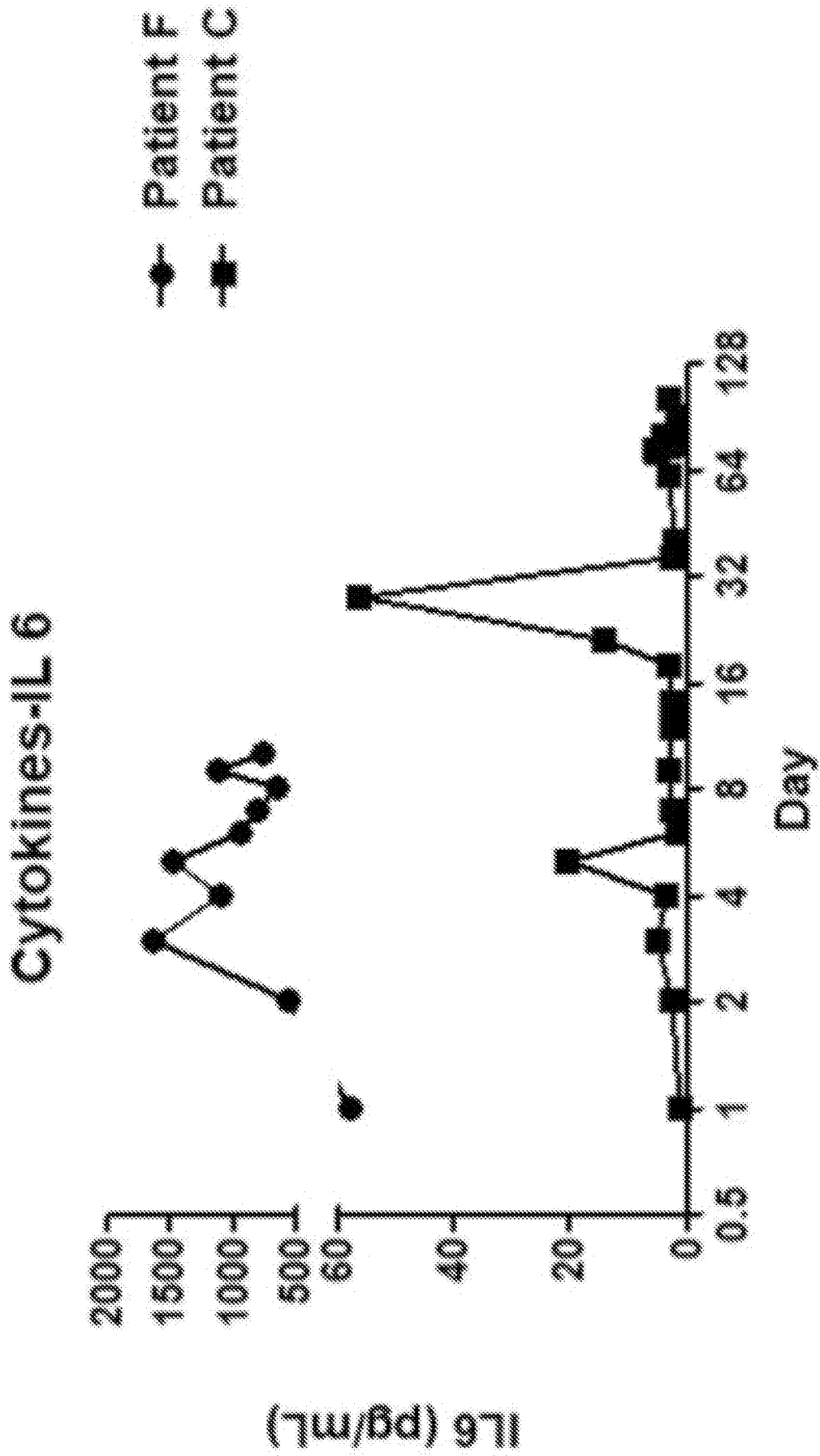


FIG. 51

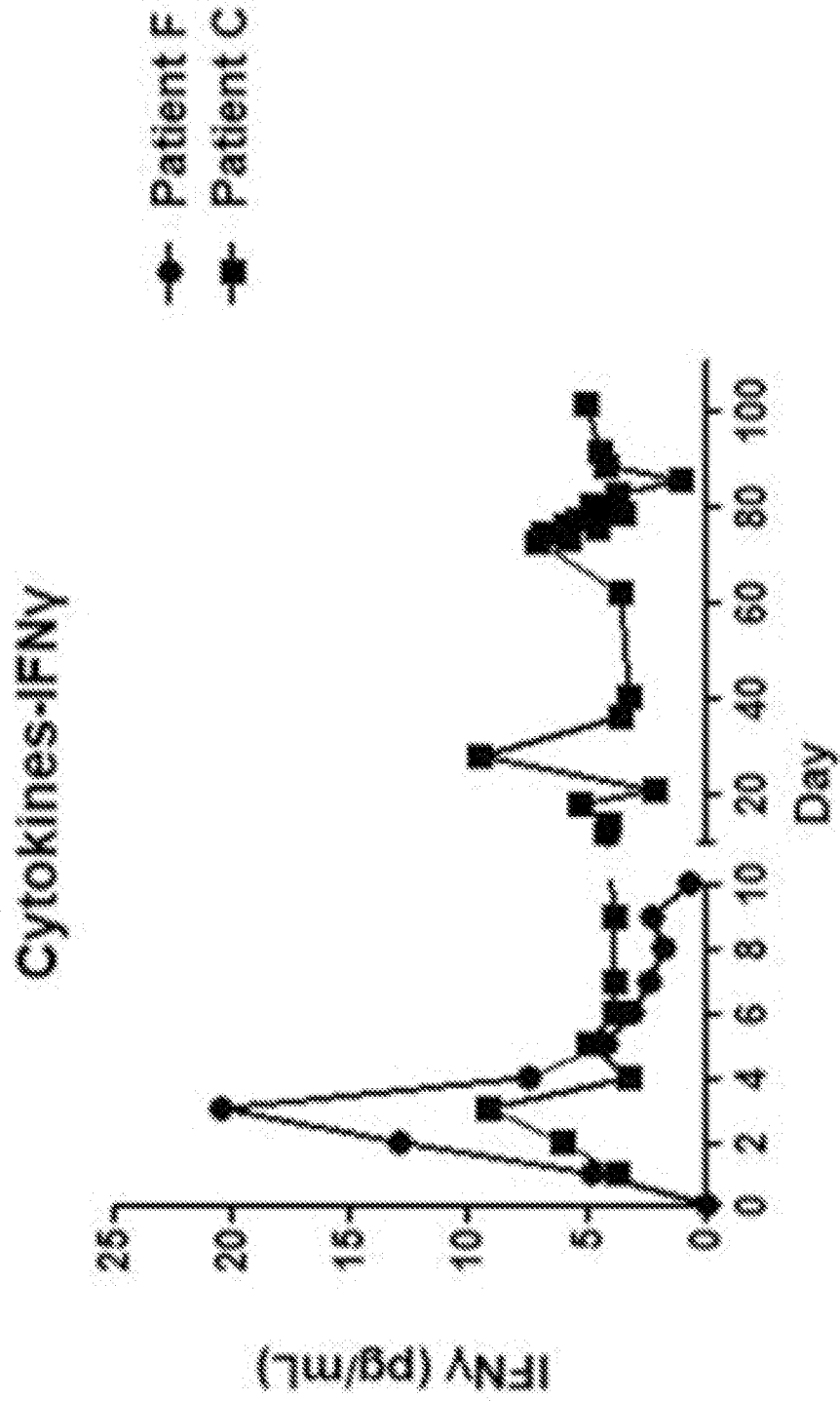


FIG. 52

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 19/13068

A. CLASSIFICATION OF SUBJECT MATTER

IPC(8) - A61K 35/17, A61K 48/00 (2019.01)

CPC - C12N 5/0636, C07K 14/705, A61K 39/0011, A61K 48/005, A61K 39/39558

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

See Search History Document

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

See Search History Document

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

See Search History Document

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2017/027291 A1 (SEATTLE CHILDREN'S HOSPITAL DBA SEATTLE CHILDREN'S RESEARCH INSTITUTE) 16 February 2017 (16.02.2017) para [0089]; para [0240]; claim 66; claim 68; claim 108	1
X	WO 2017/149515 A1 (NOVARTIS AG et al.) 8 September 2017 (08.09.2017) page 20, ln 14-27; page 244, ln 11-20 page 20, ln 14-27; page 292, ln 16-30; page 293, ln 18-27; claim 1-2; claim 12; claim 23; claim 63; claim 65; claim 82	1-3, 12-13, (17-19)/(1-3, 12-13)
Y		4, (17-19)/4
A		5, 14-16, (17-19)/(5, 14-16)
Y	US 2017/0145108 A1 (UNIVERSITY OF CHICAGO) 25 May 2017 (25.05.2017) Abstract; para [0118]-[0119]claim 1-3; claim 28	4, (17-19)/4
A	US 2014/0271635 A1 (BROGDON et al.) 18 September 2014 (18.09.2014) Abstract; para [0008]; SEQ ID NO: 11	5, (17-19)/5
A	WO 2017/172981 A2 (UNIVERSITY OF SOUTHERN CALIFORNIA) 5 October 2017 (05.10.2017) para [00506]; claim 1; page 201, SEQ ID NO: 2543; SEQ ID NO: 3448	5, 15, (17-19)/(5, 15)

 Further documents are listed in the continuation of Box C. See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

28 May 2019 (28.05.2019)

Date of mailing of the international search report

17 JUN 2019

Name and mailing address of the ISA/US

Mail Stop PCT, Attn: ISA/US, Commissioner for Patents
P.O. Box 1450, Alexandria, Virginia 22313-1450
Facsimile No. 571-273-8300

Authorized officer:

Lee W. Young

PCT Helpdesk: 571-272-4300
PCT OSP: 571-272-7774

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 19/13068

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	US 2005/0079170 A1 (LE GALL et al.) 14 April 2005 (14.04.2005) claim 19; SEQ ID NO: 5	14, (17-19)/14
A	US 2014/0227237 A1 (UNIVERSITY OF PENNSYLVANIA) 14 August 2014 (14.08.2014) claim 22; SEQ ID NO: 5	16, (17-19)/16

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 19/13068

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

-----continued on supplemental sheet-----

1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.
3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-5, 12-16, (17-19) in part, limited to SEQ ID NOs: 5, 70, 202, 215, 216

Remark on Protest

- The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- No protest accompanied the payment of additional search fees.

Continuation of Box III: Observations where unity of invention is lacking

Group I+: Claims 1-19 directed to a modified cell comprising a plurality of nucleic acids encoding a chimeric antigen receptor (CAR) binding a solid tumor antigen and encoding a CAR binding a B cell antigen; and administration of said modified cell to enhance T cell expansion and promote T-cell tumor treatment in a subject in need thereof. The modified cell will be searched to the extent that the CAR binding the solid tumor antigen binds MUC1 and comprises amino acid sequences of SEQ ID NO: 70 (Tumor associated MUC1 scFv 1), and SEQ ID NO: 216 (CAR2 of MUC1-5E5-A-IRES-hCD19-A); the CAR binding the B cell antigen binds CD19, and comprises amino acid sequences of SEQ ID NO: 5 (scFV Humanized CD19) and SEQ ID NO: 202 (CAR1 of MUC1-5E5-A-IRES-hCD19-A), and the corresponding nucleic acid sequence is SEQ ID NO: 215 (construct of MUC1-5E5-A-IRES-hCD19-A). It is believed that claims 1-5, 12-16, (17-19) (in part) limited to a modified cell comprising (1) a CAR binding MUC1 comprising the amino acid sequences of SEQ ID NO: 70 (antigen binding domain), and SEQ ID NO: 202 (CAR); and (2), a CAR binding CD19 comprising the amino acid sequences of SEQ ID NO: 5 (antigen binding domain), and SEQ ID NO: 207 (CAR), and the corresponding nucleic acid sequence SEQ ID NO: 206; encompass this first named invention, and thus these claims will be searched without fee to the extent that modified cell encompasses said CARs. Additional modified cells will be searched upon the payment of additional fees. Applicants must specify the claims that encompass any additionally elected oligonucleotides. Applicants must further indicate, if applicable, the claims which encompass the first named invention, if different than what was indicated above for this group. Failure to clearly identify how any paid additional invention fees are to be applied to the "+" group(s) will result in only the first claimed invention to be searched. An exemplary election would be a modified cell comprising a CAR that binds to the solid tumor antigen MUC1 and comprises amino acid sequences of SEQ ID NO: 70 (Tumor associated MUC1 scFv 1), and SEQ ID NO: 202 (CAR 1 of MUC1-5E5-A-IRES-CD19-B); further comprising a CAR that binds the B cell antigen CD19, and comprises amino acid sequences of SEQ ID NO: 6 (scFV CD19) and SEQ ID NO: 202 (CAR 1 of MUC1-5E5-A-IRES-CD19-B), and the corresponding nucleic acid sequence SEQ ID NO: 206 (construct of MUC1-5E5-A-IRES-CD19-B) (Claims 1-10, 12-16, (17-19) (in part)).

The inventions listed as Groups I+ do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Special Technical Features

The technical feature of each of the inventions listed as Group I+ is a modified cell with solid tumor antigen-binding CAR and B cell antigen-binding CAR recited therein. Each invention of Group I+ requires a combination of two CARs not required by any of the other inventions.

Common Technical Features

The feature shared by the inventions listed as Group I+ is a modified cell having a first CAR that binds to a tumor cell antigen and a second CAR that binds to a B-cell antigen. However, this shared technical feature does not represent a contribution over prior art, because the shared technical feature is anticipated by WO 2017/149515 A1 to Novartis Ag et al. (hereinafter 'Novartis'). Novartis discloses a modified cell (claim 1- "A cell comprising a first chimeric antigen receptor...") comprising a plurality of nucleic acids (claim 82- "method of generating the cell ... comprising introducing into said cells a first vector comprising nucleic acid encoding the first CAR... a second vector comprising nucleic acid encoding the second CAR") encoding a chimeric antigen receptor (CAR) binding a solid tumor antigen (claim 2- "the second CAR binds...a solid tumor antigen") and encoding a CAR binding a B cell antigen (claim 1- "first CAR binds to a B-Cell antigen").

Another feature shared by the inventions listed as Group I+ is (claim 18) a method of promoting T cell response in a subject in need thereof and/or treating a tumor of the subject, the method comprising administering an effective amount of the composition to the subject. However, this shared technical feature does not represent a contribution over prior art, because the shared technical feature is anticipated by Novartis (abstract "methods for treating diseases associated with expression of a tumor antigen as described herein by administration of a cell comprising a chimeric antigen receptor that binds a B-Cell antigen and a chimeric antigen receptor which binds a tumor antigen.", pg 14 ln 8-14 "In an aspect (including in any of the aforementioned aspects and embodiments), the cell is a T cell, a natural killer (NK) cell, a cytotoxic T lymphocyte (CTL), a tumor infiltrating lymphocyte (TIL), or a regulatory T cell. In another aspect, the invention provides a method for stimulating a T cell-mediated immune response to a myeloid tumor cell in a mammal, the method including administering to a mammal an effective amount of a cell as described herein").

Another feature shared by the inventions listed as Group I+ is (claim 19) a method of enhancing T cell expansion in a subject in need thereof by administering a modified cell having both a B-cell binding CAR and a solid tumor antigen binding CAR, wherein T cell expansion is greater than a T cell expansion obtained by administering T cells having the CAR binding the solid tumor antigen in the absence of the CAR binding the B cell antigen. However, this shared technical feature does not represent a contribution over prior art, because the shared technical feature is made anticipated by Novartis. Novartis teaches that T cell expansion by the modified cell is greater than a T cell expansion obtained by administering T cells having the CAR binding the solid tumor antigen in the absence of the CAR binding the B cell antigen (page 244, ln 11-20 "administering to a subject in need thereof a cell of the invention, e.g., an immune effector cell (e.g., T cells, K cells) that comprises (e.g., is engineered to express) a TA CAR described herein, and a BCA CAR described herein, that binds to a tumor antigen-expressing cell... BCA CAR on the cell of the invention allows the cell to persist longer in vivo, or proliferate to a greater degree in vivo, than an identical cell which does not express the BCA CAR, thereby allowing for the generation of persisting populations of cells expressing a TA CAR, which may effectively treat a relapse without another administration of the cells for the invention."; page 204, ln 23-26 "The present disclosure also provides vectors in which a nucleic acid of the present disclosure 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.").

As the technical features were known in the art at the time of the invention, they cannot be considered special technical features that would otherwise unify the groups.

Group I+ therefore lack unity under PCT Rule 13 because they do not share the same or corresponding special technical feature.